

**GENETIC VARIABILITY OF COMMON BEAN (*Phaseolus vulgaris* L.)
GENOTYPES GROWN IN KARAMILE, EAST HARARGE, ETHIOPIA**

M.Sc. THESIS

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February 2024

HARAMAYA UNIVERSITY, ETHIOPIA

**Genetic Variability of Common Bean (*Phaseolus vulagris* L.) Genotypes
Grown in Karamile, East Hararge, Ethiopia**

A Thesis Submitted to the School of Biological Sciences and Biotechnology

Postgraduate Programs Directorate

HARAMAYA UNIVERSITY

In Partial Fulfillment of the Requirements for the Degree of

MASTER OF SCIENCE IN BIOLOGY

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February 2024

Haramaya University, Ethiopia

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DEDICATION

I dedicate this Thesis to my beloved family and my friends for the advice and support they have given me. And for nursing me with affection and love for the dedicated partnership in the success of my life.

STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this MSc Thesis is my own work. I have followed all ethical and technical principles of scholarship in conducting studies, data collection, data analysis, and compilation of this Thesis. Any scholarly matter that is included in the Thesis has been given recognition through citation.

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BIOGRAPHICAL SKETCH

The author was born in Ethiopia Oromia Regional State, East Harerge woreda on October 10,1974 to his adored Father Diinee Ibroo and his Mother Maymuna Ahamed. He attended Elementary school in Abera Gizaw and his secondary school education in Dader Senior Secondary School May1993.After completion of his Secondary education, he joined Asella Teachers Training Institute and then Diploma distance program at Kidist Marys college. Then he joined Dire Dawa University as a summer student in 2001, and graduated with a BSc degree in Biology in October 2006.After 3 years'of service in Karramille High Schools he joined Postgraduate program school of graduate studies of Haramaya University to pursue his MSc study in Biology in 2010.

ACKNOWLEDGEMENTS

First of all, I would like to thank my God for helping me to successfully complete this work. The author is highly indebted to his major and co-advisors, Dr. Yohannes Petros and Dr. Meseret Chimdessa, respectively. Without their encouragement, insight and guidance and professional expertise the completion of this work would not have been possible.

I am very grateful to the director of Karamile Senior Secondary School for material and moral assistance in my research work which led to the implementation of the study and my friends Kelilachew Tadesse. Without their support this research would have not been completed on time.

Finally, I would like to acknowledge all members of my family most importantly my mothers Maymuna Ahamed and specially my lovely wife Iftu Mohammed and all my brothers specially Arif Diinee and Tofiq Diinee and all my Son Firomsa Abdujabar, Badhane Abdujabar and Nu'umaan Abdujabar supported me for the success of my research undertaking.

LIST OF ABBREVIATION AND ACRONYMS

ANOVA	Analysis of Variance
By	Biological yield
CSA	Central statistics Agency
CV	Coefficient of Variance
DF	Days to 50% flowering
EIAR	Ethiopian Institute of Agricultural Research
FAOSTAT	Food and Agricultural Organization statistics
GA	Genetic Advance
GAM	Genetic Advance as Percent Mean
GCV	Genotypic Coefficient of Variation
GLM	General Linear Model
ha	Hectare
HI	Harvest Index
m.a.s.l	Meters above Sea Level
NPPP	Number of pods per plant
NSPPT	Number of seeds per plants
PCV	Phenotypic Coefficient of Variation
PH	Plant height
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
SSA	Sub-Saharan Africa
SYPP	Seed yield per plant

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Genetic Variability of Common Bean (*Phaseolus vulagris* L.) Genotypes Grown in Karamile East Hararge 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 genotypes of common bean was studied. The experiment was conducted at karramille farmer's field as randomized complete block design planted in three replications. Results showed that genotypes with more yields were identified as Tinike for maximum seed yield per plants with values of (120g), Awash-melka for seed per plant (264) and for hundred seed weight(98.33g). The genetic advance as percent of mean (GAM) ranged from 1.167% for number of pods per plants to 104.15% for hundred seed weight. Genotypic coefficient of variation ranged from 2.275 (days of flowering) to 54.663 (Hundred seed weight) while phenotypic coefficient of variation ranged between 2.548 (days of flowering) and 59.187 (Hundred seed weight). While High genotypic coefficients of variations(GCV) were observed for plant height (45.31),harvest index(26.6938) ,hundred seed weight (54.66), above ground dry biomass(42.44), number of seed per plants (44.83) and seed yield per plant(45.98). High phenotypic coefficients of variations (PCV) were observed for, plant height (49.17), number of pod per plants (35.31), number of node per plant (24.05), number of seed per plants (45.78), above ground dry biomass (43.60), hundred seed weight(59.18734), harvest index (29.53),and seed yield per plant (47.77).Seed yield per plant had positive and significance different with related to biological yield (0.398) and hundred seed weight (0.349) as well as positive and highly significant difference with related to number of seed per plant (0.52) and harvested index (0.61). The genotypic path analysis had the maximum positive direct effect of biological yield (0.978) on seed yield constitutes the major portion of the total correlation between biological yield and seed yield ($r_g=0.834$). The maximum positive direct effect of harvest index (0.9078) on seed yield constitutes the major portion of the total correlation between harvest index and seed yield ($r_p=0.6155$).

Keywords: Agronomic Character, Genetic advance, Genetic variability, Heritability.

1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most consumed leguminous pulse in the world, and is a major dietary staple and source of protein in Africa and Latin America (Mamidi *et al.*, 2013). It is a diploid annual species ($2n = 2x = 22$), and is predominantly self-pollinating (De Ron *et al.*, 2015). It is an annual crop, which belongs to order Rosales, family Fabaceae, and the genus *Phaseolus*, with pinnately compound trifoliate large leaves (Katungi *et al.*, 2009). There are diverse botanical varieties of the species *Phaseolus* that vary in terms of growth habit, seed and pod characteristics, agronomic features, and response to biotic and abiotic stresses (Abebe, 2011). Cultivated forms are herbaceous annuals, which are determinate or indeterminate in growth habit. On germination, the plant is initially tap-rooted, but adventitious roots emerge thereafter, and dominate the tap root which remains 10-15 cm in length. It grows best in warm climate at temperature of 18 to 24°C (Katungi *et al.*, 2009).

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. 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 bean is the world's most important food legume for direct human consumption. Average per capita consumption of common bean in the main bean production areas is higher in Africa, estimated at 31.4kg/year (Schoonhoven and Voysest, 1991). High in nutrients and commercial potential, common bean holds great promise for fighting hunger, increasing income and improving soil fertility in Sub Saharan Africa. The crop occupies more than 3.5 million hectares in sub-Saharan, accounting for about 25% of the global production but production is concentrated in the densely populated areas of East Africa, the lakes region and the highlands of southern Africa (<http://webapp.ciat.cgiar.org/ciainfocus>). In Africa, common bean is a popular crop among small-scale farmers, given its short growth cycle (about 70 days) which permits production when rainfall is erratic. Common bean is often grown by women farmers for mainly for subsistence and markets.

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, rainfall, 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).

Common bean will be considered for this research because of its economic importance in the country serving as cash crop for smallholder farmers. It can be cultivated at times of irregular rainfall and previous reports indicated that it can grow in the low lands of Ethiopia where soils are relatively affected by salt (Alemu and Seifu, 2003). The aim of this study is to investigate the genetic diversity of *P. vulgaris* accessions collected from Haramaya Univewrsity. This will be provide information on the overall genetic variability of *P.*

vulgaries accessions which may assist in the identification and selection of the genetic materials used to obtain good yield.

