EFFECT OF SEED STORAGE TIME ON GERMINATION RATE AND EXTENTS OF MORPHOLOGICAL GENETIC DIVERSITY AND YIELD OF FABA BEAN (*Vicia faba* L.) GENOTYPES

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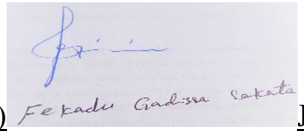
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We, the undersigned, members of the Board of Examiners of the final open defense by Solomon Abiyu have read and evaluated his thesis entitled "**effect of seed storage time on germination rate and extents of morphological genetic diversity and yield of faba bean (*Vicia faba* L.) genotypes**" and examined the candidate. This is, therefore, to certify that the thesis has been accepted in partial fulfillment of the requirement of the Degree of Master of Science in Biology

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STATEMENT OF THE AUTHOR

Here by I declare that this study is my reliance work and that all sources of materials used for this thesis has been properly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for master's degree in Biology at Madda Walabu University and is deposited at the University's Library to be made available to borrowers under rules of the Library. I solemnly dedicate that this thesis is not submitted to any other institution for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

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Solomon Abiyu

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LIST OF ACRONYMS AND

ANOVA	Analysis of Variances
CSA	Central Statistics Agency
CV	Coefficient of variation
D^2	Pair wise cluster distance
GA	Genetic advance in absolute units
GAM	Genetic advance as percentage of the mean
GCV	Genotypic Coefficient of Variation
h^2	Heritability in broad sense
R^2	Coefficient of genetic determination
RCBD	Randomized complete block design

ABBREVIATIONS

M.A.S.L	Meters above sea level
NPS	Nitrogen, phosphors and sulpher

ABSTRACT

*In Ethiopia, faba bean (Vicia faba*L.*) is an important pulse crop widely used as a source of food and cash source to the subsistence farmers. In rare case, it is used as a foreign currency earning to the country. Ecologically, it is used to improve soil fertility. However, its production and productivity are affected by different factors such as seed quality, storage time that is affected by different conditions including prolonged storage time, scarcity of available information on the extents of genetic diversity. Therefore, the present study was designed to test the effects of seed storage time and extents of genetic diversity using twenty-five faba bean samples (24 genotypes and one local check) obtained from Holeta Agricultural Research Center. The experiment was conducted at Holota agricultural research center research field under rain fed condition during the main cropping season in 2019. The experiment was laid using randomized complete block design (RCBD) with three replications. Data were collected on twenty-two traits and analyzed using SAS version 9.0 and MINITAB® Release 19. All the qualitative traits showed a wide variation among the phenotypic traits revealing importance in selection breeding. ANOVA for the 16 quantitative traits revealed a very highly significant ($P < 0.001$) variation for several traits. Likewise, high genetic advance joined with heritability and genotypic coefficient of variation was observed in several of the quantitative traits suggesting their importance in making effective selection breeding targeting their improvement. PCA also differentiate most of quantitative traits that had high contribution to the entire variation within the genotypes. The higher values in cluster distances observed shows the difference in genetic background between the materials in which some were taken from germplasm and others from seed store (released varieties). The highest yields were obtained in Geblcho, Hachalu and moti genotypes which had relatively less storage time. Thus, storage time had some profound effect on the genetic performance of faba bean genotypes and as a result, care should be taken while using seeds stored for longer periods as a seed source. In order to minimize the effects of environmental condition, multiple sites and season-based evaluation needs to be carried out. In addition, molecular markers-based testing is essential to complement the findings.*

Keywords/ phrases*: Faba bean, Genetic diversity, Genotypes, Seed storage time, Seed viability*

1. INTRODUCTION

1.1 Background of the study

Faba bean belongs to genes *Vicia* and family *Fabaceae* (Leguminosae) (Akpinar *et al*., 2001). It has a long tradition of cultivation in Old World agriculture, being among the most ancient plants in cultivation and also among the easiest to grow. Along with lentils, peas, and chickpeas, the plant is believed to be part of the eastern Mediterranean diet around 6000 BC or earlier (Muratova, 1931).

The crop is believed to be introduced to Ethiopia soon after its domestication, at around 5000 B.C. (Telaye, A. *et al*., 1994) and the country is now considered as one of the secondary centers of genetic diversity (Bond, 1976).

Worldwide, the crop has a multipurpose use and is consumed as dry seeds, green vegetable, or as processed food. Its products are a rich source of high-quality protein in the human diet, while its dry seeds, green haulm and dry straw are used as animal feeds (Sainte, 2011). Likewise, in Ethiopia, it is grown for different purposes including serving as a source of food to the people, feed to animals, cash to the farmers and foreign currency earning to the country. Thus, it ranks first in its production volume and cultivated land among pulse crops in Ethiopia and it is a valuable and the cheap source of protein in the country's diet (Teklay et al., 2014).

According to CSA (2016), faba bean is the most important pulse crop in both area coverage and volume of annual production in Ethiopia. Its production area covers from mid-altitude to highland areas with high rainfall and varied soil types. The country is ranking second, next to China, in terms of production (FAO Stat, 2017; Mussa Jarso and Gemechu Keneni, 2006) though its contribution was not more than 14.7 per cent of the amount that the top ten growing countries can contribute (FAO Stat, 2017).

It has long been cultivated as excellent source of protein and cash source for resource poor farmers (Hove *et al*., 1987). *Shiro wot*, *kikwot*, *full*, *eshet*, *kollo*, *nifro*, *gunkul*, *ashuke* and *endushdush* are the major local dishes prepared from faba bean in Ethiopia and neighboring Eritrea (Duc *et al*., 2010). The straw is used as fuel for cooking in rural community (Endale Hailu *et al*., 2014).

Besides, faba bean provides major benefits in the cropping systems and the environment due to its ability to perform symbiotic nitrogen fixation (Boddey et al., 2009; Kaur *et al*.,

2012; López-Bellido *et al*.,2006), break disease cycles in the cereal-based rotations and control weeds (Schmidtke and Rauber, 2000). Erik *et al*. (2012) suggested that the substitution of larger proportion of industrial nitrogen fertilizer by leguminous N_2-fixation could minimize considerable amount of global CO_2 emissions.

Despite of such immense importance the country is obtaining, the production and productivity of pulses in general and faba bean in particular is still far below the country's potential. For example, the average faba bean yield in the country was not more than2.1 tons per hectare (CSA, 2018).

Nowadays, the yield and area coverage are radically decreasing because of several intervening factors. Thus, use of quality seed and having pre-hand information on the extents of genetic diversity in the breeding materials are among the methods to improve the productivity of the crop. In addition, since most farmers produce seeds only once a year, knowledge of seed preservation methods for next season's generation is an important and determinant factor on how soon the seeds would lose its viability (Dawit Tadesse *et al*., 2016). Thus, scientific methods of maintaining seed viability for longer period is very essential to preserve the genetic integrity in stored samples. Simple techniques have been adopted to maintain the seed viability in both domesticated and wild sources (Ellis et al., 1991), (Vertucci and Roos, 1991).

On the other hand, seed deterioration and loss of viability is a natural phenomenon occurring during storage (Nasreen *et al*., 2000; Schmidt *et al*., 2002) and inappropriate storage medium such as room temperature has often resulted in low seed germination (Hezewijk *et al*., 1993), Müller et al., 2011). Several factors, including temperature, nature of the seeds, seed moisture content, and relative humidity influences the seed longevity during storage (Onyekwelua and Fayose (2007), Pradhan and Badola (2008). Proper storage conditions may effectively retain substantial viability in seeds over a considerable storage period (Butola and Badola 2004, Chen et al. (2007), Pradhan and Badola 2008; Mc Donald, 1999). Overall, the present study was initiated to attain the following objectives:

1.2. Objective of the study

1.2.1 General objective

The general objective of this study is to investigate the effect of seed storage time on its germination rate and to evaluate the extents of agro-morphological traits-based genetic diversity and yield in faba bean (*vicia faba*) genotypes from Ethiopia.

1.2.2 Specific objectives

- To assess the effect of seed storage time on the germination of faba bean genotypes
- To identify the extents of genetic diversity in the genotypes using standard agro-morphological traits
- To determine the effects of seed storage time on the extents of morphological genetic diversity and seed yield in the genotypes

1.3. Research questions

This research is going to answer the following basic questions:

- Is seed storage time in faba bean genotypes affecting the germination rate?
- What is the extent of agro-morphological genetic diversity in faba bean genotypes?
- What is the effect of seed storage time of faba bean on the extents of genetic diversity and morphological diversity?
- Is storage time influence the yield of faba bean?

1.4. Significance of the study

This research was aimed at studying the effect of seed storage time and its relation to the extents of genetic diversity and yield in faba bean genotypes from Ethiopia. Thus, the finding will be important to be used as baseline information in further breeding and seed storage used by breeders, farmers, and other stakeholders so that the production and productivity of the crop will be improved.

2. LITERATURE REVIEW

2.1. Botanical Description of FabaBean

Faba bean (*Vicia faba* L.)is among the pulses and together with Phaseolus bean, soya bean and lupines, belongs to the genus *Vicia* and the family *Fabaceaea*(Sitte et al., 2002).Based on its seed size, it is classified into: small seeded (*Vicia faba* minor)- roundish seeds of up to 0.6gm or 0.7gm per seed, medium to large seeded (*Vicia faba* equine)- single seeded weight less than about 1gm, and *Vicia faba* major (impressive, large and flat seeds weighting more than 1gm per seed).The synonyms "field bean" indicates the small and medium sized types, whereas "broad bean" denotes *Vicia faba* major (Persoon, 1807).

2.2. Origin and Distribution of FabaBean

Faba bean is an ancient crop and numerous studies have been performed on its origin and domestication. Despite numerous studies, little is known of the origin and domestication of faba bean (Maxted *et al*., 1991). It is believed originate in Central Asia and secondary centers of diversity are postulated in Afghanistan and Ethiopia (Hajjar and Hodgkin, 2007).

However, Cubero (1973, 1974) postulated the Near East as the center of origin to the crop from where it radiated into Europe, the North African coast and Spain, along the Nile to Ethiopia and from Mesopotamia to India. Ladizinsky(1975) reported the origin to be in central Asia. According to Muratova(1931) and Maxted(1995)the center of origin for the genus *Vicia* is South Eastern Europe and south western Asia.

2.3. Agro-ecology of Faba Bean in Ethiopia

In Ethiopia, faba bean is largely cultivated in Weyndega (mid-altitudes) ranging from 1800-2200 m.a.s.l, with an average annual rainfall of 740 mm, and mean daily temperature of 18-22ºC) and Dega zones (high altitude, above 2200 m.a.s. l, average annual rainfall of 900 mm, mean daily temperature of 10-18^{o}C) (Asfaw *et al*, 1994). Similarly, Mussa Jarso, and Gemechu Keneni, (2006) indicated that Weynadega zone (mid-altitudes ranging from1800-3000m.a.s. l),is the best agro-ecology for the crop because of ample and satisfactory chilling temperature and optimum annual rain fall (700-1100mm).In most parts of the country, it is grown from June to December under rain-fed conditions usually in rotation with cereals. Its cultivation is mostly for subsistence use (Mussa Jarso, and Gemechu Keneni, 2006).

2.3. Faba Bean Production and Productivity in Ethiopia

In Ethiopia, agriculture accounts about 42 percent of the national GDP, employs about 85 percent of the labor force and contributes around 90 percent of the export earnings of the country (CSA, 2017/2018). Faba bean is ranking first, in terms of production, among the pulses produced in the country. In addition, the country is the second world producer of faba bean.

The major producing regions are Oromia (Wollega, Shewa, Bale and Arsi administrative zones), Amhara (Gondar, Gojam, Wollo), South people Nation and Nationality, some parts of Tigray and Benishangul-Gumuz. In addition, it is grown in the pocket areas of the remaining country's highland and semi-highland regions. It is best grown within altitudinal ranges of 1800 to 3000 m above sea level (Tewodros, T. *et al*., 2015).

