



**GENETIC DIVERSITY OF FABA BEAN (*VICIA FABA* L.)
LANDRACE ACCESSIONS IN ETHIOPIA**

**BY
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DEDICATION

This thesis is dedicated to my advisor, the late Dr. Kifle Dagne and development agent worker Mr. Tesfaye Seyoum who helped me during field work but passed away by accident at the beginning of my journey.

DECLARATION

This is to certify that the dissertation prepared by **Bullo Neda Tulu**; entitled: '**GENETIC DIVERSITY OF FABA BEAN (*VICIA FABA L.*) LANDRACE ACCESSIONS IN ETHIOPIA**' and submitted in the partial fulfillment for the requirements for the Degree of Doctor of Philosophy in Biology (Applied Genetics) complies with the regulations of the University and meets the accepted standards with respect to the originality & quality.

Signature _____

Bullo Neda

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ACRONYMS AND ABBREVIATIONS

Abbreviations	Explanation
AAU	Addis Ababa University
AFLP	Amplified fragment length polymorphism
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
AZs	Administrative zones
CSA	Central statistical authority
CTAB	Cetyltrimethylammonium bromide
CV	Coefficient of variation
D ²	Squared divergence
DAP	Di-ammonium phosphate
DAPC	Discriminant analysis of principal components
DbARC	Debra Birhan Agricultural Research Center
DM	Days to 90% maturity
DMRT	Duncan's Multiple Range Test
DTF	Days to 50% flowering
EARO	Ethiopian agricultural research organization

EDTA	Ethylenediamine tetraacetic acid
EMR	Effective multiplex ratio
EtBr	Ethidium bromide
EV	Estimated variance
FAO	Food and Agriculture Organization (of the United Nations)
FAOSTAT	FAO statistics
FTC	Farmers' Training Center
GA	Genetic advance
GAM	Genetic advance as percentage of mean
GCV	Genotypic coefficient of variability
GD	Genetic diversity
Gd	Genetic distance
GI	Genetic identity
GY	Grain yield
HARC	Holeta agricultural research center
I	Shannon information index
EBI	Ethiopian Biodiversity Institute
IBPGR	International Board for Plant Genetic Resources

ICARDA	International Center for Agriculture Research in the Dry Areas
ISSR	Inter-simple sequence repeat marker
k	Selection differential
K-squared	The number of different categories squared
MCMC	Markov Chain Monte Carlo
MoA	Ministry of agriculture
MoARD	Ministry of agriculture and rural development
MSE	Mean Square of Error
NAB	Number of abundant bands
NJ	Neighbor-joining analysis
Nm	Gene flow
PAGE	Polyacrylamide gel electrophoresis
PCA	Principal Component Analysis
PCoA	Principal coordinate analysis
PCV	Phenotypic Coefficient of Variability
PhiPT	Genetic differentiation
PIC	Polymorphic information content
PVP	Polyvinylpyrrolidone

RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
SDS	Sodium dodecyl sulfate
SE	Standard error of the Mean
SRAP	Sequence-related amplified polymorphism
SNP	Single Nucleotide Polymorphism
SNNPR	South Nations and Nationalities and Peoples Region
SRAP	Sequence Related Amplified Polymorphism
SSR	Simple Sequence Repeats
TBE	Tris-borate-EDTA
TE	Tris EDTA
UBC	University of British Columbia

ABSTRACT

Faba bean is one of the most important legume species cultivated in Ethiopia for both human and animal protein source. Morphological and molecular characterization of faba bean accessions is important for future collection, conservation, and crop improvement programs. However, the genetic diversity of the Ethiopian faba bean accessions has not been comprehensively characterized. The present study was conducted to determine the genetic diversity of faba bean using morphological and ISSR markers. A total of 96 accessions including 90 landraces and six released varieties of faba bean were analyzed. Analysis of variance showed significant to very high significant differences for most of the traits. In this study phenotypic coefficient of variation, genotypic coefficient of variation, broad-sense heritability, and genetic advance as percent of mean revealed medium to high values for most traits. Traits that had a positive direct effect and positive correlation with grain yield could be used as a reliable indicator in indirect selection for higher grain yield. The D^2 analysis showed a highly significant difference ($P < 0.01$) among all intra and inter-cluster distances. Therefore, this study indicated that there is an opportunity to improve this crop through simple selection and hybridization in these accessions. Using ISSR molecular markers, the polymorphic information content, marker index, resolving power, and effective multiplex ratio showed average values of 0.32, 5.87, 7.14, and 18.34 per primer, showing high polymorphism values. The marker showed average gene diversity of 0.26, ranging from 0.15 to 0.36. The amount of polymorphism among the landrace accessions ranged from 44.91% for the Sidama population to 72.46% for the East Hararghe population, with a mean of 57.27%. AMOVA indicated 99% and 1% variation within and among populations, respectively. The current study exhibited little to moderate population differentiation and high gene flow. Both distance-based and model-based cluster analysis distinguished seven distinct

groups showing the conformity of results obtained from the study. This study exhibited high genetic diversity of collections from most of the administrative zones.

Keywords: cluster analysis, genetic advance, heritability, ISSR marker, population differentiation, principal component

1. INTRODUCTION

1.1 Background and Justification

Faba bean (*Vicia faba* L.) is an annual diploid legume ($2n = 12$) and it is a self-pollinated crop with significant levels of cross-pollination that vary greatly between cultivars (Suso *et al.*, 1996). Depending on the cultivars used, environmental factors, and the pollinating insects; the rate of out crossing ranged from 4 - 89% (Rashid and Bernier, 1994). The average degree of out crossing is about 35% (Bond and Poulsen, 1983). Faba bean is also known as the broad bean and it is a cultivated crop species belonging to the Fabaceae family (Torres *et al.*, 2006).

It is among the earliest domesticated food legumes in the world. Its domestication is believed to be around 8,000 BC in the Near East (Torres *et al.*, 2006). It is an ancient crop and numerous studies have been performed on its origin and domestication. The origin of faba bean is still in argument because archaeological remains and/or wild relatives have not yet been found (Cubero, 2011). Faba bean could not cross with its close relative *Vicia narbonensis* since it tolerates no exchange of genes and genetically isolated (Hawtin and Hebblethwaite, 1983). It is widely believed that the center of primary diversity and origin somewhere in the near and Middle East (Lawes *et al.* 1983). Vavilov (1936) discovered a primitive type of faba bean at the intersection of Himalaya and Hindu Kush, and proposed that faba bean was originated from Central Asia and then expanded westward along the mountains to Turkey, Iran, the Mediterranean, and Spain. Cubero (1974) also proposed that the primary center of origin of faba bean is in the Near East, Iraq, and Iran with four different radiations to Europe; along the North Africa coast of Spain; along the Nile to Ethiopia; from Mesopotamia to India. Vavilov also considered areas along the Mediterranean Sea and Ethiopia as the secondary centers of origin of faba bean. According to

Torres *et al.* (2006) also Ethiopia is considered to be the secondary center of the diversity of faba beans. In addition, Harlan (1969) pointed out that the secondary centers of diversity of faba beans have occurred in Afghanistan and Ethiopia. Recently, the archeological study strongly suggests that Neolithic people in Israel (the lower Galilee: Ahihud, Nahal Zippori, and Yiftah'el) first domesticated faba beans 10,000 years ago, and they were consuming as a staple food before grain began to be cultivated in the area (Caracuta *et al.*, 2015). It is believed that the crop was introduced to Ethiopia from the Middle East via Egypt around 5,000 BC, soon after its domestication (Duc *et al.*, 2010). The derivation of *Vicia faba* is not clear and its immediate ancestor is not known. That means, no wild progenitor has been found (Cubero, 1974), and successful crossing between faba bean and any other *Vicia* species has never been reported (Bond *et al.*, 1985). Nevertheless, a wide range of genetic variations still exists in the species (Lawes *et al.*, 1983). According to Muratova (1931) and Cubero (1974) based on seed characters, *Vicia faba* has been classified into four groups; major, equine, minor, and paucijuga. The large-seeded ones (major) emerged in South Mediterranean countries and China. The medium seeded types (equina) are grown throughout the Middle East, North Africa, and Australia while the small-seeded types (minor and paucijuga) are found in Ethiopia and are the favored types in North European Agriculture (Duc, 1997).

Faba bean is a globally substantial grain legume, with an annual production of 4-5 million tones worldwide in recent years (Merga *et al.*, 2019), providing the major affordable dietary source of protein to subsistence farmers and urban populations across North Africa, the horn of Africa and the Middle and Near East as well as parts of China. Thus partly compensates for the large deficit in animal protein sources (O'Sullivan and Angra, 2016). According to Muehlbauer and Tulu(1997), the whole dried faba bean seeds contain 344 calories per 100g, 10.1% moisture, 1.3g

fat, 59.4g total carbohydrate and provides a balanced diet of lysine-rich protein, carbohydrates, fiber, and phytochemicals (Burstin *et al.*, 2011) and essential amino acids (Alghamdi, 2009). The feeding value of faba bean is high and it has been considered as a meat substitute due to its high protein content of 20% to 41% (Crépona *et al.*, 2010) as compared to all other temperate and tropical pulse crops, including lentil, common bean, chickpea and pea (FAOSTAT, 2013). That is why it is called the meat of the poor. In many developing countries of Africa, Asia, and Latin America where many people cannot afford to buy meat; the faba bean is used for human nutrition, animal and poultry feed because of its high protein and other essential nutrient content (El Fiel *et al.*, 2002). Likewise, in Ethiopia, faba bean is the leading protein source for the rural people and used to make various traditional dishes (Yetneberk and Wondimu, 1994), which otherwise includes mainly cereals or root crops. It is grown primarily for its edible seeds that are used for human consumption. The mature seeds that are rich in proteins and minerals such as calcium, phosphorus as well as vitamins are consumed cooked or fresh (FAO, 2019). Yields of cereal crops following faba bean are also improved and the need for artificial nitrogen fertilizer applications is reduced for subsistence farmers (Agegnehu and Fessehaie, 2006). Chintalapati (2011) reported that faba beans maintain soil fertility, serve as fodder, a break crop to reduce cereal diseases, insect pests, and weeds. According to Marzinzig *et al.* (2018), faba bean attracts pollinators through its flowers. According to Desta (1988), faba bean can restore soil fertility through atmospheric nitrogen fixation and provides large cash for producers, and also earn foreign exchange for the country. Therefore, the crop is a good source of income for small scale farmers and fetches higher prices than cereals on the local market (Ayele and Alemu, 2006) and the country also used to earn a good share of its foreign currency from faba bean export and still

has the potential; if production is substantially improved beyond the local demand (EARO, 2000).

Ethiopia is among the major faba bean producing countries in the world ranking second next to China (FAO, 2019). In Ethiopia faba bean is mainly produced for domestic consumption and only a smaller percentage of the crop is delivered to the export market. However, still, this small portion of export volume put Ethiopia the fourth largest faba bean exporting country next to France, Australia, and the United Kingdom (FAO, 2016). In Ethiopia importance of faba bean as an export commodity increased over time; as a result, this has led to a renewed interest by farmers to increase the area under production (Sahile *et al.*, 2008). The average national yield of faba beans is about 2.1t/ha (CSA, 2018) which is very low compared to the average yield of 3.7 t/ha in major producer countries (FAOSTAT, 2017). Even though the area under production has been increased; the productivity is still very low as compared to the world average. For four decades breeders executed research on faba bean to narrow the yield gap in Ethiopia.

Faba bean breeding in Ethiopia was started in the 1950s with the prime objectives of improving grain yield, seed size, and resistance to important diseases, particularly chocolate spot (*Botrytis fabae*) (Kenehi *et al.*, 2006). In Ethiopia, previous breeding efforts developed and released, a number of improved varieties for mid and high-altitude agro-ecologies, and waterlogged vertisol areas. As a result, more than thirty-four improved faba bean varieties have been released by different agricultural research centers in Ethiopia to date. However, having all these released varieties; the national average productivity of released varieties is less than 3.5 t/ha, which is still lagging behind the crop potential 5.0 t/ha (CSA, 2014), due to several constraints. Bekele *et al.* (2006) reported the lower productivity of faba bean in Ethiopia is due to biological limitation of the crop, particularly the inherently low yielding potential of indigenous cultivars, susceptibility

to biotic and abiotic stresses such as diseases, insects, weeds, moisture deficit, high soil acidity, water logging and frost. Degago (2000) also reported the productivity of crop is far below the potential due to several yield-limiting factors such as the inherent low-yielding potential of the indigenous cultivars which is among the most productive constraints and diseases like chocolate spot, rust, and root rot and also abiotic stresses like water logging. The other factor causing the reduction in yield is a narrow genetic base in released varieties. On the other hand, the on farm and on station average yield of released faba bean varieties reaches up to 3.5 t/ha and 4.8 t/ha, respectively (National Planning Commission, 2016) indicating the existence of considerable yield gap between farmer managed and researcher managed plots. One way of confronting this challenge is with sound crop breeding programs that improve the productivity of the crop through developing varieties resistant to biotic and abiotic constraints, improving nutritional quality, and improving adaptation to different agro-ecologies. As a result, to increase the production and productivity of faba bean, identifying the variation available in the landrace materials is the first step for a successful crop improvement program. Thus, the genetic diversity in a landrace accession is important for parental selection in hybridization (Jaradat, 1991), and for planning, efficient germplasm collection, conservation, and utilization (Demissie and Bjørnstad, 1997). Hybridizations between groups with maximum genetic divergence produce higher heterosis (Singh, 1990) and desirable genetic recombination and segregation in their progeny (Chahal and Gosal, 2002).

