MADDA WALABU UNIVERSITY

COLLEGE OF NATURAL AND COMPUTATIONAL SCIENCE

DEPARTMENT OF BIOLOGY

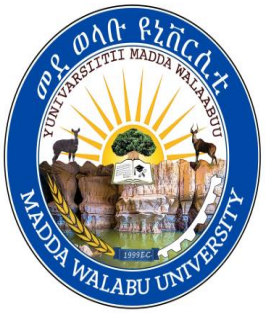
ASSESSMENT OF GENETIC DIVERSITY AMONG ETHIOPIAN FABA BEAN (*Vicia faba* L.) GENOTYPES USING AGRO-MORPHOLOGICAL TRAITS

BY:

ZEMEDKUN KASSAYE

June, 2021

Bale-Robe, Ethiopia



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BY:
ZEMEDKUN KASSAYE
ID NO. PGBSG/016/09

A Thesis Submitted to the Department of Biology College of Natural and Computational Science Madda Walabu University in Partial Fulfillment of the Requirements for the Degree of Masters of Science in Biology

June, 2021
Bale-Robe, Ethiopia

ADVISORS' APPROVAL SHEET

To: Biology department

MWU

Subject: Thesis Submission

As a major advisor, I hereby confirm that I have read and evaluated the thesis entitled **"Assessment of genetic diversity among Ethiopian faba bean (*Vicia faba* L.) genotype using agro-morphological traits"** which was conducted by Zemedkun Kassaye in partial fulfillment of the requirements for Master of Science degree in Biology. Therefore, I strongly recommend that Zemedkun has fulfilled all the requirements for the thesis and thus he can submit the final copy to the department to be presented in the upcoming open thesis defence program as per the schedule of School Graduate Studies.

With Regards!

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We, as member of the Board of Examiners of the final open defence by Zemedkun Kassaye have read and evaluated his thesis entitled "**Assessment of genetic diversity among Ethiopian faba bean (*Vicia faba* L.) genotypes using agro-morphological traits** " and examined the candidate. We hereby 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

By signature below, I declare that this thesis is my genuine work and that all sources of materials used for this thesis have been duly acknowledged.

This thesis has been submitted in partial fulfilment of the requirements for a MSc. degree in Biology at the Madda Walabu University. The thesis is deposited in the Madda Walabu University Library and is made available to borrowers under the rules of the Library. I solemnly declare that this thesis is not submitted to any other learning institution anywhere for the award of any academic degree, diploma, or certificate.

Brief quotations from this thesis may be made without special permission provided that accurate and complete acknowledgement of source is made.

Name: Zemedkun Kassaye Signature: _____ Date: _____

BIOGRAPHICAL SKETCH

The author was born in Ethiopia, Oromia administrative region, Arsi zone, Tiyo District in the village called Chebi, in 1975 E.C. He attended his elementary and junior School in the same village at Chebi Primary School, from 1981-to1988 E.C. Then, he attended his Secondary School from 1989-to1993 E.C, at Chilalo Terera Secondary School in Assela town.

After completion of the secondary school, he joined Bahr Dar University in 1994 E.C and gained BEd degree in Biology in 1997 E.C. Since 1998, he has been teaching Biology in different high schools in Arsi zone.

In 2009 E.C, he joined Madda Walabu University, School of Graduate Studies College of Natural and Computational Sciences Biology Department to pursue his MSc degree in Biology.

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LIST OF ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of Variance
APLP	Amplified fragment length polymorphism
CSA	Central Statistical Authority
DNA	Deoxy Ribonucleic acid
EGR	Economic Growth Rate
GCV	Genotypic coefficient of variation
HA	Hector
HI	Harvest Index
IBC	Institute of Bio diversity conservation
ICARDA	International Center for Agricultural Research in the Dry Area
ISSR	Inter-simple Sequence repeat
KARC	Kulumsa Agricultural Research Center
LSD	Least Significant difference
M.A.S.L	Meter above Sea level
MoA	Ministry of Agriculture
MoSHE	Ministry of Science and Higher Education
MWU	Madda Walabu University
PCA	Principal Component Analysis
PCV	phenotypic Coefficient of Variation
SAS	Statistical Analysis Software
SDS	Sodium dodecyl sulphate
SIDA	Swedish international Development Agency
SPE	Seed Production Rate
SRAP	Sequence repeat amplified polymorphism
UPGMA	unweighted Pair Group Methods with Arithmetic

ABSTRACT

Faba bean (Vicia faba L.) is a facultative cross-pollinating legume crop with remarkable nutritional value (high protein content) and plays important role in maintaining soil fertility. Despite the wide importance in serving as a source of food, nutrition and ecological importance, the productivity of faba bean in Ethiopia is affected by different factors including management practice in the field, limited information on the extents of its genetic diversity, and scarcity of information on the performance of different genotypes for selection of best performing ones for further use. Therefore, the present study was initiated to assess the genetic diversity in 18 Ethiopian faba bean genotypes using22 agro-morphological traits. The genotypes were obtained from Holleta, Kulumsa and Sinana agricultural research centers and field experiment was carried out at Kulumsa agricultural research center in Kulumsa site under rain fed condition during the main cropping season of 2020. The experiment was laid using randomized complete block design (RCBD) with three replications and two blocks each having nine plots (rows) per replication. The data, which were collected using a total of 22 agro-morphological traits, were analyzed using SAS 9.0 statistical analysis software. The results showed significant ($p < 0.05$) to highly significant ($p<0.01$, $p<0.001$) variation among the genotypes for seed yield and several yield associated traits. Mean performance values of the studied agro-morphological traits revealed a wide range of variation. Seed yield is a very essential trait and showed strong positive and highly significant correlation both at genotypic and phenotypic level for all yield components except days to 50% flowering. The range of variations in both PCV and GCV was wide implying existence of enough variation in the tested genotype and importance of most of the traits for selection and breeding of the genotypes through phenotypic selection. Principal components analysis (PCA) revealed 90.2% of the total variation among the genotypes on the first six principal components (Eigen value ≥ 0.94) revealing that several traits in these PC's had the greatest contribution to the overall variation in the genotypes and could be used as selection criteria. In addition, PCA scatter plot grouped the genotypes into four clusters implying significant amount of genetic variability among the genotype. Moreover, Cluster analysis grouped the genotypes into six major clusters each with high inter-cluster distances indicating that existence of sufficient variability among the tested genotypes and their suitability for selection and high genetic gain (heritability) for the character of interest. Overall, the study revealed a wide range of variation among the genotypes considered in most of the traits and the results generated could be used as baseline information in improving faba bean production and productivity. The genotypes such as Didea, Walki, Hachalu and Ashebeka, in that order, were high yielding genotype for further use. However, to exploit the actual extents of genetic variability using molecular (DNA based) markers are recommended.

Keywords: Agro-morphological traits, Faba bean, Genetic diversity, Genotypes, Seed yield

1. INTRODUCTION

1.1. Background of the study

Faba bean (*Vicia faba* L.) is one of the oldest and most important legume crops believed to be originated in the Near East and Middle East regions, with a large percentage of the species and wide morphological diversity occurring in the Irano-Tauranian floristic region (Bellido, 1994). It is grown by man for its remarkable nutritional value and high seed protein content (Crepona et al., 2010). The crop has a versatile use in that it is widely cultivated both for human food and animal feed. In addition, it is used in maintaining soil fertility through nitrogen fixation and greatly reduces dependence on energy consuming mineral fertilizers (Jensen et al, 2010; Kopke and Nemecek, 2010). It also reduces soil borne diseases during crop rotation in agricultural systems (Landryetal et al., 2016) and attracts pollinators through its beautiful flowers (Marzinzig et al., 2018). Annual world production of the crop reaches up to 4.3 Million tons and the total cultivated area reaches nearly2.55 Million hectares (FAO STAT, 2010).

The crop is currently produced in more than 66 countries of the world including Ethiopia. The country is considered to be the secondary mother land for the crop (Torres et al.,2006) and in terms of production, the country is among the major producers and ranks second, next to the People's Republic of China and ranks first from African countries(FAO,WHO,2019; Torres et al.,2006).In Ethiopia, the crop is mainly cultivated in mid and high-altitude areas with an elevation ranging from 1800-3000 meters above sea level, an average annual rainfall of 700-1000 mm, and mean daily temperature range of 22-10^{0}C(Mussa and Gemechu,2006*;* Asfaw et al,1994). The annual area coverage of the crop is nearly 443,966.09 hectares with the total production of 8.39 million tons and productivity of 1.91 tons ha-1 (CSA, 2016).In terms of hectarages and total national production; it ranks first among the cultivated grain legumes. However, the productivity per unit of land is still far below the potential of the country and is very low compared to the average yield of 3.7 tons ha^{-1}in major producer countries (FAOSTAT, 2017).The situation is even worse in the current scenario of climatic change that is triggering both biotic and a biotic yield limiting factors.

Assessing the extents of genetic diversity and properly managing genetic resources are important issues and major concerns in improvement programmes and conservation, both *ex-situ* (off-farm) and *in-situ* (on farm) measures (Farooq and Azam, 2002).

Different methods collectively called markers are in place to detect the extents of genetic diversity in any crop species. Genetic markers are broadly divided into molecular, biochemical and morphological markers. Several authors have reported the genetic diversity within and among populations of faba bean genotypes using different biochemical and molecular markers, including: SDS PAGE (Hou et al., 2014), random amplified polymorphic DNA (RAPD) (Yassine et al., 2014; Aziz and Oman, 2015), amplified fragment length polymorphism (AFLP) (Rebaa et al.,2017; Ammar et al., 2015), SRAP (Ammar et al., 2015; Alghamdi et al., 2012) and inter simple sequence repeat (ISSR) (Wang et al., 2012; Salazar-Laureles et al., 2015). In addition, their presence is not dependent on the growth stage of the crop and can be found in all tissues.

Morphological (classical or visible, agronomic traits) marker systems are the earliest, simple and inexpensive genetic markers which is reveal genetic diversity of crops based on phenotypic appearances (Lie et al., 2009). The marker still plays a central role in the analysis of the extents of genetic diversity in crop species, fruits, tubers and their relatives (Newbury and Ford-Lloyd, 1997).

Currently, the number of faba bean varieties released by the national research system in Ethiopia is increasing of which is 31 faba bean varieties (Meselu Y. K. 2019; MoANR, 2016). However, once released and recommended for use, the work done so far regarding continuous assessments of the level of genetic diversity on traits field performance sustainability in Ethiopian faba bean genotypes and varieties is still less because faba bean research program in the country has largely been focusing on increasing production and productivities, and identifying resistant/tolerant lines to biotic and a biotic stresses. Therefore, the present study is aimed at assessing the extents of agro-morphological traits based genetic diversity in Ethiopian faba bean genotypes collected from Sinana, Holota and Kulumsa agricultural research centers, Ethiopia.

1.2. Statement of the problem

Estimation of genetic diversity among faba bean genotypes in Ethiopia is the main concern of breeders as the effectiveness of selection depends on the proportion of heritable variations (Behailu Mulugeta, 2016). The effectiveness of plant breeding and stability of yield depends upon the nature and magnitude of existing genetic variability, the degree of heritability or transmission of the traits and genetic gain from selection (Sharifi, 2015; Behailu Mulugeta, 2016). Thus, the presence of genetic variation is a basic requirement for long-term stability of crops including genotypes resulted from selection breeding in certain ecosystem. In addition, eventual maintenance of the existing

diversity over a period of time through successive assessment and essential intervention is essential for efficient and durable utilization in breeding schemes and effective conservation (Farooq and Azam, 2002).

In Ethiopia, faba bean offers a wide importance and serves a source of food, nutrition and provides ecological importance. However, its productivity is far below the real potential of the country due to several biotic (diseases, weeds and insects), a biotic (drought, water logging and marginal management) and related factors such as edaphic stresses like soil acidity (El-Fouly, 1982; Mussa et al., 2008). Moreover, scarcity of continuous assessments on those improved and released varieties has limited the intended yield and adaptability potential in several parts of the country (Mussa et al., 2008). As a result, the average yield of those improved varieties has remained as low as 1.8 ton per hectare(CSA 2014) which is comparable to the productivity of landraces cultivated under small holder farmer but by far less as compared to the productivity in UK, which is about 30 qt/ha (Winch, 2006).

Thus, sustainable yield improvement and adaptability in crop breeding programs involves the development of varieties that resist the major biotic and a biotic constraint. In addition, refinement of integrated pest management strategies, improving adaptation to changing environments, improving nutritional quality and adaptation under different agro-ecologies and launching an integrative approach leading to effective exploitation of the genetic and environmental manipulations are important scenarios.

Performance evaluation on the level of genetic diversity and properly managing genetic resources particularly in improved varieties and genotypes is an important issues and major concerns in assuring sustainable performance related to yield and other agronomic traits. Moreover, it is important in designing *ex-situ* (off-farm) and *in-situ* (on-farm) conservation measures (Farooq and Azam, 2002). The available genetic diversity can be accessed through biological markers which could be morphological, biochemical and/or molecular. Morphological (classical or visible, agronomic traits) markers are phenotypic traits which still play a central role in the analysis of genetic variability in crop species, including legumes such as faba bean (Newbury and Ford-Lloyd, 1997).

So far, there is very limited work on the extents of agro-morphological traits based genetic diversity of Ethiopian faba bean varieties/genotypes. Thus, this research was initiated to analyze the extents of genetic diversity in the released genotypes. The information generated could be used as a baseline in

establishing traits performance sustainable improvement and conservation of this economically important legume crop.