2.4. Economic Importance of Faba Bean

Faba bean is an important grain legume used as a protein source for human and animals. Cultivated faba bean is used as human food in developing countries and as animal feed, mainly for pigs, horses, poultry and pigeons in industrialized countries (Singh *et al*., 2012).It has also valuable agronomic function because of its high capacity of N fixation and its ability to facilitate diversification of the agro-ecosystems by indirectly enhancing associated diversity of wild fauna (Köpke and Nemecek, 2010). Due to its nitrogen fixing capacity, it is used in crop rotation. It provides major benefits in the cropping systems and the environment due to its ability to perform symbiotic nitrogen fixation (Boddey et al., 2009; Kaur *et al*., 2012), break disease cycles in the cereal-based rotations and control weeds (Schmidtke and Rauber, 2000). Erik et al. (2012) suggested that the substitution of larger proportion of industrial N fertilizer by leguminous N_2-fixation could minimize considerable amount of global CO_2 emissions.

In Ethiopia it is used as a source of food to the people, feed to animals, cash to the farmers and foreign currency earning to the country. Its nutritional value and composition is comparable to that of meat due to its high protein content, which ranges from 20-41%, despite the imbalance in Sulphur containing amino acids (Ali et al., 1982; Larralde and Martínez, 1991; Crépona, *et al*., 2010).Thus, it is a crop of high economic value in complementing the cereal based Ethiopian diet (Temesgen *et al*., 2015).It also contribute a lot to income generation in small holder farmers (FAO, 2014).

2.5 Seed Storage Time and its Effect on Germination Rate

Germination is the most important function of a seed as an indicator of its viability and worth as seed. Depending on the duration and method adopted, drying and long-term storage may lead to considerable reduction in germination or to eventual death of the seeds. Before storage, if the seeds are not properly dried, the high moisture content may reduce the seed viability by promoting fungal growth. Such deterioration could further result in decline of seed germination capacity (Romanas, 1991). The seed deterioration rates may vary depending on the storage conditions, and the germination percent and/or seed viability gradually declines with increase in storage period (Yilmaz and Aksoy, 2007).

According to Delouche, (1968) and Harrington, (1972), seed longevity during storage is influenced by inheritance or the species, the quality of the seed at the time it enters storage, temperature of the storage environment; and the moisture content of the seed or ambient relative humidity. Quality seeds ensure better germination as well as better yield and thus, contribute in yield increase of as high as 30% keeping the other factors of production as constant (BARI, 1993).

2.6 Genetic Diversity Analysis in Crop Plants

Diversity in plant genetic resources (PGR) provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (yield potential and large seed, etc.) and breeders preferred traits (pest and disease resistance and photosensitivity, etc.)(Govindaraj *et al*., 2015).

Large numbers of germplasms (more than 6 million) have been maintained in the worlds Gene banks for use in breeding and conservation (Hammer *et al*., 2003). One of the purposes of breeding is to produce populations that bear better adaptation and greater fitness to a given environment. However, adaptation and adaptability (the capacity for genetic change in adaptation) are antagonistic. As adaptation in one environment is maximized, genetic information for fitness in other environments tends to be lost. Successful plant breeding, while improving adaptation, reduces variability and hence long-term adaptability and as the genetic base narrows it limits further progress in breeding (Simmonds, 1962). Genetic variability of crops can be partitioned into variability between crop cultivars and variability within a crop cultivar (the genetic differences within the population of plants that make up the cultivar).

Genetic variation in crop plants could be raised from spontaneous mutation or the accident of mechanical mixture. In addition, the amount of out crossing permitted by the breeding

system, the effectiveness of the isolation procedures used in growing seed crops, and the selection pressures governing the relative fitness of homo- and heterozygote could raise variation that is used as a raw material in selection breeding(Knowles,1969).

2.6.1. Agro-morphological traits based genetic diversity analysis

The assessment of genetic diversity within and between plant populations is routinely performed using various techniques such as morphological, biochemical (allozyme), and/or DNA (or molecular) marker systems (Yang et al, 2006).

Morphological markers are based on visually accessible traits such as flower color, seed shape, growth habits, and pigmentation. The system is relatively simple, does not require expensive technology and cost effective. However, the marker traits are often susceptible to phenotypic plasticity and thus difficult to exactly reveal the extents of genetic diversity in a given test material in the presence of environmental variation. Regardless of their limitations, they are still used in many instances (Govindaraj *et al*., 2015).

2.6.2. Diversity Analysis so far in Ethiopian faba bean genotypes

The long history of cultivation, the wide distribution across diverse environments, the mating system and responses to human selection have led faba bean to become one of the most variable species, possessing a wide spectrum of variation in plant architecture such as leaf size and shape, seed color, seed shape and size (Maalouf *et al*., 2013).

The crop prevails a high degree of genetic variability due to the presence of high percentage of out crossing (Hanelt and Mettin, 1989). A large genetic variability has already been identified in faba bean in terms of floral biology, seed size and composition, yield potential efficiency of symbiotic nitrogen fixation and tolerance to several biotic and abiotic stresses (duc *et al,* 2010).

Estimation of genetic variation in faba bean varieties in Ethiopia is the main concern of breeders as the effectiveness of selection depends on the proportion of the heritable variation. Different marker systems such as morphological, biochemical and molecular markers have typically used to assess the genetic diversity of the crop.

According to reports, the extent of genetic diversity in this species is not uniformly distributed across the country. Probably the level of genetic diversity in the original introductions may vary among regions. The nature and degree of natural and artificial manipulations after introductions, which may vary among regions, could also play an important role both in the dynamics of creation and perpetuation of genetic diversity. The concept that difference in

geographic origin should be used as an index of genetic diversity in parental selection could not reliably be used as a strategy and parental selection should rather be made based on systematic assessment of genetic distance in a specific population (Gemechu Keneni *et al*., 2005).

In Ethiopia, there are about 29 improved faba bean varieties which are adapted to different agro-ecology with varying reaction to diseases (Crop variety register, 2014). Farmers in the Ethiopia commonly used to cultivate local varieties (Thijssen *et al.,* 2008). In most cases local varieties are expected to be low yielding and susceptible to both biotic and abiotic stresses. Local landraces faba beans are highly susceptible to the disease and give low yield (Samuel *et al.,* 2008).

Ethiopia is secondary centers of diversity to faba bean due to the existence of wide genetic variability (Bond, 1976). Gemechu Keneni *et al* (2003) indicated the existence of high genetic diversity. Report by Dawit Tadesse *et al*. (1994) and Gemechu Keneni *et al*. (2005) also revealed the existence of a wealth of genetic variability among Ethiopian faba bean germ-plasms for most of the morpho-agronomic traits.

2.7. Effects of Seed Storage Time on the Extents of Genetic Diversity

Seed has been playing a critical role in agricultural development since the onset of the first domesticated crop at around 11,000 years ago. It is a carrier of genetic information that controls the maximum crop productivity, resistance to disease, and tolerance to environmental stresses (Cavatassi *et al.,* 2010; Bishaw, Z., 2004).Its quality is very essential and comprises physiological, health, physical and genetic qualities. Physiological qualities include germination, resistance to environmental conditions such as drought, soil conditions, fertility, etc. The health quality of a seed refers to the seed being free from important seed borne diseases while physical seed quality refers to freedom of seed from foreign materials such as weed seed, other species seed and inert materials. Whereas genetic quality is what establishes the production of a crop including yield, tolerance to drought, resistance to disease etc (Bishaw, Z., 2004).

In order to preserve the genetic integrity of a given seed, maintaining its viability for longer period is very essential (Bharat *et al*. 2012).Basically, deterioration of seed viability occurs when its moisture content, temperature, and storage periods become less than or above optimum during storage (Roos, 1981). Depending on the duration and method adopted, drying and long-term storage may lead to considerable reduction in germination or to eventual death

of the seeds (Romanas, 1991). Seeds of many species are delicate and lose viability after short periods of storage (Mohamed-Yasseen *et al*.1994; Walters 1998). Thus, it is of practical interest to determine how storage conditions affect germination and seedling growth in an attempt to maximize sapling production for ecological restoration and germplasm conservation (Berjak&Pammenter, 2008; Mohamed-Yasseen *et al*., 1994).

3. MATERIALS AND METHODS

3.1. Study area and its description

Holeta is situated in the Southwest direction at approximately 40kms from Addis Ababa, the capital of Ethiopia. The center is located on latitude 9^0 00'N and longitude 38^o3'E, at an altitude of 2400 m above sea level. The area receives an average annual rainfall of1144 mm, a minimum and maximum temperature of6^0C and 22^0C.

3.2. Plant Material

In the present study, a total of 26 genotypes and one local check (a total of 27 samples) were used. After germination test, only 24 well germinated genotypes and one local check were selected (***Table 1***). All the genotypes together with the local check were obtained from Holeta Agriculture Research Center, highland pulse research section seed store.

Table 1: List of genotypes used in the present study along with their storage time and condition

S/N	*Genotypes*	*Year of collection*	*Storage Condition*	*Remark*
1	Tesfa	2007	Germplasm store	
2	EH95074-9	2006	Germplasm store	
3	Woyu	2003	Germplasm store	
4	Messay	2004	Germplasm store	
5	EH940050V4	2004	Germplasm store	
6	EH99019-4	2005	Germplasm store	
7	EH00126	2006	Germplasm store	
8	EH99071-2	2006	Germplasm store	
9	EH98033-3	2006	Germplasm store	
10	EH98106-1	2007	Germplasm store	
11	EH99102-4	2007	Germplasm store	
12	NC-58-M	2010	seed store	
13	Dagaga	2012	seed store	
14	Moti	2013	seed store	
15	Geblcho	2014	seed store	
16	Obse	2015	seed store	
17	Dosha	2015	seed store	
18	Hachalu	2015	seed store	
19	Dida	2016	seed store	
20	Geblcho	2016	seed store	
21	Moti	2018	seed store	
22	Gora	2018	seed store	

23	Hachalu	2018	seed store
24	Dosha	2013	seed store
25	Local check	2018	local pot

3.3. Germination Test

Germination test was conducted at Holeta Research Centre, Highland pulse department using distilled water, clean Petri dish, and Whiteman paper. The experiment was conducted in three replication to reduce experimental error.

3.4. Field Experiment

The experiment was conducted under rain-fed conditions at Holeta Agricultural Research Center from July to December, 2019.

3.3.2. Experimental design and procedures

The field experiment was laid pit in a randomized complete block design (RCBD) with three replications. The plots were 2 m (length) × 1.2 m (width) with three seedling rows in a plot. Spacing between blocks was 1.5 m and spacing's between plots, rows, and plants were 0.6 m, 0.4m, and 10 cm, respectively. NPS fertilizer was applied at a rate of 121 kg per hectare during sowing(according to Holota agricultural research center). Weeds were controlled by hoeing and weeding.

3.4. Data Collection

3.4.1. Germination data collection and analysis

Germination data were collected after checking the germination of treated seeds from the first five days period to fourteen days by observing radical and plumule production following ISTA, (1996).

The germination % was calculated using the following formula:

$$\text{Germination } (\%) = \frac{\text{No.of germinated seeds}}{\text{Total number.of seeds sown}} \text{X } 100$$

The seed germination rate was computed using the formula:

∑n/∑D. n (Ellis and Roberts, 1980),

Where n is the number of seeds germinated on day D, and D is the number of days counted from the beginning of the test and;

Mean germination time (MGT) was calculated following Ranal& Santana (2006):

$$\mathrm{MGT} = \sum_{i=1}^{k} \mathrm{niti} / \sum_{i=1}^{nk} \mathrm{ni}$$

Where, ni is the number of seeds germinated at the time i; ti is the time from the start of the experiment to the i^{th} observation, and k is the time of last germination.