Hence, analysis of genetic diversity of faba bean accessions is important for further improvement of yields and to impart resistance to biotic and abiotic stresses, and also to avoid genetic vulnerability by widening the genetic base of variety releases. Among different germplasm, landraces are population mixtures containing a great number of different alleles due to their

genotypic diversity and have adapted to the changes in the environmental condition of their habitat (Kuckuck *et al.*, 1991). Landrace collections are reservoirs of genetic variability and are sources of many valuable genes, especially those of adaptation. The knowledge of the genetic diversity and relationships among germplasm collections of a crop is fundamental in managing and assuring the long-term success of plant breeding programs (MA *et al.*, 2009). This available genetic diversity has not been fully exploited, even though a considerable range of variation exists within populations (Lawes *et al.*, 1983). Different reports also indicated that modern varieties reduced crop genetic diversity (Tripp,1996) and thereby causing the vulnerability of the crop to biotic and abiotic stresses and failure of their ability to evolve and adapt to ever-changing climates (Keneni *et al.*, 2012). For instance, the outbreak of Irish potato blight in Iceland in the 1940s (Cox and Large, 1960), corn blight in the U.S.A in the 1970s (Bauer, 1972), and new race development of stem rust Ug99 (Singh *et al.*, 2008) and yellow rust (Landuber *et al.*, 2016) on wheat in East Africa are some of the factors of intensification of uniform improved varieties to the farming community. Thus, the diverse landraces not only have rich gene and allele content but also can help enhance any important agricultural traits in breeding programs. The potential worth of faba bean genetic diversity in landraces could not be extensively used in improvement program due to the lack of concrete information about the genetic value contained in germplasm collections. Despite more than 2,300 faba bean accessions held in the Ethiopian Biodiversity Institute (EBI), information on the magnitude and pattern of genetic diversity are scanty at morphological and molecular level. Hence, further evaluation is required to identify the full extent of phenotypic and genetic variation within these collections. The existence of a wealth of genetic variability among landrace collections has been used either for release after selection for high yield and wide or specific adaptation or crossed with exotic materials to generate superior

genotypes. For instance, varieties such as CS20DK, NC58, Bulga-70 (coll 111/77), Wayu (Wayu 89-5), and Selale (Selale Kasim 91-13) have been nationally released directly from landrace for different recommendation domains. Keneni *et al.* (2003) indicated the existence of high genetic diversity in their study of the extent and pattern of genetic diversity among the 160 faba bean landraces collected from North Wello, South Wello, North Gonder, North Shewa and Arsi zones for morpho-agronomic traits. Mulugeta (2016) also studied genetic diversity among 32 faba bean improved varieties and pipelines using both phenotypic traits and molecular markers. However, this was not extensive and a considerable amount of accessions are left untouched and a comprehensive study on faba beans, especially on molecular markers is limited.

Hence, molecular analyses in conjunction with the morphological evaluation of germplasm are recommended since these provide complementary information and increase the resolving power of genetic diversity analyses (Gomez *et al.*, 2004). Therefore, it is necessary to identify additional genetic resources in the breeding programs by using both morphological and ISSR markers. Morphological and molecular marker studies are used in genetic diversity analysis in crop improvement programs because the genetic gain from selection depends on the extent of genetic variation. To this effect, having information on the degree of genetic diversity in faba beans is critical to design an effective breeding program.

For molecular aspects, various genetic marker systems have been used in analyzing the genetic diversity and relationships between accessions in faba bean *ex situ* germplasm collections such as restriction fragment length polymorphism (RFLP) (Van de Ven *et al.*, 1990), random amplified polymorphic DNA (RAPD) (Link *et al.*, 1995), amplified fragment length polymorphism (AFLP) (Zong *et al.*, 2010), and inter-simple sequence repeat (ISSR) (Al-Ali *et al.*, 2010) markers. Molecular markers have been reported for faba bean, but they were very

limited when compared to other major crop species. Therefore, it is vital to further examine the potential and genetic diversity of the local landrace collections of faba beans in Ethiopia as a source for further breeding work. Information on the available diversity in landraces is essential for broadening the genetic base of cultivars to sustain improvement (Singh, 2005). For instance, information on the variability of landrace genotypes helps in identifying accessions with higher potential for yield, disease resistance, and nutritional qualities (Awan *et al.*, 2014).

Not only diversity, but selection is also an important activity in crop improvement programs to develop desirable genotypes with high productivity. However, the effectiveness of selection depends on the amount of variability present in the genetic material for different traits. Hence, the estimation of variability is of prime importance (Johnson *et al.*, 1955). Despite the immense potential of landraces in enhancing adaptation and resistance to major biotic (foliar diseases, insects pests, viruses and parasitic weeds) and abiotic (soil acidity, drought and water logging) stresses, little has been done so far about the variability found in faba bean. This gap can be bridged via analyzing the extent and nature of variability present in the landrace accessions for yield and yield-related traits. Mitiku (1998) also indicated the existence of considerable variation for morpho-agronomic traits in faba bean landraces in Ethiopia.

Furthermore, since grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations, in plant breeding programs, direct selection for yield per se is not very effective (Laws *et al.*, 1983). In a plant breeding program, a successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Identification of secondary traits, which are positively associated with grain yield and possess high genetic variability and high heritability, helps in formulating efficient multiple trait selection indexes, as it provides means of direct and indirect effects of

component characters (Lawes *et al.*, 1983). Singh (1990) also reported that the efficiency of selection for traits with high (80% or more) heritability was fairly easy as compared to those with low heritability (less than 40%). Hence, quantifying and determining the association of grain yield with important yield contributing traits, using correlation and path coefficient analysis is of paramount importance since it provides a better understanding of the association of different characters with grain yield (Negahi *et al.*, 2014). The study of associations between various traits is also useful to breeders in selecting genotypes possessing groups of desired traits. Path coefficient analysis also separates the correlation coefficient into the direct and the indirect effects (Dixet and Dubey, 1984). It is not sufficient for a breeder to identify secondary traits associated with primary traits, but the breeding progress from simultaneous selection for the primary and secondary traits must be proven to be superior over the selection for the primary trait alone (Banziger *et al.*, 1997). However, the works that had been done so far regarding the association and genetic advance studies in faba bean landrace accessions in Ethiopia were very limited. Hence, there is a need to bridge this gap via determining the association of seed yield with important yield-related traits and expected genetic advance for each trait at 5% selection intensity in Ethiopian faba bean landrace accessions (Johnson *et al.* 1955a).

The knowledge about the extent of genetic diversity in landrace accessions leads to better characterization and utilization in breeding (Asfaw *et al.*, 2009). Mondini *et al.* (2009) argued that a comparison of plant morphology is the simplest approach for the assessment of genetic diversity. However, morphological diversity analysis is influenced by environmental variations and cannot always distinguish between closely related individuals. On the other hand, molecular methods of identification have the distinct advantage of being independent of climatic variables, even though they could have some limitations that are the cost and time required to undertake

genetic analysis. Therefore, using both morphological and molecular aspects for genetic diversity analysis complements each other. Knowledge gathered in the areas of morphological and molecular genetic diversity has been limited as compared to a huge number of faba bean landraces collections at EBI.

Among the various marker types, ISSR is ideal for visualizing the genetic distinctiveness of faba bean accessions (Alghamdi *et al.*, 2012a). Though ISSR markers are dominant like RAPD, they are more stable and reproducible. ISSR markers are easy to use, low-cost, and methodologically less demanding compared to other dominant markers, making them an ideal genetic marker for organisms whose genetic information is lacking. For PCR it requires low quantities of template DNA and also no need of sequence data for primer construction. ISSRs are randomly distributed throughout the genome (Mishra *et al.*, 2003). Therefore, the objectives of the current study were as follow.

1.2 General Objective

To study the extent of genetic diversity and pattern of distribution using morphological and ISSR markers, and investigate association of grain yield and yield-related traits of faba bean accessions in Ethiopia.

1.3 Specific Objectives

The specific objectives of the study were;

To determine the extent of genetic variability among the accessions;

To estimate correlation and path coefficient analysis, among yield and yield-related traits to recommend useful indexes for indirect selection in faba bean breeding in Ethiopia;

To determine the morphological diversity within and between faba bean accessions;

To determine the genetic diversity within and between faba bean accessions from Ethiopia with ISSR markers;

2 LITERATURE REVIEW

2.1 Taxonomy of *Vicia faba*

The classification of pulse crops is grouped under the Leguminous family. Leguminosae also called Fabaceae family is morphologically diverse and comprise a number of trees, herbs, legume crops, and some aquatic plants (Polhill and Raven, 1981). It is the third-largest family of flowering plants behind Orchidaceae and Asteraceae and consisting of approximately 650 genera and 18,000 species (Doyle and Luckow, 2003). The Leguminosae is divided into three major groups mainly on the basis of their morphological and floral differences; the Caesalpinioideae, Mimosoideae, and Papilionoideae (Doyle and Luckow, 2003). *Vicia faba* belongs to the family Fabaceae, sub-family faboideae, tribe fabeae, and the genus *Vicia*. *Vicia* consists of about 140-190 species (Doyle and Luckow, 2003).

The wild ancestor and the exact origin of *Vicia faba* remains a mystery. In the absence of a clearly defined ancestor, there has been considerable taxonomic controversy over the placement of *Vicia faba* ($2n= 12$ (14)) within the genus. *Vicia faba* is probably most closely related to, but distinct from, subdivision *Narbonensis* species. At various stages, the species has been proposed to be in a distinct series, subdivision, subgenus, or even genus. However, in most literature investigated, the following are listed as wild relatives of *Vicia faba*: according to Westphal (1974), *Vicia .pliniana* known to grow in Algeria; Witcornbe (1982), *Vicia angustifolia*L ($2n = 12$) and *Vicia narbonensis* L. ($2n = 14$); Lawes *et al.* (1983) *Vicia galilaea*, and *Vicia hyaeniscyamiis*; Muehlbauer *et al.* (1994) *Vicia johannis*, and *Vicia bithynia*; and Tadese *et al.* (1994) as known to grow in Ethiopia, *Vicia saliva*, *Vicia villosa*, and *Vicia pancifolia*. The relationship between these wild relatives and *Vicia faba* must be distant since no artificial

hybridization between them anywhere in the world has been successful so far. Subspecies faba was further classified into var. minor (small rounded seeds of 1 cm long), var. equine (medium-sized seeds of 1.5 cm), and var. major (large broad flat seeds of 2.5 cm). Alternatively (Muehlbauer and Tullu, 1997) proposed four subspecies (minor, equina, major, and paucijuga).

2.2 Origin and geographical distribution of *Vicia faba*

Several wild species (*Vicia narbonensis*, *Vicia galilea*, *Vicia johannis*, and *Vicia hayaensiscyamus*) are taxonomically closely related to the cultivated crop, but they contain $2n = 14$ chromosomes, whereas cultivated *Vicia faba* has $2n = 12$ chromosomes (Cubero, 1974). Raina and Ogihara (1995) reported that the chromosome size and DNA content of *Vicia faba* are about double that of other species. The hybridization endeavors between cultivated *Vicia faba* and closely related wild species have failed (Hajjar and Hodgkin, 2007).

Vavilov (1936) discovered a primitive type of *Vicia faba* at the intersection of the Himalaya and the Hindu Kush and proposed that *Vicia faba* originated from Central Asia and suggested a gradual increase in the *Vicia faba*'s area expansion from Central Asia westward along the mountains of Iran, Turkey, the Mediterranean, and Spain. Duc (1997) also reported the geographical origin of *Vicia faba* is accepted as the Near East, with the Mediterranean basin as the most important center of diversity for *Vicia faba* (Maxted and Kell, 2009). China, Afghanistan, and Ethiopia have also been reported as secondary centers of diversity for *Vicia faba* (Zong *et al.*, 2009). Faba bean was cultivated and used almost 5,000 and 3,000 years ago, by Chinese and Egyptians, respectively and by the Hebrews in biblical times, and a little later by the Greeks and Romans (Singh *et al.*, 2012).

The area of the *Vicia faba* domestication is supposed either very broadly as between Afghanistan and East Mediterranean (Maxted, 2009) or the Near East which is the center of diversity where the most primitive forms of *Vicia faba* occur (Maxted *et al.*, 1991). *Vicia faba* 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 its domestication around the 5,000 years BC. Faba bean was introduced into agriculture in the Near and the Middle East either in the Neolithic or the mid to late Bronze age (Korber-Grohne, 1987), then distributed to Europe, North Africa, along the Nile to Ethiopia, from Mesopotamia to India, to China, and later to South America. The earliest forms of *Vicia faba* were small-seeded, and would currently be classified as subspecies var. *minor* or subspecies *paucijuga* (Maxted, 1991).

2.3 Types and uses of *Vicia faba*

Vicia faba is a multipurpose crop used for both food and fodder (Prolea, 2014). Its value as a food and fodder crop lies in its high protein, vitamins, minerals, and carbohydrates (Crepon *et al.*, 2010), which make it one of the best solutions to malnutrition, particularly in developing countries in Africa and parts of Asia and Latin America (Haciseferogullari *et al.*, 2003). It is used as human food in developing countries and as animal feed, primarily for pigs, horses, poultry, and pigeons in developed countries (Singh and Bhatt, 2012). It is consumed as green vegetables, dry seeds, or processed food, and its green haulm, dry seeds, and dry straw are used as animal feeds (Sainte, 2011). *Vicia faba* major is the botanical type used for human nutrition; whereas the *Vicia faba* equina and *Vicia faba* minor are the botanical types used for animal feeding (Monti *et al.*, 1991). It is a much-appreciated food legume in the Middle East, the

Mediterranean region, China, and Ethiopia (Muehlbauer *et al.*, 1997) and serves frequently as a breakfast food. The grain of *Vicia faba* contains a high protein content of 24 – 33% (Winch, 2006); then, *Vicia faba* has been considered as a meat extender or substitute and as a skim-milk substitute (Oplinger, 1982). Because their nutritional value and composition are very similar, in many ways, to that of meat and they are often called “poor man’s meat”. In Ethiopia, *Vicia faba* is one of the most popular legumes. It plays a central role in the protein diet in Ethiopia in that several traditional dishes that are famous and widespread involve faba bean. These dishes can be divided into snacks, main and side dishes, and occasional dishes (Yetneberk and Wondimu, 1994). Snacks: ‘Eshet’: fresh green faba seeds either eaten raw or roasted; ‘Kolo’: roasted dry beans; ‘Nifro’: boiled dry or fresh green beans; ‘Gunkul’: seeds soaked and sprouted and roasted; ‘Ashuk’: seeds roasted first and then soaked; ‘Endushdush’: seeds soaked first and then roasted. Main dishes: ‘Shiro Wet’: dehulled seeds ground and made into stew; ‘Kik Wet’: dehulled and split beans boiled and made into stew; ‘Ful’: dehulled and boiled and spiced and minced with butter and eaten for breakfast. Side dishes: ‘Siljo’: flour fermented paste; Occasional dishes: ‘gulban’: dehulled, split, and broken faba bean seeds boiled together with cereal seeds such as corn and white or yellow sorghum eaten spiced from Good Friday to the eve of Easter Sunday. During the fasting period in an Ethiopian Orthodox church tradition called ‘Tsome Fillisete’, ‘Tsome arbea’, ‘Tsome Tahsas’, and ‘Tsome Hawariat’ (which are in August, end of February-April, mid-November-beginning of January and June-July, respectively), two uncooked spicy vegetable dishes are made using *Vicia faba*. The first is ‘Hilibet’, a thin, white paste of *Vicia faba* flour mixed with pieces of onion, green pepper, garlic, and other spices based on personal taste. The second is ‘siljo’, a fermented, sour, spicy thin yellow paste of *Vicia faba* flour.