1.3. Objectives of the study

1.3.1. General Objective

The general objective of this study was to assess the genetic diversity Ethiopian faba bean genotypes collected from Holota, Kulumsa and Sinana Agricultural Research Centers, Ethiopia using agro-morphological traits

1.3.2. Specific objectives

- To determines the extents of genetic variability within and between the genotypes.
- To identify yield and yield associated traits among the genotypes.
- To identify faba bean variety that is/are superior in desirable agronomic characters for use in further breeding/crossing programs.

1.4. Significance of the Study

The study provides important baseline information for further faba bean breeding and to keep sustainability of traits performance. Furthermore, it provides baseline information to *ex-situ* and *in-situ* conservation measures to conservation experts, community, and farmers in the study area and elsewhere in the country within the same range of agro-geographical location. Besides, the study will be used as a supporting document for further in-depth study regarding sustainability of released varieties over years and locations.

2. LITRATUREREVIEW

2.1. Botanical Description of Faba Bean

The term faba bean (*Vicia faba* L.)has been accepted to refer to the three types of faba bean species: the large seeded *Vicia faba* major (broad bean), medium seeded type *Vicia faba* equine and the smaller seeded *Vicia faba* minor (field and/or horse bean).In fact, all the three types belong to the same species and are only distinguished on the basis of seed size and weight per seed such that large and flat seeds weighting more than 1gm,medium less than about 1gmand round seeds up to 0.6gm or 0.7gm,respectively(Hanelt and Mettin,1989; Harlan, 1969).

2.2. Origin, Distribution and Production of Faba Bean

The exact geographical origin of faba bean is not clearly known but the high rainfall regions of central Asia and the Mediterranean regions have been proposed as possible centers of origin (Metayer, 2004).On the other hand, Vavilov (1936) discovered a primitive type of faba bean at the intersection of Himalaya and Hindu Kush, and proposed Central Asia as the center of origin. In addition, he suggested a gradual increase in faba bean's area expansion from Central Asia westward along the mountains to Iran, Turkey, the Mediterranean and Spain. He also concluded that areas along the coast of the Mediterranean Sea and Ethiopia could be the secondary origin of the crop. Cubero (1974) also reported Near East, Iraq and Iran as the primary centers of origin and Afghanistan and Ethiopia as the secondary centers of origin.

Faba bean has spread across the globe due to its wide adaptability. It grows well in the frosty northern areas of Europe as well as in the arid climates of the Middle East and Africa. It is chiefly produced in Europe, Asia and North America, extending to temperate South America and tropical East Africa (Allkin et al., 1986) and reached Ethiopia soon after domestication around 5000 B.C. Among the world faba beans producing countries, China is the leading which gives East Asia the largest share in world total area harvested (38%) and total production (42%), (Akibod and Maredia, 2011).

As a secondary center of diversity for the crop (Bond, 1976; Yohannes, 2000) and Ethiopia is one of the major producers for faba bean occupying the largest area coverage and volume of annual production of all pulses. It is largely grown in the highland (1800-3000 m.a.s.l) parts of the country

(Gemechu et al., 2003) though the crop is extremely diverse in terms of cultivation methods, uses, and the range of environments.

2.3. Morphology and Phenology of Faba Bean

Faba bean is an annual plant with strong, erect and hollow stem. The height of the plant varies with cultivar and environment, but in the range of 50-200cm.Depending on the genotype, the main stem develops several nodes (17 to 22 nodes) the first leaf may arise on the first or second node above the soil surface. Alternate pinnate leaves consisting of two to six leaflets arise at each node. The leaflets are rounded or oval, up to 6-8 cm long and 2-4 cm broad. The inflorescences are borne on short axillaries racemes and they bear between 1 and 6 papilionaceous flowers. These flowers are large (up to 3-4 cm long), white or white with black/dark purple spots (Singh et al., 2012).

The fruit is a dehiscent cylindrical pod, up to 10 cm long and 1-2 cm in diameter. The pods are green when young and turn to dark brown or black at maturity. The pods contain 3-4 oblong-oval seeds (beans) that have a distinctive hilum on their short side (McVicar et al., 2013; Muehlbauer et al., 1997).

Most faba beans have indeterminate growth in which the plant continues its vegetative growth while forming flowers and pods. The vegetative nodes at the top of the plant may compete with flowers and developing pods for assimilate (Chapman and peat, 1978). The roots system of faba bean consists of a tap root with secondary roots (bond et al., 1985).

The first flowering node is influenced both by photoperiod and temperature; date of flowering and the position of the first flowering node were reduced as the photoperiod increases, indicating quantitative long day response (Evans, 1959). Low temperature vernalization or cool growing conditions have been shown to accelerate flower initiation (Saxena and Wassimi, 1979).

The first pod is normally produced at the 5^{th}-9^{th} node but it varies with genotype and environment (Adisarwanto, 1988). The distribution of pods along the stem is also influenced by genotype and environment.

Pods are short and erected in V. minor (3-4 ovules/ pod), and long and hanging in V. major types (8-12 ovules/ pod). V. equina types are intermediate having 4 to 8 ovules/ pod. Like many legumes, only 15 % flowers develop pods. The seed-set is frequently higher on the bottom podding nodes of a stem and in proximal pods of a raceme (Singh, 2015).Within the pod, abortion is reported to be

greater at position proximal to the peduncle. As pods mature, they turn black, as eventually do the stems and leaves of the plant.

During maturity, the lower leaves become darken and drop, pods turn black and dry progressively up the stem (Hekneby et al., 2006; Singh et al., 2013).

Physiological maturity is defined as the time when the seeds reach maximum dry weight, after which the weight of the seed remains constant and the moisture content falls (Dvies and Willians, 1986), however, Stipnagel (1984) proposed that maturity can be defined as a stage when all pods are hard and black. Seed size of faba bean usually ranges between 200mg to 300mg per seed though it varies with genotypes.

2.4. Reproductive Development

Vegetative growth and reproductive development occur concurrently. Reproductive development is indicated at axillary meristems. The first reproductive nod usually coincides with a change from being four leaflets to six leaflets (Evans, 1959).

The stem continues to grow during flowering and a large number of floral nodes can be produced. Vegetative growth terminates when the whole plant begins to senesce, which coincides with pod ripening. Mature pods are usually concentrated at the lower reproductive nodes and at the lower (proximal) position of the racemes (Peat, 1982).

The distribution of pods along the stem can be affected to some extent by the environment. The number of pods that reach maturity is always lower than the number of flowers initiated (Kambal, 1969a, Peat, 1987). Abscission may vary from 36 to 94% of the flowers initiated, depending on cultivar and season (Smith and Kambal, 1982; Clifford et al, 1990).

Pollination does not guarantee successful fertilization and seed development. The growth pollen tubes through the style have been shown to have direct effects on further development of the flower (Peat, 1982). A number of factors such as in adequate number of pollen grains, insufficient number of pollen tubes for the enhancement growth, failure of some tubes to reach the ovules,

defects in the structure or physiology of the ovary and extreme temperature have been found to have effects on the development of a flower in to a pod (Stodderd,1985). However, young pods may cease to grow and abscise despite successful pollination and fertilization (Champman et al.,

1978). Internal competition for assimilates within the plant, particularly between young pods and the vegetative apex and water stress is a major factor in pod abscission (Peat, 1982).

2.5. Inception of Faba Bean Breeding in Ethiopia

In Ethiopia, faba bean breeding program started early in the 1960's with the establishment of Arsi Rural Development Unit (ARDU) followed by Debrezeit Agricultural Research Center, under Haramaya University, the then Alemaya College of Agriculture. It was established with the main objectives of improving productivity of the crop through developing and promoting improved cultivars that tolerate both biotic and a biotic stresses and copes with different agro-ecologies and cropping systems of the country. Special focuses have been made to improve grain yield, diseases and water logging resistance/tolerance and increase seed size in response to market demand (Asfaw et al., 1994).

Even though Ethiopian Institute of Agricultural Research was established in 1958,faba bean research efforts in general and breeding works in particular was started later at a very few research centers and some locations based on separate efforts. Strong and well-organized breeding effort started in mid 1980's when research collaboration started among different research centers at different locations and the program was further strengthened by technical supports from ICARDA (Asfaw et. al., 1994). Thus, 1980's is regarded as the commencement of hybridization of faba bean in Ethiopia because of the first crossing attempt at Holeta Agricultural Research Center to transfer chocolate spot resistance from parental materials introduced from ICARDA into other adapted parents with good agronomic traits. Thus, this center is considered as the country's major contributor in improving faba bean varieties for improved productivity and production.

2.6. Faba bean production climate zone in Ethiopia

Faba bean is one of the oldest domesticated and third most important cool-season food legumes in the world (Torres et al., 2006) and is commonly produced as a winter annual in subtropical areas. It takes about four to five months for maturity depending on the growing conditions of the area (Macleod and Sweetingham, 1999; Mussa et al., 2008). In Ethiopia faba bean is cultivated in Weyndega (mid-altitude ranging from 1800-2200 m.a.s.l, receiving average annual rainfall of 740 mm, and having mean daily temperature of 18-22^{0}C) and Dega (high altitude, above 2200 m.a.s.l, average annual rainfall of 900 mm, mean daily temperature of 10-18^{0}C)zones (Asfaw et al, 1994). It is grown from

June to December in rotation with cereal crops like wheat and tef due to its nitrogen fixing capacity (Gorfu and Feyissa, 2006).Apart from its adaptation and distribution, mostly subsistence farmers grow faba bean under rain-fed conditions.

2.7.Faba bean germplasm source

International Center for Agricultural Research in the Dry Areas (ICARDA) is the largest international center having global mandate for faba bean germplasm because of drought and heat waves that are having significant effects on the productivity of faba bean in rain fed areas with a Mediterranean type of climate. It houses nearly 9,320 germplasm accessions of faba bean in its Gene Bank that is shared regularly with various partners of National Agricultural Research Systems (NARS) and Advanced Research Institutes (ARIs) in order to identify suitable cultivars for different countries. As a result, around 69 faba bean improved varieties were released in different countries mainly Egypt, Ethiopia, Australia, Sudan, China, Tunisia, Turkey and Yemen. So far, in particular in Ethiopia, a total of 199 improved pulse varieties were released by the national research system, of which 31 faba bean varieties (Meselu Y. K. 2019; MoANR, 2016).

Between 1994 and 2002, on average, more than 2500 germplasm accessions/lines and breeding materials of faba bean have been annually evaluated in Ethiopia (Mussa et al., 2008). Out of these, 60% was from hybridization, 20% was from collection and 15% from introduction**.** In the past decade, about 31 improved faba bean varieties have been released and adapted to different agro-ecology with varying reaction to diseases (Degye Goshu et al., 2019; Crop variety register issue No.18, 2016).

2.8.Major Importance of Faba Bean

Faba bean plays an important and diverse role in the farming systems and in diets of subsistence farmers in poor countries, and hence qualified as an ideal crop for reducing poverty and hunger, improving human health and nutrition, and enhancing ecosystem resilience. Its major benefits are presented below:

2.8.1. As a source of human nutrition and animal feed

Faba bean has an important place in the human diet in developing countries and as both food and animal feed, mainly for pigs, horses, poultry and pigeons in developed countries (Singh and Bhatt, 2012 a).In some parts of the world because of its high protein content, it can be used as a vegetable, green or dried, fresh or canned (Gasim and Link, 2007).The bean is also considered as a extender of meat, coffee and as a skim-milk substitute when it eaten roasted (Yitayih and Azmeraw, 2017).

Faba bean seeds contain relatively high protein that can nourish human with almost all essential elements required for life such as, carbohydrates, vitamins B, antioxidants and minerals (Etemadiet al., 2019). The antioxidant properties of phenolic compounds may provide excellent dietary source for natural antioxidant for chronic diseases prevention and health promotion (Oomah et al., 2006).

Protein content in different varieties varies from22 to 33(Winch,2006)and the amino acid profile has a high lysine content (5.4-6.8%) that are not present in sufficient quantity in staple cereal crops (Giller, 2001). Genetic characterization of faba bean revealed sufficient variability in seed yield and its components combined with appropriate amount and variability of carbohydrate, fibber, and protein contents and quality that determines the taste and cooking qualities for consumption (Gasim et al., 2015).

2.8.2. Environmental and Economic significance

Faba bean is the highest nitrogen-fixing annual legume that can fix more than 90% of its own nitrogen requirements. Such capability made it an excellent rotational crop with cereals to help reduce soil pathogens and improve or supply nitrogen to the next cereals(Thomas et. al., 2011).For example; rotation of wheat per faba bean compared to continuous wheat copping found to reduce the incidence of crown rot pathogen (*Fusarium pseudograminearum*) by approximately 10% in the following wheat crop (Moore et al., 2003 and Verrell et al.,2005).The effectiveness of faba bean nodule in nitrogen fixation depends on the variety of the crop, the physical and chemical properties of soil and rhizobia that found in the soil (Argaw and Mnalku, 2017).Moreover, faba bean has a great capacity of solubilising and thus facilitating the availability of insoluble phosphorus for other associate crops, there by improves soil physical environment and soil microbial activity (Rashid et al., 2016).