3.4.2. Data on field experiments

Field data were collected either on plant basis (i.e. from five random plants) or on plot basis using the descriptor lists of IBPGR and ICARDA (1985) as follows;

Data collected on plot basis:

a) Days to flowering (DTF): Number of days from planting to 50% of plants bears flower

b) Days to maturity (DTM): The number of days from sowing to the stage when 90% of the plants in a plot have reached physiological maturity.

c) Seed filling period (SFP): The number of days from flowering to maturity (i.e. the number of days to maturity minus the number of days to flowering).

d) Hundred seed weight (HSW)(g): The weight of hundred seeds taken randomly from the harvest seed lots of each plot

e) Seed yield per plot (grain yield) (SY/P): Grain yield in *gram* from the harvestable plot area. It was adjusted to 10% moisture level to give adjusted yield.

f) Seed production efficiency (**SPE**): Seed filling duration divided by duration of vegetative period and then multiplied by grain yield

g) Biomass weight per plot (BMPP in g/m2): Whole above ground plants parts on the plot were harvested, sun dried and weighted.

h) Harvest index (HI): according to Manfred (1993) and Rkmhay (1995) harvest index was calculated by the ratio of grain yield to above ground biological yield.

i) Economic growth rate (EGR): It is the ratio of seed weight per plot to seed filling duration and then multiplied by 100.

j) Seed yield per hectare (SYPH): Seed yield (g) from the specified harvestable plot area and adjusted to its recommended (10%) moisture content. The value was converted to Kg/ha and used for analysis.

k) Leaf size: was scored by visual observation on each plot by considering three leaf sizes small, medium, and large

l) Leaf shape: was scored based on visual observation from the plot by considering shapes such as narrow, intermediate, and rounded .

m) Pod attitude: recorded based on erect, horizontal, pendent and mixed

n) Seed shape: was recorded based on visual observation of the seeds such as oblong, semi spherical, semi oval.

o) Seed size: was scored small, medium and large

p) Seed coat color: recorded based on visual observation of the seed coat green, yellow and brown

Data collected on plant bases:

A sample of five randomly sampled and tagged individual plants were used per plot. The traits are presented below:

a) **Leaf length (LL) (cm):** Length from the base to the tip of the leaf. Three leaves from top, middle and bottom of the plant were taken and averaged.

b) **Number of pods per plant (NP/PL):** The average numbers of pods counted from samples of five plants taken randomly from each plot.

c) **Numbers of seeds per pod (NS/P):** The total number of seeds per plant divided by the total number of pods on the same plant and averaged over five plants taken randomly from each plot.

d) **Plant height (PH) (cm):** The average height of five plants taken randomly from each plot measured at physiological maturity.

e) **Height to the first poding node (HFPN) (cm):** The average height from ground to the first pod bearing nodes of five randomly selected plants from plots measured at physiological maturity.

f) **Pod length (PL):** Exterior distance of fully matured pod from the pod apex to the peduncle as measured in centimetres. Three pods from top, middle and bottom will be taken and averaged.

h) **Internode length (IL)**: Three internodes per plant of five randomly selected plants will be measured and averaged.

3.4.3. Statistical analysis on field experiments

3.4.3.1 Analysis of qualitative traits

For qualitative traits, percentage of each cladistic (trait) observed in different accessions showing phenotypic deficiency or richness (number of phenotypes per trait) and evenness (frequency of each phenotype) across accessions, were determined using MINITAB® Release 19.

3.4.3.2. Statistical analysis for quantitative traits

The quantitative data were subjected to statistical analysis using Statistical Analysis Computer Software (SAS version 9.0) (Rayne *et al*., 2012) and MINITAB® Release 19. Mean separation was made 5% probability level using the LSD method.

Analysis of variance (ANOVA)

After checking homogeneity and normality, analysis of variance (ANOVA) with statistical analysis software (SAS) computer version 9.1.3 was used for partitioning the total variation according to the following model:

Mijs=μ + ri + rj(s) + Gs + (τxl) is+ξrgs Where,

Mijs = morphological differences of **i**th treatment (storage period) under **j**th replication at sth storage period

μ = Grand mean; **r**i = the effect of ith treatment; **r**j(s) = the effect of replication j within storage time s; **G**s = the effect genotype; (**rxg**)is = the interaction effects between treatment and genotype; and ξ rgs = pooled error.

Correlation analysis and treatment means will be compared using least significance (LSD) at 5% probability level (Fisher, 1935).

Table 2: ANOVA model for randomized complete block design (RCBD)

Source ofVariation	**Df**	**Mean square**	**Expected mean square**
Replication	(r-1)	MSr	σ2e + gσ2 r+ bσ2r
Genotype	(g-1)	MSg	σ2e + rσ2g+ bσ2g
Block	(b-1)	MSb	σ2e + rσ2b+ gσ2b
Error	(r-1) (g-1) (b-1)		
Total	rgb-1	-	**-**

Df -degrees of freedom; **r** = number of replications; and **g** = number of samples/accessions

b- Number of blocks MSb-mean square of block **MSr** = mean square of replication; **MSg**= mean square of samples. **MSe** = mean square of error

3.4.3.3. Estimating coefficient of variation

Estimation of genotypic and phenotypic variance components and their coefficients of variation per storage were done based on the methods by Singh and Chaudhary (1985), and Allard (1960). Accordingly,

Phenotypic variance (δ^2p) per year= $\delta^2Y + \delta^2e$ where, δ^2p = phenotypic variance; δ^2Y = phenotypic variance and δ^2e = error variance

Phenotypic variance (δ^2g) per genotype= (MSg – MSe)/r where, MSg = mean square of genotype, MSe is mean square of error and r is the number of replications

Phenotypic Coefficient of Variation (PCV) per year= ($\sqrt{\delta^2Y}/m$) x 100 where, PCV = phenotypic coefficient of variation; m= population mean for the trait considered

Phenotypic Coefficient of Variation (PGCV) per genotype= ($\sqrt{\ }\delta^2g/m$) x 100 where, PGCV = phenotypic per genotype coefficient of variation.

Broad sense heritability per location was estimated according to Allard (1960) as Heritability per location (H^2) = (δ^2g/δ^2p) x 100 Where, δ^2g = genotypic variance and; δ^2p = phenotypic variance.

Expected genetic advance under selection assuming the selection intensity at 5% was also be computed following Allard (1960) as: **GA = (K) (δp) (H^2)** where, GA = expected genetic advance; K= selection differential that varies depending up on the selection intensity and

stands at 2.056 for selecting 5% of the genotypes. δp = phenotypic standard deviation and, H^2= heritability in broad sense

Genetic advance as percent of mean was obtained as; **GA (% of mean) = (GA/m) x 100**
Where, GA= genetic advance; m = population mean for the trait considered

Estimation of phenotypic and genotypic correlation coefficients

Correlation coefficient measures the mutual relationship between various traits and determines the component character on which selection can be based for improvement in yield (Singh and Chaudhary, 1985). The phenotypic and genotypic coefficients of correlation for
The traits measured in the study were estimated using Pearson Simple Correlation which deals with association between any two traits. Phenotypic correlation is the observable correlation between two variables, which include both genotypic and environmental effects, and genotypic correlation is the inherent association between two variables. Phenotypic and genotypic correlation coefficients between two traits were determined by using PROCCANDISC procedure of SAS software following the variance and covariance components (Singh and Chaudhary, 1985; Sharma, 1998).

Phenotypic and genotypic correlation coefficients were tested for their significance using the formula suggested by Robertson (1959), using the t- table at (g-2) degrees of freedom at 5% and 1% level of significance; g is the number of genotypes (treatments) used in the study.

Cluster and distance analysis

Cluster analysis was done using SAS Software version 9.1.3 and number of clusters was determined by using points where local peaks of Pseudo F-statistics join with small values of the Pseudo t^2 statistics followed by a larger Pseudo t^2 for the next cluster fusion.

Genetic distance between pair of clusters was calculated using the generalized Mahalanobis's D^2 statistics based on the recommendation of (Singh and Chaudhary, 1996). The D^2 statistics measures the force of differentiation at intra-cluster and inter-cluster levels (Singh, 2007). Hence, genetic distance between clusters as standardized Mahalanobis's D2 statistics (Mahalanobis, 1936) was calculated as follow:

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

Where, D^2ij is distance between class i and j; Xi and Xj are the vector means of the traits for the i^{th} and j^{th} groups cov^{-1} = the inverse of pooled error variance and covariance matrix.

The D^2 value obtained for pairs of clusters were considered as the calculated value of Chi-squire ($\chi 2$) and will be tested for significance at 5% and 1% level of probability against the tabulated values of $\chi 2$ for p degrees of freedom, where p is the number of characters considered. Principal components analysis (PCA) and factor analysis was conducted for combined and standardized accession means using MINITAB® Release 19 statistical software.

4. RESULTS AND DISCUSSIONS

4.1 Results

A total of 26 faba bean genotypes and one local check (a total of 27 samples) were used for germination test. For genetic diversity analysis, a total of 24 well germinated faba bean genotypes and one local check (a total of 25 samples) were used. Twenty-two qualitative (six) and quantitative (sixteen) agro-morphological traits were used to analyze the patterns of genetic variation during the main growing season (July – November/ 2019) of the crop. The main results are presented below under separate headings.

4.1.1. Effects of seed storage time on germination rate of the seeds

The effect of seed storage on germination were measured in terms of percent germination, mean germination time and germination rate. Registration of germination started on 5th day of planting and continued up to 14th day. The result show moderate range of germination percentage the highest being 100% in Hachalu and the smallest is 46.7% in EH940050V4 and EH99019-4.These genotypes are spent 15 and 14years respectively since collection. The smallest mean germination time was recorded for Moti (9.31) and the highest for Obse (12.5). These two genotypes spent 1 and 4 years respectively. The germination rate is nearly similar across the genotypes and the local check with the highest being 0.10 in Dosha, Hachalu, Moti and Gebelcho, all of which spent four years after collection. Two genotypes, Tesfa-1 and EH95070-9 failed to germinate; both were 17 years old. As a result, they were not given entry code and thus, excluded from further analysis.

Table3: Percent of germination, mean germination time and germination rate of the tested faba bean genotypes

S/N	Genotype	entry code	year of release	germination percentage	MGT (mean germination time	germination rate/day
1	Tesfa-1		2002	not germinated	-	-
2	EH95070-9		2002	not germinated	-	-
3	Tesfa	15	2007	53.33	11.45	0.08
4	EH95074-9	16	2006	63.33	12.67	0.08
5	Woyu	18	2003	66.70	12.43	0.09
6	Messay	3	2004	50.00	11.77	0.09
7	EH940050V4	8	2004	46.70	13.00	0.08
8	EH99019-4	7	2005	46.70	10.82	0.09
9	EH00126	14	2006	60.00	10.87	0.09
10	EH99071-2	5	2006	63.30	12.00	0.09

11	EH98033-3	10	2006	63.30	11.10	0.08
12	EH98106-1	21	2007	63.30	10.50	0.08
13	EH99102-4	12	2007	76.70	11.00	0.09
14	NC-58-M	17	2010	66.60	11.63	0.08
15	Dagaga	23	2012	76.60	10.73	0.09
16	Moti	24	2013	83.30	10.37	0.10
17	Geblcho	19	2014	80.00	10.60	0.10
18	Obse	13	2015	56.70	12.50	0.09
19	Dosha	4	2015	96.70	10.03	0.10
20	Hachalu	20	2015	73.30	12.33	0.10
21	Dida	9	2016	93.30	10.63	0.09
22	Geblcho	2	2016	90.00	10.43	0.10
23	Moti	1	2018	90.00	9.31	0.10
24	Gora	11	2018	90.00	11.33	0.09
25	Hachalu	22	2018	100.00	10.20	0.09
26	Dosha	6	2013	80.00	10.73	0.09
27	Local check	25	2018	90.00	11.34	0.09

4.1.2. Patterns of genetic diversity

4.1.2.1Qualitative traits and their distributions

The frequency of qualitative traits grouped into leaf, pod and seed characteristics were recorded and the number of observed traits (richness) and frequency (evenness) is presented in ***Table 4***.

4.1.2.1.1. Leaf characters

Two leaf characters such as leaf size and shape were recorded. Accordingly, most of the genotypes (64.00%) bear medium sized leaves followed by small sized (24.00%). Smaller number of the tested genotypes (12.00%) had larger sized leaves. With regards to leaf shape, three characters such as narrow, intermediate and rounded phenetic traits were considered. Accordingly, genotypes with intermediate leaf shape were more frequent (64.00%) than those with rounded (20.00%) and narrow (16.00%) leaf shapes **(*Table 4*).**

4.1.2.1.2. Pod characteristics

Only pod attitude was recorded. Accordingly, collections with erect pod were dominant (72.00%) followed by those bearing horizontal pod arrangement (20.00%). Genotypes having mixed pod arrangement were smaller (8.00%)(***Table 4***).