Regarding the nutritional qualities, immature faba bean has essential vitamins and antioxidants. It also contains high amounts of vicine and convicine, components that are medicinally important (Ray and Georges, 2010). These two anti-nutritional factors cause favism which is glucose-6 phosphate dehydrogenase deficiency. About 400 million people are affected by this disease and it is one of the most common human enzyme deficiencies worldwide (Ray *et al.*, 2015). Hence, a robust molecular marker would be recommended to reduce levels of vicine and convicine in faba bean accessions. The accumulation of anti-nutritional component that is tannin in faba bean seed and the seed coat creates problems for consumption both in food and feed. Tannins reduce protein digestibility and negatively affect the taste and are usually relatively low in faba bean. *Vicia faba* can also contain Levodopa-the aromatic amino acid L-3, 4-dihydroxyphenylalanine which is a precursor of the neurological factor dopamine. This biochemical compound is used to treat Parkinson's disease. Faba bean has relatively large amounts of L-DOPA which can account for up to 7% of the dry weight of pod tissue (Burbano *et al.*, 1995).

In addition to its use as food for humans and animals, *Vicia faba* plays a critical role in some agricultural systems due to the ability to have symbiotic relationship with nitrogen-fixing bacteria to fix atmospheric nitrogen under a broad spectrum of environmental conditions. This facilitates diversification of the agro ecosystem in both time and space, which also may indirectly enhance associated diversity of wild flora and fauna, as well as soil microbes, which may, in turn, impact the sustainability of agricultural systems (Kopke and Nemecek, 2010). Faba bean is also an important crop for sustainable agriculture on unfavorable land (Alghamdi *et al.*, 2012). It is also used as a component of crop rotations, something that has been very much neglected in modern cropping, at a time when there is an urgent need to minimize the impact of emissions of undesirable gasses, chemical fertilizers on the environment, and reduces the

production cost of the subsequent cereal crops such as Wheat, Barley and Rice (Kopke and Nemecek, 2010).

2.4 Importance and production of *Vicia faba*

The world production of faba bean reaches 4.3 million tons from a total cultivated area of 2.6 million hectares (FAOSTAT, 2012). Faba bean seeds contain relatively high proteins, carbohydrates, vitamins B, antioxidants, and minerals. According to Monti and Grillo (1983), Picard (1977), Griffin and Lawes (1978), and Hulse (1994), the average ranges protein content for world faba bean are close to each other; 22-37%, 26-41%, 23-38%, and 23 – 39%, respectively. In Ethiopia, figures for protein contents are much lower than those given elsewhere. It is generally between 22 and 29%. Carbohydrate contents vary from 51% to 68%, of which major proportions are contributed by starch which varies from 41% to 53% (Cerning *et al.*, 1975). This world faba bean production is concentrated in nine major agro-ecological regions as; the Mediterranean basin, the Nile valley, Ethiopia, Central Asia, East Asia, Oceania, Latin America, Northern Europe, and North America (Bond *et al.*, 1985). Faba bean production ranks fourth in the world as an important food legume after, garden pea, chickpea, and lentils (Kaur *et al.*, 2014). The world-leading producing countries for faba beans are China, Ethiopia, Australia, France, Morocco, Egypt, and the United Kingdom (FAOSTAT, 2014). Ethiopia is the leading producer of faba beans in Africa accounting for 56% of the production (FAOSTAT, 2014). In Ethiopia, faba bean is widely grown in the mid and highland altitudes (1,800 – 3,000 m.a.s.l.), where the mean rainfall ranges from 650 to 1,500 mm and serves as a multi-purpose crop leading the other pulse crops in areas and production (CSA, 2017). Faba bean grows in several eco-geographical regions of the country, including Arsi and Bale highlands, Central highlands (South-West, West, and North Shewa), Tigray, North, and South Wollo, North and South

Gonder, East and West Gojam, Wollega, Guji highlands, Hadiya, Sidama and Gamogofa (Singh *et al.* 2013). Amhara and Oromia regions are the major faba bean producing regions. Within the regions, some zones such as West Shewa, North Shewa, South Wollo, and East Gojam are identified as major production areas of faba bean (Bereda, 2009). The area coverage and production volume of faba beans ranked first among the pulse crop in Ethiopia. It accounts for about 36% of the country's pulse production (IFPRI, 2010). Faba bean area coverage and total production is estimated to be 0.44 million hectares and 839 million kilograms, respectively which ranked the first among the pulse crops and the seventh following the cereal crops such as Teff (3 million hectares, 5.2 billion kilograms), Barley (0.95 million hectares, 2.1 billion kilograms), Wheat (1.6 million hectares, 4.6 billion kilograms), Maize (2.1 million hectare, 8.4 billion kilograms), Sorghum (1.9 million hectares, 5.1 billion kilograms), and Finger millet (0.46 million hectares, 1 billion kilograms) (CSA, 2017). Faba bean is used in crop rotation with major cereal crops like wheat, teff, barley, and other crops due to its nitrogen-fixing ability (IFPRI, 2010). In Ethiopia, the average yield of faba bean under smallholder farmers is not more than 1.8 t ha⁻¹ which is far below the crop potential that is greater than 5 t ha⁻¹ (CSA, 2013), even though there are high yielding varieties greater than 2 t/ha) (MoA, 2011). This has been attributed to different biotic and abiotic stresses (Jarso *et al.*, 2008).

Faba bean is an important component of crop production in smallholder agriculture that provides an economic advantage to farming communities as an alternative source of protein and cash income. It also serves as a break crop in the cereal-based rotations thus playing a significant role in improving the productivity of the soil by fixing atmospheric nitrogen. Schmidtke and Rauber (2000) reported that the amount of atmospheric nitrogen fixed through symbiosis in faba bean exceeds that of peas. Yields of cereal crops following faba bean are therefore improved, thus

reducing the need for artificial nitrogen fertilizer for subsistence farmers (Lindemann and Glover, 2003). As the faba bean is familiar with the Ethiopian feeding culture, the majority of the seed produced would be consumed domestically and only a smaller percentage of the crop is delivered to the export market. According to Bereda (2009), Ethiopia is among the top faba bean exporting countries, even if the export volume is very small. Thus, Ethiopia is the fourth exporting country of faba bean next to France, Australia, and the United Kingdom (FAOSTAT, 2014). Sahile *et al.* (2008) reported that the area of faba bean under production has increased by Ethiopian farmers due to the rising of faba bean as an export commodity.

2.5 Production constraints of *Vicia faba* in Ethiopia

The productivity of faba bean in Ethiopia is still far below its potential due to abiotic and biotic factors. Among these diseases are the most important biotic factors causing faba bean yield reduction (Degago, 2000). More than 17 pathogens have been reported so far on faba beans from different parts of the country. Diseases in the major faba bean growing regions are faba bean rust (*Uromyces viciae-fabae*), chocolate spot (*Botrytis fabae*), aschochyta blight (*Aschochyta fabae*), faba bean necrotic yellows virus, and black rot (*Fusarium solani*) (Gorfu and Beshir, 1994). Recently, the new gall-forming disease is threatening the crop with typical symptoms of green and sunken on the upper side of the leaf and bulged to the backside of the leaf, and finally develops light brownish color lesion, chlorotic galls, and progressively broaden to become circular or elliptical uneven spots. In addition, biotic stresses are parasitic weeds (*Orobanche and Phelipanche spp*), rust (*Oromyces fabae*), powdery mildew (*Microsphaera penicillata var. ludens*), and soil born diseases (*Fusarium root rots*), in western Asia, North Africa, East Africa (Hailu *et al.*, 2014).

The major abiotic stresses affecting faba bean production are soil acidity and aluminum toxicity. In areas where soil acidity is a problem, the potential and the actual productivity of a crop are different. Soil acidity has a dramatic impact on the most chemical and biological processes of a crop. Faba bean grows best in soils with a pH ranging from 6.5 to 9. (Jensen *et al.*, 2010), and is considered to fare poorly at a pH value of 5 or less (French and White, 2005). But, below 4.5 pH value some accessions remain productive (Singh *et al.*, 2012), with a critical soil pH value of 4.0 below which assimilation of major ions decreases (Schubert *et al.* 1990), and net H⁺ release and root growth cease (Yan *et al.*,1992). Nowadays the soil acidity is problematic since it limits the usage of faba beans in some cropping systems. Besides the simple matter of low pH, soil acidity is associated with the high availability of Al³⁺, which is stressful or toxic to many plants. Acid soil can be managed by the application of lime and the effect of Al³⁺ toxicity is ameliorated by the use of P-containing fertilizers (Atemkeng *et al.*, 2011). However, faba bean tolerates water logging better than other grain legumes such as chickpeas, field peas, lupins, and lentils. As compared to other grain legumes faba bean also tolerates acid soil.

2.5 Breeding history of *Vicia faba* in Ethiopia

In Ethiopia, faba bean breeding was started in the 1950s with the main purpose of enhancing the production and productivity of faba bean varieties suitable for different agro-ecologies of the country (Keneni *et al.*, 2006). Emphasis has been given to improve grain yield, disease resistance, water logging resistance, and increase seed size in response to the market demand (Telaye *et al.*, 1994). Until the mid-1980's breeding works were limited to a few research centers, even though, the institute of agricultural research was established in 1958. Strong and well-organized breeding works were started after research collaboration among different research centers and especially when the program was further strengthened by technical support from

ICARDA (Telaye *et al.*, 1994) in the 1980s. The main objective of the launching faba bean hybridization in Ethiopia in the mid-1980s at Holeta Agricultural research center was to cross chocolate spot resistance material introduced from ICARDA with adapted parents with other good agronomic traits and this center contributed a major role in releasing faba bean varieties involved in increasing production and productivity in the country.

2.6 Genetic diversity, heritability and genetic advance in faba bean

2.6.1 Genetic diversity

For the development of an effective crop improvement program, the existence of genetic diversity is a prerequisite. According to Falconer and Mackay (1996), genetic diversity is the occurrence of variability among individuals because of differences in genetic composition. If the traits of two individuals are measured in a similar environment and showed different expressions, this indicates the variations would be caused by genetic variation (Falconer and Mackay, 1996). Genotypic variation is the component of variation caused by the genetic differences among individuals within a population. Therefore, genotypic variation among individuals is essential for plant breeders in crop improvement and this can buffer against seasonal fluctuation (Sharma, 1998). Phenotypic variation is observable variation present in traits that include both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions (Singh and Chaudhary, 1977). Hence, phenotypic variation is the result of genotypic variation and environmental variation (Falconer and Mackay, 1996). Singh (2007) suggested that the presence of variability among individuals within a population can be estimated by using the following three ways: (1) simple measures of variability, such as range, mean, variance, standard deviation, coefficient of variability, and standard error, (2) by estimating the various components of variance and (3) by measuring the genetic diversity (e.g. D^2 statistics). In

faba bean, high estimates of variability have been reported for a number of attributes by Peyman (2015) and Keneni and Jarso (2002). According to Burton and Devane (1953), the variability that exists in the populations is measured by genotypic and phenotypic coefficients of variation. If the environmental variance is greater than the genotypic variance, it indicates, the contribution of the environment was greater in the phenotypic expression of that trait. Abdul-ariz *et al.* (2015) reported a higher genotypic coefficient of variation in thousand seed weight and moderate with the number of seeds per plant in faba bean. They also reported a low genotypic coefficient of variation for the number of pods per plant, number of seeds per pod, and seed yield per plant. Mulualem *et al.* (2013) also found the high genotypic coefficient of variation for biomass and the number of pods per plant in their study of genetic variation, heritability, and correlation in some faba bean. Abdul-ariz *et al.* (2015) reported a higher phenotypic coefficient of variation with the number of pods per plant, thousand seed weight, and moderate for the number of seeds per pod and seed yield per plant. A high phenotypic coefficient of variation was also reported for days to flowering, number of pods per plant, and thousand seed weight by Alghamdi (2007). Mulugeta (2016) also reported intermediate GCV (>10%) for pod length (13.71%), pod width (11.28%), number of pods per plant (17.14%), number of seeds per plant (16.12%), thousand seed weight (14.22%), seed production efficiency (12.14%) and economic growth rate (15.09%). While low genotypic coefficients of variability (>5% and <10%) for leaf length (6.59%), leaf area (9.41%), leaf area index (6.64%), plant height to the first pod (8.48%), number of branches per plant (8.81%), biomass weight per plot (9.64%), seed yield per plot (8.54%), harvest index (6.98%) and grain filling period (5.52%) were observed. He also reported the highest PCV (>20%) for traits like leaf area index (22.02%), number of branches per plant (68.57%), number of pods per

plant (68.57%), number of seeds per plant (27.22%), thousand seed weight (25.87%), seed production efficiency (20.95%) and economic growth rate (28.20%).