Faba bean is characterized by producing large amount of biomass that can be tilled back into the soil as green manure and straw. It is also used as fuel in Sudan and Ethiopia (Tewodros et al., 2015).It

reduces cost of fertilizer for the following cereal crop production for small holder farmers by adding nitrogen. Studies have shown a net global warming potential index (GWP)of 114 when using fertilizers as compared to41 for a legume-based system (Robertson et al., 2000).The limited resources of fossil energy and the increased emissions of the greenhouse gasses: CO_2 andN_2Othrough the use of industrially produced nitrogen fertilizer make a N-fixing legume crop like faba bean an attractive option and a component of future cropping systems as it is renewable, clean and environment friendly(Giller, 2001; Jensen and Hauggaard Nielsen, 2003).Its high protein content provides higher prices compared to cereals and are increasingly grown to supplement farmers' incomes (Gowda et al., 1997).

2.9.Faba Bean Production Constraints in Ethiopia

In Ethiopia, the average yield of faba bean under small -holder farmers is not more than 1.8ton/ ha (CSA, 2014), despite the availability of high yielding varieties which give more than 2 tons/ha (MoA, 2012). Such low productivity of the crop is attributed to susceptibility to biotic and a biotic stress and lack of sustainable performance over years (Mussa et al, 2008). The major constraints include climatic factors such as temperature and light (Asfaw et al.,1990), agronomic practices such as plant density, and unfavourable climatic condition like drought, salinity, excessive soil moisture (excessive water logging), inadequate supply of nutrients, distribution of assimilates and hormones imbalance (El-Fouly,1982).

2.9.1. Impact of moisture and excessive biomass production

Faba bean yields are considered to be relatively unstable and there has been concern regarding its excessive biomass growth and the intra plant competition for resources that could reduce yield and harvest index. Grashoff (1990) state that abundant water during and after flowering stimulated vegetative growth, but reduced final seed yield compared to mild water shortage during flowering followed by generous water after flowering. This effect may partly explain the reduced yield and harvest index associated with excessive vegetative growth as lower parts of the canopy receive less light in such circumstances. Thus, since faba beans are poor competitors with weeds, particularly in the seedling stage integrated weed control is essential for successful crop production including selecting fields with light weed pressure (Ali et al., 2000).

2.9.2. High temperature and frost

Faba bean is sensitive to drought (Habib Rahman et al., 2007) and it requires a large amount of moisture to maintain turgor in the fleshy stem and broad leaves (Bond et al., 1994). High temperatures affect a number of growth processes which may significantly reduce yield in legumes. The critical periods of drought sensitivity is during flowering and pod-filling periods (El Nadi, 1969). The optimum temperature for flowering is reported to be 22 – 23°C, and a temperature over 28°C cause significant yield loss (El Nadi, 1969 and Bishop et al., 2016).Frost (temperatures below 1°C) is a major a biotic stress and damages the reproductive structures of the crop production particularly, in the flowering, early pod formation and pod-filling stages (Maqbool et al., 2010).

2.9.3. Time of sowing

In indeterminate crops including grain legumes, the relationship between time of sowing and physiological maturity is more complex as crops continue vegetative growth while reproduction is occurring. In the case of faba bean, determinate cultivars exist, however they have lower yields and smaller seed weight (Baginsky et al., 2013). Thus, sowing time for faba bean is still important and does not differ due to the limited range of maturities available in suitably adapted varieties and have noted that earlier sowing increased the length of the flowering and pod filling phase which contributed to higher yield through greater pod number and greater seed weight. As a result, time of sowing is the main method of managing frost, heat and late season moisture stress (Matthews et al., 2015).

2.9.4. Pest and disease

Among the biotic category, diseases are important limiting factors that hinder the production of food-legume crops as a whole and specifically, faba bean in Ethiopia (Berhanu et al, 2006). Among the major faba bean disease causing pathogens, fungi are the largest and perhaps the most important group affecting all parts of the plant at all stages of growth (Nigussie et al., 2008). The low productivity may also be attributed to the inherently low yielding potential of the local varieties grown by the farmers.

The major diseases affecting faba bean production in the country are chocolate spot (*Botrytis fabae*), Ascochyta blight (*Ascochyta fabae*) and faba bean rust (*Uromyces viciae-fabae*) which are prevalent in prolonged wet seasons (ICARDA, 2008). Chocolate spot and rust became the important diseases worldwide. Faba bean leaf roll virus (FBLRV) and faba bean necrotic yellow virus (FABNV)are also

diseases associated with faba bean (Foead, 2011). According to the research results from Holeta and Debrezeyit ARC, chocolate spot and rust caused yield loss of 34.1% and 14 -21%, respectively (Asfaw et al., 1993). Hence, control measure is very important to minimize loss due to these diseases. Among many ways to control faba bean diseases, identification and utilization of resistant genotypes is believed to be most practical, economical and environmentally save measure for farmers (Asfaw et al., 1994).

2.10. 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) .

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). 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).

2.10.1. Agro-morphological traits based genetic diversity analysis

Genetic variation among faba bean genotypes is imperative for their efficient utilization in plant breeding schemes and effective conservation. Agro-morphological marker systems are the earliest, relatively simple and inexpensive genetic markers which lie on phenotypic appearance (Vos et al., 1995).Even though, morphological and agronomic traits bear limited use in covering the genome, and highly affected by environmental factors and developmental stage of the plants, they are still routinely used and plays a central role in the analysis of genetic variability in crop species, fruits, tubers and their relatives (Newbury and Ford-Lloyd, 1997). Several reports have been there on Ethiopian faba bean varieties (Tafere et al., 2012; Girma and Haila, 2014; Mitiku and Wolde, 2015; Elshafei et al, 2019; Tadele et al. 2011; Gemechu and Musa, 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).

3. MATERIALS AND METHODES

3.1. Description of the Study Site

Field experiment was conducted at Kulumsa Agricultural Research Center (KARC) which is found in Arsi Administrative Zone, Oromia National Regional State, Ethiopia under rain fed conditions during the main cropping seasons (from July to December, 2020). The soil condition in the research farm is dark-clay loam with soil pH of 6.0. It is located at170kms South of Addis Abeba with coordinates: $8^0$2`N and $39^0$10`E, with an altitude of 2200 meter above sea level, The area receives an average minimum and maximum temperature of 10^0C and $22^0$and average annual rainfall of 800 mm. The area is one of the major mid-altitude pulse production areas. The KARC is Center of Excellence to wheat (wheat for East Africans: Ethiopia, Kenya, Uganda, Tanzania), malt barley and coordinates highland pulse crops such as faba bean, field pea research nationally**.**

3.2. plant Material

A total of 18 faba beans genotype including local seed (**Table 1**) were obtained from the Highland pulse production and productivity department's seeds store of Holota, Sinana and Kulumsa Agricultural Research Centers.

Table 1: List of faba bean genotypes their pedigree, year of release and collection centers

S/N	Names	Pedigree	Year of release	Collected from
1	Tumsa	EH99051-3	2010	Holeta
2	Gora	EK01024-1-2	2013	Holeta
3	Hachalu	EH00102-4-1	2010	Holeta
4	CS-20-DK	CS-20-DK	1978	Holeta
5	Dosha	COLL 155/00-3	2009	Holeta
6	Ashebeka	EH01075-4	2015	Holeta
7	Gebelcho	EH96009-1	2006	Holeta
8	Walki	EH96049-2	2008	Kulumsa
9	Moti	EH95078-6	2006	Holeta
10	Alloshe	--	2017	Sinana
11	Tosha	--	2019	Sinana
12	Moyben	--	2019	Sinana
13	Shalo	EH011-22-1	2000	Sinana
14	Mosisa	EH99077	2013	Sinana
15	Numan	--	2016	Kulumsa
16	Didea	ICB2717-1xR-878-3	2014	Kulumsa
17	Degaga	R-878-3	2002	Kulumsa
18	Local seed	Local Variety	-	Ketar variety

Broken lines (--) shows pedigree information not available in the sample

3.3.Experimental design

The experiment was laid using a randomized complete block design (RCBD) with three replications and two blocks. Each block per replications consisted of nine rows (plot) with 4 m width by 18.4 m length = 73.6 m^2 (2 x 73.6 m^2 area of replication).Spacing between replications, plots, rows, and plants was 1m, 0.5m, 40cm, and 10cm respectively. The genotype was assigned randomly to the plot at each replication. Management practices including application of NPS fertilizer was applied at a rate of 121kg per hectare (Faba bean production guideline, 2018). In addition, all the necessary field management practices were carried regularly and weeds were controlled by hoeing and weeding.

3.4.Data collection

Agro-morphological data were collected using a total of 22 quantitative morphological traits following IBPGR and ICARDA (1985).Data recording was performed on both plot bases (for phonological data *viz* days to 50% flowering, 90%maturity, above the ground biological yield (gm) and seed yield (gm)) and on plant bases (through randomly sampling of five middle plants from each plot). Data were recorded at the correct developmental stage and physiological maturity. The details 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) Leaf width (LW) (cm): Width across the leaf at its widest point of the central leaflet of the trifoliate leaf. Three leaves from top, middle and bottom of the plant were taken and averaged.

c) Leaf area (LA) (cm2): This was calculated by leaf area estimation model as described by Peksen (2007) and three leaves per plant were measured and averaged LA=0.919+0.682LW; Where **L**= leaf length and **W** = leaf width

d) **Leaf area index** (**LAI**): This was calculated by the formula LAI=Leaf Area x Number of leafs per plant Area covered by plant

e) **Number of pods per plant (NPPL):** The average numbers of pods counted from samples of five plants taken randomly from each plot.

f) **Numbers of seeds per plant (NSPPl):** The total number of seeds per pod on the same plant

g) **Numbers of seeds per pod (NSP):** 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.

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

i) **Height to the first podding 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.

j) **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 was taken and averaged.

k) **Pod width (PW)**: Three pods per plant of five randomly selected plants were measured at the centre of pod using a calliper.

l) **Internode's length (IL)**: Three internodes per plant of five randomly selected plants were measured and averaged.

m) **Number of branches per plant (NBPL):** Numbers of branches per plant was counted from basal and mediated nodes.

Data collected on plot basis and their descriptions are indicated as follow: -

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) Thousand seed weight (TSW)(g): The weight of thousand seeds taken randomly from the harvest seed lots of each plot

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

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 where harvested, sun dried and weighted.

h) Harvest index (HI %): is the ratio of grain yield to above ground biological yield and then multiplied by 100

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

3.5. Data Analysis

3.5.1. ANOVA and Correlation Coefficients

After checking homogeneity and normality, the data were subjected to analysis of variance (ANOVA) with statistical analysis software (SAS) computer version 9.1.3, according to the following model:

$\mathbf{M_{ijs}=\mu + r_i + r_j + G_s + \xi_{rgs}}$ Where,

$\mathbf{M_{ijs}}$ = morphological differences of i^{th} genotypes under j^{th} replication

μ = Grand mean; **r**i = the effect of i^{th} genotypes; **r**j = the effect of replication j; **G**s = the effect genotype; and ξ rgs = pooled error.

Correlation analysis and treatments means was compared using least significance difference (LSD) at 5% probability level (Fisher, 1935).

3.5.2. Estimating Coefficients of Variation

Estimation of genotypic and phenotypic variance components and their coefficients of variation were done following Singh and Chaudhary (1985), and Allard (1960). Accordingly,

Genotypic variance ($\delta^2 g$) = (MSg – MSe)/r where, MSg = mean square of genotype, MSe is mean square of error and r is the number of replications

Phenotypic variance ($\delta^2 p$) = $\delta^2 g + \delta^2 e/r$

Where, $\delta^2 p$ = phenotypic variance; $\delta^2 g$= genotypic variance and $\delta^2 e$ = error variance

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

Genotype coefficient of variation (GCV) per = ($\sqrt{\delta^2 g}/m$) x 100 where, GCV = genotype coefficient of variation.

Heritability (H^2) = ($\delta^2 g/\delta^2 p$) x 100 Where, $\delta^2 g$ = genotypic variance and; $\delta^2 p$ = 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.

The correlation coefficients between the quantitative traits were calculated according to Adler and Rosller (1961).

3.5.3. Estimating phenotypic and genotypic correlation coefficients

The phenotypic and genotypic correlation coefficients for the traits measured were estimated using PROC CANDISC procedure of SAS software following the variance and covariance components (Singh and Chaudhary, 1985; Sharma, 1998). Their significance was tested using the formula suggested by Robertson (1959), using the t- table at (v-2) degrees of freedom at 5% and 1% level of significance; v is the number of varieties (treatments) used in the study.

3.5.4. Cluster Analysis

Cluster analysis was made using SAS Software version 9.1.3. Principal component analysis (PCA) is made using the MINTAB statistical computer package, version 14.00.Following Sneath and Sokal (1973), record of all the quantitative traits were pre-standardized to means of zero and variance of unit to avoid bias due to differences in measurement scales. Un-weighted Pair Group Methods with

Arithmetic-average (UPGMA) based average linkage method of agglomerative hierarchical clustering was made for the genotypes. Appropriate 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 D^2 statistics (Mahalanobis, 1936) was calculated as follow:

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

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 will be 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.

4. RESULTS AND DISCUSIONS

4.1. Results

4.1.1. Analysis of variance (ANOVA)

Analyses of variance revealed a statistically significant differences ($P<0.05$) for all the quantitative traits considered except leaf length and pod width which showed a non-significant variation (**Table 2**). Replication showed a non-significant variation for all the traits considered except three such as internodes length, plant height to the first podding nod and number of branches per plant that showed a significant ($P<0.05$) variation. Block effect revealed a non-significant variation for all the traits considered. Similarly, the effects of block within replication (block replication interaction) showed a non-significance variation for most of the quantitative traits considered except four traits: economic growth rate ($p<0.01$), plant length, number of seeds per plant, number of seeds per pod and harvest index ($p<0.05$).