4.1.2.1.3 Seed characters

Three seed characters such as seed shape, seed size and seed coat color were recorded. In the case of seed size, three phenetic traits such as small, medium and large were recorded. Accordingly, genotypes with medium sized shape was dominant (48.00%), followed by small (28.00%) and large sized (24.00%). For seed shape, three phenetic traits were observed. Most of the genotypes (56.00%) had flattened seed shape followed by those having mixed (28.00%) and round (16.00%) seed shapes. In the case of seed coat color, three phenetic traits were considered. Accordingly, genotypes with brown seed coat color were dominant (64.00%), followed by those having yellow (28.00%) and green (8.00%) coat colors, in that order (***Table4*****).**

***Table 4*:** Characters, frequency and percent coverage of qualitative morphological traits in the tested 24 faba bean genotypes and one local check.

Group character	**Individual trait**	**Score**	**Phenotypic characters**	**Number of accessions (frequency)**	**% of accessions possessing a phenotype**
Leaf characteristics	Leaf size	1	Small	6	24.00
		2	Medium	16	64.00
		3	Large	3	12.00
	Leaf shape	1	Narrow	4	16.00
		2	Intermediate	16	64.00
		3	Rounded	5	20.00
Pod characteristics	Pod attitude	1	Erect	18	72.00
		2	Horizontal	5	20.00
		3	Pendent	0	0.00
		4	Mixed	2	8.00
Seed character	Seed size	1	Small	7	28.00
		2	Medium	12	48.00
		3	Large	6	24.00
	Seed shape	1	Flattened	14	56.00
		2	Round	4	16.00
		3	Mixed	7	28.00
	Seed coat color	1	Green	2	8.00
		2	Yellow	7	28.00
		3	Brown	16	64.00

4.1.2. Analysis of the quantitative traits

4.1.2.1 Analysis of variance (ANOVA)

Analyses of variance between treatments are presented on (***Table 5***). The result revealed that the genotypes (treatments)tested showed a significant ($P<0.05$) to highly significant ($P<0.01$ and 0.001) variation for all the traits except plant height (**PH**), number of pods per plant (**NPPP**), number of seed per plant (**NSPP**) and harvest index (**HI**) which showed a non-

significant variation. Similarly, the variation due to replication is significant in half of the traits considered. Accordingly, Days to maturity (**DM**), Leaf length (**LL**), Internode length (**IL**), Height to the first poding nod(**HFPN**), Number of seeds per plant (**NSPP**), and seed filing period(**SFP**) showed a significant ($P<0.05$) and highly significant ($P<0.001$) variation. The effect of block within replication is non-significant for all the traits considered except Biomass weight per plot (**BMWPP**).

Detection in the coefficient of genetic determination (R^2) revealed that most traits had higher records with Hundred seed weight (**HSW**), Pod length (**PL**) and Economic growth rate (**ECGR**) being the highest (>0.8). Plant height (**PH**) is the only trait with lower (0.46) coefficient of genetic determination. Similarly, the coefficient of variation (CV) seems moderate and within the acceptable range except in plant height (**PH**) that showed the highest record **(*Table 5*).**

***Table5*:** Analysis of Variance (ANOVA) for the 16 quantitative traits evaluated using the 25 faba bean samples

Variables	Rep (2)	Block(Rep) (8)	Trt (20)	MSE (40)	CV (%)	R2
DF	5.69	2.56	43.23**	6.59	4.13	0.79
DM	53.85***	3.55	9.23**	4.01	1.43	0.68
PH	0.38	0.25	0.20	0.21	42.33	0.46
LL	4.92***	0.11	0.84**	0.38	9.71	0.65
IL	2.98***	0.24	0.42*	0.24	11.42	0.63
PL	0.08	0.30	0.84***	0.29	0.08	0.82
HFPN	120.84**	19.24	45.81*	27.26	13.95	0.58
NPPP	5.18	6.81	7.69	4.43	22.70	0.59
NSPP	0.63***	0.04	0.06	0.05	7.83	0.62
BMWPP	0.24	0.18*	0.38***	0.08	21.06	0.78
SEY	14260.39	2778.74	68396.11***	10433.44	24.04	0.79
HSW	43.74	27.45	427.81***	23.76	7.23	0.92
SFP	48.89*	8.13	37.25**	10.26	4.11	0.71
HI	0.01	0.01	0.01	0.01	24.95	0.55
SepHa	13704221.00	9632649.30	14164720.90*	9721543,00	13.95	0.53
ECGR	46085.03	5769.74	123230.68***	17518.02	24.45	0.81

** (significant at p<0.05) ** (highly significant at p<0.01) *** (highly significant at p<0.001); DF(days to 50% flowering), DM(days to physiological maturity),PH(plant height),LL(leaf length),IL(internod length),PL(pod length),HFPN(height to the first poding nod),NPPP(number of pod per plant),NSPP(number of seed per pod), BMWPP(biomass weight per plot),SEY(seed yield),HSW(hundred seed weight),SFP(seed filing period),HI(harvest index),SepHa(seed production per plot per hector),ECGR(economic growth rate),Rep(replication),Trt(treatment), MSE(mean square error), CV(coefficient of variation), R^2(coefficient of genetic determination)*

4.1.2.2. Phenotypic and genotypic variations

The phenotypic (δ^2p) and genotypic (δ^2g) variance estimates showed a wide range of variations in the traits considered. Accordingly, δ^2p ranged from 0.08 in harvest index (HI) to 2224707.14 in seed yield per hector (**SYPH**). Similarly, δ^2g ranged from 0.00 in plant height (PH) and harvest index (HI) to 2221589.20 in seed yield per hector (**SYPH**).

Similarly, both phenotypic (PCV) and genotypic (GCV) coefficients of variation showed a wide range of variations in the traits considered. In this regard, PCV ranged from 1.54 in days to maturity (**DM**) to 87.50 in harvest index (**HI**). Likewise, GCV score ranged from 0.00 in harvest index to 70.02 in seed yield per hectare (**SYPH**). Five traits such as biomass weight per plot (**BWPP**), seed yield per hectare (**SYPH**), seed yield per plot (**SYPP**), hundred seed weight (**HSW**), and economic growth rate (**EGR**) scored high PCV and GCV. Harvest index (**HI**) and number of pods per plant (**NPPP**) scored higher PCV with no eventual higher GCV.

In general, the GCV and PCV scores are medium to high and the difference between the two is wide in most of the traits with PCV higher than the corresponding GCV score in all the traits considered.

4.1.2.3. Estimates of heritability in broad sense and genetic advance

Estimate of heritability in broad sense (H^2%) revealed a wide range of variations (1.08 in plant height to 99.86% in seed production per plot per hectare) among all the traits considered. According to (Singh 2001), if heritability of a character is very high, i.e., 80% or more, selection for that character could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relatively small contribution of the age of the seed to the phenotype. Whereas, for characters with low heritability, i.e., 40% or less, selection may be considerably difficult or impractical due to the masking effect of the environment. Considering this bench-mark, heritability estimates in the present study is high for seed production per plot per hectare (99.89%), economic growth rate (99.75%), seed yield per hectare (99.65%), hundred seed weight (97.65%) and days to flowering; moderate for height to the first poding nod (63.99) and days to physiological maturity (56.62). The estimate is very low (<40%) for plant height(1.08%), harvest index(0.00), number of seed per pod (2.22%), Inter nod length(15.52%), leaf length(27.06%), biomass weight per plot(34.88%), pod length(39.09%) and number of pod per plant(43.70%).

Genetic advance under selection (GA) refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Estimates of genetic advance (GA) among the traits revealed a wider variation (0.00 in harvest index to 3070.54 kg /ha in seed production per plot per hectare).

Genetic advance as percent of mean (GAM) was high for economic growth rate (87.19%), seed yield (82.24%) and seed yield per plot per hectare (144.25). However, the estimate is low for harvest index (0.00%), plant height (1.35%) and number of seed per pod (0.75%).

Table 6: Variance components for the 16 quantitative traits evaluated using the 25 faba bean samples

Traits	MSg	Mse	Trait Mean	δ²e	δ²g	δ²p	GCV%	PCV%	Hb%	GA	GAM
DF	43.23	6.50	61.73	2.55	18.37	20.92	6.95	7.40	87.81	8.25	13.37
DM	9.23	4.01	139.87	2.00	2.61	4.61	1.16	1.54	56.62	2.50	1.79
PH	0.20	0.21	1.11	0.47	0.00	0.47	6.31	61.26	1.08	0.02	1.35
LL	0.84	0.38	6.37	0.62	0.23	0.85	7.54	14.44	27.06	0.51	8.03
IL	0.42	0.24	4.31	0.49	0.09	0.58	6.96	17.63	15.52	0.24	5.63
PL	0.84	0.20	6.35	0.50	0.32	0.82	8.98	14.33	39.02	0.73	11.50
HFPN	45.81	27.26	37.42	5.22	9.28	14.50	8.15	10.18	63.99	5.01	13.39
NPPP	7.69	4.43	9.27	2.10	1.63	3.73	13.81	20.82	43.70	1.73	18.71
NSPP	0.06	0.05	2.86	0.22	0.01	0.23	2.45	16.43	2.22	0.02	0.75
BMWPP	0.38	0.08	1.32	0.28	0.15	0.43	29.55	50.00	34.88	0.47	35.86
SEY	68396.11	10433.44	424.87	102.14	28981.34	29083.48	40.07	40.14	99.65	349.40	82.24
HSW	427.81	23.76	67.46	4.87	202.03	206.90	21.06	21.32	97.65	28.87	42.79
SFP	37.25	10.26	77.95	3.20	13.50	16.70	4.71	5.25	80.83	6.80	8.72
HI	0.01	0.01	0.32	0.08	0.00	0.08	0.00	87.50	0.00	0.00	0.00
SEpppHa	14164720.90	9721542.50	2128.57	3117.94	2221589.20	2224707.14	70.02	70.26	99.86	3070.54	144.25
ECGR	123230.68	17518.02	541.43	132.36	52856.33	52988.69	42.46	42.52	99.75	472.09	87.19

Sg = *mean of squares of genotype, MSe= mean of square error, δ²e = variance due to age of seed, δ²g = genotyhpic variance, δ²p = phenotypic variance, GCVg= enotypic coefficient of variation, PCV = phenotypic coefficient of variation Hb (%) = Broad sense Heritability; GA = Genetic Advance; GAM = Genetic advance as percent of mean*

4.1.2.4. Analysis of correlation coefficients

Analysis of correlation coefficient (**Table7)** was performed to find out the inter-relationship between the studied pair of traits. Analysis of pair wise correlation coefficients in the 16 quantitative traits used in the present study is presented in (**Table7)**. In this regard, genotypic and phenotypic correlation coefficients between seed yield per hectare of land and all the remaining traits are presented below:

Accordingly, seed yield per hectare showed a highly significant ($p<0.001$) and positive genotypic correlation with biomass weight per plot (**BMWPP**) (**0.86)** and economic growth rate (**ECGR**) (**0.99)** and significant ($p<0.01$) positive correlation with hundred seed weight (**HSW**) (0.63), harvest index (**HI**) (0.68) and seed yield per plot per hectare **SEPPPHa**)(0.66).