It is assumed that common bean was introduced to Ethiopia in the 16th century by the Portuguese and since then, become an important component of the human diet (Imru, 1985; Zelalem, 2005). Moreover, it is among the most important food legumes produced in Ethiopia (Zelalem, 2005; Kasaye, 2006). In addition, it has become an export crop for more than 40 years with a rapidly increasing export value, highlighting its importance among major pulse crops (Asfaw *et al.*, 2009). The crop is highly preferred by Ethiopian farmers because of its fast maturing characteristics that enables households to get cash income required to purchase food and other household needs when other crops have not yet matured (Teame *et al.*, 2017). Its suitability for double or triple production per year enabled its production on offseason free lands and relatively cheaper labor force. Its reasonable protein content (22%) made it the poor man's meat securing more than 16.7 million rural people against hidden hunger (Zelege *et al.*, 2016).

Common Bean is locally known as Boloke also known as dry bean haricot bean and french bean are an annual leguminous plant with chromosome number $2n=22$ that belongs to the genus *Phaseolus* with pinnately compound trifoliate large leaves. It is largely a self-pollinated plant though cross-pollination is possible if the stigma contacts with pollen coated bee when extended. Seeds are non-endospermic and vary greatly in size and color from the small black wild type to the large white, brown, red, black or mottled seeds of cultivars, which are 7-16 mm long (Cobley and Steele, 1976). Common bean is an important part of human diet in Ethiopia. It is among the most important food legumes produced in the country, which has been cultivated as a field crops for a very long time (Amare, 1987). Moreover, it has been an export crop for more than 40 years. Common bean stands out among the pulses and is also known as the poor man meat due to its high protein content, which compensates for the deficiency that could have occurred in a population with low income (Teshome and Kirkby, 1990).

Common bean is an annual crop which belongs to the family Fabaceae. It grows best in warm climate at temperature of 18 to 24°C (Teshale *et al.*, 2005). Common bean is one of the principal grain legumes of eastern and southern Africa, occupying more than 4 million

hectare annually and providing food for more than 100 million people (Wortmann *et al.*, 1998). It is the second most important source of dietary protein and the third most important source of calories for lower income African households after cassava and maize (Broughton *et al.*, 2003). In Ethiopia, common bean is grown predominantly under smallholder producers as an important food crop and source of cash. The crop grows well between 1400 and 2000m above sea level. In 2011/12, total common bean production in the country Therefore, to overcome the above stated problems and to familiarize smallholder farmers with new technologies, there is need to evaluate widely grown, well-performed common bean varieties to target area.

Although a common bean is largely grown in Ethiopia the national average yield of common bean is low ranging from 0.5 to 0.8 tone ha⁻¹, which is far below the corresponding yield recorded at research sites (2.5 up to 3 tones ha⁻¹) using improved varieties (EPPA, 2004). The low national mean yield observed for common bean could be attributed to various constraints related to low adoption of improved agricultural technologies, draught, and lack of improved varieties, poor cultural practices, disease and environmental degradation (Lagase *et al.*, 2006). Studies of heritability and genetic advance enable the breeders to use the best genetic stock for improving the crop (Mangi *et al.*, 2008). The succession of any breeding program depends up on the amount of genetic variability existing in the germplasm and it is prerequisite to have a good knowledge of heritability and genetic advance present in different yield associated parameters (Waqar ul Haq *et al.*, 2008).

1.1. Objectives of the Study

1.2. General Objective

To assess the genetic variability of traits for common bean varieties in Karamile.

1.3. Specific Objectives

1. To estimate the magnitude of genetic variability for yield and yield related characters in *common bean* accessions from Haramaya University.

2. To estimate the extent of correlation among yield components themselves and with the yield of *common bean*.
3. To assess the direct and indirect effects of the different characters on yield of *common bean* through path coefficient analysis.

2. LITERATURE REVIEW

2.1. Origin and Domestication of Common Bean

Common bean is a dicotyledonous plant that belongs to the family Fabaceae. The species evolved from a wild-growing vine ancestor in the highlands of Middle America and the Andes (Gepts and Debouck, 1991). Middle America is the origin of races Durango, Jalisco, and Mesoamerica, and the Andes is the origin of races Chile, Nueva Granada, and Peru (Singh *et al.*, 1991). There are two types of common bean: dry and snap. Dry beans are harvested once the seeds are fully mature and dry whereas snap beans are harvested while the pods are immature and fleshy. For dry beans, there are market classes developed based on the color, shape, and size of the bean. Voysest and Dessert (1991) list 59 known market classes of dry beans. Pinto is one market class with a plump, medium sized seed with a cream background and brown mottling.

2.2. Nutritional Benefits of Common Bean

Beans have been consumed for thousands of years and have an excellent nutritional profile as Geil and Anderson (1994) found after conducting an extensive review. Dry beans contain 21-25% crude protein, are rich in amino acids such as lysine, but are moderately deficient in sulfur containing amino acids such as methionine and tryptophan. The carbohydrate content of dry beans is 60-65%, composed mainly of starch with small amounts of monosaccharide and disaccharides. Carbohydrate in the form of fiber is 3-7% in cooked beans, composed primarily of cellulose and hemicelluloses. Beans are cholesterol free and very low in fats. Of the fat that is present, 16% is saturated and 84% is unsaturated. Beans are an excellent source of minerals. A single cup serving of cooked dry beans contains 29% of the of the US recommended dietary allowance of iron for females, and 55% for males, 20-25% of phosphorus, magnesium, manganese, potassium, and copper, and 10% of calcium and zinc.

2.3. The common bean in Ethiopia

2.3.1. The Common Bean as a Dietary Component in Ethiopia

Production of common bean is expanding slowly, based on population growth, with highest usage in poor developing countries, where beans provide an alternative to meat as a source of low-cost protein. Beans are well suited to low input systems as they can be stored for long periods without refrigeration and provide an excellent nutritional complement to maize, which is one of the most important grain cereals (Ayele, 1990; Ferris and Kagnazi, 2008). The common bean is high in starch, protein and dietary fiber and is an excellent source of minerals and vitamins including iron, potassium, selenium, molybdenum, thiamine, vitamin B6, and folic acid. Dry beans will keep for 3–4 years if stored in a cool, dry place, but as time passes, its nutritive value and flavor degrades and cooking times lengthen as they desiccate and harden. Dried beans are almost always cooked by boiling, often after having been soaked for several hours. While the soaking step is not essential it shortens the cooking. Common beans take longer to cook than most pulses, and depending on the variety, cooking times vary from one to four hours (Ferris and Kagnazi, 2008). There is a growing domestic and regional demand for red beans. In the future, there is potential to expand into new export markets as there are trends for richer consumer segments in industrialized countries to adopt vegetarian diets. In Ethiopia there are strong cultural bonds with pulse crops which are closely associated with the dietary customs of the majority Orthodox Christian community. Moreover, most traditional vegetarian dishes are prepared from highland pulses, such as chickpeas, split peas, faba beans and lentils. Phaseolus beans are considered to be a lower value and lower esteem pulse crop, but there is increasing interest in Phaseolus beans, particularly among the low income segments for reasons of food security and income generation (Ferris and Kagnazi, 2008; Karanja *et al.*, 2011).