Suso *et al.* (1993) reported a significant difference in days to flowering among Spanish faba bean cultivars. Other studies showed that faba bean genotypes had a long time to flowering when grown under irrigation conditions than those grown under rain-fed conditions (Della, 1988). Talal (2012) also reported significant variation in days to flowering between nineteen landrace genotypes. Al- Refaee *et al.* (2004) reported that the date of fruit setting among faba bean genotypes varied significantly. Fruit setting is affected by genetic makeup and environmental factors. According to Talal (2013) also significant variation in days to fruit setting among nineteen landrace faba bean genotypes was observed. According to Nanda *et al.* (1988) study on twenty-five faba bean genotypes cultivated under irrigation conditions, significant differences were observed for days in pod formation. The environmental factors affecting fruit sets are mainly related to changes in temperature and rainfall. Della (1988) reported that the plant height of faba bean genotypes varied significantly under rain-fed conditions. According to Suso *et al.* (1993), an important trait discriminating among different geographic regions was plant height. According to Talal (2013), significant variation in plant height was observed. Della (1988) reported that faba bean genotypes varied significantly in different environmental conditions for the lowest pod height. The study by Terzopoulos *et al.* (2003) on 55 faba bean genotypes found that the lowest pod height ranged from 2 to 24 cm. Suso *et al.* (1993) reported that late flowering faba bean genotypes gave a high position of the lowest pod-bearing node corresponding to the region growing in. Talal (2012) also reported significant variation in the lowest pod height among accessions. Silim and Saxena (1992) reported that the number of branches was different among the faba bean accessions. Talal (2012) reported significant variation in the number of

branches on the main stem. Suso *et al.* (1993) found that genotypes varied significantly in pod length. The report on 1,500 faba bean germplasm by Li-juan *et al.* (1993) on its agronomic and yield traits from different provinces in China indicated pod lengths were less than 10 cm and 24% of the germplasm exceeded 7.6 cm. Talal (2012) reported that significant variation in pod length was observed. According to Al-Rifae *et al.* (2004) seed size highly affects pod width. Talal (2012) reported that significant variation in pod width was observed. Hassan and Ishaq (1972) reported that genotypes variation in their pod number per plant. Talal (2012) also reported significant variation in pods number per plant. Suso *et al.* (1996) reported significant differences in seed number per pod among twelve faba bean genotypes. The report on 1,500 accessions by Li-juan *et al.* (1993) from different provinces of China also indicated that the number of seeds per pod ranged from 1.7 to 2.9. According to Abdelmola and Abuanja (2007) as compared to the environmental factors, the number of seeds per pod was influenced by genetic factors. Talal (2013) reported that a significant variation in the number of seeds per pod. Della (1988) found that seeds' weight varied considerably among the genotypes. Talal (2012) reported that significant variation in 100-seed weight.

2.6.2 Heritability

Heritability is the measure of the value of selection for specific traits and an index of their transmissibility (Phoelman and David, 1995). It is defined as the share of the phenotypic variance in a population attributed to hereditary factors. It determines to which degree the difference between phenotypes results from genetic causes. Heritability is used to show which degree a trait is inherited from the offspring generation. This magnitude suggests the extent to which improvement can be achieved through selection. Heritability in a broad sense is the proportion of the total genetic variability to the total phenotypic variance (Allard, 1960), whereas

heritability in a narrow sense is the ratio of additive genetic variance to phenotypic variance (Falconer and Mackay, 1996). Heritability value ranges from zero to 1 where zero indicates all the variation resulted from the environment and 1 indicates all variations are caused by the genetic composition of an individual's population. Practically, it is very difficult to determine the presence, amount, or types of genetic variability in conditions where phenotypic expressions are strongly influenced by the environment (Welsh, 1990). The greater the proportion of the total variability that is due to the environment, the more difficult will it be to select for inherited differences. Singh (1990) categorized heritability into very high heritability ($> 80\%$), moderate-high heritability (50 - 80%), intermediate heritability (40 – 50%), and low heritability ($< 40\%$). Therefore, selection for characters with a heritability of more than 80% should be fairly efficient than low heritability ($< 40\%$). This indicates that small environmental variability in relation to genotypic differences because there is a close correspondence between genotype and phenotype and a relatively small contribution of the environment to phenotype. For traits with low heritability, selection may be difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Poehlmon and David (1995) suggested the influence of the environment on the trait with high heritability is very low and the increasing value of broad-sense heritability could serve as an indicator of selection based on phenotype, particularly when it is accompanied by relatively high variability and genetic advance. Hence, heritability indicates the effectiveness with which the selection of genotypes can be based on phenotypic performance. Sufficiently very high heritability values were reported by Peyman (2015) for traits like pod length and pod width in genetic variation in seed yield and some of the agro-morphological traits in faba bean genotypes. Alghamdi (2007) also reported moderately high heritability values for traits such as plant height, number of pod per plant, number of seed per plant, number of seed per

pod, biomass weight per plot, thousand seed weight, and seed yield. Abdel Aziz *et al.* (2015) found moderate heritability for seed yield per plant and thousand seed weight of faba bean genotypes and also reported low heritability of traits: number of pods per plant, number of seeds per plant, and the number of seeds per pod. Alghamdi (2007) reported the highest estimates of broad-sense heritability for days to flowering, number of pods per plant, number of seeds per plant, and days to maturity. Mulugeta (2016) also reported high broad-sense heritability values for traits like pod length (92.2%), leaf width (81.03%), and pod width (81.03%) and moderately high heritability values for characters such as leaf length (71.88%), leaf area (79.09%), plant height to first pods (69.78%), plant height (74.19%), number of pods per plant (79.15%), number of seeds per plant (78.79%), number of seeds per pod (60.80%), biomass weight per plot (72.79%), thousand seeds weight (62.41%), seed production efficiency (63.88%) and economic growth rate (62.31%).

The selection of superior genotypes based on the yield alone is less efficient due to the complexity of the yield and its dependence on its components (Sindhu *et al.*, 1985). The direct selection was also ineffective due to the larger environment-genotype interaction (Yassin, 1973). For a breeding program to be successful there must be genetic differences between the individual plants of the breeder's collection of material. Then the breeder will be able to select the desired combination of genes. Many desirable traits such as yield, protein content, and quality are under the control of many genes and environmental factors. The most important selection parameters in crop improvements are heritability and genetic advance. The estimation of heritability together with genetic advance is more useful to predict the gain according to selection than the estimation of heritability alone. Kalia and Sood (2004) working in faba bean found high heritability and high genetic advance for pod yield per plant which indicated high additive gene action and

possibly of the trait improvement through selection. The same result was obtained by Dawwam and Abdel Aal (1991) and Ramgiry (1997). High heritability and low genetic advance, which suggest a dominant effect, were found in protein and ascorbic acid contents, and hence these characters can be improved by hybridization (Kalia and Sood, 2004). Johnson *et al.* (1955) showed that the estimation of heritability together with the coefficient of variation is usually useful to the resulting effect of selection than heritability alone. This was mainly because heritability is a ratio of genotypic and phenotypic variances and varies according to the sample size, the environment, and the character of the population.

2.6.3 Expected genetic advance

According to Allard (1960), the improvement in the mean genotypic value of the selected plants over the base population measures the expected genetic gain from selecting the best performing genotypes for a given character. Johnson *et al.* (1955) categorized genetic advance into > 20 high, 10 - 20 medium and < 10 low. Johnson *et al.* (1955) reported broad sense heritability along with genetic advances are usually more useful than heritability alone in predicting the resultant effect of selecting the best individuals. Bakhiet *et al.* (2015) reported high genetic advances with high heritability for traits: days to flowering, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, and seed yield per plot. Keneni and Jarso (2002) reported high broad-sense heritability along with high genetic advance as percent of the mean for seed yield per plot and thousand-grain weight in faba bean genotypes. For the number of pods per plant, Kalia and Sood (2004) reported high heritability and high genetic advance. Mulugeta (2016) reported a relatively high genetic advance as percent of the mean for leaf area (23.99%), pod length (30.37%), pod width (28.75%), number of pods per plant (44.71%), number of seeds

per plant (41.42%), biomass weight per plot (23.02%), thousand seed weight (33.26%), seed production efficiency (27.75%) and economic growth rate (36.20%).

2.7 Correlation and path coefficient analysis

2.7.1 Correlation coefficient

Both correlation and path analysis will give a better insight into the cause and effect relationship between different pairs of characters. In crop improvement correlation was significant as studied by different authors. According to Gomez and Gomez (1984), the correlation coefficient is the measure of the degree of linear association between two variables. That means the association between two variables, regardless of the influence of other related characters. Correlations between characters are frequent features of plant breeding and may arise from linkage or developmental genetic interaction, with or without purely phenotypic components (Bond, 1976). The ultimate expression of yield in crop plants is usually dependent upon the action and interaction of a number of important characters and these characteristics are generally interrelated or correlated and its value can be either negative or positive. Correlations of characters with yield are useful in crop breeding to identify criteria for indirect selection, to provide reliable information on the nature, extent, and direction of selection (Sharma, 1998). Correlation helps breeders to identify the characters that could be used as selection criteria in a breeding program. Correlations in quantitative genetics can be grouped into phenotypic, genotypic, and environmental correlations. Phenotypic correlations (r_p) are the association between two characters that can be directly observed and measures the extent to which the two observed characters are linearly related. Genetic correlation (r_g) is the associations of breeding values (i.e additive genetic variance) of the two characters and measures the extent to which degree the same genes or closely linked genes cause co-variation (simultaneous variations) in

two different characters. The genotypic correlation coefficient provides a measure of genetic association between traits in order to identify the important traits. An environmental correlation (r_e) is the correlation of environmental deviations together with non-additive genetic deviations (i.e. dominance and epistatic genetic deviations) (Sharma, 1998). Abdalla *et al.* (2015) reported a positive and significant association between seed yield per plot and thousand seed weight. Tadese *et al.* (2011) found the number of pods per plant; the number of seeds per pod, thousand seed weight had a positive and significant association with seed yield per plot for faba bean. A report by Alghamdi (2007) revealed a positive and highly significant correlation between the number of pods per plant and the number of seeds per plant and seed yield per plot. Abdella *et al.* (2015) reported a positive and significant phenotypic relationship between the number of pods per plant and traits: plant height, seed yield per plot, number of seeds per plant, and thousand seed weight. Oral *et al.* (2011) found a positive and highly significant association between harvest index and seed yield per plot. The report from different authors suggested days to flowering had a positive and highly significant phenotypic association with plant height, seed yield (Peyman, 2015). Mulualem *et al.* (2013) found a positive and highly significant phenotypic relationship between days to flowering and days to maturity. Mulualem *et al.* (2013) reported a positive and significant phenotypic association between days to maturity and the number of branches per the main stem and thousand seed weight. According to Mulugeta (2016), seed yield showed strong and highly significant positive genotypic correlation with leaf width, leaf area, pod width, plant height, harvest index, economic growth rate and seed production efficiency. He also reported yield showed a significant positive genotypic correlation with thousand seed weight, leaf length, leaf area index, pod length, number of pods per plant, and seed filling period. Seed yield also showed positive and highly significant phenotypic correlation

coefficients with leaf length, leaf width, leaf area index, pod width, internode length, plant height, number of pods per plant, number of seeds per plant, biomass per plot, harvest index, thousand seeds weight, and seed filling period for faba bean. According to Mulugeta (2016), the number of branches per plant showed a highly significant positive association with leaf area index and the number of pods per plant. The number of pods per plant signified a strong and positive, highly significant genotypic correlation coefficient with the number of seeds per plant and also showed a positive significant association with harvest index per plot. The number of pods per plant revealed positive highly significant phenotypic correlation coefficient with leaf width, leaf area, leaf area index, internode length, number of branches per plant, number of seeds per plant, seed yield per plot, harvest index per plot, seed production efficiency, crude protein content and significant association with biomass weight per plant. There is a positive correlation between the number of seeds per pod and the length of the pods or 100-seed weight whereas there is a negative correlation between days to flowering and days to maturity (Karakoy *et al.*, 2014).

2.7.2 Path coefficient analysis

The grain yield of faba bean depends on many related traits. Identifying the extent and nature of the relationship between traits, especially the effect of each trait on yield is the first step towards selecting the best plant breeding components. Interrelationships among traits help in formulating a scheme of multiple trait selection. The correlation coefficient could show the linear relationship between them. However, path analysis would elucidate direct and indirect relationships among these traits, and hence on the basis of that, the breeder could select the most effective traits to evaluate and release varieties. Indirect selection is also important when desirable characters have low heritability. Tadese *et al.* (2011) in faba beans reported that using path analysis, the number

of pods per plant, seeds per pod, thousand seed weight, stand percent, and plant height had a high positive direct effect on grain yield. Azarpour *et al.* (2012) reported in the study of path coefficient analysis of seed yield and its components in faba bean that the maximum value of direct effect was related to plant height on seed yield. Path analyses have been observed to differ among the genotypes. Since yield is controlled by a number of traits, phenotypic path analysis of these component characters is essential for increasing the grain yield performance.

2.8 Importance of genetic diversity in plant breeding

Plant genetic resources are important for future food security. Crop germplasm diversity provides material to produce new improved crop varieties. The total gene pool of a species includes landraces, advanced breeding lines, popular cultivars, and wild and weedy relatives. Variation and differentiation among landraces contribute to the diversity of cropping systems. Vavilov (1951) recognized the importance of genetic diversity for the improvement of crops and organized comprehensive germplasm collections from their origin. Since then, major crop germplasm collections have increased in the world (Brown, 1989).

Before modern plant breeding, farmers cultivated a large number of crop landraces. Due to modern plant breeding programs, within-species diversity has been lost because uniform varieties have taken the place of traditional varieties and landraces. Also, natural disasters, deforestation, road laying, environmental pollution, and change in dietary habits are other factors that negatively influence the situation. Approximately 75% of the U.S. department of agriculture's listed germplasm has been lost in the last 80 years according to the rural advancement foundation international (Upadhyaya, 2010). The diverse landraces, exotic and wild relatives not only have rich gene but also can help enhance some important agricultural traits in breeding programs.

Breeders prefer to use parental lines from their breeding study. Actually elite inbred lines are often thought to be the best genetic resources because each line contains a good combination of genetic traits (Troyer, 1990). Although plant breeders are aware of the lack of diversity in their germplasm and the potential worth of wild and landrace, they do not tend to use such resources because of a lack of concrete information about the genetic value contained in large germplasm collections and because such materials are known to contain many undesirable alleles.