In addition, the extent of correlations is higher ($r>0.5$) for all of these traits. Likewise, seed yield per hectare showed a highly significant ($p<0.001$) positive phenotypic correlation with hundred seed weight (0.52), harvest index (0.61), economic growth rate (0.99) and biomass weight per plot (0.75) and significant ($p<0.01$) positive correlation with inter node length (0.28) and seed production per plot per hectare (0.41), except the last two others revealed a strong correlation ($r>0.5$)

***Table 7*:** Genotypic (**above diagonal**) and phenotypic (**below diagonal**) pair wise correlation coefficients for the 16 quantitative traits considered

Variables	DF	DM	PH	LL	IL	PL	HFPN	NPPP	NSPP	BMWPP	SEY	HSW	SFP	HI	SEPPPHa	ECGR
DF	**1.00**	**0.29**	**-0.27**	**0.62*** **	**-0.29**	**-0.15**	**-0.12**	**0.27**	**0.02**	**0.03**	**0.12**	**0.10**	**-0.86*** **	**0.12**	**0.23**	**0.22**
DM	0.17	**1.00**	**-0.58****	**0.52****	**-0.34**	**0.31**	**0.27**	**-0.15**	**0.42***	**0.25**	**0.14**	**0.30**	**0.16**	**-0.08**	**0.12**	**0.13**
PH	-0.13	-0.12	**1.00**	**-0.05**	**0.22**	**-0.14**	**-0.24**	**-0.01**	**-0.22**	**-0.09**	**-0.06**	**-0.11**	**0.03**	**-0.05**	**-0.04**	**-0.07**
LL	0.47***	0.17	-0.03	**1.00**	**-0.33**	**0.13**	**-0.05**	**0.07**	**0.21**	**0.19**	**0.18**	**0.18**	**-0.39**	**0.03**	**0.31**	**0.24**
IL	-0.16	-0.42**	0.16	0.08	**1.00**	**0.33**	**0.07**	**-0.15**	**-0.16**	**0.47****	**0.35**	**0.27**	**0.14**	**0.00**	**0.10**	**0.30**
PL	-0.17	0.10	-0.01	0.05	0.29**	**1.00**	**0.52****	**-0.48****	**0.37**	**0.42****	**0.21**	**0.74*** **	**0.25**	**-0.13**	**0.03**	**0.17**
HFPN	-0.14	0.02	-0.13	-0.05	-0.05	0.30**	**1.00**	**-0.49****	**0.04**	**0.13**	**-0.07**	**0.43****	**0.19**	**-0.17**	**-0.23**	**-0.10**
NPPP	0.27**	-0.07	0.01	0.19	0.10	-0.30**	-0.34**	**1.00**	**0.03**	**-0.07**	**-0.02**	**-0.53****	**-0.32**	**0.06**	**0.06**	**0.01**
NSPP	0.04	0.05	0.07	0.33**	0.23	0.27**	-0.15	0.17	**1.00**	**0.06**	**-0.21**	**0.02**	**0.10**	**-0.39**	**-0.06**	**-0.25**
BMWPP	0.09	0.08	-0.08	0.18	0.29**	0.37**	-0.05	0.00	0.22	**1.00**	**0.86*** **	**0.64****	**0.02**	**0.28**	**0.59****	**0.84*** **
SEY	0.15	0.06	-0.11	0.20	0.28**	0.15	-0.14	0.17	0.04	0.75***	**1.00**	**0.63****	**-0.06**	**0.68****	**0.66****	**0.99*** **
HSW	0.07	0.18	-0.02	0.11	0.19	0.69***	0.22	-0.36**	0.06	0.55***	0.52***	**1.00**	**0.02**	**0.28**	**0.36**	**0.61****
SFP	-0.74***	0.41**	0.07	-0.32**	-0.12	0.16	0.07	-0.29**	-0.04	0.00	-0.13	0.04	**1.00**	**-0.19**	**-0.18**	**-0.17**
HI	0.15	-0.03	-0.09	0.04	0.06	-0.18	-0.10	0.24**	-0.15	0.02	0.61***	0.13	-0.20	**1.00**	**0.29**	**0.69****
SEPPPHa	0.14	0.06	0.03	0.20	0.06	-0.06	-0.17	-0.08	0.07	0.32**	0.41**	0.21	-0.10	0.17	**1.00**	**0.68****
ECGR	0.25**	0.01	-0.11	0.25**	0.27**	0.12	-0.15	0.20	0.03	0.74***	0.99***	0.51***	-0.23	0.62***	0.42**	**1.00**

*Numbers with no superscript = non-significant; * (significant at p<0.05); ** (highly significant at p<0.01); *** (highly significant at p<0.001)*

4.1.2.5. Principal components analysis (PCA)

Principal components analysis, conducted using the standardized data for all the16 quantitative traits revealed that the first six principal axes (Eigen value ≥ 0.97) accounted for 87.5% of the total variation (***Table8***). The first principal component (PC1) accounted for 30.3% of the total variance and had high contributing factor loadings from seed yield (0.432), seed production per plot per hectare (0.430), biomass weight per plot (0.415) and economic growth rate (0.412). The second PC axis accounted for the total variation 19.5% and differentiated among accession on the basis of height to the first poding node (-0.413), seed filing period(-0.403),pod length(-0.401) and number of pod per plant(0.313). The third PC axis contributed 15.4% of the total variation had high contributing factor loadings from days to physiological maturity (-0.509), days to 50% flowering (-0.415), plant height (0.407), inter node length (0.378) and leaf length (-0.367). The fourth PC axis accounted for 9.1% of the total variation and differentiated accessions on the bases of number of pod per plant (-0.529), number of seed per pod (-0.403), hundred seed weight (0.391) and height to the first poding node (0.315). The fifth PC axes accounted for 7.2% of the total variation and differentiated largely on the bases of plant height (0.588), leaf length (0.538), harvest index (-0.402) and number of seed per pod (0.247). The sixth PC accounted for 6.1% of the total variation and differentiated on the base of seed filling period (0.554), inter node length (-0.388), days to 50% flowering (-0.362) and harvest index (0.344).

***Table8*:** Principal Component's analysis (PCA) for the 16 quantitative traits used in the present study

Traits	PC1	PC2	PC3	PC4	PC5	PC6
DF	-0.06	0.29	-0.42	0.04	-0.13	-0.36
DM	0.04	-0.22	-0.51	-0.15	-0.12	0.22
PH	-0.02	0.09	0.41	0.09	0.59	0.09
LL	0.05	0.13	-0.37	0.22	0.54	0.32
IL	0.24	-0.14	0.38	-0.15	-0.04	-0.39
PL	0.23	-0.40	-0.04	0.01	0.12	-0.24
HFPN	0.06	-0.41	-0.06	0.32	-0.20	-0.10
NPPP	-0.12	0.31	-0.02	-0.53	0.06	-0.08
NSPP	-0.06	-0.30	-0.24	-0.40	0.25	-0.10
BMWPP	0.42	-0.02	-0.04	-0.23	0.07	-0.09
SEY	0.43	0.12	-0.02	-0.14	-0.02	0.10
HSW	0.33	-0.10	-0.14	0.39	0.20	-0.15
SFP	0.03	-0.40	0.15	-0.26	-0.07	0.55
HI	0.20	0.24	0.13	0.21	-0.40	0.34
SYPH	0.43	0.13	-0.03	-0.13	-0.02	0.11

ECGR	0.41	0.22	-0.05	-0.05	0.00	0.02
Eigenvalue	*4.84*	*3.11*	*2.47*	*1.45*	*1.15*	*0.9725*
Proportion	*0.30*	*0.20*	*0.15*	*0.09*	*0.07*	*0.061*
Cumulative	*0.30*	*0.50*	*0.65*	*0.74*	*0.81*	*0.875*

Outliers are those data points that lie outside the overall pattern of distributions. In this study there was no extreme outlier in the data (***Figure 1***). According to the outlier plot, the accessions number 9(Dida(2012)) and number 23(Dagaga) were far than others and seems to be outliers.

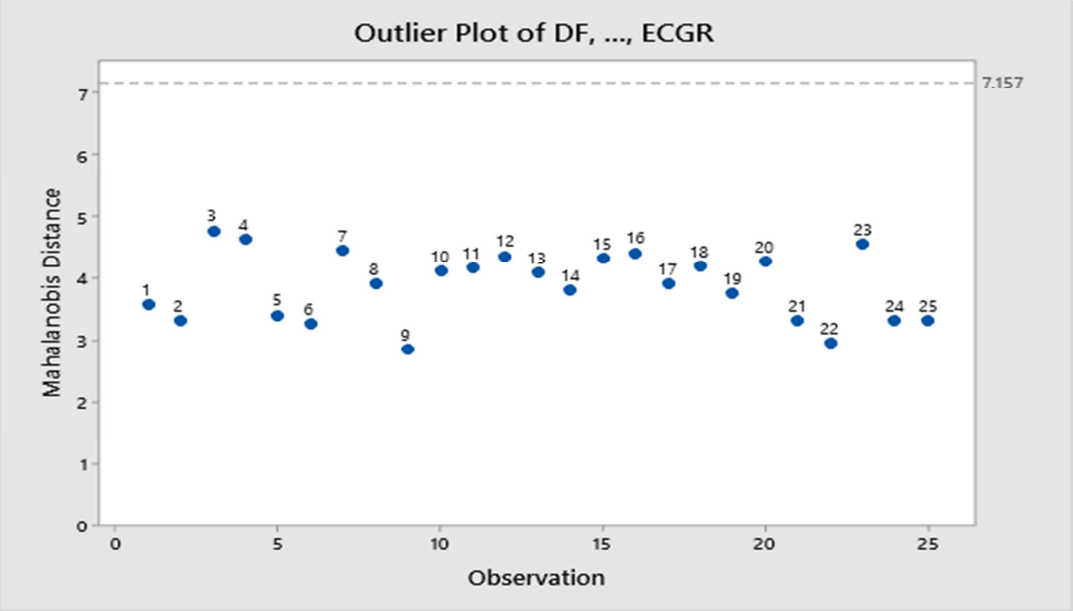


Figure 1: PCA outlier plot showing the distribution of 25 samples in terms of the 16 quantitative traits

PCA score plot roughly revealed four clusters (C1, C2, C3 and C4) in which collections were observed to seem outliers (***Figure 2***). Each of the four clusters consisted nearly equal number of genotypes. Genotype number 18(NC-58-M(2010)) was far apart than others. Genotypes 18, 3,17,8 and 5 were highly and negatively contributed to PC1.

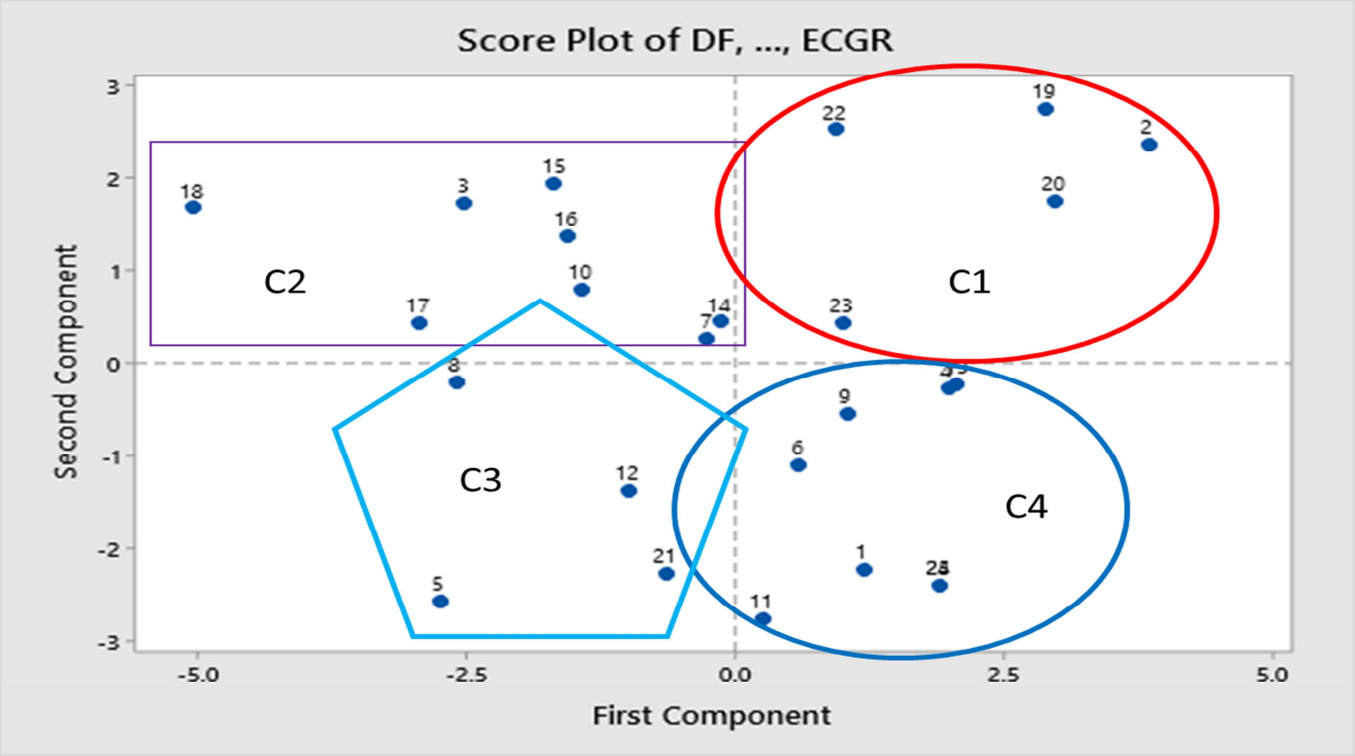


Figure2: PCA score plot of the 16 quantitative traits used

PCA loading plot again showed strong correlation among the traits such as inter node length, hundred seed weight, biomass weight per plot, seed yield, seed production per plot per hectare, economic growth rate and harvest index. Similarly, the traits: seed filling period, height to the first poding node, days to physiological maturity and pod length are correlated with each other. Leaf length had positive association but slightly contribute to the variation. Other traits such as number of pod per plant, days to 50% flowering and plant height are inter correlated with each other but negatively correlated with seed filling period, height to the first poding node and days to physiological maturity and slightly correlated with other traits (***Figure3*).**