Among the traits considered, more than half scored a high (>0.8) coefficient of genetic determination (R^2).Leaf length and plant heights revealed the highest (each 0.93) record. The lowest R^2 (0.54) was recorded in leaf length. Similarly, the coefficients of variation (CV) seem moderate and within the acceptable range except in number of branches per plant (***NBPPl***), seed production efficiency (***SPE***), and seed yield per plot (***SYP***) (each nearly 25%) (***Table2***).

Table 2: Analysis of Variance (ANOVA) for the18 faba bean genotypes evaluated using the22 morphological traits

Variables	Rep (**2**)[a]	Block(**1**)	Block(Rep) (**2**)	Trt (**17**)	MSE (**40**)	CV (%)	R^2	Mean
LL	1.63	0.79	2.07	2.39	1.44	14.95	0.54	8.03
LW	0.09	0.03	0.02	0.98***	0.09	7.04	0.88	4.16
LA	3.94	3.12	3.66	93.58***	6.01	10.01	0.91	24.48
LAI	341.02	15.25	1031.69	7319.34***	739.16	14.45	0.86	188.17
PL	0.26	0.05	0.84***	2.09***	0.14	5.17	0.91	7.29
PW	0.00	0.00	0.00	0.07	0.00	4.24	0.93	1.36
IL	0.35*	0.05	0.08	0.23***	0.08	5.92	0.64	4.91
PHFN	20.01*	2.02	12.96	24.51***	4.21	6.56	0.79	31.27
PH	12.92	1.86	4.35	330.01***	15.43	3.70	0.93	106.20
NBPPl	0.57*	0.26	0.09	0.20*	0.12	25.98	0.59	1.31
NPPPl	10.94	0.19	9.55	52.27***	4.76	8.88	0.87	24.57
NSPPl	22.82	9.40	141.83*	409.57***	32.18	9.73	0.89	58.29
NSPPod	0.03	0.00	0.05*	0.10***	0.01	4.81	0.82	2.37
DTF	0.46	0.13	3.72	4.98**	1.73	2.36	0.66	55.69
DTM	1.80	0.28	0.79	2.81***	0.68	0.68	0.73	121.52
SFP	0.50	0.03	5.83	8.33***	2.38	2.35	0.70	65.83
SPE	35680.03	829302.92	1100406.34	2415860.17***	322366.78	25.88	0.84	2194.18
TSW	3093.61	3813.46	7234.93	25096.25***	3266.97	9.12	0.83	626.62
EGR	28.40	102.30	287.91**	651.24***	62.23	14.11	0.87	55.92
BMPP	294777.20	1608507.81	2024246.15	5315183.26***	878764.90	19.31	0.81	4855.32
SYPP	34220.80	319257.10	415870.69	974169.34***	132977.49	24.06	0.84	1515.55
HI	0.94	2.91	17.94*	66.43***	5.12	7.55	0.89	29.96

*[a] number in bracket showed degree of freedom*** = Highly significant (p<0.001),** = Highly significant (p<0.01),* =Significant (p<0.05), numbers with outs inscribes = Non-significant, CV = Coefficient of variation ,R^2 =coefficient of determination, LL=leaf width ,LA=leaf area ,LAI=leaf area index ,PL=pod length ,PW=pod width ,IL=inter nodes length ,PHFN=plant height to first nodes, NBPPl =number of branch per plant, Pl = Pod length, PW = Pod width, NPPPL = Number of pods per plant, NSPPL= Number of seed per plant, NSPPod = Number of seed per pod, DTF = Days to flowering, DTM = Days to maturity, SFP = Seed filling period, SPE = Seed production Efficiency, TSW =Thousand seed weight, EGR=economic growth rate, BMPP=biomass weight per plot, SYPP = Seed yield per plot, HI = Harvest index*

4.1.2. Estimation of variance components

4.1.2.1. Phenotypic and genotypic variances and coefficient 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 0.03in pod width to 2567959.90in biomass per plot. In the same manner, δ^2g ranged from 0.02 in pod width to 1695799.30in biomass per plot. Likewise, estimates of both PCV (0.98% to 47.57%) and GCV (0.70% to 39.9%) showed a wide range of variations. In this regard, PCV ranged from 0.98% in days to maturity to 47.57% in seed production efficiency. Likewise, estimate of GCV score ranged from 0.70% in days to maturity to 39.90% in seed production efficiency. Leaf width, leaf area, leaf area index, number of pods per plant, number of seeds per plant, seed production efficiency, thousands seed weight, economic growth rate, biomass per plot, seed yield per plot and harvest index scored a higher estimate of both PCV and GCV(Table3). In contrast, leaf length and number of branches per plant scored higher PCV estimate. In general, PCV estimate was slightly higher than their corresponding GCV values in all the traits. ***(Table3***).

4.1.2.2. Heritability in broad sense and genetic advance as a percent of mean

Estimates of heritability in broad sense and genetic advance as a percent of mean for the tested genotypes using the 22 quantitative traits are presented in***Table3***.Accordingly,estimate of the Heritability in broad sense (H^2%) ranged from 18.57% (in number of branches per plant) to 88.72% (in plant length). In this regard, five traits: leaf area (84.49%), pod length (83.66%), pod width (88.10%), plant height (88.72%) and harvest index (80.52%) scored a sufficiently higher heritability estimate. Significant number of the traits considered: leaf width (79.64%), leaf area index (77.24%), plant height to the first nodes (61.27%), number of pod per plant (77.09%), number of seed per plant (79.36%), number of seed per pod (67.47%), seed production efficiency (70.36%), thousands seed weight (69.56%), economic growth rate (75.80%), biomass weight per plot (66.04%),seed yield per plot (69.93%),dates to flowering (40.48%), dates to maturity (51.52%) and seed filing period (48.02%) scored moderately higher to medium heritability estimates. The remaining three traits: leaf length (18.96%), inter nodes length (33.37%) and number of branches per plant (18.57%) scored a lower estimate.

Estimates of genetic advance (GA) among the traits (***Table3***)revealed a wider range of variation (0.14 in number of branches per plant to 2175.72 kg/ha in biomass weight per plot).Genetic advance as percent of mean (GAM) also showed a wide range of variation(1.03% in days to maturity to 68.82% in seed production efficiency) (***Table 3***).A relatively high genetic advance as percent of mean was observed in leaf area (42.94%), leaf area index (47.24%), seed production efficiency (68.82%), economic growth rate (44.92%), biomass weight per plot (44.81%) and seed yield per plot (63.04%).Conversely, the lower estimate was recorded in leaf length (6.43%), inter nodes length (4.95%), dates to flowering (2.53%), dates to maturity (1.03%) and seed filing period (3.22%).

Table 3: Variance components for the 22 quantitative traits evaluated using the 18faba bean genotypes

Traits	MSg	MSe	Trait Mean	δ^2e	δ^2g	δ^2p	GCV%	PCV%	H^2%	GA	GAM
LL	2.39	1.44	8.03	1.42	0.33	1.76	7.18	16.50	18.96	0.52	6.43
LW	0.98	0.09	4.16	0.08	0.32	0.40	13.51	15.13	79.64	1.03	24.78
LA	93.58	6.01	24.48	5.68	30.93	36.61	22.72	24.72	84.49	10.51	42.94
LAI	7319.34	739.16	188.17	713.04	2419.80	3132.84	26.14	29.75	77.24	88.89	47.24
PL	2.09	0.14	7.29	0.14	0.72	0.86	11.63	12.71	83.66	1.59	21.87
PW	0.07	0.00	1.36	0.00	0.02	0.03	11.23	11.96	88.10	0.30	21.67
IL	0.22	0.08	4.91	0.08	0.04	0.13	4.17	7.22	33.39	0.24	4.95
PHFN	24.51	4.21	31.27	4.29	6.78	11.07	8.33	10.64	61.27	4.19	13.40
PH	330.01	15.43	106.20	14.29	112.43	126.72	9.98	10.60	88.72	20.53	19.34
NBPPl	0.20	0.12	1.31	0.12	0.03	0.14	12.49	28.98	18.57	0.14	11.06
NPPPl	52.27	4.76	24.57	4.69	15.80	20.50	16.18	18.43	77.09	7.18	29.21
NSPPl	409.57	32.18	58.29	32.19	123.78	155.96	19.09	21.43	79.36	20.38	34.96
NSPPod	0.10	0.01	2.37	0.01	0.03	0.04	6.93	8.43	67.47	0.28	11.70
DTF	4.98	1.73	55.69	1.70	1.16	2.86	1.93	3.03	40.48	1.41	2.53
DTM	2.81	0.68	121.52	0.68	0.73	1.41	0.70	0.98	51.52	1.26	1.03
SFP	8.33	2.38	65.83	2.39	2.21	4.60	2.26	3.26	48.02	2.12	3.22
SPE	2415860.17	322366.78	2194.18	322939.50	766612.00	1089551.50	39.90	47.57	70.36	1509.99	68.82
TSW	25096.25	3266.97	626.62	3295.40	7530.10	10825.50	13.85	16.60	69.56	148.80	23.75
EGR	651.24	62.23	55.92	62.89	196.94	259.83	25.10	28.83	75.80	25.12	44.92
BMPP	5315183.26	878764.90	4855.32	872160.60	1695799.30	2567959.90	26.82	33.00	66.04	2175.72	44.81
SYPP	974169.34	132977.49	1515.55	132771.30	308749.00	441520.30	36.66	43.84	69.93	955.33	63.04
HI	66.43	5.12	29.96	5.10	21.09	26.19	15.33	17.08	80.54	8.47	28.28

MSg= mean of squares of genotype; MSe= mean of square error;δ^2e = variance due to environment;δ^2g = genotypic variance;δ^2p = phenotypic variance; GCV= genotypic coefficient of variation; PCV = phenotypic coefficient of variation;H^2 (%) = Broad sense Heritability; GA = Genetic Advance ;GAM = Genetic advance as per cent of mean

4.1.3. Analysis of correlation coefficients

Analysis of pair wise correlation coefficients in the 22 morphological traits was used to find out the inter-relationship between the studied pair of traits (Table 4). The result indicated that , seed yield per hectare, an important agronomic trait showed a highly significant ($p<0.001$) positive genotypic correlation with harvest index (0.87), biomass weight per hectare (0.10), seed production efficiency (0.10), leaf area index (0.85), leaf width and leaf area with the same recorded (0.81). In addition, seed yield per hectare showed highly significant ($p<0.01$) positive genotypic correlation with seed filing period (0.74), number of branches per plant (0.70) and plant height (0.68).In contrast, it showed highly significant ($p<0.01$) negative genotypic association with days to 50% flowering(-0.76). In the same way, it revealed a significant ($p<0.05$) positive genotypic correlation with number of seed per pod (0.49), plant height to the first podding node (0.58),pod length (0.60) and leaf length (0.54).In general, it showed a stronger genetic correlation coefficient ($r>0.5$) with ten quantitative traits. Similarly, seed yield per hectare showed a highly significant ($p<0.001$) positive phenotypic correlation with harvest index(0.86), biomass weight per plot (0.97),seed production efficiency (0.10), seed filing period (0.58), number of seed per pod (0.49), number of branches per plant (0.50), plant height (0.62), pod width (0.51),leaf width (0.69), leaf area (0.71), leaf area index (0.80).On the other hand, it showed a highly significant ($P<0.001$) negative phenotypic correlation with day to 50% flowering (-0.63).In general, it showed a stronger correlation ($r>0.5$)with eight quantitative traits(***Table 4***).