2.9 Ways of studying the diversity

There are three major ways to study crop diversity: a morphological, biochemical, and molecular analysis. These techniques are used in the detection and analysis of genetic diversity. Therefore, each of these markers is described below.

2.9.1 Morphological markers

Morphological marker systems are the earliest, simple, and inexpensive genetic markers that lie on phenotypic appearance (Vos *et al.*, 1995). It is the oldest method and considered the first step in the description and classification of germplasm (Hedrick, 2005). Its estimations are more dependent on the environment and are more subjective than other measurements (Li *et al.*, 2009). However, morphological traits that exhibit continuous variation between individuals in a population often obscure the evaluation of genetic diversity. Thus, the very plastic nature of morphological traits, in turn, needs extra time and resources for evaluation in the field and greenhouse (Bretting and Widrlechner, 1995). Moreover, pleiotropism and a multi-factorial basis to morphological traits further hide the characterization of the plant populations (Rahman *et al.*, 2010).

Faba bean morphological markers include plant height, fat, protein, starch content, seed weight, color, shape, size, number of pods per plant, number of seeds per pod, flowering time, and days to maturity. These phenotypic traits give us valuable information about crop plant domestication. Morphological diversity is demonstrated by statistical comparisons of relationships among agronomical and morphological traits. Moreover, a correlation can exist between these morphological traits. For example, there is a positive correlation between the number of seeds per pod and the length of the pods or 100-seed weight whereas there is a negative correlation between days to flowering and days to maturity (Karakoy *et al.*, 2014).

2.9.2 Biochemical markers

Biochemical markers are protein-based polymorphism markers. The most commonly used biochemical marker systems for the study of genetic diversity and relationships in faba bean species are isozyme (Kaser and Steiner, 1983) and protein markers using Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS PAGE) (Sultana and Ghafoor, 2008). SDS-PAGE is a useful tool for identifying the genetic diversity of wild and cultivated plant species (Farshadfar, 2008). SDS gel electrophoresis allows the separation of proteins in denatured conditions. The molecular weight is the basis of the migration of polypeptides. A detergent that denatures protein by wrapping around the polypeptide backbone is an anionic SDS. In doing so, SDS confers a negative charge to the polypeptide in proportion to its length. As a result, polypeptides become the rod of negative charge with equal densities or charge per unit length. Sultana and Ghafoor (2008) concluded for seed proteins, SDS-PAGE on 9.4% acrylamide in a large gel based on seed protein could be used as a useful tool for intra-specific diversity study in crop species. SDS-PAGE based on seed storage proteins has proven to be a simple and effective method for distinguishing the cultivars of the largest cross-fertilized pasture grasses and legumes

despite their high innate genetic variability (Vapa *et al.*, 1997). Variation in the number of bands, width, and intensity of bands was observed in different peas (*Lathyrus sativus*) of the same geographical origin (Dellagatta *et al.*, 2002).

2.9.3 Molecular markers

In plant breeding, the efficient utilization of genetic diversity among faba bean genotypes, and its effective conservation are very important. DNA-based molecular markers have several advantages over the conventional phenotypic markers since their presence is not dependent on the growth stage of the crop and can be found in all tissues (Mondini *et al.*, 2009). Most molecular markers are selectively neutral because they are usually located in non-coding regions of DNA (Collard *et al.*, 2005). The primary advantages of molecular markers are their numerous in number than morphological markers and they are not influenced by environmental factors. In addition, such markers do not change with the physiology of the organism. It is a sequence of DNA or a gene, which is situated on a chromosome (Schulmann, 2007). Molecular techniques make it possible to analyze numerous characters, which are also independent, whereas morphological analysis provides fewer characters, often of dubious homology. Thus, the molecular approach is more objective than morphological approaches. Though morphological and agronomic traits are routinely used to access genetic diversity, they are not enough to cover the genome, are affected by environmental factors, and development stage-dependent. Evaluating and assessing the genetic diversity of *Vicia faba* germplasm provide reliable information on molecular markers; ISSR (Terzopoulos and Bebeli, 2008; Alghamdi *et al.*, 2011), RAPD (Link *et al.*, 1995; Alghamdi, 2008; Yassine *et al.*, 2014), SSR (Pozarkova *et al.*, 2002; Gong *et al.*, 2010, 2011; Ma *et al.*, 2011; Kaur *et al.*, 2012; Yassine *et al.*, 2014), SRAP (Alghamdi *et al.*, 2012), and AFLP (Zeid *et al.*, 2003). Hence, molecular techniques are the most

advanced and, possibly, the most effective means for understanding the basis of genetic diversity. They are efficient and accurate tools with which genetic variation can ultimately be identified and assessed in a rapid and careful manner. Several molecular marker systems have been developed and are applied to a range of crop species. These include Randomly Amplified Polymorphic DNA (RAPD) (El-Danasoury *et al.*, 2008; Basheer-Salimia *et al.*, 2013), Amplified Fragment Length Polymorphism (AFLP) (Zeid *et al.*, 2003; Zong *et al.*, 2009; Duc *et al.*, 2010), and Simple Sequence Repeats (SSR) (Zeid *et al.*, 2009; Kaur *et al.*, 2012). The main limitations of these methods are low reproducibility and dominance of RAPD, high cost and dominance of AFLP analysis, and the necessity to know the flanking sequences to develop species-specific primers for SSR polymorphism and high cost of development of SSR (Jabbarzadeh *et al.*, 2010). An alternative to these molecular markers is the inter-simple sequence repeat (ISSR) marker which is a method that overcomes most of the technical limitations that the above-mentioned techniques have (Terzopoulos and Bebeli, 2008). ISSR is simple, fast, and cost-efficient as well as it does not need sequences to be amplified for primer construction, and thus it is a tremendously useful molecular marker in genetic diversity, phylogeny, genomics, and evolutionary studies (Aguilera *et al.*, 2011). The limitations of ISSR markers are dominant markers and band staining can be weak. ISSR analysis has been successfully documented to determine genetic diversity and relationships in numerous economic legume species such as cowpea (Ajebade *et al.*, 2000), common bean (Sadeghi and Cheghamirza, 2012), lentil (Joshi, 2013), chickpea (Bhagyawant and Srivastava, 2008), Mung bean (Singh *et al.*, 2013), in addition to faba bean (Terzopoulou and Bebeli, 2008). ISSR markers are also used to study the genetic diversity of crops like coffee (Tesfaye *et al.*, 2014), linseed (Ziarovska *et al.*, 2012), sesame (Teshome *et al.*, 2015), barley (Varshney *et al.*, 2007), and rice (Girma *et al.*, 2010). Sofalian *et*

al. (2008) also reported that ISSR markers could differentiate the local varieties collected from different regions and these molecular markers are efficient tools for estimating intraspecific genetic diversity in wheat. Besides, this marker could be efficiently used to evaluate genetic variation in the wheat germplasm (Sofalian *et al.*, 2009). Hence, Song *et al.* (2002) and Fahmy *et al.* (2008) concluded that ISSR markers could be used as highly informative markers for genome mapping and gene tagging because of the evolutionary rate of change within microsatellites is considerably higher than many other regions DNA markers.

3. MATERIALS AND METHODS

3.1. Genetic diversity, association and morphological diversity study

3.1.1. Planting material

The plant material used in this study consisted of a total of ninety-six accessions of faba bean (*Vicia faba* L.), which were ninety landrace accessions obtained from Ethiopian Biodiversity Institute (EBI) along with six released varieties obtained from Holetta Agricultural Research Center (HARC) and Debre Birhan Agricultural Research Center (DbARC)). Among the Ethiopian Regional States, Oromia, Amhara, SNNPR, and Tigray are the first four leading faba bean categories in area and production from where landrace collections obtained in this study. The accessions were originally collected from 14 administrative zones (AZs) of Ethiopia, which covers an altitudinal range of 1,562 to 3,130 m.a.s.l, and collection sites were also the basis for studying. The origin, names, and numbers of accessions are presented in Table 1. In addition, the geographic regions, from which sampling was done for the landrace accessions are shown in fig. 1 below.

Table 1: List of accessions, collection regions, and sites for the 96 faba bean (*Vicia faba* L.) accessioned in the study

S/N	Accession Code	Region	Zone	Latitude	Longitude	Altitude
1	26400	Amhara	East Gojam	10-36-25-N	37-41-41-E	2792.00
2	26428	Amhara	East Gojam	10-14-14-N	38-03-24-E	2439.00
3	27279	Amhara	East Gojam	10-27-00-N	37-03-00-E	2400.00
4	229871	Amhara	East Gojam	10-45-00-N	35-04-00-E	2420.00
5	229869	Amhara	East Gojam	10-36-00-N	37-41-00-E	2510.00
6	25006	Amhara	East Gojam	10-14-00-N	38-03-00-E	2450.00
7	25017	Amhara	East Gojam	10-45-00-N	38-04-00-E	2370.00
8	212565	Amhara	North Shewa Amhara	09-39-00-N	39-00-00-E	2670.00
9	212567	Amhara	North Shewa Amhara	09-39-00-N	39-00-00-E	2630.00
10	212572	Amhara	North Shewa Amhara	10-15-00-N	39-15-00-E	2630.00
11	212578	Amhara	North Shewa Amhara	10-15-00-N	39-35-00-E	3100.00
12	212580	Amhara	North Shewa Amhara	10-10-00-N	39-42-00-E	3130.00
13	208085	Amhara	North Shewa Amhara	09-49-00-N	38-53-00-E	2300.00
14	208114	Amhara	North Shewa Amhara	10-23-00-N	39-12-00-E	1983.00
15	229299	Amhara	North Shewa Amhara	10-24-00-N	39-12-00-E	1970.00
16	229310	Amhara	North Shewa Amhara	09-39-00-N	39-00-00-E	2140.00
17	212566	Oromiya	North Shewa Oromia	09-39-00-N	39-00-00-E	2630.00
18	25003	Oromiya	North Shewa Oromia	09-38-00-N	39-05-00-E	2490.00
19	25010	Oromiya	North Shewa Oromia	09-38-00-N	39-10-00-E	2870.00
20	25018	Oromiya	North Shewa Oromia	09-38-05-N	39-10-04-E	2440.00
21	25022	Oromiya	North Shewa Oromia	09-38-10-N	39-10-05-E	2480.00
22	229303	Oromiya	North Shewa Oromia	09-38-15-N	39-10-10-E	2140.00
23	29526	Oromiya	East Hararghe	09-21-34-N	41-33-11-E	2428.00
24	29527	Oromiya	East Hararghe	09-20-27-N	41-33-07-E	2436.00
25	29531	Oromiya	East Hararghe	09-29-17-N	42-13-13-E	2432.00
26	29532	Oromiya	East Hararghe	09-25-26-N	41-42-12-E	2512.00
27	29536	Oromiya	East Hararghe	09-18-49-N	41-45-18-E	2530.00
28	29533	Oromiya	East Hararghe	09-25-24-N	42-42-13-E	2512.00
29	29535	Oromiya	East Hararghe	09-25-28-N	42-92-02-E	2489.00
30	29537	Oromiya	East Hararghe	09-18-49-N	41-45-18-E	2530.00
31	30008	Oromiya	West Arsi	06-59-18-N	39-13-54-E	2437.00
32	30011	Oromiya	West Arsi	06-51-32-N	38-58-54-E	2628.00
33	30015	Oromiya	West Arsi	07-09-39-N	39-32-21-E	2500.00
34	30016	Oromiya	West Arsi	07-09-39-N	39-32-21-E	2500.00
35	30014	Oromiya	West Arsi	07-00-33-N	39-21-06-E	2364.00
36	30017	Oromiya	West Arsi	07-00-19-N	39-21-26-E	2369.00
37	231293	Oromiya	Arsi	08-09-00-N	39-14-00-E	2200.00
38	219089	Oromiya	Arsi	07-47-00-N	39-54-00-E	2410.00
39	27052	Oromiya	Arsi	07-12-00-N	38-37-00-E	2300.00
40	25009	Oromiya	Arsi	07-40-00-N	39-50-00-E	2350.00
41	219355	Oromiya	Arsi	07-00-00-N	38-00-00-E	1730.00
42	25259	Oromiya	West Shewa	08-54-00-N	38-35-00-E	2000.00
43	25260	Oromiya	West Shewa	08-54-00-N	38-35-00-E	1960.00
44	25274	Oromiya	West Shewa	08-26-00-N	37-55-00-E	1830.00
45	25264	Oromiya	West Shewa	08-60-00-N	38-38-00-E	2350.00
46	25270	Oromiya	West Shewa	08-57-00-N	38-35-00-E	2000.00