2.3.2. The common bean in Ethiopia from marketing

Common bean is grown throughout Ethiopia and is an increasingly important commodity in the cropping systems of smallholder producers for food security and income. Farmers grow a wide range of bean types, in terms of color and size, but the most common types are the pure red and pure white beans. Most of the beans produced, traded and consumed in the domestic Ethiopian bean markets are the medium and small red beans, where as white beans are virtually all exported (Ferris and Kagnazi, 2008; Karanja *et al.*, 2011).

In Ethiopia, common bean is one of the most important cash crops and source of protein for farmers in many lowlands and mid-altitude zones. Between the periods from 2007-2010, the country's export earnings from the crop was estimated to be over 85 % of export earnings from pulses, exceeding that of other pulses such as lentils, faba bean and chickpea (Negash, 2007; Katungi *et al.*, 2010). Overall, common bean ranks third as an export commodity in Ethiopia, contributing about 9.5 % of total export value from agriculture (FAOSTAT, 2010). Total national production was estimated at 421,418 ton in 2008, with a market value of USD 132,900,609 million (FAOSTAT, 2010; Katungi *et al.*, 2010). During the 2012/13 growing season, the production was estimated at 463,008.49 ton and this has a 19.3% increment from the previous growing season, i.e. 2011/12 (CSA, 2013). According to Buruchara *et al.* (2011), since 1996, over 550 new bean varieties have been released by the alliance across Africa, many of which have gone on to transform beans from a subsistence crop to a cash crop, such as the white pea bean in Ethiopia, which grew from an annual export industry of USD 8.5 million in 2004 to USD 50 million in 2010. On the other hand, this market is a foreign exchange annual value in the range of USD 25–30 million in 2012-13 (Ronner and Giller, 2013).

2.4. Production Constraints

Common bean is an important food and cash crop in Kenya and Ethiopia. In Kenya, about 417,000 metric tons of common bean were produced in 2007, an equivalent of US\$ 199,743,000 million (FAOSTAT, 2010). Consumption and contribution of common bean to human nutrition in Kenya is relatively high. Per capita consumption is estimated at 14 kg per year, but can be as high as 66 kg/yr in western parts of the country (Spilsbury *et al.*, 2004; Buruchara, 2007). The crop is the most important pulse and ranks second after maize as a staple food crop grown by more than 3 million households. Similarly, in Ethiopia, common bean is one of the most important cash crops and source of protein for farmers in many lowlands and mid-altitude zones. The country's export earnings is estimated to be over 85 % of export earnings from pulses, exceeding that of other pulses such as lentils, horse (faba) bean and chickpea (Negash, 2007). Overall, common bean ranks third as an export commodity in Ethiopia, contributing about 9.5 % of total export value from agriculture (FAOSTAT, 2010). Total national production was estimated at 421,418 ton in 2008, with a market value of US\$ 132,900,609 million (FAOSTAT, 2010).

Common bean is also highly preferred by Ethiopian farmers because of its fast maturing characteristics that enables households to get cash income required to purchase food and other household needs when other crops have not yet matured (Legesse *et al.*, 2006). Two types of common bean are grown: the canning type primarily grown for export market dominates the Oromiya region (Northeast rift valley), and the cooking type primarily grown for food in the Southern National Nationality Peoples' region, south of lake Ziway (Alemu and Bekele, 2005). Significant amounts of the cooking type are exported to the neighboring countries particularly Kenya (Ferris and Kaganzi, 2008).

2.5. Genetic Variability

Variability is the occurrence among individuals due to differences in their genetic composition and /or the environment in which they are raised (Falconer and Mackay, 1996). If the character expression of two individuals can be measured in an environment identical for both, differences in expression will be result from genetic control and hence such variation is called genetic variation (Welsh, 1990, Falconer, *et al*, 1996). The study of variability and heritability is of primary importance for an efficient breeding program as it provides a genetic basis for effective selections. The type of selection and progress from selection for a particular character depends, in part, on the magnitude of heritability estimates. This is because the expected response under selection is a function of heritability, variation and selection intensity [(Ajibade, S. R. (2000).]

Genetic variability is a measure of the tendency of individual accessions in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response environment and genotype. Genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction. Variability is an important factor in evaluation as it affects an individual's response to environmental stress and thus can lead to differential survival of organisms with in a population due to natural selection of the fit variants (Burt and Austin, 2000).

Assessing the causes and magnitude of variation is the key to success in crop improvement program, as difference will be always exist among individuals in a plant population and selection in breeding programs are based on measurements of phenotypic traits. Genotypic variability is measured through analysis of variance, simple measurements like range, mean, standard deviation and coefficient of variation and estimation of diversity (Singh, 1991).

The breeding methodology to be adapted for the improvement of a crop mainly depends upon the amount of genetic variability present in the crop. It is of immense importance that the hybrids are obtained only from desirable parental combination. Therefore, it is very important to select the desirable parents, which could transmit high yield and other economic traits to the progeny. Combining ability analysis would help in the selection of parents and crosses for improvements of the crop (Falconer, 1981).

2.6. Heritability

The effectiveness of selection is dependent upon genetic variability present in the germplasm and the extent to which it is heritable. In crop improvement, the genetic component of variation is important as only this component is transmitted to the next generation which is heritability. According to Hanson *et al.* (1956), heritability in broad sense is the ratio of genotypic variance to total variance in non-segregating population. Thus, heritability denote the proportion of phenotypic variance that is due to genotype which is heritable. Thus information on the extent of heritability is very important to plant breeders for it gives an indication on effectiveness with which selection of genotypes and can be based on phenotypic performance of qualitative characters (Kirschbaum *et al.*, 2002).

Heritability can be increased by diversifying the genetic background, i.e., by using only out breed individuals', who are able to increase the variance, and or by minimizing environmental effects, which decreases the variance. Smaller heritability, on the other hand, can be generated by using inbred individuals which decreases the variance or individuals reared in very diverse environments, which increases the variance. Due to such effects, different populations of environments, which increases the variance? Due to such effects, different population of species might have different heritability's even for the same traits (Cattel, 1960).

Theoretically, heritability can range from one where all variation is due to genetic, to zero where all the variation results from the environment. Actual heritability value will be fall same where between this extreme values. It is very difficult to determine the presence, amount type of genetic variability if phenotypic expressions are strongly influenced by the environment. According to Fischer *et al.*, (1932) definition heritability in “broad sense” as the ratio between genotypic variance as a whole and that due to phenotypic. Later, Hanson *et al.*, (1956) suggested heritability in “broad sense” as the ratio of genotypic variance to total variance. But broad sense heritability does not give a clear picture of transmissibility of variation from one generation to the next generation. It’s utility in plant improvement program was limited since the genetic variation included is fixable additive effect and non-fixable dominance and epistatic effect. Thus, heritability in “narrow sense” was defined as the ratio of additive genetic variance to phenotypic variance. Selection for trait having high heritability would be very effective as there would be a close correspondence between genotype and phenotype, but heritability estimates along with expected genetic advance are considered to be more useful in predicting the outcome of selecting the best individuals (Lush, 1949).

2.7. Correlation coefficient

The correlation coefficient analysis measures the mutual relationship between various characters and it determines the component traits on which selection can be relied upon to effect the improvement. There are three types of correlations viz., phenotypic, genotypic and environmental correlation. Phenotypic correlation is the observable correlation between two variables and includes both genotypic and environmental effects. Genotypic correlation on the other hand, the inherent association between two variables may be either due to pleiotropic action of genes or linkage, more likely both or developmental induced relationships (Crossa *et al.*, 1990).