Table 4. Estimates of pairwisegenotypic (**above diagonal**) and phenotypic (**below diagonal**) correlation coefficientsinthe 22 quantitative traits considered to study the 18 Ethiopian faba bean genotypes

Variable	**LL**	**LW**	**LA**	**LAI**	**PL**	**PW**	**IL**	**PHFN**	**PH**	**NBPPl**	**NPPPl**
LL	1	0.57*	0.65**	0.66**	0.46	0.16	-0.04	0.31	0.63	0.53**	-0.12
LW	0.38**	1	0.96***	0.94***	0.63**	0.53*	0.22	0.45	0.62**	0.62**	-0.04
LA	0.44**	0.95***	1	0.99***	0.67**	0.45	0.19	0.53*	0.71**	0.58*	-0.09
LAI	0.48**	0.87***	0.94***	1	0.70**	0.48*	0.22	0.55*	0.71**	0.66**	-0.06
PL	0.35*	0.53***	0.59***	0.61***	1	0.60**	0.15	0.36	0.47*	0.52*	0.01
PW	0.08	0.48**	0.42**	0.45**	0.54***	1	0.39	0.12	0.32	0.50*	-0.01
IL	-0.13	0.24	0.20	0.18	0.03	0.29*	1	0.22	0.13	0.36	0.52*
PHFN	0.24	0.34*	0.42**	0.43**	0.34*	0.09	-0.01	1	0.69*	0.19	-0.30
PH	0.40**	0.57***	0.67***	0.68***	0.44**	0.31*	0.08	0.60***	1	0.27	-0.26
NBPPl	0.39**	0.33*	0.33*	0.41**	0.33*	0.32*	0.17	0.05	0.16	1	0.37
NPPPl	-0.08	-0.04	-0.10	-0.07	-0.03	-0.04	0.34*	-0.28*	-0.22	0.30*	1
NSPPl	-0.03	0.06	0.00	0.05	0.11	0.10	0.33*	-0.17	-0.14	0.35**	0.92***
NSPPod	0.11	0.24	0.22	0.31*	0.37**	0.33*	0.08	0.21	0.13	0.21	0.08
DTF	-0.58***	-0.49***	-0.50***	-0.56***	-0.29*	-0.45**	-0.09	-0.14	-0.51***	-0.38**	0.03
DTM	0.12	0.21	0.24	0.15	0.29*	0.14	0.39**	0.11	0.05	0.22	0.34*
SFP	0.53***	0.50**	0.53***	0.53***	0.39**	0.43**	0.29**	0.17	0.43**	0.43**	0.17
SPE	0.45**	0.70***	0.73***	0.81***	0.50***	0.52***	0.27*	0.41**	0.64***	0.52***	0.12
TSW	0.19	0.34*	0.33*	0.37**	0.52***	0.58***	0.12	-0.15	0.07	0.36**	0.20
EGR	0.04	0.21	0.16	0.21	0.32*	0.36**	0.30*	-0.22	-0.09	0.44**	0.76***
BMPP	0.40**	0.67***	0.70***	0.79***	0.50**	0.50***	0.25	0.51***	0.67***	0.47**	0.07
SYPP	0.41**	0.69***	0.71***	0.80***	0.50**	0.51***	0.25	0.43**	0.62***	0.50***	0.11
HI	0.32*	0.59***	0.58***	0.64***	0.37**	0.48**	0.13	0.20	0.39**	0.48**	0.08

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

Table4. Continued…

Variable	NSPPl	NSPPod	DTF	DTM	SFP	SPE	TSW	EGR	BMPP	SYPP	HI
LL	-0.10	-0.07	-0.65**	0.12	0.56*	0.57*	0.19	-0.00	0.60	0.54*	0.34
LW	0.10	0.25	-0.63**	0.18	0.58*	0.81***	0.40	0.25	0.79***	0.81***	0.69**
LA	0.01	0.22	-0.68**	0.25	0.65**	0.82***	0.36	0.17	0.79***	0.81***	0.66**
LAI	0.05	0.28	-0.71**	0.25	0.68**	0.86***	0.39	0.22	0.84***	0.85***	0.69**
PL	0.16	0.42	-0.45	0.40	0.57*	0.60**	0.64**	0.40	0.60**	0.60*	0.41
PW	0.14	0.38	-0.60**	0.18	0.55*	0.60**	0.74**	0.50	0.60*	0.57	0.53
IL	0.54*	0.21	-0.25	0.51*	0.47*	0.45	0.19	0.48*	0.47	0.44	0.25
PHFN	-0.16	0.28	-0.23	0.13	0.25	0.55*	-0.16	-0.20	0.65**	0.58*	0.32
PH	-0.166	0.13	-0.67**	0.11	0.57*	0.70**	0.06	-0.12	0.74**	0.68**	0.42
NBPPl	0.41	0.22	-0.64**	0.34	0.68**	0.71*	0.53*	0.55*	0.68**	0.70**	0.63**
NPPPl	0.93***	0.15	0.06	0.45	0.21	0.09	0.20	0.76**	0.06	0.08	0.02
NSPPl	1	0.50*	-0.00	0.45	0.25	0.26	0.34	0.89***	0.25	0.26	0.17
NSPPod	0.46**	1	-0.11	0.16	0.18	0.45	0.46	0.59**	0.47*	0.49*	0.42
DTF	-0.08	-0.23	1	-0.13	-0.83***	-0.81***	-0.42	-0.18	-0.72**	-0.76**	-0.71**
DTM	0.34*	0.09	-0.08	1	0.66**	0.33	0.48*	0.53*	0.32	0.29	0.09
SFP	0.25	0.23	-0.83***	0.62***	1	0.80***	0.59**	0.43	0.72**	0.74**	0.58*
SPE	0.30*	0.47**	-0.71***	0.20	0.67***	1	0.45	0.40	0.97***	0.10***	0.86***
TSW	0.31	0.38**	-0.33*	0.35*	0.45**	0.44**	1	0.72**	0.37	0.41	0.44
EGR	0.87***	0.51***	-0.16	0.36**	0.33*	0.42**	0.72***	1	0.36	0.39	0.34
BMPP	0.26	0.47**	-0.58***	0.16	0.55***	0.10***	0.38**	0.37**	1	0.10***	0.75**
SYPP	0.31*	0.49***	-0.63***	0.16	0.59***	0.10***	0.42**	0.43**	0.97***	1	
HI	0.24	0.43**	-0.61***	0.02	0.50***	0.84***	0.42**	0.38*	0.71***	0.86***	1

*Numbers with no superscript = non-significant; * (significant at p<0.05); ** (highly significant at p<0.01); *** (highly significant at p<0.001) LL=leaf width ,LA=leaf area ,LAI=leaf area index ,PL=pod length ,PW=pod width ,IL=inter nodes length ,PHFN=plant height to first nodes, NBPPl =number of branch per plant, Pl = Pod length, PW = Pod width, NPPPL = Number of pods per plant, NSPPL= Number of seed per plant, NSPPod = Number of seed per pod, DTF = Days to flowering, DTM = Days to maturity, SFP = Seed filling period, SPE = Seed production Efficiency, TSW =Thousand seed weight, EGR=economic growth rate, BMPP=biomass weight per plot, SYPP = Seed yield per plot, HI = Harvest index*

4.1.4. Principal components analysis (PCA)

Estimate of the relative contributions of the traits to the principal components were conducted using standardized data. The first six principal components (Eigen value ≥ 0.94) accounted for 90.2% of the total variation (***Table5*)**.The first principal axis (PC1) accounted for 49.4% of the total variance and this variation were contributed by traits: leaf width (0.259), leaf area (0.263), leaf area index (0.274), plant height (0.205), number of branches per plant (0.234), number of seed per pod (0.134), days to 50% flowering (-0.243),seed filing potential (0.255), seed production efficiency (0.294), biomass weight per plot (0.285), seed yield per plot (0.289) and harvest index (0.240). The second PCs accounted for 18.1% of the total variation and differentiated among the genotypes on the basis of plant height (-0.262), thousand seed weight (0.222), number of pods per plant (0.425), number of seed per plant (0.433) and economic growth rate (0.424). The third PC axis contributed 7.1% of the total variation with larger contributing factor loadings from pod width (0.336), inter nodes length (-0.376), plant height to the first podding nodes (-0.414), number of pod per plant (-0.251) and thousand seed weight (0.494).The fourth PC axis accounted for 6.4% of the total variation and differentiated treatment on the bases of internodes length (-0.376), leaf length (0.370), plant height to the firs podding nodes (-0.285), number of seed per pod (-0.615), days to maturity (0.267), seed filing period (0.319) and harvest index (0.387). The fifth PC axis accounted for 4.9% of the total variation and traits that caused this variation were pod length (0.413), plant height to the firs podding nodes (-0.273), number of branches per plant (0.238), days to 50% flowering (0.239),days to maturity (0.565) and harvest index (0.387).The sixth PC axis accounted for 4.3% and the source of variation loadings were leaf width (0.203), leaf length (0.323), leaf area (0.214), leaf area index (0.213), days to 50% flowering (0.263),pod width (-0.419), internodes length (-0.483) (***Table 6***).

Table 5.Eigen values, proportion and cumulative variation of the six principal axes

Eigen value	10.875	3.980	1.555	1.418	1.081	0.940
Proportion	0.494	0.181	0.071	0.064	0.049	0.043
Cumulative	***0.494***	***0.675***	***0.746***	***0.810***	***0.860***	***0.902***

Table 6. Principal components (PC) analysis for the 22 quantitative traits used in the present study

Variable	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
LL	0.185	-0.194	0.012	0.370	0.029	0.323
LW	0.259	-0.116	0.039	-0.013	0.061	0.203
LA	0.263	-0.156	-0.001	0.041	-0.039	0.214
LAI	0.274	-0.138	-0.005	0.021	-0.013	0.213
PL	0.221	0.009	0.231	-0.070	-0.413	0.231
PW	0.202	0.075	0.366	-0.148	-0.033	-0.419
IL	0.132	0.239	-0.376	0.032	-0.032	-0.483
PHFN	0.148	-0.233	-0.414	-0.285	-0.273	-0.008
PH	0.205	-0.262	-0.181	0.020	-0.144	-0.060
NBPPl	0.234	0.112	0.056	0.202	0.238	0.133
NPPPl	0.041	0.425	-0.251	0.198	0.168	0.188
NSPPl	0.088	0.433	-0.216	-0.050	0.132	0.221
NSPPod	0.134	0.176	0.031	-0.615	-0.073	0.138
DTF	-0.243	0.106	-0.134	-0.224	-0.239	0.263
DTM	0.126	0.244	-0.153	0.267	-0.565	-0.069
SFP	0.255	0.056	0.016	0.319	-0.134	-0.238
SPE	0.294	-0.033	-0.099	-0.061	0.115	-0.081
TSW	0.177	0.222	0.494	-0.011	-0.199	-0.042
EGR	0.145	0.424	0.089	-0.065	0.024	0.152
BMPP	0.285	-0.053	-0.170	-0.116	0.046	-0.037
SYPP	0.289	-0.035	-0.118	-0.129	0.140	-0.050
HI	0.240	-0.026	0.075	-0.170	0.387	-0.103

LL=leaf width ,LA=leaf area ,LAI=leaf area index ,PL=pod length ,PW=pod width ,IL=inter nodes length ,PHFN=plant height to first nodes, NBPPl =number of branch per plant, Pl = Pod length, PW = Pod width, NPPPL = Number of pods per plant, NSPPL= Number of seed per plant, NSPPod = Number of seed per pod, DTF = Days to flowering, DTM = Days to maturity, SFP = Seed filling period, SPE = Seed production Efficiency, TSW =Thousand seed weight, EGR=economic growth rate, BMPP=biomass weight per plot, SYPP = Seed yield per plot, HI = Harvest index

The relative intensity of contribution of each component to the overall diversity in the 18 Ethiopian faba bean genotypes was presented n ***Figure 1***. There was a sharp decline in pattern and contribution from PC1 to PC2 and then a slight decline from PC2 to PC3and onwards. This shows that the morphological traits that cause variation in the first three PC's (PC1 – PC3) had the greatest contribution to the overall variation in the studied faba bean genotypes.

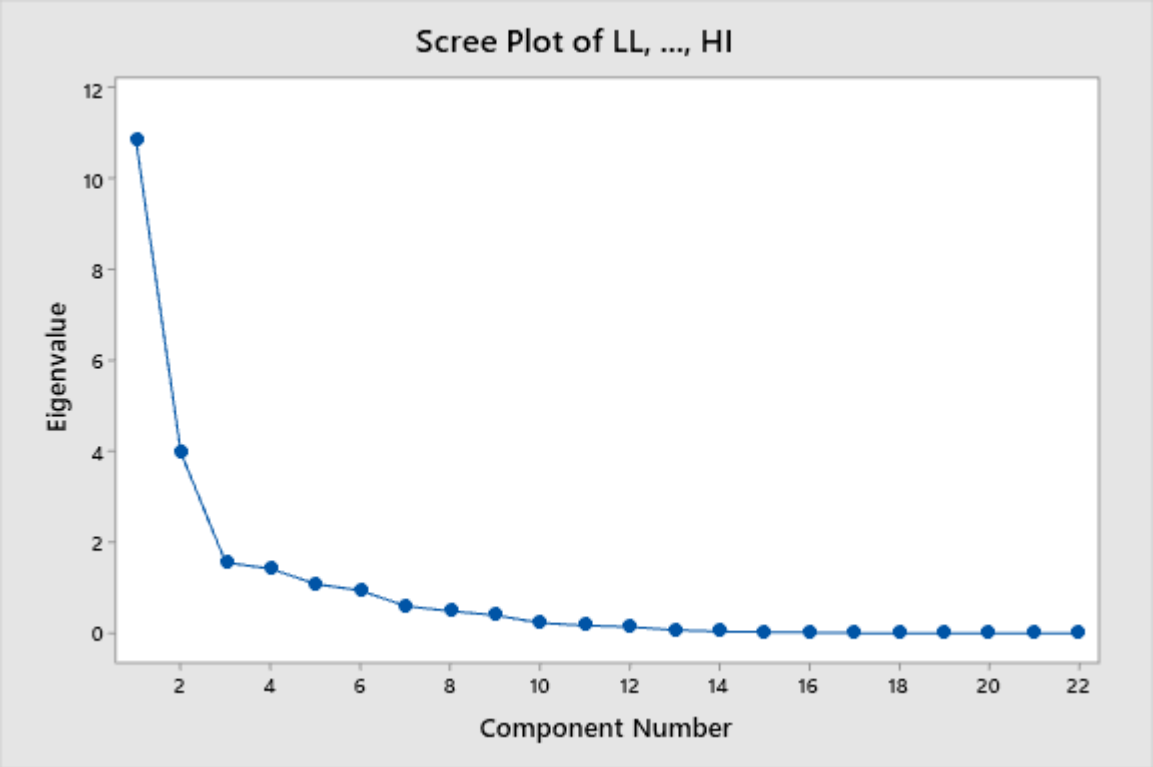

Figure 1: PCA screen plot contribution of the 22 morphological traits in each principal axis to overall variation in the genotypes.