S/N	Accession Code	Region	Zone	Latitude	Longitude	Altitude
47	28770	Oromiya	Bale	71-13-70-N	40-37-09-E	2073.00
48	28771	Oromiya	Bale	07-56-34-N	40-37-36-E	2070.00
49	28772	Oromiya	Bale	07-10-50-N	40-43-03-E	1921.00
50	28773	Oromiya	Bale	07-24-28-N	40-30-18-E	1984.00
51	28774	Oromiya	Bale	07-24-28-N	40-30-18-E	1984.00
52	28776	Oromiya	Bale	07-24-27-N	40-14-57-E	2393.00
53	28777	Oromiya	Bale	07-22-44-N	40-13-48-E	2414.00
54	30021	Oromiya	Bale	07-23-56-N	40-19-19-E	2402.00
55	30022	Oromiya	Bale	07-14-27-N	40-13-41-E	2380.00
56	30023	Oromiya	Bale	07-14-48-N	39-49-11-E	2502.00
57	27929	SNNPR	Benchmaji	06-52-37-N	35-52-07-E	2053.00
58	27931	SNNPR	Benchmaji	06-58-46-N	35-46-05-E	2019.00
59	235709	SNNPR	Benchmaji	05-17-00-N	37-29-00-E	2150.00
60	28103	SNNPR	Gedeo	06-03-47-N	38-14-39-E	2558.00
61	28104	SNNPR	Gedeo	06-04-04-N	38-14-39-E	2549.00
62	26883	SNNPR	Gedeo	06-12-71-N	38-19-05-E	2589.00
63	26885	SNNPR	Gedeo	06-12-44-N	38-19-52-E	2813.00
64	26886	SNNPR	Gedeo	06-13-37-N	38-19-07-E	2555.00
65	26882	SNNPR	Gedeo	06-15-13-N	38-17-30-E	1880.00
66	26887	SNNPR	Gedeo	06-13-17-N	38-20-01-E	2549.00
67	26860	SNNPR	Gedeo	05-28-22-N	37-53-13-E	1778.00
68	26861	SNNPR	Gedeo	05-33-07-N	37-54-17-E	1625.00
69	26859	SNNPR	Gedeo	05-32-41-N	37-04-25-E	1641.00
70	26862	SNNPR	Gedeo	05-32-33-N	37-54-27-E	1644.00
71	28109	SNNPR	Sidama	06-28-08-N	38-29-59-E	2744.00
72	28110	SNNPR	Sidama	06-28-48-N	38-30-18-E	2782.00
73	28113	SNNPR	Sidama	06-27-26-N	38-27-47-F	2752.00
74	28112	SNNPR	Sidama	06-27-12-N	38-27-16-E	2791.00
75	26853	SNNPR	Segen	05-41-10-N	37-54-01-E	2551.00
76	26888	SNNPR	Segen	05-41-03-N	37-54-20-E	2553.00
77	26854	SNNPR	Segen	05-41-17-N	37-54-05-E	1895.00
78	26889	SNNPR	Segen	05-41-39-N	37-54-15-E	1624.00
79	26855	SNNPR	Segen	05-41-27-N	37-54-09-E	1871.00
80	26858	SNNPR	Segen	05-26-37-N	37-24-21-E	1562.00
81	25290	SNNPR	Kembata	06-28-50-N	38-30-20-E	2790.00
82	25292	SNNPR	Kembata	06-27-00-N	38-29-00-E	2325.00
83	25298	SNNPR	Kembata	06-27-10-N	38-29-15-E	2420.00
84	25299	SNNPR	Kembata	06-26-99-N	38-28-98-E	2220.00
85	25310	SNNPR	Kembata	06-26-90-N	38-28-92-E	2100.00
86	25303	SNNPR	Kembata	06-26-70-N	38-28-80-E	2150.00
87	220076	Tigray	Central Tigray	14-08-00-N	38-54-00-E	1920.00
88	220079	Tigray	Central Tigray	14-10-00-N	38-56-00-E	2750.00
89	16599	Tigray	Central Tigray	14-14-36-N	38-56-57-E	2058.00
90	220086	Tigray	Central Tigray	14-05-00-N	38-14-00-E	1950.00
91	Moti	Released	Released			1800-3000
92	Bulga-70	Released	Released			2300-3000
93	Hachalu	Released	Released			2300-3000
94	Lalo	Released	Released			
95	Dagim	Released	Released			
96	Walki	Released	Released			

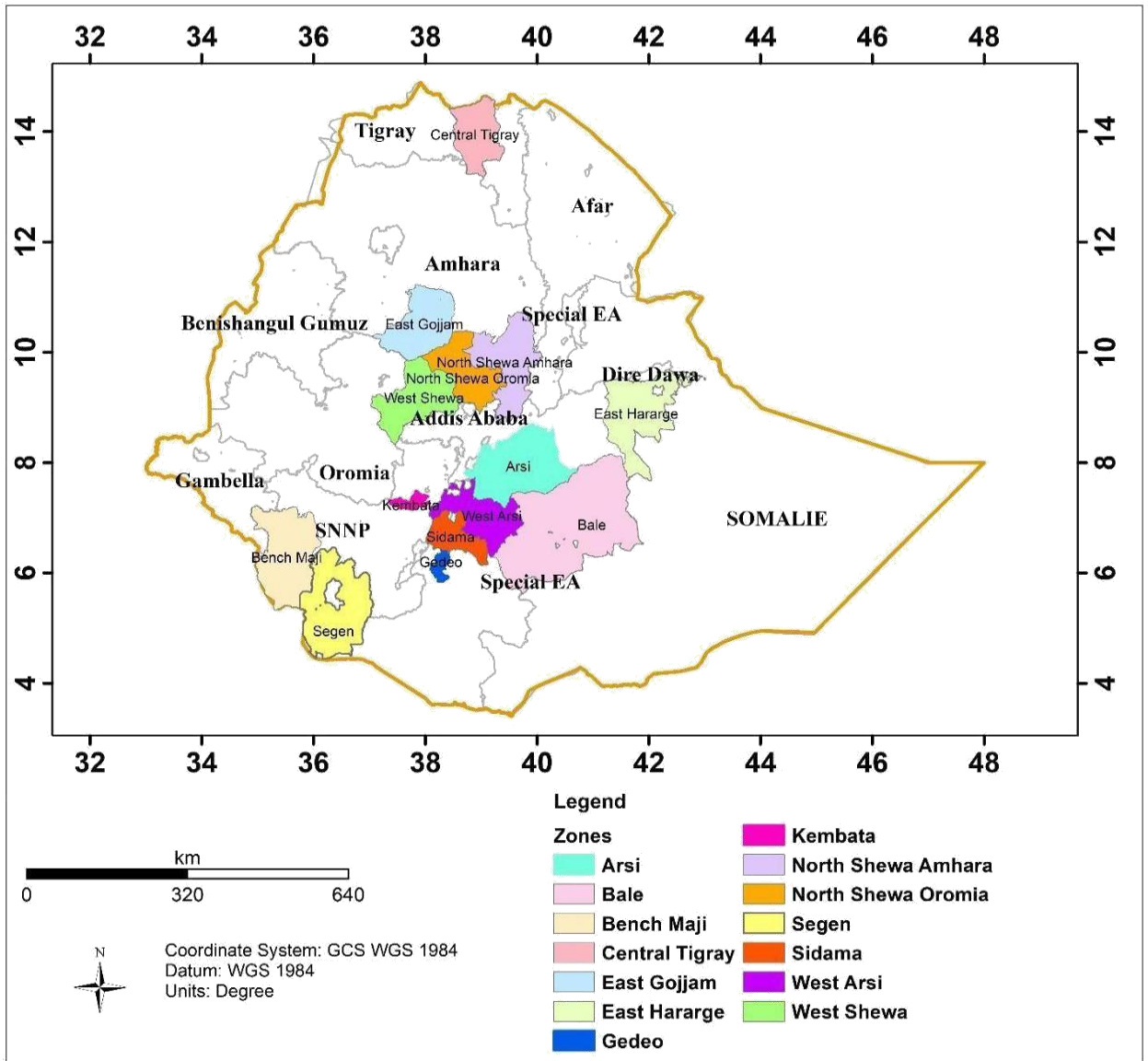


Figure 1. Map of Ethiopia showing the collection sites

3.1.2 Description of the study area

The experiment was conducted at Farmers’ Training Center (FTC); Girar Jarso and Degem districts of North Shewa Zone during 2018 and 2019. The planting were done at the main cropping seasons from June to December, at specific sites Koticho Safani and Ali Doro Abo, respectively. Koticho Safani is located 106 km away from Addis Ababa in central Ethiopia toward the north direction and 6 km from the nearby town Fiche toward the south direction. It is

situated at 9° 76' 67" N latitude and 38° 73' 33" E longitude with 2,784 meters above sea level (m.a.s.l). The average minimum and maximum temperatures of the area are 8.19°C and 20.42°C, respectively. It is also characterized by clay soil with 16% sand, 66% clay, and 18% silt in texture and a pH value of 5.88 (Dugassa, 2018). The site receives an annual mean rainfall of 1,126.65 mm most falling between April to September with peaks in July and August. Ali Doro Abo is located 142 km away from Addis Ababa in central Ethiopia toward the north direction and 18 km from the nearby town Degen toward the north direction. It is situated at 9° 81' 83" N latitude and 38° 63' 33" E longitude with 3,086 m.a.s.l. In addition, the average temperatures range from a minimum of 8.10 to 8.23°C to a maximum of 20.30 to 20.52°C and characterized by clay soil and a pH value of 6. Its mean annual rainfall is 883.18 mm which occurs mainly from June to September growing season. The total annual rainfall and temperature data of both locations for the years 2002 to 2018 are presented in appendices I, II, III, IV, and V.

3.1.3 Experimental design and field management

The experimental design was laid out in 4 x 24 (4 incomplete blocks in replication and 24 plots in an incomplete block) alpha-lattice designs (Patterson and Williams, 1976) with two replications. The accessions were sown within the second and third week of June 2018 and 2019 respectively at both Girar Jarso and Degem districts. Planting was done by placing one seed per hill. Each plot consists of one row of 2 m length with a spacing of 0.4 m between rows (accessions) and 0.1 m between plants. All plants in a single row were used to collect data on grain yield and other traits. Redomil gold was sprayed ten days before the flowering date to control chocolate spots. At planting, 46 kg Phosphorus pentoxide per ha and 18 kg Nitrogen per ha were applied in a form of DAP since the recommended rate of fertilizer for faba bean is 100 kg DAP per ha (MoARD, 2007). Sowing was done by hand drilling at a seed rate of 20 seeds per row. Weeding was done as per the recommendation adopted for the area.

3.1.4 Data collection for phenotypic variability and association study

3.1.4.1 Data collected for genetic variability

Based on the faba bean descriptors (IBPGR, 1985) the following data were collected on a plot or plant basis.

1. Days to 50% flowering (DTF): the number of days taken by each accession from the day of sowing to the day on which 50% of the plants in the harvestable rows of a plot opened their first flower in a plot.
2. Days to 90% maturity (DM): the number of days from sowing to the stage when 90% of the plants in a plot reach physiological maturity i.e. when the plants become yellowish (showing sign of senescence).

3. 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).
4. Thousand seed weight (TSW): the weight of thousand seeds taken randomly from the harvested seed lots of each plot that was measured at 10% seed moisture content and expressed in gm.
5. Seed yield per plot (SYPP): the weight of seeds that were harvested from all the plants in the harvestable rows of a plot, in gm.
6. The number of pods per plant (NPPPL): the number of fertile pods from five randomly taken plants that were counted and averaged.
7. Plant height (PH): the height of the plant from the ground surface to the tip of the main guide that was recorded in cm from five plants randomly taken from each plot at physiological maturity and averaged.
8. The number of seeds per pod (NSPP): 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.
9. The number of branches per plant (NBPPL): numbers of branches per plant were counted on five randomly taken plants and the average was used.
10. Pod length (PL): measured on five randomly selected pods, which was measured as the distance between the edges of each pod and the average was used.
11. Pod width (PW): it was measured for five randomly selected pods, at the center of the pod using a caliper and the average was used.

12. Grain yield (GY): the seed yield in gram per plot was measured and then converted to per hectare (ton/hectare) basis at 10% seed moisture content.

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

14. Leaf width (LW): width across the leaf at its widest point of the central leaflet of the trifoliolate leaf. Three leaves from the top, middle, and bottom of the plant were taken and averaged in cm.

15. Leaf area (LA): this was calculated by leaf area estimation model as described by Peksen (2007) and three leaves per plant were measured and averaged in cm^2 .

$LA=0.919+0.682LW$; Where L= leaf length and W= leaf width

16. Numbers of seeds per plant (NSPPL): the total number of seeds per plant averaged over five randomly selected plants.

17. Internode length (IL): three internodes per plant of five randomly selected plants were measured and averaged.

18. The number of pods per node (NPPN): number of pods on three nodes per plant of five randomly selected plants were counted and averaged.

19. Lowest pod height (LPH): the average height from ground to the first pod-bearing nodes of five randomly selected plants from plots measured at physiological maturity in cm.

3.1.4.2 Data collected for association study

The associations of eighteen independent traits such as days to 50% flowering, days to 90% maturity, seed filling period, thousand seed weight, seed yield per plot, number of pods per plant, plant height, number of seeds per pod, number of branches per plant, pod length, pod width, leaf length, leaf width, leaf area, internode length, number of pods per node, lowest pod height, and number of seeds per plant with grain yield per hectare, as the dependent variables were used.

3.1.5 Data analysis for phenotypic variability and association study

3.1.5.1 Data analysis for variability study

Analysis of variance (ANOVA) was carried out according to Gomez and Gomez (1984) for each environment separately to determine the differences among the accessions. Accessions, replications and blocks within replications were considered random. Further analyses were carried out for traits that showed statistically significant differences among the accessions and for those traits that showed homogeneity of error variances; to estimate the combined analysis of variance over locations and years since the environment enormously affects faba bean yield. Grain yield is also influenced by the year and location (Pilbeam *et al.*, 1990). Error mean squares from each environment for significant traits were tested for homogeneity of variance to ensure that the combined analysis of variance across environments was appropriate or not using Bartlett's test. For statistical analysis, grain yield from a net plot area of 0.8 m² was harvested and converted into ton per ha base at 10% standard grain moisture content was used. Finally, statistical analysis was carried out using the R-software program (version 3.1.1).

3.1.5.1.1 Phenotypic and genotypic variability

The variability present in the accessions was estimated by simple measure, namely, range, mean, standard error, phenotypic and genotypic variance, and coefficient of variation. The genotypic and phenotypic variances were obtained from the analysis of the variance table according to Comstock and Robinson (1952). Partitioning of the total variation into components due to genotype (σ^2g), environment (σ^2e), and genotype by environment interaction (σ^2ge) deviations were performed by assuming observed mean squares equal to their expected mean squares as suggested by Singh and Chaudhary (1985) and Sharma (1998).

3.1.5.1.2 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variability were computed as per the method suggested by Burton and De Vane (1953).

Genotypic coefficient of variability:

$$GCV = \frac{\sqrt{\sigma^2g}}{\bar{X}} \times 100$$

Phenotypic coefficient of variability:

$$PCV = \frac{\sqrt{\sigma^2p}}{\bar{X}} \times 100$$

The estimates of GCV and PCV were categorized based on the scale given by Sivasubramanian and Madhava Menon (1973).