Lack of the knowledge of interrelationships among various traits and the practice of unilateral selection for agronomic traits frequently end up with less than optimum result in plant breeding. Correlation does not mean having equal causation. To be correlated only means that two variables are related. We cannot say that one of them causes the other

variable to change. The other seems to change in predictable way (Panse, 1940). Correlation coefficients range from -1.00 to +1.00.

A correlation coefficient of -1.00 tells that there is a perfect negative relationship between the two variables. This means that as values of one variable increase there is a proportional decrease in values of the other variable. In other word, as one variable goes up, the other goes down (Cernaand Beaver, 1990). A correlation coefficient of +1.00 tells that there is a perfect positive relationship between the two variables. This means that as the values of one variable increase there is a predictable increase in values of the other variables.

2.8. Genetic Advances

Genetic advance is the measure of expected genetic progress that will be the result from selecting the best performing accession being evaluated for improvement in the mean genetic value of the selected plants over the base population for a given character so; improvement in the performance of the selected over the original population can be termed as genetic advance. The presence of genetic variability and heritability estimates will be helpful to the breeder to estimate genetic advance in the populations (Allard, 1960).

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 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. It is clear that the heritability estimated either “broad sense” or “narrow sense” is useful only for the population or genotypes under consideration as these estimate vary with the set of genotypes considered. The estimates of genetic advance help in understanding the type of gene action involved in the expression of polygenic characters (Kassaye, 2006).

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The study was conducted at Gorogutu Woreda karamille which is situated 400km east the of Addis Ababa, Ethiopia. The coordinates for Karamile town are 290 26' 48 north latitude and 270 42' 29 east longitudes, with an altitude of 1610m above sea level. Karamille is located in Gorogutu district of East Hararge Zone of Oromia Regional State. The experiment were conducted during the cropping season (April, 2023) under rain fed conditions. The area receives rain two and more than two times in a year which suitable to produce crops in once in a year. The temperature of the area is characterized by cold and warm which suitable for different crops including vegetables and root crops.

3.2. Experimental materials

The experiment consists of sixteen improved varieties of common bean obtained from Haramaya University research center

Table 1: description of common bean genotypes

NO.	Genotypes
1	Awash-1
2	Awash-2
3	Awash-melka
4	Ayenew
5	Babile
6	Chercher
7	Dursitu
8	Fadis
9	Gofta
10	Haramaya
11	Hirna
12	Kufanzik
13	Nasir
14	Raro SAB632
15	SER-19
16	Tinike

3.3. Experimental design

The field experiment were laid out in a randomized complete block design (RCBD) with three replications. Common bean accessions were collected on March 2023 from Haramaya University research center and planted in five rows per plot with spacing of 40cm length with row-to-row distance of 30 cm and plant-to-plant distance of 20cm. Each replication was consist sixteen plot and each plot consist five rows and each rows contain 25 plants. The experimental plot size were 1.5m x 1.5m (1.5m²) which has 5 rows and the two outer most rows at both ends of the plots were treated as border leaving three middle rows of each of the genotypes for data collection. The spacing between rows and plant was be 30cm and 20cm respectively. Bean seeds used in experiment were obtained from Haramaya University

Research Center. Common bean was sown on April, 2023. The experimental field were prepared by using farm plough and it was ploughed three times, the first at the beginning of January 2023, the second at the beginning of March and the third for planting in April 2023.

3.4. Agronomic practices

The land was prepared through ploughing, and after which disc harrow was used to level the seedbed and break the clods. Sowing of seeds were done by hand. The seeds were sown during rainy season and irrigation would not be used. Weeding was done by hand-hoeing during the growing period of the beans to control weeds. Any insect pest were controlled using insect pest during growing periods of the beans.

3.5. Method of Data Collection

The pre- and post-harvesting observations were recorded from randomly selected five plants from each genotype in each replication for all characters studied except days to germination, days to flowering and days to maturity, which were determined from the whole plot. Altogether 12 agronomic and morphological traits of sampled plants and seeds were recorded according to *Phaseolus vulgaris* L. descriptor (Debouck and Hidalgo, 1986), at the correct growth stage of the plant for each character.

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

1. Seed yield and its components

1.1. Seed yield: The average seed yield in grams obtained from five randomly taken plants in each plot.

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

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

Harvested index (HI)= seed yield (g)/ biological yield (g)

1.4. Pods per plant: The number of pods per plant were counted from five randomly taken plants from the middle three rows and expressed as an average for each plot.

1.5. Number of Seeds per plant (NSPP): Number of seeds per pod were recorded by counting the total number of seeds in a pod from twenty randomly sampled pods taken from the five randomly selected plants.

1.6. Hundred seed weight: Determined from the average 100-seeds mass at (12-14%) moisture content of the seed and expressed in grams.

2. Morphological traits

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

2.2. Plant height: The plant heights of five randomly taken plants from each of the three middle rows were measured from the ground level to the tip of the plant at physiological maturity and expressed as an average of heights of five plants per plot.

2.3. Number of nodes per plants (NNPP): Number of nodes per plants were recorded by counting the total number of nodes in a plants from five randomly selected plants.

3. Phenological traits

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

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

3.3. Days of germination: days to the germination (emergence) of 50% of the plants in a plot.

3.6. Data Analysis

3.6.1. Analysis of Variance

Data on phenological parameters, growth parameters, yield, and yield components were subjected to analysis of variance (ANOVA). Analysis of variance (ANOVA) was conducted using SAS version (SAS, 2004) computer software following SAS statement for complete randomized block design (CRBD) to test the presence of significant difference among

genotype. All collected data were subjected to analysis using the SAS (statistical Analysis system). The analysis of variance was also performed using the GLM procedure of SAS Statistical Software. All the measured variables were subjected to analysis of variance (ANOVA) following Gomez and Gomez (1984). The General Linear Model (GLM) of SAS Statistical Package Version 9.2 Software (SAS, 2009) was employed for the analysis. The model for experimental design used in randomized block design can be expressed as follows.

Table 2: The skeleton for analysis of variance for randomized block design

Source variation	d.f	Sum of squares	Mean square	F-Calculated
Replication	(r-1)	SSr	MSr	MSr/Mse
Genotypes	(g-1)	SSg	MSG	MSG/Mse
Error	(r-1)(g-1)	SSe	Mse	
Total	(rg-1)			

NB: d.f= degree of freedom, r = number of replications, g = number of genotypes, MSG = mean square due to genotypes, MSe = error mean square,

3.6.2. Phenotypic and Genotypic Variation

The variability was estimated using range, mean, standard error, phenotypic and genotypic variance and coefficient of variation. The resulting component of variance were used to compute the phenotypic and genotypic variation and genetic advances suggested by Brutton and Devance (1953).