PCA score plot roughly grouped the entire genotypes into four clusters (C1-C4) (***Figure 2***). Each of the four clusters consisted nearly equal number of genotypes. Cluster 1(C1) consisted of Hcahalu, Gora, Ashebeka, numan and didea. PC2 consisted of local seed, Gebelcho, Tosha and Mosisa. The third PCs consists Degaga, Shalo, Cs-20 DK, Alosha, Moti and Tumsa.The fourth PCs contained Dosha, Moyben, and Weleki genotypes.

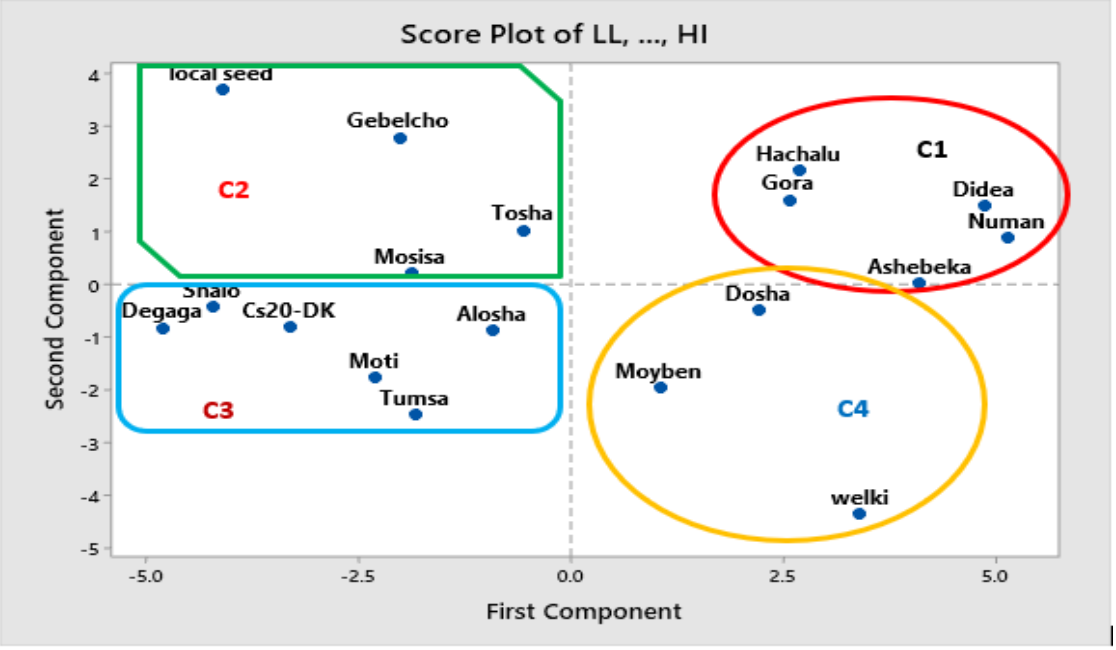

Figure 2: PCA score plot of relative position and distribution of the studied Ethiopian faba bean genotypes

PCA loading plot again revealed a strong and positive association among most of the traits considered except days to 50% flowering (DTF) that showed a negative association with almost all the traits (***Figure3).***

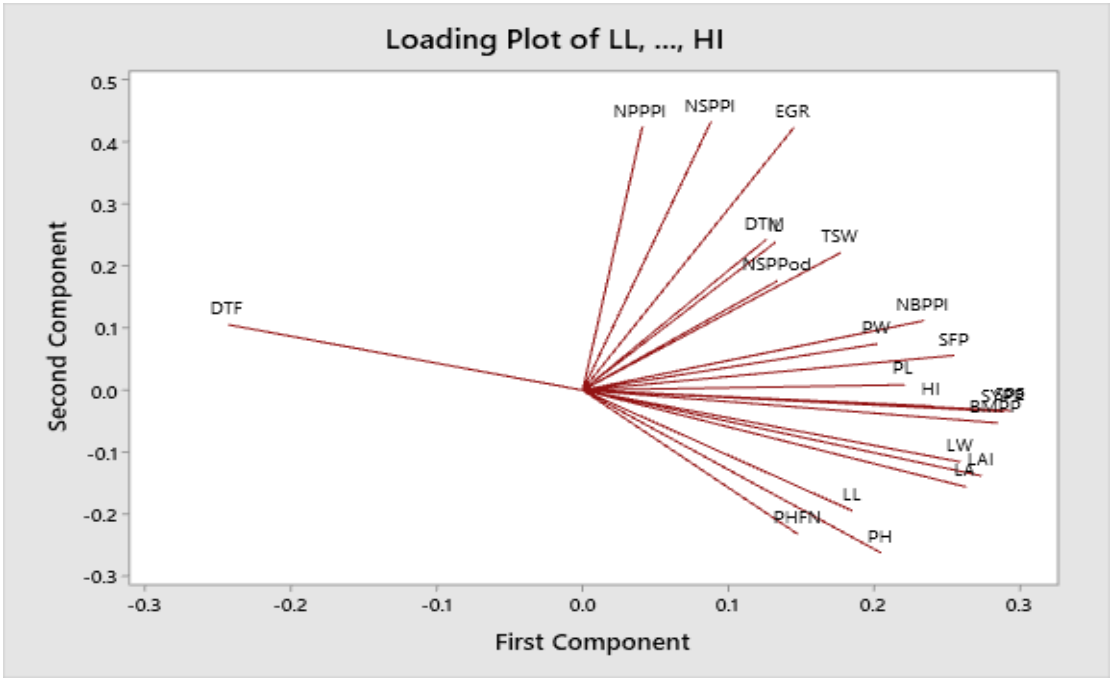

Figure 3: PCA loading plot of relative magnitude of correlation among the 22 traits considered

PCA bi plot revealed that the genotypes were evenly distributed in principal component axis. All the considered traits had strong and positive correlation to each other to the contribution of variation except days to 50% flowering which is negatively correlated to the traits and positive correlation to number of pods per plant (***Figure4).***

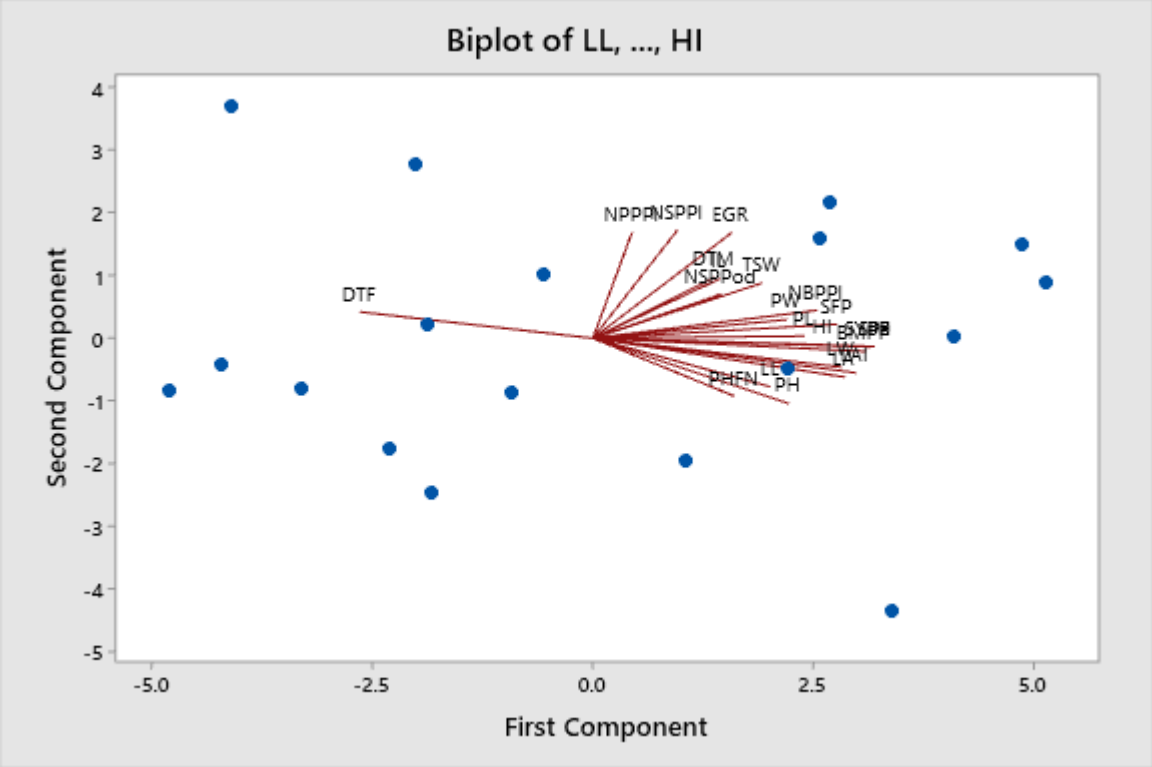

Figure 4: PCA bi plot of distribution of genotype and their correlation with the morphological traits

4.1.5. Cluster analysis based on mean values of the traits considered

The cluster analysis performed by using the 18 genotypes' mean performances evaluated using the 22 quantitative traits grouped the genotype into six major clusters (**Figure 5**; **Table7**).

Cluster I is monophyletic and consisted only one genotype (local seed). The highest mean value was contributed by number of pods per plant (32.40).Cluster II is consisted three genotypes and accounted closer to 16.67%of the total samples. The cluster holds the highest mean value for leaf length (9.41), leaf area (34.26cm^2), plant height to the first podding nodes (37.53cm), plant height (125.47cm), number of seed per plant (82.87), days to maturity (123.33days), seed

production efficiency (3580.55), economic growth rate (82.23), biomass weight (7187.33kg ha^{-1}) and seed yield(2358.27kg ha^{-1})

Cluster III contained four genotypes (22.22% of the total genotypes) and characterized by highest mean performance from days to 50% flowering (57.67days.Cluster IV consisted of five genotypes which is highest number of genotypes per cluster and accounts about 27.78% of the total samples. It was characterized by high values for harvest index (38.42) and low mean value from plant height to the first podding nodes (26.60cm), number of branches per plant (0.93), number of seed per pod (2.11), number of seed per plant (17.47) and seed filing period (63.67).Cluster V consisted of two genotypes.

Cluster VI consisted of three genotypes and characterized by high in mean values leaf area (34.52cm^2), leaf area index (275.60), pod length (8.53cm), inter nodes length (5.34), seed filing period (70.00) and thousands seed weight (838.79).

Table.7. Grouping of the 18 faba beans genotypes based on Mahalanobis (D^2) distance were Calculated using the 22 trait's contribution in each genotype to the clusters

Cluster	Number of treatments (trt) with in Cluster	Name of genotypes
I	1	Local seed
II	3	Welki, Didea, Hachalu
III	4	Cs20DK, Moti,Tumsa,Gebelcho
IV	5	Tosha, Mosisa, Alosha,Dosha, Moyben
V	2	Shalo, Degage
VI	3	Ashebeka, Numan, Gora

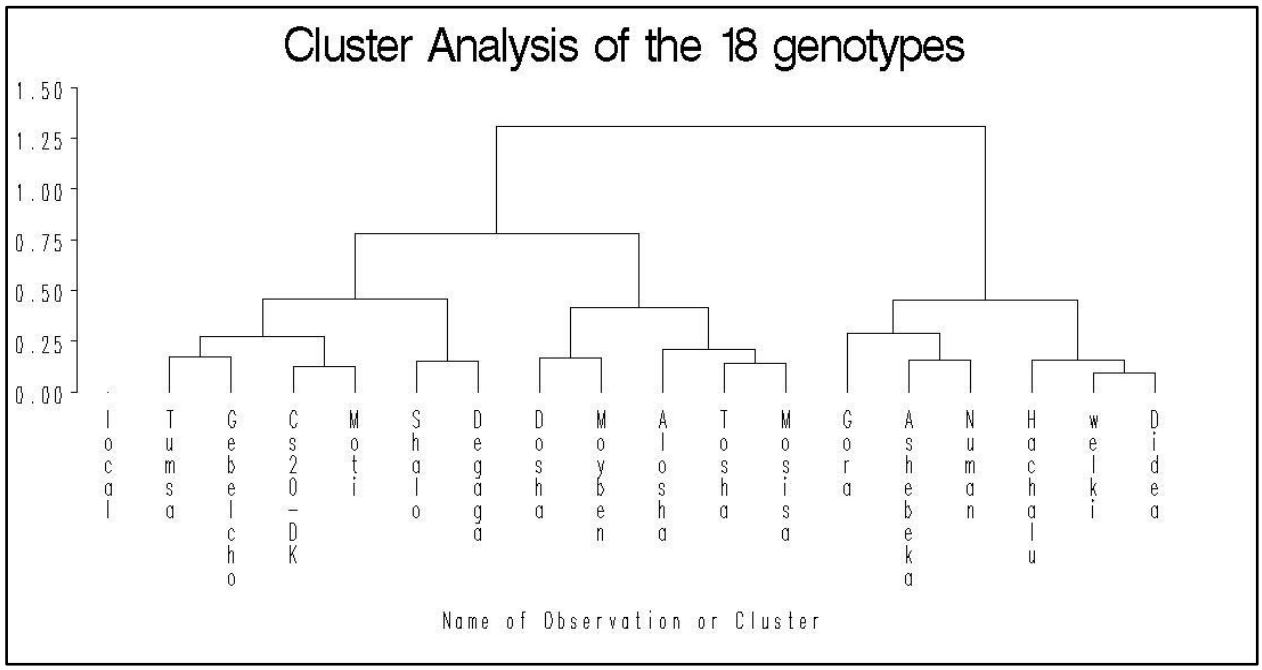

Figure 5: Dendrogram of the18 faba bean genotypes constructed using mean performance of the 22 quantitative traits.