Where σ^2g = genotypic variance, σ^2p = phenotypic variance, \bar{x} = general mean of the trait

3.1.5.1.3 Estimation of heritability

Heritability (h_b^2) in a broad sense for all traits was computed using the formula adopted by Lush (1940) as:

$$h_b^2 = \sigma^2_g / \sigma^2_p \times 100$$

Heritability was categorized as low, medium, and high as given by Johnson *et al.* (1955).

3.1.5.1.4 Estimation of expected genetic advance

Genetic advance (GA) for each trait was computed using the formula adopted from Johnson *et al.* (1955) and Allard (1960).

$$GA = (k) (\sigma_p)^* (h_b^2)$$

3.1.5.1.4 Genetic advance as percentage of mean

$$GA \text{ (as \% of the mean) (GAM)} = (GA / \bar{x}) \times 100$$

Where, k= selection differential (k = 2.06 at 5% selection intensity)

σ_p = phenotypic standard deviation

h_b^2 = heritability in broad sense

\bar{x} = Grand mean

Genetic advance as percent of the mean was categorized as a low, medium, and high as given by Johnson *et al.* (1955).

3.1.5.2 Data analysis for association study

3.1.5.2.1 Correlation coefficient analysis

Phenotypic and genotypic correlation coefficients were calculated using `spar11` statistical package following the formula described by Miller *et al.* (1958) as:

$$r_{pxy} = \frac{\text{cov } pxy}{\sqrt{(\sigma^2 px)(\sigma^2 py)}}$$

$$r_{gxy} = \frac{\text{cov } gxy}{\sqrt{(\sigma^2 gx)(\sigma^2 gy)}}$$

Whereas: r_{pxy} = phenotypic correlation coefficients between traits x and y

r_{gxy} = genotypic correlation coefficients between traits x and y

r_{exy} = environmental correlation coefficients between traits x and y

$\text{cov } pxy$ = phenotypic covariance between traits x and y

$\text{cov } gxy$ = genotypic covariance between traits x and y

$\text{cov } exy$ = environmental covariance between traits x and y

$\sigma^2 px$ = phenotypic variance of the first trait

$\sigma^2 py$ = phenotypic variance of the second trait

$\sigma^2 gx$ = genotypic variance of the first trait

The phenotypic correlation coefficient was tested for their significance using the formula suggested by Sharma (1998).

$$t = \frac{r_p}{\sqrt{\frac{1-r_p^2}{n-2}}} \quad \text{where, } n = \text{number of accessions,}$$

However, the coefficients of correlation at a genotypic level were tested for their significance using the formula described as indicated by Robertson (1959).

$$t = \frac{rg_{xy}}{SErg_{xy}} \quad \text{where } SErg_{xy} = \sqrt{\frac{1-r^2g_{xy}}{2h^2_x * h^2_y}}$$

$SErg_{xy}$ = standard error of genotypic correlation coefficient between traits x and y

h^2_x = heritability for trait x

h^2_y = heritability for trait y

The calculated absolute t value was tested against the tabulated t- value at g-2 degree of freedom for both phenotypic and genotypic correlations. Where g is the number of genotypes.

3.1.5.2.2 Path coefficients analysis

Path coefficient analysis was carried out using the genotypic correlation coefficients to determine the direct and indirect effects of the yield components and other morphological traits on grain yield. Path coefficient analysis was calculated using the formula spar11 statistical package suggested by Dewey and Lu (1959) to determine the direct and indirect effect of different variables on grain yield based on the following relationships.

$$r_{ij} = P_{ij} + \sum r_{ik}P_{kj} \quad \text{where,}$$

r_{ij} = Mutual association between the independent trait (i) and dependent trait, grain yield (j) as measured by the genotypic correlation coefficients.

P_{ij} = Components of direct effects of the independent trait (i) as measured by the genotypic path coefficients and

$\sum r_{ik} P_{kj}$ = Summation of components of indirect of a given trait (i) on a given dependent trait (j) via all other independent traits (k).

3.1.5.3 Genetic diversity analysis using morphological data

3.1.5.3.1 Multivariate analysis

Multivariate analysis is a technique used for the characterization and grouping of accessions evaluated for different traits. The data were pre-standardized to a mean zero and variance of unity before computing cluster analysis and principal component analysis so as to avoid differences in scales used for recording data on different traits (Sneath and Sokal, 1973). Description of accessions collection for different useful traits is an important prerequisite for effective and efficient utilization of accessions collection in the improvement program. The means of each trait of the 96 accessions were used for cluster analysis. Differences in traits have been considered as simple indicators of genetic similarities or differences in crop accessions. Deviation-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent accessions into different groups. The extent of diversity present between accessions determines the extent of improvement gained through selection and hybridization. The chance of improving the accessions through selection and hybridization is based on the distances of the two accessions from each other. Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis, 1936) by using the R-software program (version 3.1.1).

3.1.5.3.2 Estimation of squared distance

Squared distance (D^2) for each pair of accessions combinations were computed using the following formula:

$$D^2_{ij} = (X_i - X_j) S^{-1} (X_i - X_j)$$

Where, D^2_{ij} = the square distance between any two accessions i and j , X_i and X_j = the vectors for the values for accession i^{th} and j^{th} accession, and S^{-1} = the inverse of the pooled variance-covariance matrix.

3.1.5.3.3 Cluster analysis

The agglomerative hierarchical cluster analysis approach based on the squared distance (D^2) values was used to examine the assembling pattern of the 96 faba bean accessions based on their similarity with respect to the corresponding means of all the 19 traits studied. Cluster analysis was done by the average linkage method and the number of clusters was determined based on pseudo-F and t^2 values. The points where local peaks of the pseudo-F-statistic join with small values of the pseudo t^2 statistic followed by a larger pseudo t^2 for the next cluster combination were used to determine the number of clusters.

3.1.5.3.4 Estimation of intra and inter-cluster squared distances

Average intra and inter-cluster D^2 values were estimated using the formula $\frac{\sum D^2_i}{n}$, where

$\sum D^2_i$ is the sum of the distance between all possible combinations (n) of the accessions included in a cluster. Significance of the squared distances for each cluster was tested against the tabulated χ^2 values at p degree of freedom at 1% and 5% probability level where p = number of traits used for clustering accessions.

3.1.5.3.5 Principal component analysis (PCA)

Principal component analysis (PCA) was used to find out the trait which accounted more for the total variation among the accessions. Principal components based on correlation matrixes were calculated using the R-software program (version 3.1.1). The traits with large absolute values closer to unity within each principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). In this analysis, only PCs with Eigen values greater than one are considered as important. According to Johnson and Wichern (1988), a trait eigenvector greater than half divided by the standard deviation of the Eigen value of the respective PC was employed as a general guideline for weighing the relative significance of traits constituting the PCs.

3.2 Molecular genetic diversity and population structure study

3.2.1 Plant materials

Planting materials (seeds) were obtained from the Ethiopian Biodiversity Institute (EBI), Holeta Agricultural Research Center (HARC), and Debre Birhan Agricultural Research Center (DbARC). A total of 96 faba bean accessions including six released varieties were grown in a greenhouse at the plant genetic laboratory in Addis Ababa University (AAU) for DNA extraction. A total of 10 plants per accession were planted in a pot in a greenhouse in January 2019 G.C for DNA extraction. The accessions that were used in the laboratory experiment are also as illustrated in Table 1 above.

3.2.2 Genomic DNA extraction

The youngest and the lightest green leaves of three-week-old seedlings were collected separately from randomly selected individual plants of each accession and dried in silica gel. Genomic

DNA extraction of faba bean plants was performed from a bulked leaf tissue sample of five plants of each accession based on a method developed by Borsch *et al.* (2003), which involves a modified CTAB method (Puchooa, 2004) employing triple extraction for each sample tissue so as to get optimum quality and quantity of genomic DNA (the first extraction was selected based on high band intensity and less smear). Five plants from each accession were used in this experiment to produce 200 mg amount of fresh leaf tissue and then, 50 mg of dried leaf samples were collected from five representative plants and put in 2 ml labeled Eppendorf-caps containing two autoclaved beads with 5 mm diameter and ground with Mixer Mill (Retsch GmbH, Germany) for four minutes at a frequency of 30 Hz/sec. Total genomic DNA was isolated from about 50 mg of the fine ground leaf sample. A total of 700 µl of CTAB solutions (Consisted of 4 ml (0.5 M EDTA), 10 ml (1 M Tris-HCl), 2 g CTAB and 1 g PVP), 40 ml (5 M NaCl) were added to each ground sample. After mixing the CTAB solutions with the sample, it was incubated at 65°C for 30 min in a water bath and was centrifuged at 13000 rpm for 7 min. After taking the supernatant, 600 µl chloroform was added and centrifuged at 13000 rpm for 7 min and this step was repeated for better cleanup of the genomic DNA. Cooled (4 °C) Iso-propanol (2/3 of volume) was added to the solution and allowed to freeze for 2 h at -20°C and then centrifuged at 13000 rpm for 15 min. The supernatant was poured off and then the tubes were placed upside down on a paper towel to remove remaining Iso-propanol drops and then the pellet was air-dried for 30 min at room temperature. The DNA pellet was washed with 200 µl of 70% ethanol and centrifuged at 13000 rpm for 15 min, then aspirated and the DNA pellet was dried at room temperature for 15 min. The DNA pellet was suspended in 100 µl of TE (1x, p.a. grade), and was precipitated in ammonium acetate and after thoroughly mixing the solution, 300 µl of 100% ethanol was added and again kept at -20°C for more than 2 h. After centrifuging the solution at

13000 for 35 min, the fluid was carefully aspirated and again 200 µl of 70% ethanol was added and centrifuged at 13000 for 15 min followed by aspirating the liquid and drying the pellet at room temperature and the pellet was dissolved in 100 µl TE. The precipitation step was repeated by using sodium acetate and finally, the pellet was dissolved in 100 µl of TE and stored at -20°C.

3.2.3 DNA quantification and quality test

The isolated DNA samples were visualized using 0.8% agarose gel electrophoresis under UV light to test the quantity and quality of the DNA template. In addition, the quantity and quality of DNA extracts were also determined by using a NanoDrop spectrophotometer (Thermo Scientific™, Vantaa, Finland) by reading their absorbance at 260 nm wavelength. Then, the extracts with high band intensity, lesser smear, and high concentration were selected for PCR amplification based on the absorbance ratio at 260/280 reading. All DNA samples were stored at -20°C.

3.2.4 Primer selection and optimization

A total of 17 ISSR primers obtained from the University of British Columbia (primer kit UBC 900) were selected based on published experimental results made by different authors on faba bean (Abdul-Razzak *et al.*, 2012; Merji *et al.*, 2012; Wang *et al.*, 2012; Salazar-Laureles *et al.*, 2014) and other related crops like chickpea (Bhagyawant and Srivastava, 2008), lentil (Fikiru *et al.*, 2007; Meenakshi *et al.*, 2013) and mung bean (Singh *et al.*, 2013) (Table 2). Five representative landrace accessions, which were expected to represent a high level of genetic diversity were selected based on morphological analysis to screen primers for their amplification, polymorphism, and reproducible bands. According to DNA quantity and quality results, dilution of genomic DNA to the amount of 80 ng/µl was made for all samples for running of PCR to

screen primers and optimize the reaction condition. Accordingly, nine primers that showed polymorphic and reproducible bands were selected and these primers include six di-nucleotides, one tetra-nucleotides, and two penta-nucleotides repeat motives.

3.2.5 PCR amplification and gel electrophoresis

The polymerase chain reaction (PCR) amplification was conducted in a Biometra 2003 T3 Thermocycler (Applied Biosystem, USA) considering initial denaturation cycle at 94°C for 4 min, followed by 40 cycles of denaturation at 94°C for 15 s, 1 min annealing phase at primer specific temperature, and 1.30 min extension at 72°C; with a final extension of 7 min at 72°C. The lid temperature was held at 105°C. Finally, the PCR products were stored at 4°C until gel electrophoresis. The optimum PCR reaction components were 17.2 µl ddH₂O, 2.5 µl 10x PCR buffer, 2.5 µl MgCl₂ (25mM), 1 µl dNTPs (1.25mM), 0.4 µl primer (20pmol/ul), 0.4 µl Taq polymerase (5U/ul) and 1 µl template DNA (80 ng /ul). The ISSR-PCR products were separated by horizontal gel electrophoresis chamber (SGV-2626T-02, CBS Scientific, San Diego, California, USA) using 0.866% (w/v) agarose with 40ml 1xTBE buffer and 10 ul amplification product of each sample with 2 ul loading dye (6xloading dye) was loaded on the gel. Fifteen wells comb was used for each ISSR gel slab. DNA marker of 100 bp was loaded on the first lane of the gel as a size standard or to estimate the molecular weight and the other lanes were loaded with DNA templates. Electrophoresis was conducted at 100 V for about 1:30 - 2:00 h in 1X TBE buffer. The DNA was stained for 30 min with (10mg/ml) ethidium bromide (EtBr) which was mixed with 450 ml distilled water and destained for 30 min and bands were detected using BIO-RAD Gel Doc.followed by taking the band images.