Phenotypic and genotypic variances were estimated as per the formula provided by Burtone and Devane (1953):

Environmental variance, σ^2_e = error mean square = MSe

Where:

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ^2_{gl} = genotype by location interaction variance

σ^2_e = environmental variance

$$\sigma^2_g = (\sigma^2_t - \sigma^2_e) / r$$

Where, σ^2_g = genotypic variance, σ^2_t = mean square of treatment, σ^2_e = error mean square and r = number of replication.

$$\sigma^2_p = (\sigma^2_g + \sigma^2_e)$$

Where, σ^2_p = phenotypic variance

According to (Singh, 2000) the phenotypic and genotypic coefficient of variance are expressed by the following formula:

$$GCV (\%) = (\sqrt{\sigma^2_g / \bar{x}}) \times 100$$

Where, GCV = genotypic coefficient of variance, \bar{x} = mean value of the trait. Or \bar{X} is population mean for the character

$$PCV (\%) = (\sqrt{\sigma^2_p / \bar{x}}) \times 100$$

Where PCV = phenotypic coefficient of variance.

3.6.3. Heritability (Estimation of heritability in broad sense H^2 (%))

Heritability in broad sense for all traits were computed by adopting the formulae presented by Allard (1960). Heritability in broad sense (H^2) estimated as $H^2 (\%) = (\sigma^2_g / \sigma^2_p) \times 100$ or

$$H^2 = [\sigma^2_g / \sigma^2_p] \times 100$$

Where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance.

3.6.4. Expected Genetic Advance from selection (GA)

Genetic advance for all traits were computed by adopting the formulae presented by Allard (1960) and GA as percentage of the mean expected from selection of the best 5% of the genotypes were estimated as: Expected genetic advance (GA) = $H^2 \times k \times \sigma_p$ or

Genetic advance under selection, assuming the selection intensity of 5% was calculated using the formula adopted by Jonson *et al.*, (1955) and Allard (1960).

$$GA = (k) \cdot (\sigma_p) (H^2)$$

Where, GA = expected genetic advance, K = the selection differential (K= 2.06 at 5% selection entity), σ_p = phenotypic standard deviation, H^2 = heritability in broad sense.

Expected genetic advance as percentage of mean (GAM). Genetic advance as percent of mean were calculated to compare the extent of predicted advances of different traits under selection using formula:

$$GAM = (GA/X) 100$$

Where, GAM = genetic advance as percent of mean

GA = genetic advances under selection

X = mean value . According to Johnson *et al.* (1955) Genetic advance as percent of mean were classified as low (0-10%), moderate (10-20%) and high (>20%).

3.6.5. Phenotypic and Genotypic Correlation

The correlation coefficient among all possible characters' combinations at phenotypic (r_p) and genotypic (r_g) level was estimated employing formula Al-Jibouri *et al.*, (1995).

$$r_g = Gcov_{x,y} / \sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})} \quad \text{Where, } r_g = \text{genotypic correlation coefficient}$$

$G_{covx.y}$ = genotypic covariance between variables x and y

σ^2_{gx} = genotypic variance for variable x

σ^2_{gy} = genotypic variance for y

$$r_p = P_{covx.y} / \sqrt{(\sigma^2_{px} \cdot \sigma^2_{py})}$$

Where, r_p = phenotypic correlation coefficient

$P_{covx.y}$ = phenotypic covariance between variables x and y

σ^2_{px} = Phenotypic variance for variable x

σ^2_{py} = Phenotypic variance for variable y
The coefficient of correlation was tested for their statistical significance by using t- test as;

$$t = r \sqrt{(n-1) / \sqrt{(1-r^2)}}$$

Where, n= number of treatment, r= replication. The calculated value of t compared with t table value at n-2 degrees of freedom at 1 and 5 percent level of significance.

4. RESULTS AND DISCUSSION

4.1. Quantitative characters

The present study deals with a field experiment carried out with 16 varieties common bean to evaluate variability in morphological characters, extent of genetic variability. The results obtained in the present investigation and the discussions were given below.

4.1.1. Mean and range trait performance of genotypes

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 germination, days to flowering, days to maturity, plant height, pods per plant, seed yield per plant, pod length, node per plants, seed per plant, hundred seed weighted, above ground dry biomass, and harvest index. Sixteen 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 while other characters showed low to fairly high range values. This result is supported by the findings of (Berecha, 2015) who observed high range of variation for seed yield per plant, hundred seed weight, seeds per plant, plant height, days to maturity and days to flowering.

In the present study, the genotype of Haramaya (6.33) took the shortest days to germination, while Tinike took the longest days to germination with mean of 7.875. The genotype of Haramaya (40.33) took the shortest days to flowering while Chercher (45) took the longest days to flowering with mean of 43.54. The genotype SAB 632 (89) took the shortest days to maturity while Haramaya took the longest (106) with mean of 95.25. The genotype Haramaya had maximum heights of plants 168.9cm while the genotype Fadis (32cm) had the minimum value for plant height. Tinike had maximum seed yield per plant (120g), while Awash 2 minimum seed yield per plant (21.33g) genotype. The genotype (Awash melka) had the maximum hundred seed weighted (98.33g) while Awash 2 had minimum hundred seed weighted (11.66g).

The genotype Fadis had the maximum harvest index with value (0.89g) while Awash-2 genotype had minimum harvest index with value 0.24. 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 above ground dry biomass (biological yield), pods per plant and their considerable potential for improvement of common bean. The mean performances of each of the accessions are presented in Table 3. It showed wide ranges of means for the studied agro morphological traits except a few traits which revealed narrow mean range of variation among tested genotypes.

Table 3. Minimum, maximum, mean values and CV for the 12 characters of 16 common beans accessions.

Traits	Minimum score	Maximum score	Mean	CV
DE	6	9	7.875	8.79
DF	41	45	43.54	1.148
DM	89	106	95.25	4.508
NPPP	13.2	33.17	23.760	30.84
PL	9.60	12.18	10.810	15.258
PH	32.4	168.9	65.425	19.095
NNPP	3.8	5.6	4.666	24.611
NSPP	39.4	264	131.470	9.270
SYPP	21.33	120	55.437	12.955
BY	50.66	191.66	93.833	9.978
HSW	11.66	98.33	39.604	22.695
HI	0.24	0.89	0.602	12.622

DF=Days to flowering, DM=Days to maturity, PH=Plant height, NPPP=Number of pods per plant, SYPP=Seed yield per plant, HSW=hundred Seed weight, BY= biological yield, HI=Harvest index DE: days of emergence PL: pod length, NSPP: number of seed per plant, NNPP: number of node per plant.

4.1.2. Analysis of Variance

Data obtained for the 12 quantitative traits from 16 common bean accessions were subjected to analysis of variance and revealed highly significant differences among the accessions for all the traits studied. The mean squares due to various sources of variation for different traits are presented in Table 4. The results obtained from present investigation revealed that there was considerable genetic variability in the experimental materials, which could be exploited through systemic breeding and selection approaches.

The analysis of variance computed for 12 agro-morphological traits revealed that, the mean square due to genotypes were highly significant ($p < 0.01$) for days to emerging, days of flowering, days of maturation, plant height, number of seed per plant, biological yield, hundred seed weight, harvested index and seed yield per plant. However, non-significant difference observed on number of pod per plant, plant length and number of nod per plant (Table 4). The analysis of variance indicated the presence of variability among common bean genotypes which can be exploited through selection to improve the crop for desired traits for further common bean breeding program. Several previous studies reported similar significant variations among common bean accessions from different parts of the world (Zelalem, 2005; Kassaye, 2006; Lima *et al.*, 2012; Berecha, 2015; Zelalem, 2015). More importantly, the observed variation among accessions showed the importance of evaluating and maintaining genetic resources for improvement of common bean productivity and other desirable traits. Analysis of variance indicated significant to highly significant ($P < 0.05$ and 0.01) differences among genotypes for all of the studied traits (Table 4), this indicates the presence of considerable genetic variability among the tested common bean genotypes for various characters suggested that the genotypes were genetically diverse and could be a good opportunity for breeders to select genotypes for trait of interest.