Table 8: Genotypes under each cluster and contribution of the traits mean performance to each genotype in the cluster grouping.

Trt	LL	LW	LA	LAI	PL	PW	IL	PHFN	PH	NBPPl
local	6.83	3.24	16.06	105.27	6.83	1.19	5.10	28.33	91.53	1.07
Welki	9.41	5.19	34.26	267.65	7.02	1.33	5.16	37.53	125.47	1.47
Didea	9.38	4.58	30.28	254.79	8.44	1.28	5.23	33.73	121.20	1.73
Hachalu	8.37	4.43	26.21	204.88	7.14	1.37	5.07	32.73	111.07	1.33
Cs20-DK	7.17	3.58	18.39	137.94	6.06	1.32	4.96	32.93	110.87	1.13
Moti	8.80	4.41	27.44	196.41	7.50	1.28	4.71	29.27	110.07	0.93
Tumsa	7.91	4.02	22.60	176.00	7.73	1.27	4.22	33.20	112.20	1.20
Gebelcho	7.10	4.00	20.31	151.66	5.97	1.30	5.02	29.00	83.13	1.47
Tosha	7.05	4.37	21.86	152.05	7.17	1.48	4.96	27.53	99.93	1.20
Mosisa	7.39	3.46	18.35	136.78	6.91	1.29	5.02	32.07	99.47	1.27
Alosha	8.30	4.17	24.49	193.84	7.67	1.36	4.63	32.53	99.60	1.33
Dosha	9.08	4.64	29.77	242.08	7.45	1.36	4.75	28.53	103.80	1.67
Moyben	8.87	3.92	24.66	185.53	7.47	1.39	4.79	33.53	117.00	1.07
Shalo	7.62	3.56	19.43	141.38	7.24	1.15	4.71	29.80	90.07	1.10
Degaga	7.22	3.20	16.72	120.03	5.11	1.20	4.68	26.60	100.80	0.93
Ashebeka	6.74	5.05	34.52	275.60	8.53	1.56	5.14	35.27	114.47	1.27
Numan	9.23	4.97	32.21	255.15	8.62	1.66	4.84	29.40	114.00	1.80
Gora	8.11	4.11	23.02	190.00	8.40	1.77	5.34	30.87	106.93	1.53

Table 8 continued…..

Trt	NSP Pod	DTF	DTM	SFP	SPE	TSW	EGR	BMPP	SYPP	HI
local seed	2.39	57.33	122.67	65.33	702.47	576.77	67.31	2500.00	509.87	20.42
Welki	2.19	54.00	121.33	67.33	3516.55	464.60	28.99	7187.50	2346.43	32.58
Didea	2.49	54.67	123.33	68.67	3580.55	654.91	74.09	7083.33	2358.27	32.88
Hachalu	2.71	55.67	121.67	66.00	3310.80	652.81	82.23	6875.00	2319.12	33.58
Cs20-DK	2.21	56.33	120.00	63.67	1306.23	504.13	43.69	3750.00	946.67	25.17
Moti	2.06	57.00	121.33	64.33	1132.96	588.70	43.18	3541.67	821.39	22.99
Tumsa	2.46	56.67	120.67	64.00	1617.49	600.47	42.02	4270.83	1199.03	27.79
Gebelcho	2.36	57.67	122.33	64.67	1535.12	684.51	69.72	3854.17	1155.22	29.85
Tosha	2.43	55.67	120.67	65.00	2188.39	650.50	61.74	4583.33	1557.74	33.84
Mosisa	2.11	56.33	122.00	65.67	1983.24	537.27	45.66	4375.00	1398.92	31.53
Alosha	2.52	56.67	120.33	63.67	1828.14	567.80	50.65	4895.83	1406.33	28.68
Dosha	2.35	53.67	120.00	66.33	2844.92	661.26	60.38	5000.00	1918.23	38.42
Moyben	2.50	54.67	122.00	67.33	2618.53	698.90	45.25	5312.50	1749.00	33.00
Shalo	2.27	57.33	121.33	64.00	856.14	597.51	44.17	2812.50	638.54	22.87
Degaga	2.21	55.67	120.67	65.00	1116.97	514.20	38.27	3020.83	787.34	25.87
Ashebeka	2.66	55.33	122.33	67.00	3376.83	714.01	63.93	6250.00	2313.91	36.88
Numan	2.24	53.00	123.00	70.00	3260.24	838.79	74.25	6041.67	2029.09	33.15
Gora	2.55	54.67	121.67	67.00	2719.63	771.98	71.02	6041.67	1824.74	29.85

4.1.6. Genetic distance between clusters

Genetic distance between the six clusters was presented in ***Table 9***. The maximum inter-cluster distance was recorded between clusters 6 and 2 (D^2=172.06) followed by clusters 5 and 2 (D^2=134.44) while, the minimum inter cluster distance was between cluster 2 and 1 (D^2=20.14). The highest intra cluster distance was observed clusters 2 and cluster 3 (4.28 in each) and the lowest intra cluster distance was recorded for in cluster 1 (2.89).

Table 9: Inter and intra (diagonal element, bold) cluster distance of the six clusters constructed for the18 faba bean genotypes using the 22 quantitative traits

CLS	1	2	3	4	5	6
1	**2.89**					
2	20.14	**4.28**				
3	49.34	91.27	**4.28**			
4	12.68	48.46	21.71	**3.46**		
5	68.75	134.44	28.77	29.03	**3.46**	
6	96.24	172.06	34.26	47.38	34.04	**3.46**

CLS = Clusters

4.2. Discussions

4.2.1. Patterns of variation in the studied genotypes

The studied genotypes revealed that statistically significant differences in most of the traits. Similar results have been reports by Alghamdi (2007), Sharifi (2014) and Ammar et al. (2015).Such significant differences among the genotypes reveal the presence of substantial variation which gives a good opportunity for further improvement through selection breeding. Some traits such as leaf length and pod width showed a non-significant variation among the genotypes indicating their less importance in improvement programs of the genotypes. The present result disagrees with that of Akash et al. (2017 who reported pod

width as essential trait for improvement of faba bean accessions. Similarly, BehailuMulugeta (2016) and Abdullah, (2018) reported number of branches per plant and thousands seed weight as an important trait in faba bean improvement program.

The effect of blocking and replication showed no significant variation among the genotypes suggesting the genetic bases of the variations and smaller environmental effects.

4.2.2. Traits mean performance, seed yield and yield associated traits

The mean performance values of the 22 morphological traits considered revealed a wide range of variation. Similar report has been made by Kumari (1996) suggesting wide variability in both phenotypic and genotypic values that are useful to identify promising genotypes for yield potential and quality. Moreover, the wide difference among the genotypes could be attributed to genetic difference and thus selection could be effective for different breeding objectives.

From among the traits considered, yield is very essential and several breeding attempts could be directed towards its improvement. In the present study, all the tested genotypes revealed a highly significant ($P<0.001$) variation. Accordingly, Didea was the best genotype with highest average seed yield of 2358.27kg/ha, followed by wolki (2346.43 kg/ha), Hachalu (2319.12kg/ha) and Ashebeka (2313.91 kg/ha). The result is in line with the reports of Yirga and Zinabu (2019), BehailuMulugeta (2016), and Kubure et al. (2016) who reported a promising higher yield in the genotypes. The result suggests stability of the genotypes in mean performances regardless of their year of release. On the contrary, Shalo (638.54 kg/ha), Degaga (787.34 kg/ha) and Moti (821.39 kg/ha) showed a lower performance unlike the report by Degife and Kiya (2017) for Moti. This decrease in yield might be attributed to environmental variants and the genotype's adaptive potential to different eco-logical conditions. Yet, there are reports suggesting lower performance of Shallo and Degaga genotypes (Girma and Haile, 2014).

4.2.3. Patterns of phenotypic and genotypic variations

Genotypic and phenotypic coefficients of variation were reported as the major tools to measure the variability that exists in a given population (Burton and Devane,1953).In this

regard, the wide range of variations in both PCV and GCV revealed importance of the most of the traits considered for selection and breeding of faba bean genotypes. The slightly higher PCV estimate over the corresponding GCV values in all the traits and the relative narrow gap between them indicates the small environmental effects on the traits and once again assure the genetic base of the variations which is expected in genotypes that are under breeding scheme for so long. There have been similar reports by Yirga and Zinabu (2019) BehailuMulugeta (2016) and Kubure et al. (2016) on different According to Sharifi (2015), sufficiently high heritability value shows minimal influence of environment response on detectable traits and separate heritable components. In this regard, the present study revealed five traits such as leaf area (84.49%), pod length (83.66%), pod width (88.10%), plant height (88.72%) and harvest index (80.52%) having high broad sense heritability value (>80%). The result suggests their relative importance in further selection breeding of faba bean genotypes because of small contribution of the environment to the resulted phenotypes. Likewise, moderately high and medium broad sense heritability value for several of the traits considered reveal their relative importance in faba bean yield improvement selection. Whereas, for characters with low heritability (<40%) such as leaf length (18.96%), inter nodes length (33.37%) and number of branches per plant (18.57%) selection may be considerably difficult or impractical due to the masking effect of the environment and thus testing should be done over multiple locations and years. Similar results have been reported by Alghamdi (2007), Mellion et al. (2012) and Teferen et al.(2013) for several of the traits faba bean genotypes and varieties.

4.2.4. Trait's heritability and genetic advance

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. According to Singh (2001) heritability of a character could be quantified as very high (≥ 80%), high (≥60-79 %), moderate (>40-59%) and low (≤40%). Singh (2001), and Swarup and Chaugale (1962) reported that high heritability alone is not always an indicator of genetic gain. Moreover, higher estimates of heritability along with high genetic advance (GA) and genetic coefficient of variation (GCV) provide good scope for further improvement through phenotypic selection(Burton,1952; Singh and

Chaudhary,1985).In this view, the present study exhibited high heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean (GAM) in several quantitative traits such as leaf area, leaf area index, number of seeds per plant, seed production efficiency, economic growth rate, biomass weight per plot and seed yield per plot. This indicates that these traits are largely controlled by additive gene effects thereby, simple selection (heritability) based on these traits could be effective for improving those characters (genetic parameters).

4.2.5. Correlation analysis of yield and yield components

Pair wise correlation coefficient analysis determines the magnitude and degree of relationship between two traits. Association between traits could be due to genotypic correlation, which is attributed to linkage between genes or pleiotropic gene effect (Shafique et al., 2016), or due to environmental correlation, or both (Falconer and Maccky, 1996). With this view, the correlations between seed yield and yield components in the present study revealed a positive and highly significant association. Accordingly, the trait revealed a strong association harvest index (rg = 0.87 and rph = 0.86), biomass weight (rg=0.10 and rph=0.97), seed production efficiency (rg and rph=0.10), leaf width (rg=0.81 and rph=0.69), leaf area (rg=0.81 and rph=0.71)and leaf area index (rg=0.85 and 0.80).The result is in close agreement with Alghamdi (2007); Gemechu and Musa (2003); Ulukan et al. (2003); Abdelmula et al. (2007); Tadele et al. (2011); Sharifi (2014);and BehailuMulugeta (2016).Thus, improving those traits will simultaneously improve seed yield in faba bean or selecting genotypes of high mean value for those traits will increase the productivity of faba bean and breeders could use them as selection criterion. On the other hand, seed yield revealed a highly significant but negative association with days to 50% flowering (rg = -0.76 and rph = -0.63) suggesting that, early maturing faba bean genotypes could provide more yield.

4.2.6. Principal component's analysis (PCA)

Principal component analysis (PCA) is used to understand sources of variance among the study samples and to find out the characters which accounted more to the total variation. In

the present study, the first six principal components (Eigen value ≥ 0.94) accounted for 90.2% of the total variation among the tested faba bean genotypes suggesting nearly six genotypic groups of the entire genotypes. Several traits, for example; seed per pod, seed filing potential, seed production efficiency, biomass weight per plot etc. have contributed for the largest variation in the first principal components suggesting that selection based on these morphological traits may be effective because of the higher comparative variability.

The patterns of variation in screen plot revealed a sharp decline from PC1 to PC3showing that the morphological traits that cause variation in these PC's had the greatest contribution to the overall variation in the studied faba bean genotypes. Likewise, loading plot graph demonstrate positive association among the traits except one showing their relative importance in improving the genotypes. Score plot distinguished the genotypes into four clusters implying significant amount of genetic variability among the tested genotypes and thus good opportunity in breeding programs.

4.2.7. Patterns of grouping in the genotypes

Cluster analysis has a power to tell us how genotypes are genetically similar to each other or different from each other by grouping them into clusters. In this regard, the tested genotypes were grouped into 6 major clusters. Different members within a cluster being assumed to be more closely related with each other than those members in the other clusters in terms of the traits under consideration. The maximum inter-cluster distance was recorded between clusters 6 and 2 (D^2=172.06) and, 5 and 2 (D^2=134.44). Such a high inter cluster distances indicate that faba bean genotypes in each cluster are still bearing sufficient variability and thus selection between clusters could bring high genetic gain for the character of interest and vice versa. Consistent with results presented here, Elshafei et al. (2019) reported eighteen genetically different faba beans were evaluated for their yields and yield components during successive growing seasons and the genotypes were grouped into five diversity classes.

5. CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusions

The present study generated baseline information that could be used in slowing down some of these challenges such as lack of sustainability in the current scenario of climate change. Most of the traits considered revealed a wide range of variation in the genotypes and could be used for selection breeding and conservation program. Wide significance of the traits was once again confirmed from strong association revealed from correlation (both phenotypic and genotypic) analysis and PCA loading plot. In this regard, seed yield, one of the important traits showed a strong association with most of the traits.

With regards to the variation in the tested genotypes, they are largely governed by genetic components and are largely heritable as revealed by PCV, GCV and broad sense heritability estimates. Sufficiently high heritability value shows minimal influence of environment response on detectable traits and separate heritable component. Similarly, the high heritability coupled with seven traits; leaf area, leaf area index, number of seed per plant, seed production efficiency, economic growth rate, biomass weight per plot and seed yield per plot indicates inheritance of the traits and their being controlled by few major genes or possessed additive gene effects. Therefore, simple selection (heritability) based on these traits could be effective for improving those characters (traits) and can be used as selection criteria of high yielding genotype.

The genotypes were grouped into6 major clusters but the within and between cluster distance was sufficiently larger suggesting possibility to cross hybridize most of the genotypes for the desired traits including yield.

5.2. Recommendations

- The present study results showed existence of genetic variations among the studied faba bean genotypes and generated supportive information on the seed yield and yield correlated traits in field performance of the genotypes for breeder, researcher and farmers.
- Further research needs to be carried out at multiple locations and seasons to clearly indicate the interaction effects of those traits so that the resulting genetic variation could be sustainable and credible.
- Efficient yield product is the central objective in crop production. Thus, in order to forward deserving justification on the actual extents of genetic diversity and for promising selection targeting yield potential of the genotypes more markers such as molecular markers (DNA based)are essential.

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7. Appendices

Appendix 1. Table 1.Correlation coefficient seed yield and yield associated

Variable	LL	LW	LA	LAI	PL	PW	IL	PHFN	PH	NBPPl	NPPPl	NSPPl	NSPPod	DTF	DTM	SFP	SPE	TSW	EGR	BMPP	SYPP	HI
LL	1	0.57*	0.65**	0.66**	0.46	0.16	-0.04	0.31	0.63	0.53**	-0.12	-0.10	-0.07	-0.65**	0.12	0.56*	0.57*	0.19	-0.00	0.60	0.54*	0.34
LW	0.38**	1	0.96***	0.94***	0.63**	0.53*	0.22	0.45	0.62**	0.62**	-0.04	0.10	0.25	-0.63**	0.18	0.58*	0.81***	0.40	0.25	0.79***	0.81***	0.69**
LA	0.44**	0.95***	1	0.99***	0.67**	0.45	0.19	0.53*	0.71**	0.58*	-0.09	0.01	0.22	-0.68**	0.25	0.65**	0.82***	0.36	0.17	0.79***	0.81***	0.66**
LAI	0.48**	0.87***	0.94***	1	0.70**	0.48*	0.22	0.55*	0.71**	0.66**	-0.06	0.05	0.28	-0.71**	0.25	0.68**	0.86***	0.39	0.22	0.84***	0.85***	0.69**
PL	0.35*	0.53***	0.59***	0.61***	1	0.60**	0.15	0.36	0.47*	0.52*	0.01	0.16	0.42	-0.45	0.40	0.57*	0.60**	0.64**	0.40	0.60**	0.60*	0.41
PW	0.08	0.48**	0.42**	0.45**	0.54***	1	0.39	0.12	0.32	0.50*	-0.01	0.14	0.38	-0.60**	0.18	0.55*	0.60**	0.74**	0.50	0.60*	0.57	0.53
IL	-0.13	0.24	0.20	0.18	0.03	0.29*	1	0.22	0.13	0.36	0.52*	0.54*	0.21	-0.25	0.51*	0.47*	0.45	0.19	0.48*	0.47	0.44	0.25
PHFN	0.24	0.34*	0.42**	0.43**	0.34*	0.09	-0.01	1	0.69*	0.19	-0.30	-0.16	0.28	-0.23	0.13	0.25	0.55*	-0.16	-0.20	0.65**	0.58*	0.32
PH	0.40**	0.57***	0.67***	0.68***	0.44**	0.31*	0.08	0.60***	1	0.27	-0.26	-0.166	0.13	-0.67**	0.11	0.57*	0.70**	0.06	-0.12	0.74**	0.68**	0.42
NBPPl	0.39**	0.33*	0.33*	0.41**	0.33*	0.32*	0.17	0.05	0.16	1	0.37	0.41	0.22	-0.64**	0.34	0.68**	0.71*	0.53*	0.55*	0.68**	0.70**	0.63**
NPPPl	-0.08	-0.04	-0.10	-0.07	-0.03	-0.04	0.34*	-0.28*	-0.22	0.30*	1	0.93***	0.15	0.06	0.45	0.21	0.09	0.20	0.76**	0.06	0.08	0.02
NSPPl	-0.03	0.06	0.00	0.05	0.11	0.10	0.33*	-0.17	-0.14	0.35**	0.92***	1	0.50*	-0.00	0.45	0.25	0.26	0.34	0.89***	0.25	0.26	0.17
NSPPod	0.11	0.24	0.22	0.31*	0.37**	0.33*	0.08	0.21	0.13	0.21	0.08	0.46**	1	-0.11	0.16	0.18	0.45	0.46	0.59**	0.47*	0.49*	0.42
DTF	-0.58***	-0.49***	-0.50***	-0.56***	-0.29*	-0.45**	-0.09	-0.14	-0.51***	-0.38**	0.03	-0.08	-0.23	1	-0.13	-0.83***	-0.81***	-0.42	-0.18	-0.72**	-0.76**	-0.71**
DTM	0.12	0.21	0.24	0.15	0.29*	0.14	0.39**	0.11	0.05	0.22	0.34*	0.34*	0.09	-0.08	1	0.66**	0.33	0.48*	0.53*	0.32	0.29	0.09
SFP	0.53***	0.50**	0.53***	0.53***	0.39**	0.43**	0.29**	0.17	0.43**	0.43**	0.17	0.25	0.23	-0.83***	0.62***	1	0.80***	0.59**	0.43	0.72**	0.74**	0.58*
SPE	0.45**	0.70***	0.73***	0.81***	0.50***	0.52***	0.27*	0.41**	0.64***	0.52***	0.12	0.30*	0.47**	-0.71***	0.20	0.67***	1	0.45	0.40	0.97***	0.10***	0.86***
TSW	0.19	0.34*	0.33*	0.37**	0.52***	0.58***	0.12	-0.15	0.07	0.36**	0.20	0.31	0.38**	-0.33*	0.35*	0.45**	0.44**	1	0.72**	0.37	0.41	0.44
EGR	0.04	0.21	0.16	0.21	0.32*	0.36**	0.30*	-0.22	-0.09	0.44**	0.76***	0.87***	0.51***	-0.16	0.36**	0.33*	0.42**	0.72***	1	0.36	0.39	0.34
BMPP	0.40**	0.67***	0.70***	0.79***	0.50**	0.50***	0.25	0.51***	0.67***	0.47**	0.07	0.26	0.47**	-0.58***	0.16	0.55***	0.10***	0.38**	0.37**	1	0.10***	0.75**
SYPP	0.41**	0.69***	0.71***	0.80***	0.50**	0.51***	0.25	0.43**	0.62***	0.50***	0.11	0.31*	0.49***	-0.63***	0.16	0.59***	0.10***	0.42**	0.43**	0.97***	1	0.87***
HI	0.32*	0.59***	0.58***	0.64***	0.37**	0.48**	0.13	0.20	0.39**	0.48**	0.08	0.24	0.43**	-0.61***	0.02	0.50***	0.84***	0.42**	0.38*	0.71***	0.86***	1

Appendix 2. Table 2. Mean performance of studied traits

Trt	LL	LW	LA	LAI	PL	PW	IL	PHFN	PH	NBPPl	NPPPl	NSPPl	NSPPod	DTF	DTM	SFP	SPE	TSW	EGR	BMPP	SYPP	HI
Tumsa	7.91	4.02	22.60	176.00	7.73	1.27	4.22	33.20	112.20	1.20	18.07	44.43	2.46	56.67	120.67	64.00	1617.49	600.47	42.02	4270.83	1199.03	27.79
Gora	8.11	4.11	23.02	190.00	8.40	1.77	5.34	30.87	106.93	1.53	23.73	61.73	2.55	54.67	121.67	67.00	2719.63	771.98	71.02	6041.67	1824.74	29.85
Hachalu	8.37	4.43	26.21	204.88	7.14	1.37	5.07	32.73	111.07	1.33	30.60	82.87	2.71	55.67	121.67	66.00	3310.80	652.81	82.23	6875.00	2319.12	33.58
Cs20-DK	7.17	3.58	18.39	137.94	6.06	1.32	4.96	32.93	110.87	1.13	25.10	55.20	2.21	56.33	120.00	63.67	1306.23	504.13	43.69	3750.00	946.67	25.17
Dosha	9.08	4.64	29.77	242.08	7.45	1.36	4.75	28.53	103.80	1.67	26.00	60.87	2.35	53.67	120.00	66.33	2844.92	661.26	60.38	5000.00	1918.23	38.42
Ashebeka	6.74	5.05	34.52	275.60	8.53	1.56	5.14	35.27	114.47	1.27	23.07	59.93	2.66	55.33	122.33	67.00	3376.83	714.01	63.93	6250.00	2313.91	36.88
Gebelcho	7.10	4.00	20.31	151.66	5.97	1.30	5.02	29.00	83.13	1.47	28.00	65.93	2.36	57.67	122.33	64.67	1535.12	684.51	69.72	3854.17	1155.22	29.85
welki	9.41	5.19	34.26	267.65	7.02	1.33	5.16	37.53	125.47	1.47	19.33	76.67	2.19	54.00	121.33	67.33	3516.55	464.60	28.99	7187.50	2346.43	32.58
Moti	8.80	4.41	27.44	196.41	7.50	1.28	4.71	29.27	110.07	0.93	22.93	47.13	2.06	57.00	121.33	64.33	1132.96	588.70	43.18	3541.67	821.39	22.99
Alosha	8.30	4.17	24.49	193.84	7.67	1.36	4.63	32.53	99.60	1.33	22.73	57.13	2.52	56.67	120.33	63.67	1828.14	567.80	50.65	4895.83	1406.33	28.68
Tosha	7.05	4.37	21.86	152.05	7.17	1.48	4.96	27.53	99.93	1.20	25.27	61.40	2.43	55.67	120.67	65.00	2188.39	650.50	61.74	4583.33	1557.74	33.84
Moyben	8.87	3.92	24.66	185.53	7.47	1.39	4.79	33.53	117.00	1.07	17.47	43.60	2.50	54.67	122.00	67.33	2618.53	698.90	45.25	5312.50	1749.00	33.00
Shalo	7.62	3.56	19.43	141.38	7.24	1.15	4.71	29.80	90.07	1.10	20.93	47.27	2.27	57.33	121.33	64.00	856.14	597.51	44.17	2812.50	638.54	22.87
Mosisa	7.39	3.46	18.35	136.78	6.91	1.29	5.02	32.07	99.47	1.27	26.33	55.60	2.11	56.33	122.00	65.67	1983.24	537.27	45.66	4375.00	1398.92	31.53
Numan	9.23	4.97	32.21	255.15	8.62	1.66	4.84	29.40	114.00	1.80	27.23	61.33	2.24	53.00	123.00	70.00	3260.24	838.79	74.25	6041.67	2029.09	33.15
Didea	9.38	4.58	30.28	254.79	8.44	1.28	5.23	33.73	121.20	1.73	31.13	77.60	2.49	54.67	123.33	68.67	3580.55	654.91	74.09	7083.33	2358.27	32.88
Degaga	7.22	3.20	16.72	120.03	5.11	1.20	4.68	26.60	100.80	0.93	21.87	48.40	2.21	55.67	120.67	65.00	1116.97	514.20	38.27	3020.83	787.34	25.87
local seed	6.83	3.24	16.06	105.27	6.83	1.19	5.10	28.33	91.53	1.07	32.40	42.07	2.39	57.33	122.67	65.33	702.47	576.77	67.31	2500.00	509.87	20.42
Trait mean																						
LSD (5%)	0.90	0.44	4.20	38.83	0.67	0.11	0.24	2.30	7.78	0.26	3.14	8.75	0.14	1.16	0.79	1.44	743.13	72.09	11.33	1132.07	473.58	3.60

Appendix 3: figure 1: Stepwise experimental procedure from land preparation to harvesting of faba bean at Kulmsa agricultural research center Land Preparation and sowing (A, B), Management practice (C), Data Collection (D), Harvesting(E) and Seed Weight(F).

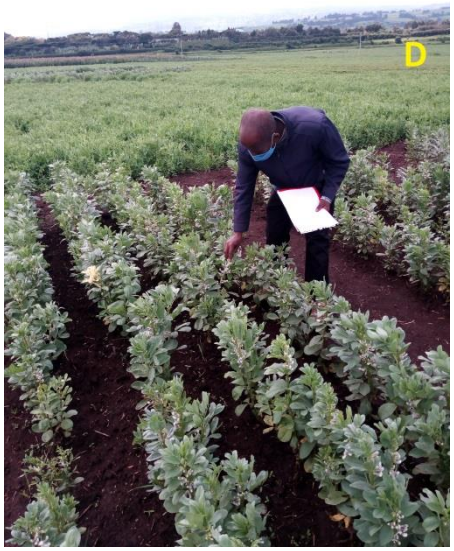

Photo By:-Zemedkun.Kassaye