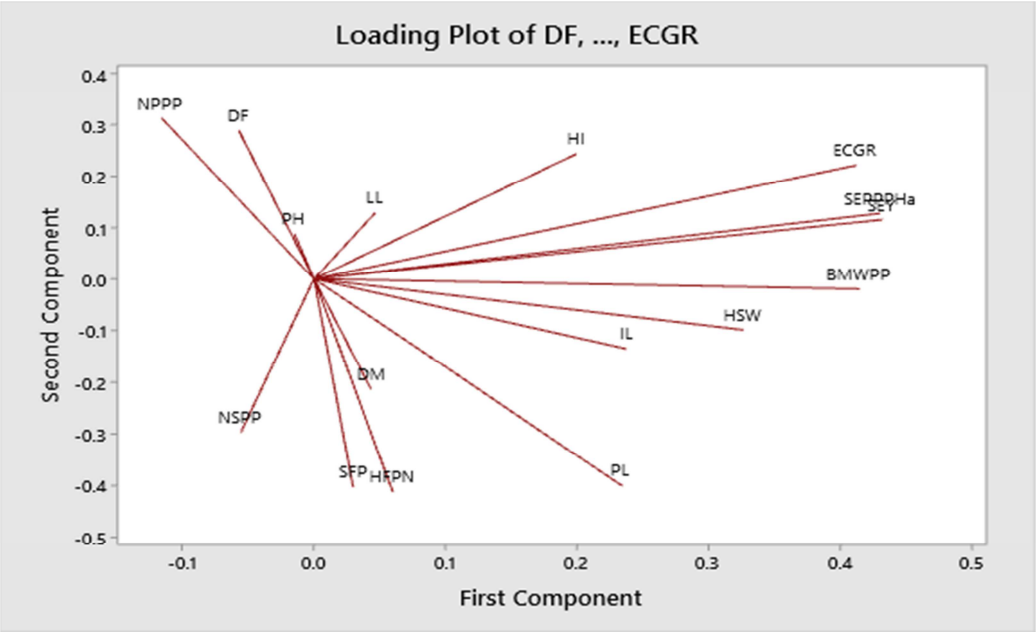


Figure3: PCA loading plot of the 16 quantitative traits used in its commutation

A PCA biplot shows both PC scores and loadings of variables. In the present study 32% of the genotypes made layover on the first axis and the traits most contribute to these were number of pod per plant, days to 50% flowering, and plant height. 20% of the varieties made layover on the second axis and the other 48% of the varieties made on the third and fourth quadrant (***Figure 3***)

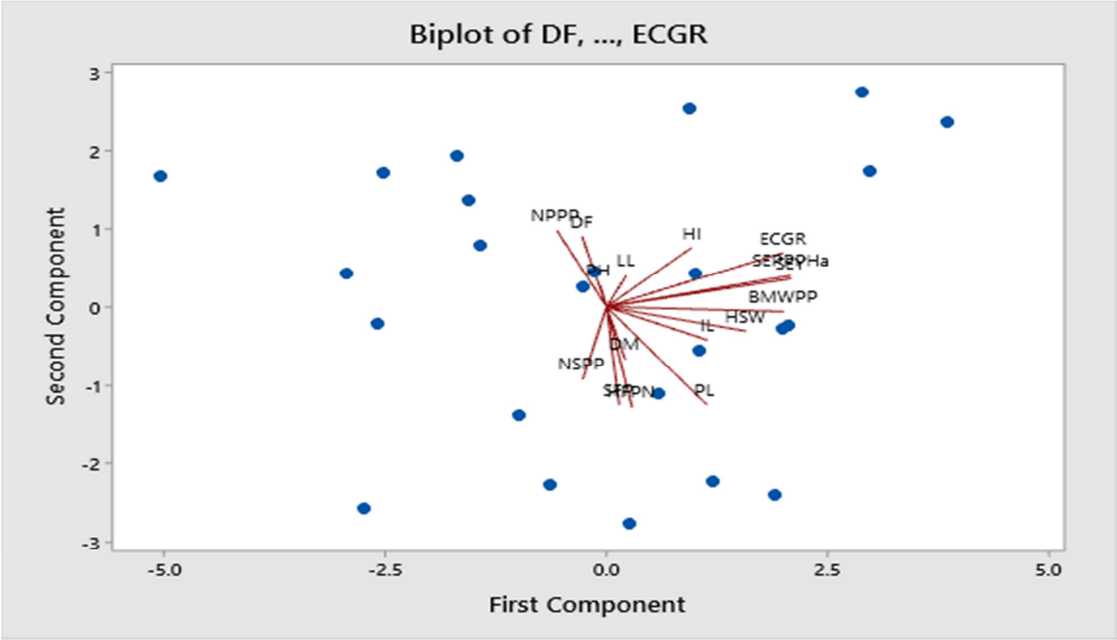


Figure 4: PCA Biplot of the 16 quantitative traits used

4.1.2.6 Cluster Analysis based on quantitative traits

Cluster analysis for the entire genotypes was performed using mean data of all the 16 quantitative traits. Accordingly, the entire genotypes were grouped into three major clusters (I, II and II). Cluster I composed of 9 or 36% of the total samples genotypes. All of the genotypes under these clusters were released varieties and had higher seed production ranges per hectare (1841.15 Kg/Ha – 2325.63Kg/Ha). The cluster holds the highest mean from number of seed per pod (3.13), seed filling period (84.33), pod length(7.65cm),leaf length(7.30cm), inter node length(4.97 cm) and harvest index (0.56) and the lowest mean value from leaf length(5.60cm) and inter node length(3.89cm) (***Table 9***).

Cluster II contained only three genotypes that only accounted for 12% of the total samples. This cluster also consist all the released varieties with the highest mean value from seed yield per hectare (3042.83Kg/Ha), economic growth rate (978.06), seed yield(730.28Kg/Ha) and biomass weight per plot (2.03m) and the lowest mean value from number of seed per pod (2.53).

Cluster III contained all the remaining 13 genotypes that constitute 52% of the total genotypes. Except two genotypes (Gora andNC-58-M), all are germplasms with 9-16 years. This cluster consist of the highest mean value from plant height (2.28m) and hundred seed weight (83.88gm) and the lowest mean value of days to physiological maturity (135 days), plant height (0.88m), inter node length (3.43cm), height to the first poding node (31.58cm), biomass weight per plot (0.60Kg), seed yield (207.29Kg/Ha), hundred seed weight (35.22gm), seed filling period (73.67), harvest index (0.23), seed production per plot per hectare (826.79 Kg/Ha) and economic growth rate (428.72) (***Table 10***).

Table 9: Pattern of clustering in the 25 faba bean samples based on the 16 quantitative traits used

Cluster	No of genotypes	Entry codes
I	9	Moti (2018),Moti(2013),Dosha(2015),Dagaga(2012),Obse(2015),Hachalu(2018),Dosha(2013), Dida(2016)
II	3	Geblcho(2016),Geblcho(2014), Hachalu(2015)
III	13	Messay(2004),NC-58-M(2010),EH9400S0V4(2004),EH99019-4(2005), Gora(2018),EH98106-1(2007),EH99102-4(2007),EH98106-1(2007), EH00126(2006),EH99071-2(2006),Woyu (2003)

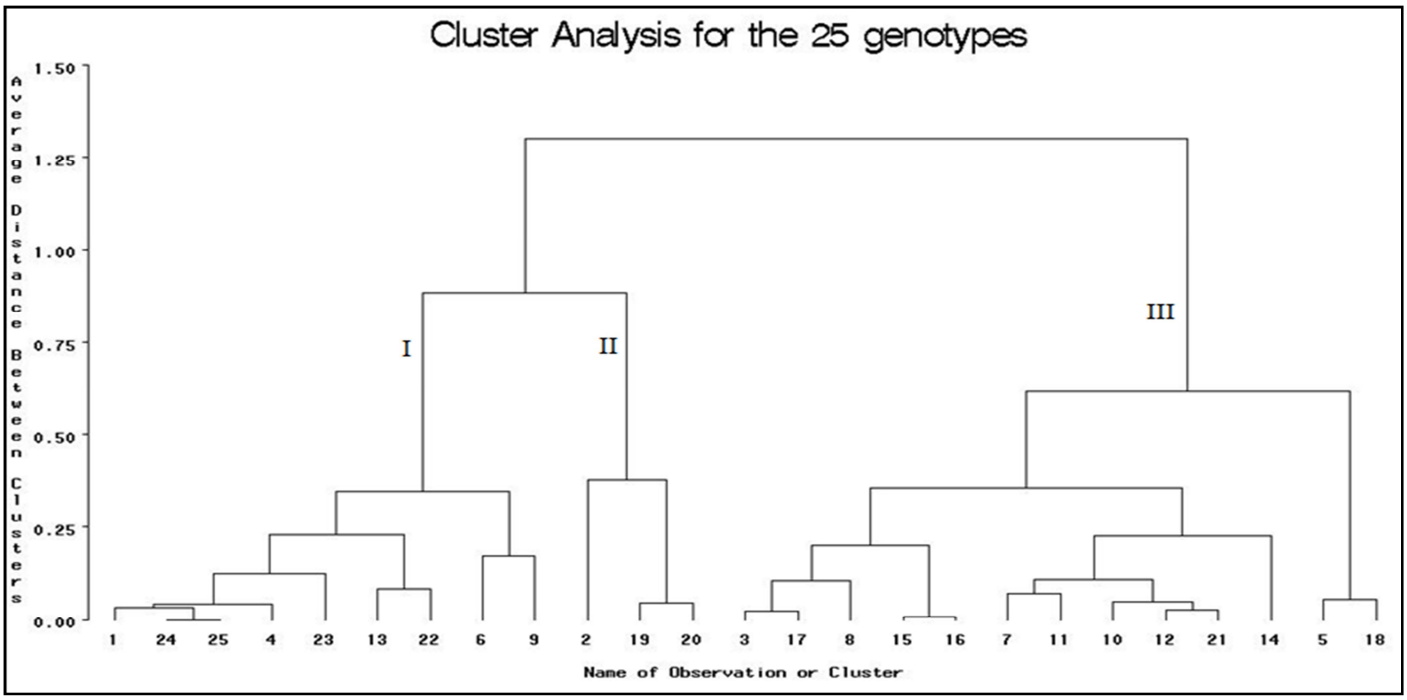


Figure 5: Clustering of the 25 faba bean samples; numbers arranged in horizontal position represents the codes and are equivalent to the entry codes given in ***Table 1***