Table 4: Combined Analysis of Variance is a report that combined the results of multiple reports in to single reports.

Source of variation	Rep	Gnts	Error	CV%
Degree of freedom	2	15	30	
Days of emergence	0.092	1.861**	0.479	8.79
Days of flowering	1.939	3.194**	0.25	1.148
Days of maturation	0.092	77,66**	18.43	4.505
Number of pod per plants	0.092	103.72	53.7	30.8
Pods length	0.458	4.911	2.72	15.25
Plants height	44.314	2792.6**	156.08	19.09
Number of node per plants	0.0001	1.230	1.23	24.6
Number of seed per plants	35.23	10572.8**	148.56	9.270
Biological yield	1.361	4846.6**	87.66	9.97
Hundred seed weight	42.45	1486.8**	80.79	22.7
Harvest index	0.007	0.0833**	0.0057	12.6
Seed yield per plants	4.5	2001.5**	51.583	12.9

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively df =Degree of freedom, DF=Days to flowering, DM=days to maturity, PH=Plant height, NPPP=Number of pods per plant, SYPP=seed yield per plant, HSW=hundred Seed weight, BYG=above ground dry biomass and HI=Harvest index, PL= plant length, DE= days to germination, NSPP= number of seed per plants, NNPP= number of node per plants CV=Coefficient of variations.

4.1.3. Genotypic and phenotypic variations

Estimation of genotypic variance (σ^2_g), phenotypic variance (σ^2_p) and environmental variance (σ^2_e) of different traits for sixteen common bean genotypes are given in the (Table 5). The progress of breeding for such agronomic traits is determined by magnitude and nature of their genotypic and phenotypic variability. In present study genotypic coefficient of variation is lower in magnitude than phenotypic coefficient of variation on all 12 agro-morphological traits. Genotypic coefficient of variation ranged from 2.275 (days of flowering) to 54.663 (Hundred seed weight) while phenotypic coefficient of variation ranged between 2.548 (days of flowering) and 59.187 (Hundred seed weight). According to Knight (1979) PCV and GCV values greater than 20% are regarded as high, values between 10% and 20% to be medium whereas values less than 10% are considered to be low. The PCV values were relatively higher than the GCV values for all the studied traits, which indicated the influence of environmental factors in the expression of the traits. Several authors reported similar findings (Alemayehu, 2010; Ahmed and Kamaluddin, 2013; Ejigu *et al.*, 2018). According to Deshmukh *et al.* (1986), genotypic and phenotypic coefficient of variations can be categorized as low (<10%), medium (10-20%) and high (>20%). Based on this delineation PCV and GCV recorded in this study, High genotypic coefficients of variations(GCV) were observed for plant height (45.312), harvest index(26.693) ,hundred seed weight (54.663), above ground dry biomass(42.446), number of seed per plants (44.836) and seed yield per plant(45.988) while Moderate genotypic coefficients of variations (GCV) were observed for number of pod per plant (17.18063) , While low genotypic coefficients of variations (GCV) were observed for days to flowering (2.275), and days to maturity (4.664), days to germination (8.618) , pod length (7.903) and number of pod per plant(3.689). This result agrees with the findings (Berecha, 2015) reported that high genotypic variance for seed yield per plants and seed yield in common bean genotypes. High phenotypic coefficients of variations (PCV) were observed for, plant height (49.171), number of pod per plants (35.310), number of node per plant (24.052) number of seed per plants (45.785), above ground dry biomass (43.603), hundred seed weight(59.187), harvest index (29.528), and seed yield per plant (47.7784). While Moderate phenotypic coefficients of variations(PCV) were observed for, days to germination (12.310) and plants length (17.183). While low

genotypic coefficients of variations (PCV) were observed for days to flowering (2.548), and days to maturity (6.487). Higher magnitude difference between phenotypic and genotypic coefficient of variation were observed in number of pod per plant, number of node per plant, pod length and low magnitude difference in day of flowering, number of seed per plant and biological yield. The observed moderate to high differences between genotypic and phenotypic coefficient of variation noticed for most of the traits indicates higher sensitivity to environmental influence. On the other hand the low or close values for genotypic coefficient of variation and phenotypic coefficient of variation for most of the traits indicated that the less magnitude of environmental variances (Ghosh et, al, 2010).

Table 5. Estimation of genetic (δ^2_g), phenotypic (δ^2_p) and environmental (δ^2_e) components of variances broad sense heritability (H^2), phenotypic (PCV), genotypic (GCV) coefficients of variability, and expected genetic advances (GA), and as percent of the mean

Traits	Mean	σ^2_g	σ^2_p	δ^2_e	GCV	PCV	(H^2b)	GA	GAM
DE	7.87	0.46	0.93	0.47	8.61	12.31	49.01	0.98	12.44
DF	43.54	0.98	1.23	0.25	2.27	2.54	79.69	1.82	4.19
DM	95.25	19.74	38.18	18.43	4.66	6.48	51.70	6.59	6.92
NPPP	23.76	16.66	70.39	53.72	17.18	35.31	23.67	4.09	17.24
PL	10.81	0.73	3.45	2.72	7.90	17.18	21.15	0.81	7.49
PH	65.42	878.84	1034.93	156.08	45.31	49.17	84.91	56.35	86.14
NNPP	4.66	0.029	1.25	1.23	3.68	24.05	2.35	0.05	1.16
NSPP	131.47	3474.76	3623.32	148.56	44.83	45.78	95.89	119.08	90.58
BYG	93.83	1586.31	1673.98	87.66	42.44	43.60	94.76	79.98	85.24
HSW	39.60	468.67	549.46	80.79	54.66	59.18	85.29	41.24	104.15
HI	0.60	0.0258	0.031	0.005	26.69	29.52	81.72	0.29	49.78
SYPP	55.43	649.98	701.56	51.58	45.98	47.77	92.64	50.62	91.31

DF=Days to flowering, DM=Days to maturity, PH=Plant height, NPPP=Number of pods per plant, SYPP=Seed yield per plant, HSW=hundred Seed weight, BY= biological yield, HI=Harvest index DE: days of emergence PL: pod length, NSPP: number of seed per plant, NNPP: number of node per plant.

4.1.4. Broad Sense Heritability

In the present study, estimated heritability in broad sense ranged from (2.353) for number of node per plant to (95.899) for number of seed per plants (Table 5). As demonstrated by Robinson *et al.* (1949), heritability can be categorized as low (0-30%), moderate (30-60%) and high (60% and above). Based on this category, high heritability estimate were observed for most of the traits studied except for days of emergence and days to maturity which had moderate heritability values. And number of pods per plants, pods length and number of nodes per plants which had low heritability values. This result is consistent with the previous report of (Ankit *et al.*, 2017). Estimates of heritability had indicated in (table 5). High heritability estimates from 60-97% were obtained for days to flowering,(79.699), Plant height(84.918) seeds per plant(95.899), harvest index(81.721), seed yield per plant(92.64), hundred seed weight(85.296) and biological yield(94.763) . This result agrees with at reported by Berecha (2015) who has reported similar results that seeds per plant, seed yield per plant, harvest index, and biological yield had high heritability estimate in common bean genotype. Moderate heritability from 20-50% was observed for days to germination (49.0147), days to maturity (51.7097), number of pod per plants (23.673) and plant length (21.155). Very low broad sense heritability reveals the ineffectiveness of direct selection for the improvement through selection (Obilana and Fakorade, 1980;Snowder *et al.*, 2005). If heritability of a character is very high around 80% or more, selection for such character is fairly easy. This indicates that there would be a close correspondence between genotypic and phenotypic variation due to relatively small contribution of the environment to the phenotypic expression of the trait (Singh *et al.*, 1990).

4.1.5. Estimate of expected genetic advance as percent of mean

Genetic advance measures the expected genetic progress that would result from selecting the best performing genotypes for a character being evaluated (Allard, 1999). According to Johnson *et al.* (1995) heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. Selection based on those traits with a relatively high genetic advance as a percent mean would result in the improvement of the performance of the genotypes for the traits. The calculated genetic advance as percent of

mean (GAM) ranged from 1.167% for number of pods per plants to 104.15% for hundred seed weight (Table 5). According to Johnson *et al.* (1955), genetic advance as percent of mean can be categorized as low (0-10%), moderate (10- 20%), and high (20% and above). According to this category, high GAM were recorded for hundred seed weight (104.15%), plants height(86.14%) number of seeds per plant (90.581 %), seed yield per hectare (91.319%), biological yield(85.242%) and harvest index(49.782%). Plants suggested that, selection could be effective for these traits and the possibility of improving common bean seed yield through direct selection for yield related traits. On the other hand, moderate GAM were recorded for days to emergence(12.447%) and pods per plants(17.245%) whereas, low GAM were recorded for days to maturity (6.920 %), days to 50% flowering(4.190%), number of node per plants(1.167%) and pods length (7.499 %). Similarly, Ejigu *et al.* (2018) reported similar finding.

According to Johnson *et al.* (1995) heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. This study revealed that, while evaluating 16 genotypes of common bean in the present study, high heritability with high genetic advance for number of seed per plant, biological yield, hundred seed weight and harvested index. Similar finding have reported by (Ankit *et al.*, 2017; Ejigu *et al.*, 2018). indicating that this trait could be predominantly governed by additive gene action and selection of this could be more effective for desired genetic improvement (Jay Prakash and Ram 2014).

4.2. Genotypic and phenotypic correlation coefficient

The results of genotypic and phenotypic correlation coefficients are presented in (Table 6) . Yield generally, is a complex polygenic trait and difficult to improve directly. Estimating its genotypic and phenotypic correlation coefficient with yield related traits is important to utilize the available variability through selection. Phenotypic correlation can be directly observed and includes both genotypic and environment effects and therefore differ under different environmental condition. Genotypic correlation refers to the inherent or heritable association between two variables. In this study correlation of seed yield with other traits was performed and result showed that genotypic correlation was lower in magnitude than the

corresponding phenotypic correlation for most of the studied traits. Correlation analysis measures association between variables and can be positive or negative, significant or non-significant (Pavlov *et al.*, 2015).

4.2.1. Phenotypic Correlation Coefficients and Genotypic Correlation Coefficients

This study revealed that phenotypic correlation ranged from -0.155 for correlation of day of emergence with seed yield per plant to 0.52 for the correlation number of seed per plant with seed yield per plant (Table 6). Seed yield had a negative and non-significant correlation with day of emergency, day of flowering, day of maturation, number of pod per plants and pod length. This suggested that, selection of late maturing genotypes for high performance of these traits reduce seed yield. Such negative and non-significant phenotypic correlation of seed yield per plant with day of emergency, days of flowering and days of maturation was also obtained in the experiment conducted by Wolde and Negash (2022).

On the other hand seed yield showed positive and non-significant difference with related to number of node per plant (0.271) and plant height (0.105). It also showed positive and significance different with related to biological yield (0.398) and hundred seed weight (0.349) as well as positive and highly significant difference with related to number of seed per plant (0.52) and harvested index (0.61). This indicated that, any improvement of these traits would result in a substantial increment on seed yield per hectare. This result agrees with previously reported findings (Roy *et al.*, 2006). Number of nodes showed positive and highly significant at ($p \leq 0.01$) correlation with pod length. Harvest index showed positive and highly significant ($p \leq 0.01$) correlation with number of seed per plant. seed yields per plant showed positive and highly significant ($p \leq 0.01$) correlation with number of seed per plants and harvest index. and showed positive and significant with hundred seed weight and biological yield.

The study revealed that genotypic correlation ranged from -0.22 for correlation of number of node per plant with seed yield per plant to 0.83 for the correlation of biological yield with seed yield per plant table 6. Seed yield had positive highly significant correlation with biological yield and positive non-significant correlations with day of maturity (0.011), plant height (0.388), number of seeds per plant (0.402), number of pod per plant (0.199) and

harvested index (0.391) at genotypic level. Similar previous finding of Karasu and Oz (2010) who revealed that positive correlation of seed yield with number of seed per plant, plant height and number of pod per plant were concurred with the present result. The positive association of seed yield with these traits suggested that the traits could be used as selection criteria for high seed yield.

The study also shown that seed yield negative non-significant different correlation with day of emerging (- 0.03), days of flowering (- 0.09), pod length (- 0.11), number of node per plant (- 0.22) and hundred seed weight (- 0.16). This result indicated that, early maturing genotypes could provide higher seed yield per hectare than late maturing genotypes, which might be due to the effect of terminal moisture stress on late maturing genotypes. Similarly, Alemayehu (2014) reported significant negative correlation of seed yield with days to maturity.

Table 6. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients for 12 traits of 16 common bean genotypes.

Trait	DE	DF	DM	NPPP	PL	PH	NNPP	NSPP	BYG	HSW	HI	SYPP
DE	1	0.06	0.13	-0.02	-0.31	-0.22	0.19	-0.10	0.04	0.12	-0.23	-0.15
DF	0.15	1	0.26	0.17	-0.08	0.04	0.28	0.04	0.01	-0.03	-0.21	-0.11
DM	-0.27	-0.40	1	-0.07	0.147	0.06	0.19	-0.08	0.24	-0.17	-0.38*	-0.09
NPPP	-0.7**	0.02	0.16	1	0.029	0.24	0.112	0.32*	0.34*	-0.12	-0.196	-0.01
PL	0.24	0.36	-0.15	-0.43	1	-0.01	0.46**	0.01	0.027	0.09	-0.048	-0.06
PH	-0.47	-0.6**	0.6**	0.23	-0.29	1	0.048	0.209	0.152	0.18	0.147	0.11
NNPP	-0.27	0.16	-0.46	0.16	0.40	-0.40	1	0.032	0.216	0.13	-0.012	0.27
NSPP	-0.5*	0.27	-0.03	0.83**	-0.28	0.07	0.17	1	0.37*	0.34*	0.40	0.52**
BYG	-0.27	-0.19	0.23	0.31	-0.21	0.56*	-0.22	0.42	1	0.155	-0.35*	0.39*
HSW	-0.19	0.39	-0.14	0.21	0.30	-0.24	0.33	0.38	-0.25	1	0.307	0.34*
HI	0.31	0.03	-0.38	-0.13	0.08	-0.17	0.06	0.01	-0.15	0.04	1	0.61**
SYPP	-0.02	-0.40	0.011	0.19	-0.11	0.39	-0.22	0.40	0.83**	-0.16	0.39	1

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ probability level respectively. DF=Days to flowering, DM=Days to maturity, PH=Plant height, NPPP=Number of pods per plant, SYPP=Seed yield per plant, HSW=hundred Seed weight, BY= biological yield, HI=Harvest index DE: days of emergence PL: pod length, NSPP: number of seed per plant, NNPP: number of node per plant.