Table 10: Clusters, genotypes under each cluster and contribution of the traits in each genotype to the clusters

	Genotype	Year of release	DF	DM	PH	LL	IL	PL	HFPN	NPPP	NSPP	BMWPP	SEY	HSW	SFP	HI	SEPPPHa	ECGR
	Moti	2018	58.00	142.33	1.12	6.78	3.89	6.64	39.33	7.33	3.07	1.63	504.93	75.44	84.33	0.31	2103.86	598.73
	Moti	2013	58.00	140.67	1.15	5.60	4.89	7.65	39.79	9.07	2.93	1.70	530.48	70.03	82.67	0.30	2105.04	611.14
	Dosha	2015	58.00	138.33	0.99	5.83	4.56	6.27	42.74	7.20	2.73	1.43	509.48	70.61	80.33	0.56	2122.83	634.34
	Dagaga	2012	58.00	138.67	1.10	5.60	4.97	5.81	35.19	12.73	2.87	1.80	530.48	58.47	80.67	0.29	2210.33	657.62
	Obse	2015	58.00	139.67	1.17	7.04	4.49	7.22	32.27	9.63	2.93	1.50	550.31	80.44	81.67	0.37	2292.96	673.85
	Hachalu	2018	66.00	141.33	1.11	7.30	3.97	5.96	32.68	12.07	2.87	1.53	558.15	65.98	75.33	0.36	2325.63	740.91
	Dosha	2013	58.00	138.67	1.12	6.21	4.72	6.61	38.80	9.13	2.87	1.47	441.88	68.85	80.67	0.30	1841.15	547.78
	Dida	2016	66.00	141.67	1.11	7.07	4.23	6.93	38.90	9.20	3.13	1.57	473.26	79.45	75.67	0.30	1971.93	625.46
I	Local check	2018	58.00	140.67	1.15	5.60	4.89	7.65	39.79	9.07	2.93	1.70	530.48	70.03	82.67	0.30	2105.04	611.14
	Geblcho	2016	66.00	140.67	1.08	7.10	4.32	6.19	32.61	9.87	2.87	2.03	730.28	80.55	74.67	0.36	3042.83	978.06
II	Geblcho	2014	66.33	139.67	1.07	6.44	4.06	5.97	36.20	9.00	2.53	1.67	655.79	83.22	73.33	0.39	2732.46	894.26
	Hachalu	2015	64.00	140.00	1.14	6.27	4.80	5.79	35.83	7.80	2.67	1.50	651.55	74.59	76.00	0.43	2714.79	857.30
	Messay	2004	58.00	135.00	2.28	6.26	4.47	5.49	31.58	9.40	2.73	0.87	286.84	52.28	77.00	0.33	1195.21	372.51
	NC-58-M	2010	66.00	141.33	0.96	5.75	4.12	5.13	32.49	9.07	2.80	0.94	286.51	45.71	81.00	0.30	1193.78	353.71
	EH940050V4	2004	60.67	140.00	1.01	6.65	3.95	5.68	39.66	9.60	2.67	0.97	265.64	56.24	79.33	0.28	1106.85	334.86
	EH99019-4	2005	67.33	140.33	1.09	6.59	4.73	6.44	39.47	9.87	2.87	1.60	354.94	65.44	73.00	0.28	1475.92	486.22
	Gora	2018	58.00	141.67	1.14	7.07	4.30	6.99	45.20	7.20	2.73	1.20	359.50	83.88	83.33	0.30	1497.92	431.40
	EH98106-1	2007	63.33	140.67	1.04	6.29	4.03	6.99	44.00	7.60	3.07	1.27	331.55	79.38	77.33	0.26	1381.46	428.72
	EH99102-4	2007	64.00	142.33	0.88	6.04	4.11	6.93	36.12	7.47	2.93	1.13	336.22	66.99	78.33	0.30	1400.92	429.22
III	EH98106-1	2007	63.33	140.67	1.04	6.29	4.03	6.99	44.00	7.60	3.07	1.27	331.55	79.38	77.33	0.26	1381.46	428.72
	EH98106-1	2007	63.33	140.67	1.04	6.29	4.03	6.99	44.00	7.60	3.07	1.27	331.55	79.38	77.33	0.26	1381.46	428.72
	EH00126	2006	65.33	139.00	1.08	6.49	4.29	6.89	41.83	9.60	2.73	1.07	387.81	74.77	73.67	0.36	1615.88	526.42
	EH99071-2	2006	61.33	140.67	1.01	6.36	4.37	6.48	40.67	7.80	3.07	0.87	198.43	64.19	79.33	0.23	826.79	250.13
	Woyu	2003	66.00	141.33	0.93	6.57	3.43	4.69	34.39	13.40	3.00	0.60	207.29	35.22	78.33	0.35	863.71	264.64
	Tesfa	2007	65.33	139.00	1.08	6.49	4.12	5.13	32.49	9.60	2.73	1.07	286.51	74.77	73.67	0.30	1193.78	526.42
	EH95074-9	2006	58.00	139.00	1.08	6.49	4.12	5.13	32.49	9.60	2.73	1.07	286.51	74.77	73.67	0.30	1193.78	526.42

4.1.2.7. Distance between clusters

Genetic distance between the three clusters is presented in ***Table11***. The largest distance was recorded between cluster III and cluster II (D^2=205.09) and the second was between cluster II and III (D^2=202.16).

Table11: Within (diagonal element or in bold) and between Cluster distance

Cls	1	2	3
1	**2.04**		
2	93.87	**4.24**	
3	47.92	205.09	**1.31**

4.2 Discussions

Faba bean is the cheap source of protein in Ethiopia and it is mostly cultivated in highland areas of the country. In the present study, a total of 25 faba bean samples (24 genotypes and one local check) were taken from Holota Agricultural research center, pulse department seed and germplasm store and tested. Implications of the results obtained are discussed under the following sections:

4.2.1. Variation in the qualitative morphological traits

The present study revealed a wide range of variations in most of the qualitative traits considered. For example: there is a huge gap between the frequency of medium sized and larger sized leaf sizes. Likewise, all the remaining group of characters and eventually phenetic traits revealed large variation in frequency distribution. Similar result has been reported by Thomas et al., (2016).Such wide variation in qualitative traits could be attributed genetic variations among the tested genotypes that eventually used for selection.

4.2.2. Patterns of variation in the quantitative morphological traits

Most of the traits used (fourteen of the total sixteen) revealed a significant ($p< 0.001, 0.01, 0.05$) variation among the tested genotypes. The result is in line with the reports by Lemma Diriba (2018), Munqezand Shtaya(2013),Gemechu Keneni *et al*., (2006) and Kubure*et al.*, (2016). Such significant variation reveals the existence of genetic variation among the genotypes and importance of the traits for further selection breeding. Four traits: plant height, number of pods per plant, number of seed per pod and harvest index showed a non-significant variation among the genotypes revealing less importance of the traits for selection of the genotypes. Similar result has been reported by Behailu Mulugeta(2016) for number of pod per plant and harvest index. However, Gemechu Keneni *et al.,* (2005) and Lemma Diriba (2018) had reported a contradicted result in Ethiopian faba bean genotypes for the traits.

Likewise, higher to intermediate GCV (>10%) were observed in biomass weight per plot, seed yield per hectare, hundred seed weight, economic growth rate, seed production per plot per hectare (higher or >20%), and number of pod per plant (intermediate or10% <GCV <20%). The delineation is based on Sivasubramanian and Madhavamenon(1973) that suggest the ranges from 0-10% as low, 10-20% as moderate, and >20% as high. Genotypic and phenotypic coefficients of variation were reported as the major tools used to measure the variability that exists in a given population

(Burton and Devane, 1988). All the GCV values were lower than the corresponding PCV values suggesting that the variation is due to environmental influence which could be attributed to test at a single field location or the age of the seed used in the experiment. The result is in agreement with the reports by Tafere *et al*., (2013) and Abdulaziz *et al*., (2015).

4.2.3. Estimates of heritability in broad sense and genetic advance

According to Singh (2001), heritability can be categorized into very high (≥80%), moderately high (60–79%), medium (40–59%), or low (<40%). Accordingly, six traits such as days to 50% flowering, seed yield, hundred seed weight, seed filing period, seed production per hectare per plot and economic growth rate had high broad sense heritability (Hb) which could suggest less influence of the environmental condition on the traits. Therefore, faba bean breeders may make superior genotypes selection based on their phenotypic performance. Similar result was reported by Sharifi (2015). Moderately high heritability was observed in height to the first poding nod and days to physiological maturity. Medium heritability was observed in number of pods per plant. Other traits such as plant height, harvest index, number of seeds per pod, inter node length, leaf length, biomass weight per plot and pod length had low heritability. Heritability estimates are expected to be lower in poor environments where heritability is masked due to a greater genotype by environment interaction (Abdulaziz*et al*., 2015; Tafere Mulualem *et al*., 2013; Mellion*et al*., 2012; Alghamdi, 2007).

Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence, knowledge about heritability coupled with genetic advance and genotypic coefficient of variations are most useful (Abebe T et al., 2017). In this view, the present study revealed high to medium heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean (GAM)in number of pod per plant, biomass weight per plot, seed yield, hundred seed weight, seed production per plot per hectare and economic growth rate. This indicates that the traits are simply inherited in nature and controlled by few major genes or possessed additive gene effects. Therefore, simple selection based on these traits could be effective for improving those characters. Similar result was reported by Abdulariz et al. (2015).

4.2.4. Patterns of relationship between the traits considered

Pair wise correlation coefficient measures the mutual relationship between various traits and determines the components on which selection can be based for improvement of the desired character (Singh, 2007). It is useful to perform efficient selection for multiple traits at a time. With this view, seed yield, one of the most important agronomic traits, showed a positive and strong genotypic and phenotypic correlation with inter node length, hundred seed weight, harvest index, biomass weight per plot and economic growth rate implying that improving these traits will improve the production of faba bean genotypes. Tafere Mulualem et al. (2013) and Abdallaet al. (2015) reported a positive and strong correlation between thousand seed weight and seed yield in faba bean.

4.2.5. Patterns of grouping

PCA is used to identify traits that contribute to most of the observed variations within a group of genotypes. Accordingly, the first six PCs (eigen value greater >0.97) accounted for 87.5% of the entire diversity in the 25 samples considered. According to Rencher(2002),the first principal component is the linear combination with maximal variance; the second principal component is the linear combination with maximal variance in a direction orthogonal to the first principal component, and so on. In the first three PCAs, seed yield, biomass weight per plot, economic growth rate, first poding node, seed filling period, pod length, number of pod per plant, days to physiological maturity, days to flowering, plant height, inter node length and leaf length were found to be an important characters and had high contribution to the entire variation within the genotypes. The result agrees with Yahia *et al.* (2012) and Gemechu Keneni *et al.*, (2005).

Cluster analysis revealed roughly three different groups of faba bean genotypes but with no clear differentiation among the genotypes based on their storage time and varietal back grounds. However, the higher values in cluster distances observed shows the difference in genetic background between the materials in which some were taken from germplasm and others from seed store (released varieties). There are several reports suggesting overlapping of faba bean verities and germplasms (Gemechu Keneni *et. al.,* 2005; Al-barri and Shtaya, 2013; Yahia *et al*., 2012; Chaieb*et al*., 2011).

4.2.6. Effects of seed storage time on faba bean yield

When seeds are stored under various conditions, life processes can terminate in individual seeds at different times. According to Woodstock (1973), there is no sharp line of demarcation between life and death in seeds. Rather, seed death is a gradual and cumulative process as more and more cells die until certain critical parts of the seed become unable to perform their essential function. Moore (1955) reported that seed life becomes less and less vigorous as the never-ceasing aging process moves onward toward death; but even long before death the seed becomes questionable or worthless for planting purpose, especially under field conditions that are not highly favorable for germination and seedling development. In the present study, most of the quantitative traits performed less in aged seeds (genotypes). For example; low seed yield per hectare observed in EH99071-2(198.4 Kg/Ha), Woyu(207Kg/Ha), EH9400S0V4 (265.64Kg/Ha),NC-58-M (286.51Kg/Ha)and Messay (286.84Kg/Ha) were stored for 13, 16,15,9 and 15 years, respectively. Similarly, all the genotypes that had greater than nine years of age were grouped under cluster three. Seed longevity in faba bean was reported to be different between cultivars (James *et al*., 1967).As reported by Walter et al.,(2005), the length of storage time is strongly influenced by environmental and genetic factors such as storage temperature and seed moisture content.