5. SUMMARY, CONCLUSION AND RECOMMENDATION

5.1. Summary

Common bean is the world's most important food legume for direct human consumption. High in nutrients and commercial potential, common bean holds great promise for fighting hunger, increasing income and improving soil fertility in Sub Saharan Africa. Common bean is an important part of human diet in Ethiopia. It is among the most important food legumes produced in the country, which has been cultivated as a field crops for a very long time. So this study were conducted to determine the genetic variability, heritability and interrelationship of traits for common bean varieties in karamile. The research was conducted on 16 common bean varieties collected from Haramaya Agricultural Research Center with three replications under Randomized Complete Block Design. This study generally indicated that there was significant genetic variability or divergence among the varieties for most of the traits considered. Thus, there is enormous opportunity in the improvement program of the common bean through direct selection. The experiment were use sixteen improved varieties of common bean obtained from Haramaya University research center and planted on the field using randomized complete design (RCBD). Then the data were collected based on Seed yield and its components, Morphological traits and Phenological traits from sample plants that used randomly from plots.

Genotypic coefficient of variation ranged from 2.275 (days of flowering) to 54.663 (Hundred seed weight) while phenotypic coefficient of variation ranged between 2.548 (days of flowering) and 59.187 (Hundred seed weight). High genotypic coefficients of variations(GCV) were observed for plant height (45.3120),harvest index(26.693), hundred seed weight(54.66306), above ground dry biomass(42.446), number of seed per plants (44.836) and seed yield per plant(45.988). While Moderate genotypic coefficients of variations (GCV) were observed for number of pod per plant (17.180), While low genotypic coefficients of variations (GCV) were observed for days to flowering (2.275), and days to

maturity (4.664), days to germination (8.618), pod length (7.903) and number of pod per plant (3.689). High phenotypic coefficients of variations (PCV) were observed for, plant height (49.171), number of pod per plants (35.310), number of node per plant (24.052), number of seed per plants (45.785), above ground dry biomass (43.603), hundred seed weight (59.1873), harvest index (29.528), and seed yield per plant (47.778). While Moderate phenotypic coefficients of variations (PCV) were observed for days to germination (12.310) and plants length (17.183). While low genotypic coefficients of variations (PCV) were observed for days to flowering (2.54), and days to maturity (6.487).

Heritability in broad sense ranged from (2.353) for number of node per plant to (95.8999) for number of seed per plants. High heritability estimates from 60-97% were obtained for days to flowering (79.699), Plant height (84.918), seeds per plant (95.899), harvest index (81.721), seed yield per plant (92.64), hundred seed weight (85.296) and biological yield (94.763). High genetic advance as a percent mean would result in the improvement of the performance of the genotypes for the traits. The genetic advance as percent of mean (GAM) ranged from 1.167% for number of pods per plants to 104.15% for hundred seed weight. Seed yield per plant had positive and significant phenotypic correlation different with related to biological yield (0.398) and hundred seed weight (0.349) as well as positive and highly significant difference with related to number of seed per plant (0.52) and harvested index (0.61). Seed yield had positive highly significant correlation with biological yield and positive non significant correlations with day of maturity (0.04), plant height (0.388), number of seeds per plant (0.402), number of pod per plant (0.199) and harvested index (0.391) at genotypic level.

5.2. CONCLUSION

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. Knowledge of relationship among yield and yield related traits is important in plant breeding for several reasons; it is possible

to fully perceive the diversity of breeding material, to identify traits that determine successful growth and performance of genotypes under certain ecological conditions. Hence, the present study was carried out to assess the genetic variability and associations of yield and yield related traits in common bean. Common bean is the most important crop for our people as a cash and food crops, the research on evaluation must be conducted. The data obtained from this study could be useful for common bean (*Phaseolus vulgaris* L.) breeders and seed producers in order to increase seed yield. Totally, they should be focused on the genotypes which have high amount of number seed per plant and harvest index.

5.3. RECOMMENDATION

The present study was conducted only for a single season on a single location in karramille, so the future researcher must conduct on different locations for many seasons to evaluate the best varieties of common bean.

- Further studies on common bean genotypes with large sample size to get consolidated information that is essential in breeding programs.
- Studies involving multi-location may be much more important to identify the genotypic and phenotypic expression of these yield and yield related traits among this common bean.
- Encourage the farmers to use the varieties that gave a good yield in the study conducted to improve the yield.

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7. APPENDIX

Table 1. Mean performance of genotypes at karramile.

Genotypes	DE	DF	DM	NPPP	PL	PH	NNPP	NSPP	SYPP	BYG	HSW	HI
Awash 1	8	43.66	99.33	21.6	14.3	51.6	4.2	98.73	35	65	60	0.54
Ser 19	8	43	89	25.2	9.77	52.2	5.2	113.86	40	79.33	58.33	0.51
Dursitu	6.66	43.33	89	33.17	10.56	61.36	5.6	229	80	103.3	15	0.53
A/ melka	7	44.66	93.66	31.6	10.23	53.86	5.2	264	42.66	66	98.33	0.66
Ayenew	8.33	43.33	102.6	22.2	9.79	86.93	4.13	126.86	70	105	22.3	0.67
Nasir	7.66	43	96	28.2	10.63	72	4.4	168.93	56	79	41.66	0.70
Babile	8.33	44	91.33	19.7	11.77	61.6	4.2	96	68.66	81.33	28.33	0.84
CHerche	7	45	96	30.6	11.19	43.06	4.8	172.53	45	86	61.66	0.53
Hirna	8	44.66	97	16.06	11.92	70.86	4.06	46.26	26.66	54.66	45	0.49
Tinike	8.66	44	93.66	19.3	11.46	65.93	4.26	169.6	120	191.6	48.33	0.63
Fadis	8.66	43.33	89	16.3	10.57	32.4	5.4	58.8	45.33	50.66	15	0.89
SAB 632	8.66	43	89	13.2	12.18	42.4	4.93	64.6	36.66	59.33	45	0.62
Haramay	6.33	40.66	106	27.53	9.72	168.8	4.26	128.33	75	160	23.33	0.47
Kufanizi	7.33	43	97	25.7	9.60	62.53	4.66	104.66	40	85	27	0.48
Gofta	8.33	43	96	27.1	10.01	74.2	3.86	151.2	84.66	100.6	35	0.84
Awash 2	8.66	43.66	99.33	21.5	9.66	52	3.8	110.33	21.33	87.66	11.66	0.24

DE= Days to emergence DF=Days to 50% flowering, DM=Days to 90% maturity, PL=Pods length, PH=Plant height, NNPP= number of nodes per plants NPPP= number of pods per plant, NSPP=Seeds per pods, SYPP=seed yield per plant, HSW=100 Seed weight, BYG= biological yield, HI=Harvest index.

8. APPENDIX FIGURES



Fig1. Photo taken during preparation the land and snowing the common beans.



Fig 2. Photo capturing during germination of common beans.

when flowering of common bean begin



Fig 3. most of common beans flowering



Fig 4. maturation of common bean begin



Fig 5. most of common beans begin maturation



Fig 6 And 7. harvest the common beans



harvesting the common beans