Even though, Seed storage is an essential step for the long-term preservation of plant genetic resources, maintaining seed viability for longer period is very essential to preserve the genetic integrity in stored samples. (Ellis et al. 1991, Vertucci and Roos 1991). In the present study there is no clear indication of storage time on genetic variation. But less performance of aged seeds to quantitative traits indicate loss of genetic integrity.

5. CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusions

Current faba bean production in Ethiopia is very much less than the actual potential of the country. One of the reasons to declining production is lack of quality seed, one of the raw materials for improvement mechanisms of crop production. The present study generated baseline information that could be used as a starting material for its breeding and improvement. Thus, a wide range of variation in all the qualitative traits considered could signal the importance of those traits for selection breeding. Similarly, significant variations in most of the quantitative traits considered could be exploitable in improvement of the crop at large.

The high genetic advance coupled with heritability and genotypic coefficient of variation observed in height to the first poding node, hundred seed weight, seed yield/ha and economic growth rate could reveal the high importance of these traits for selection breeding. This is because larger extents of heritability coupled with genetic advance and genotypic coefficient of variations is most useful to indicate the amount of genetic improvement that would result from selection of individual genotypes.

Grouping of the genotypes showed high difference among the clusters suggesting large difference in seed performance to morphological and yield in narrow sense or in genetic background between aged seeded genotypes and the recent ones.

5.2. Recommendations

- The present study generated valuable information that could supplement the awareness among farmers, breeders and researchers on the effect of prolonged seed storage time of faba bean on its germination and yield.
- In order to come up with a concrete justification on the extents of genetic diversity and effects of seed storage time on seed yield and other indices, larger number of verities with even more storage time should be tested at multiple locations and seasons.

- Further research needs to be carried out to clearly indicate the effects of environmental factors on the extents of genetic diversity.
- More advanced markers systems such as molecular markers need to be carried out to show the actual extents of genetic diversity in the genotypes.

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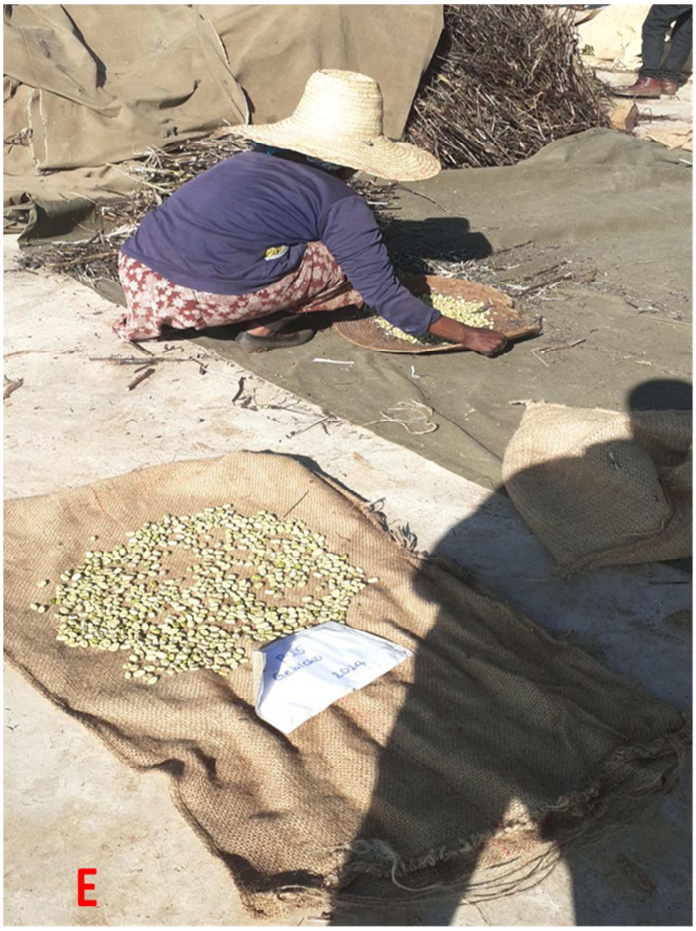
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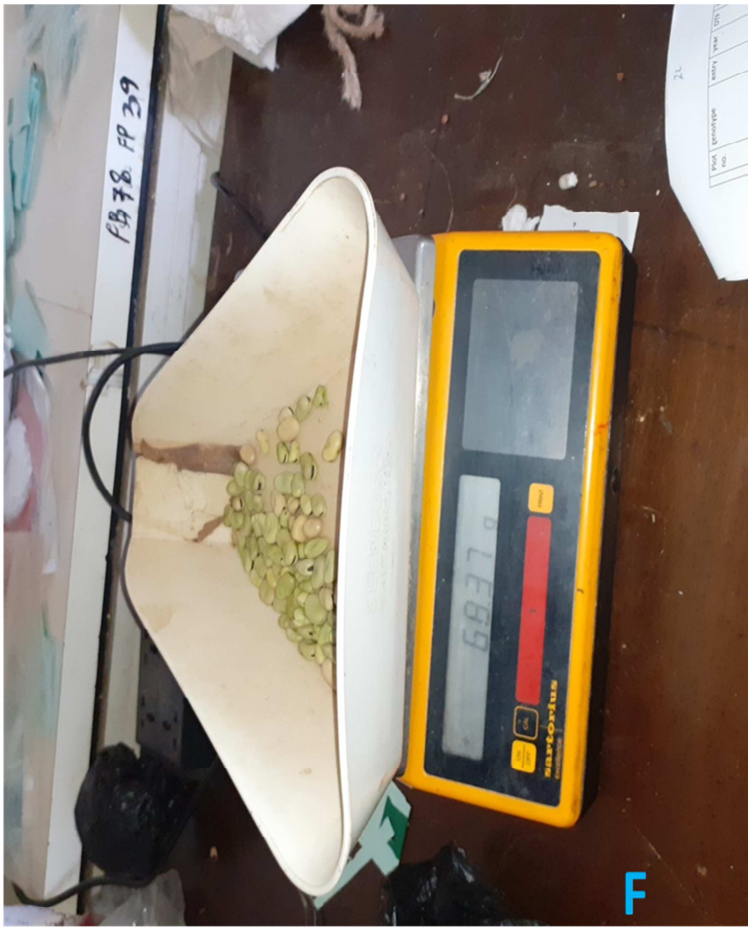
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7. APPENDICES

Appendix 1: Figure 1: Photos showing experimental activities including land preparation (A), matured faba bean samples (B),management (C), data collection (D), clearing the harvested seed (E), and measuring seed weight (F) at Holota agricultural research center.







Photos taken by Solomon Abiyu (2019)

Appendix 2: Table 1: Combined mean performance values for 16 characters along with their LSD at 5% of the 25 faba bean accessions evaluated at Holota Agricultural research center highland pulse research field

Trt	Y.R	DF	DM	PH	LL	IL	PL	HFPN	NPPP	NSPP	BMWPP	SEY	HSW	SFP	HI	SEPPPHa	ECGR
Moti	2018	58.00	142.33	1.12	6.78	3.89	6.64	39.33	7.33	3.07	1.63	504.93	75.44	84.33	0.31	2103.86	598.73
Geblcho	2016	66.00	140.67	1.08	7.10	4.32	6.19	32.61	9.87	2.87	2.03	730.28	80.55	74.67	0.36	3042.83	978.06
Messay	2004	58.00	135.00	2.28	6.26	4.47	5.49	31.58	9.40	2.73	0.87	286.84	52.28	77.00	0.33	1195.21	372.51
Dosha	2015	58.00	138.33	0.99	5.83	4.56	6.27	42.74	7.20	2.73	1.43	509.48	70.61	80.33	0.56	2122.83	634.34
EH99071-2	2006	61.33	140.67	1.01	6.36	4.37	6.48	40.67	7.80	3.07	0.87	198.43	64.19	79.33	0.23	826.79	250.13
Dosha	2013	58.00	138.67	1.12	6.21	4.72	6.61	38.80	9.13	2.87	1.47	441.88	68.85	80.67	0.30	1841.15	547.78
EH99019-4	2005	67.33	140.33	1.09	6.59	4.73	6.44	39.47	9.87	2.87	1.60	354.94	65.44	73.00	0.28	1475.92	486.22
EH940050V4	2004	60.67	140.00	1.01	6.65	3.95	5.68	39.66	9.60	2.67	0.97	265.64	56.24	79.33	0.28	1106.85	334.86
Dida	2016	66.00	141.67	1.11	7.07	4.23	6.93	38.90	9.20	3.13	1.57	473.26	79.45	75.67	0.30	1971.93	625.46
EH98033-3	2006	63.33	137.67	0.88	5.76	4.20	6.49	34.32	10.80	2.93	1.00	340.63	66.73	74.33	0.34	1419.29	458.24
Gora	2018	58.00	141.67	1.14	7.07	4.30	6.99	45.20	7.20	2.73	1.20	359.50	83.88	83.33	0.30	1497.92	431.40
EH99102-4	2007	64.00	142.33	0.88	6.04	4.11	6.93	36.12	7.47	2.93	1.13	336.22	66.99	78.33	0.30	1400.92	429.22
Obse	2015	58.00	139.67	1.17	7.04	4.49	7.22	32.27	9.63	2.93	1.50	550.31	80.44	81.67	0.37	2292.96	673.85
EH00126	2006	65.33	139.00	1.08	6.49	4.29	6.89	41.83	9.60	2.73	1.07	387.81	74.77	73.67	0.36	1615.88	526.42
Tesfa	2007	65.33	139.00	1.08	6.49	4.12	5.13	32.49	9.60	2.73	1.07	286.51	74.77	73.67	0.30	1193.78	526.42
EH95074-9	2006	58.00	139.00	1.08	6.49	4.12	5.13	32.49	9.60	2.73	1.07	286.51	74.77	73.67	0.30	1193.78	526.42
NC-58-M	2010	66.00	141.33	0.96	5.75	4.12	5.13	32.49	9.07	2.80	0.94	286.51	45.71	81.00	0.30	1193.78	353.71
Woyu	2003	66.00	141.33	0.93	6.57	3.43	4.69	34.39	13.40	3.00	0.60	207.29	35.22	78.33	0.35	863.71	264.64
Geblcho	2014	66.33	139.67	1.07	6.44	4.06	5.97	36.20	9.00	2.53	1.67	655.79	83.22	73.33	0.39	2732.46	894.26
Hachalu	2015	64.00	140.00	1.14	6.27	4.80	5.79	35.83	7.80	2.67	1.50	651.55	74.59	76.00	0.43	2714.79	857.30
EH98106-1	2007	63.33	140.67	1.04	6.29	4.03	6.99	44.00	7.60	3.07	1.27	331.55	79.38	77.33	0.26	1381.46	428.72
Hachalu	2018	66.00	141.33	1.11	7.30	3.97	5.96	32.68	12.07	2.87	1.53	558.15	65.98	75.33	0.36	2325.63	740.91
Dagaga	2012	58.00	138.67	1.10	5.60	4.97	5.81	35.19	12.73	2.87	1.80	530.48	58.47	80.67	0.29	2210.33	657.62
Moti	2013	58.00	140.67	1.15	5.60	4.89	7.65	39.79	9.07	2.93	1.70	530.48	70.03	82.67	0.30	2105.04	611.14
local check	2018	58.00	140.67	1.15	5.60	4.89	7.65	39.79	9.07	2.93	1.70	530.48	70.03	82.67	0.30	2105.04	611.14

L.S.D(5%)	***3.97***	***3.26***	***0.78***	***0.95***	***0.81***	***0.77***	***8.36***	***3.61***	***0.36***	***0.50***	***156.80***	***8.11***	***5.17***	***0.13***	***5114.75***	***204.78***