Table 2. Lists of primers, their sequence, repeat motif, and annealing temperature

No.	Primer	Sequence from 5'-3'	Repeat Motif	Annealing temp. (°C)
1	810	5'GAGAGAGAGAGAGAGAT3'	(GA)8T	45
2	812	5'GAGAGAGAGAGAGAGAG3'	(GA)8G	45
3	815	5'CTCTCTCTCTCTCTG3'	(CT)8G	42
4	824	5'TCTCTCTCTCTCTCG3'	(TC)8G	48
5	834	5'AGAGAGAGAGAGAGAGYT3'	(AG)8YT	43
6	835	5'AGAGAGAGAGAGAGAGYC3'	(AG)8YC	48
7	840	5'GAGAGAGAGAGAGAGAGYT3'	(GA)8YT	42
8	841	5'GAGAGAGAGAGAGAGAYC3'	(GA)8YC	43
9	844	5'CTCTCTCTCTCTCTRC3'	(CT)8RC	43
10	848	5'CACACACACACACARG3'	(CA)8RG	47
11	853	5'TCTCTCTCTCTCTCRT3'	(TC)8RT	45
12	861	ACCACCACCACCACC	(ACC)6	55
13	864	5'ATGATGATGATGATGATG3'	(ATG)6	39
14	873	5'GACAGACAGACAGACA3'	(GACA)4	45
15	876	5'GATAGATAGACAGACA3'	(GATA)2(GACA)2	36
16	880	5'GGAGAGGAGAGGAGA3'	(GGAGA)3	45
17	881	5'GGGTGGGGTGGGGTG3'	(GGGTG)3	47

Source: Primer kit 900 (UBC 900)

3.2.6 Data scoring and analyses

ISSR markers were dominant markers and each locus was considered as a bi-allelic locus with one null allele and one amplifiable. ISSR bands were scored manually for each individual sample from the gel photograph. Each ISSR band was considered as an independent locus and polymorphic bands were scored as present (1) or absent (0) or ambiguous '?' data for all primers and the 96 individual samples. A binary matrix of accessions on rows and molecular data on columns was constructed. Only clearly reproducible bands were scored and difference in band

intensity was not considered. Data analysis was conducted using only the polymorphic bands. Scored data were directly entered into the computer for making analysis by using different software.

Primarily, the potential of the marker for estimating the genetic variability of faba bean was examined by assessing the marker informativeness through band scoring. Hence, the number of scored bands (NSB), number of polymorphic bands (NPB), number of private bands (NPvB), number of rare bands (NRB), number of common bands (NCB), and number of abundant bands (NAB) were recorded to detect marker informativeness prior to diversity analysis. Besides, polymorphic information content (PIC), marker index (MI), resolving power (RP), and effective multiplex ratio (EMR) parameters of the ISSR markers were calculated using GenAlEx 6.5 software (Peakall and Smouse, 2006). The PIC value for each amplified fragment was calculated as $PIC_i = 2f_i(1-f_i)$, PIC_i being the individual PIC of marker i , f_i the frequency of fragments present in the marker per accession, and $1-f_i$ the frequency of absent fragments (Pirani *et al.*, 2013). The MI was obtained using the following formula: $MI = PIC \times n \times np / (np + nm)$, n being the average number of fragments per primer, np the number of polymorphic fragments, and nm the number of the monomorphic fragment (Varshney *et al.*, 2007). The RP of each primer was calculated as follows: $RP = \sum I_b$, where I_b is the level of information of each fragment. The I_b can be represented as an interval of 0-1 by the following formula: $I_b = 1 - (2 \times |0.5 - f_i|)$ (Prevost and Wilkinson, 1999).

The population indices such as polymorphic loci (P), observed alleles (N_a), effective alleles (N_e), genetic diversity (GD), Shannon information index (I), expected heterozygosity (h), unexpected heterozygosity (uh), genetic distance (Gd), genetic identity (GI), genetic differentiation (PhiPT), gene flow (N_m), principal coordinate analysis (PCoA), and analysis of

molecular variance (AMOVA) were also measured by using GenAlEx 6.5 software (Peakall and Smouse, 2006). The Neighbor-joining dendrogram method of Saitou and Nei (1987) has constructed clustering using the R package POPPR software (Kamvar *et al.*, 2014). The degree of population differentiation was calculated with PhiPT. According to Wright (1978), and Hartl and Clark (1997), a PhiPT value greater than 0.25 is referred to as very great PhiPT, a PhiPT within 0.15 to 0.25 is referred to as a large PhiPT, a PhiPT within 0.05 to 0.15 is referred to as moderate PhiPT, and values lying within 0.00 to 0.05 are considered little PhiPT. Waples (1987) and Caccone (1985) categorized N_m into three that are $N_m \geq 1$ is referred to as high (then there will be little genetic differentiation among populations), N_m value within 0.25 – 0.99 is referred to as intermediate, and N_m value within 0.00 – 0.25 is referred to as low. Based on Wright (1951) if $N_m > 1$, the PhiPT is little, and if $N_m < 1$, the PhiPT is high. If $N_m > 1$, PhiPT does not result from genetic drift only, but if $N_m < 1$ it results from genetic drift only (Slatkin, 1987).

In this study, STRUCTURE and DAPC used to analyze the population structure of 96 accessions appeared to provide complementary information. To infer the population structure of faba bean accessions, STRUCTURE 2.3.4 software was used according to Pritchard *et al.* (2000). The structure analysis was run 5 times for each K value (K = 1 to 10) using a burn-in period of 50,000 with 100,000 Markov Chain Monte Carlo (MCMC) iterations, assuming an admixture model and uncorrelated allele frequencies. The most probable value of K for each test was detected by ΔK (Evanno *et al.*, 2005), using the web-based program Structure Harvester (Earl, 2012). CLUMPP v.1.1.2 (Jakobsson and Rosenberg, 2007) was used to align cluster assignment from independent runs using the in-files generated by structure Harvest. Bar plots were generated with average results of runs for the most probable K value, using DISTRUCT v.1.1 (Rosenberg, 2004). If a genotype membership coefficient was ≥ 0.80 , it was considered to belong to a group

while if its membership coefficient was < 0.80 , a genotype was considered as admixed. Discriminant analysis of principal components (DAPC) was also measured by the Adegenet R package software (Jombart *et al.*, 2010). DAPC is a multivariate method designed to identify and describe clusters of genetically related individuals (Jombart *et al.*, 2010).

4 RESULTS

4.1 Genetic diversity, association and morphological diversity study

4.1.1 Analysis of variances

The analysis of variance for different traits at Girar Jarso and Degem districts during the 2018 and 2019 main cropping seasons are presented in Tables 3 and 4, respectively. At Girar Jarso in 2018, significant differences among the accessions ($P < 0.001$) were observed for traits internode length, lowest pod height, plant height, number of pods per plant, pod width, number of seeds per plant, days to maturity, seed yield per plot, thousand seed weight, and grain yield. The traits leaf length, number of branches per plant, and pod length revealed significant difference ($P < 0.01$), and leaf area and number of pods per node showed significant difference ($P < 0.05$). On the other hand, leaf width, days to flowering, number of seeds per pod, and seed filling period showed non-significant differences. At Girar Jarso in 2019, all of the traits exhibited significant differences ($P < 0.001$) except pod width and leaf width that revealed, significant ($P < 0.01$) and significant ($P < 0.05$) difference, respectively (Table 3).

At Degem in 2018, significant differences among the accessions ($P < 0.001$) were revealed for traits leaf length, leaf width, leaf area, days to flowering, number of pods per plant, pod length, number of seeds per plant, days to maturity, seed filling period, seed yield per plot, and thousand seed weight. The traits number of pods per node, pod width, and grain yield showed significant differences ($P < 0.01$), and internode length, lowest pod height, plant height, and number of seeds per pod showed significant differences ($P < 0.05$). On the contrary, the number of branches per plant showed a non-significant difference. At Degem in 2019, all of the traits showed significant differences ($P < 0.001$) among the accessions (Table 4).

Results obtained from the test of homogeneity for an error of variance exhibited the calculated chi-square test (X^2) value surpasses the corresponding tabular (X^2) value at 5% and 1% level of significance for most traits (Table 5). Therefore, the hypothesis of homogeneous variance was rejected according to Gomez and Gomez (1984).

Table 3. Analysis of variance for nineteen traits of 96 faba bean accessions tested at Girar Jarso district during 2018 and 2019 main cropping season

Trait	Girar Jarso 2018					Girar Jarso 2019				
	Mean square					Mean square				
	Rep (1)	Accession (95)	Bl (Rep) (6)	MSE (89)	CV	Rep (1)	Accession (95)	Bl (Rep) (6)	MSE (89)	CV
LL	2.98	1.33**	0.89	0.70	17.84	0.00	2.26***	0.96	0.23	8.69
LW	1.06	0.44	0.57	0.35	25.28	0.01	0.74*	0.20	0.09	12.91
LA	247.09	8.20*	11.37	5.31	28.94	0.01	26.20***	10.78	2.94	17.51
DTF	13.02	9.09	5.17	6.58	5.17	0.52	15.27***	0.42	0.38	1.05
NPPN	0.14	0.22*	0.18	0.14	27.11	0.00	0.13***	0.08	0.02	9.29
IL	0.49	1.86***	0.75	0.80	31.87	0.41	3.03***	2.50	0.27	13.20
LPH	52.40	56.33***	22.19	21.61	20.96	13.03	116.27***	42.69	11.12	9.47
PH	1404.5	478.30***	168.10	104.70	20.56	190.50	1212.70***	1522.50	71.70	8.72
NPPPL	75.00	23.04***	8.88	8.59	34.49	6.62	115.08***	14.04	8.72	21.61
NSPP	0.03	0.47	0.31	0.46	32.93	0.01	0.22***	0.04	0.03	7.67
NBPPL	0.26	0.47**	0.26	0.26	164.40	0.05	0.56***	0.21	0.10	66.76
PL	0.74	1.92**	0.61	1.06	20.96	0.03	1.44***	0.29	0.13	6.57
PW	1.74	0.67***	0.08	0.25	12.61	120.08	0.54**	0.53	0.33	20.78
NSPPL	100.63	120.66***	14.25	32.39	26.43	0.40	664.10***	147.10	40	20.13
DM	99.19	109.89***	10.30	21.05	3.68	10.08	266.46***	5.21	0.46	0.48
SFP	234.08	76.90	12.95	59.77	10.31	0.52	256.97***	0.42	0.38	0.75
SYPP	111	3319***	827	1136	45.56	33	5595***	21998	1431	28.43
TSW	1789	15573***	3693	3255	12.40	2857	15411***	3498	3319	12.48
GY	0.00	0.77***	0.19	0.15	35.10	0.12	0.82***	1.31	0.19	24.57

Table 4. Analysis of variance for nineteen traits of 96 faba bean accessions tested at Degem district during 2018 and 2019 main cropping season

Trait	Degem 2018					Degem 2019				
	Mean square					Mean square				
	Rep (1)	Accession (95)	Bl (Rep) (6)	MSE (89)	CV	Rep (1)	Accession (95)	Bl (Rep) (6)	MSE (89)	CV
LL		2.60***	0.02	0.01	1.61	27.64	2.59***	0.02	0.02	1.86
LW	4.07	0.75***	0.00	0.00	1.76	3.71	0.75***	0.01	0.01	2.98
LA	1.52	39.65***	0	0	0.33	1.28	39.52***	0	0	0.38
DTF	5046	13***	1	1	1.33	5016	13***	1	1	1.37
NPPN	0.93	0.15**	0.12	0.09	19.54	6.26	0.22***	0.04	0.03	10.45
IL	3.88	2.37*	1.15	1.61	24.06	83.03	2.94***	1.22	0.51	12.34
LPH	67.69	100.97*	57.52	67.65	24.85	7587	186***	16	20	11.12
PH	136.70	293.80*	418.60	185.30	15.30	39820	551***	51	72	7.99
NPPPL	94.92	42.71***	19.97	17.68	30.82	1652.50	68.30***	4.20	8.20	17.75
NSPP	0.04	0.24*	0.20	0.15	17.23	0.22	0.34***	0.06	0.07	11.63
NBPPL	0	0.62	0.52	0.44	78.48	3.26	0.69***	0.13	0.14	39.86
PL	3.71	2.23***	0.17	1.12	17.65	4.87	2.68***	0.20	0.34	9.74
PW	1.02	0.63**	0.75	0.37	15.50	148.67	0.55***	0.10	0.20	14.25
NSPPL	210.42	235.15***	57.07	82.66	30.04	6401	321***	47	34	16.59
DM	24395	65***	4	3	1.13	24245	65***	4	3	1.13
SFP	7292	78***	4	2	1.48	7256	78***	5	2	1.50
SYPP	29552	3970***	1116	1568	27.85	31431	3120***	470	579	16.93
TSW	1121462	25243***	1036	1394	6.82	1179376	27805***	532	1038	5.82
GY	2.95	0.39**	0.20	0.21	26.96	4.15	0.33***	0.04	0.07	14.95

Table 5. Bartlett test of homogeneity of variances for each trait

Trait	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	DM	SFP	SYPP	TSW	GY
K-squared	7.08	0.12	43.65	182.92	37.46	12.823	81.50	63.63	88.45	87.439	11.91	29.75	64.16	108.93	45.92	23.91	31.45	52.54	44.38
df	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
p-value	0.07	0.99	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

4.1.2 Mean, range and estimation of genetic parameters

4.1.2.1 Mean and range

The range and mean performances of nineteen traits for the accessions evaluated in this study are presented in Table 6. The mean performances of the 96 accessions for 19 traits are presented in appendices VI, VII, VIII, and IX for Girar Jarso in 2018, Girar Jarso in 2019, Degem in 2018, and Degem in 2019, respectively. The result of the range of parameters suggested that there were considerable differences observed in all of the 19 traits. The Duncan's Multiple Range Test (DMRT) was used for the mean comparison (Appendix X). The 96 faba bean accessions studied showed a wide range of variability for most of the traits. Overall grain yield for accessions ranged from 0.29 to 3 t/ha. Accession 29531 resulted in the highest mean grain yield (3 t/ha) in all environments. The accessions 25298 and 26859 gave the lowest grain yield with values of 0.29 t/ha and 0.66 t/ha at Girar Jarso in 2018 and in 2019, respectively. At Degem during 2018 and 2019 main cropping season accession 25018 gave the lowest grain yield of 0.64 t/ha. The mean performance of grain yield of the 96 faba bean accessions in this study was 1.09 t/ha at Girar Jarso in 2018, 1.79 t/ha at Girar Jarso in 2019, 1.69 t/ha at Degem in 2018, and 1.71 t/ha at Degem in 2019. The result revealed 40.6%, 46.9%, 48.9%, and 41.7% of the accessions gave above the grand mean of 1.09 t/ha, 1.79 t/ha, 1.69 t/ha, and 1.71 t/ha at Girar Jarso in 2018, Girar Jarso in 2019, Degem in 2018, and Degem in 2019, respectively. The high yielding accession 29531 had a yield advantage of 11.46%, 26.04%, and 26.04% as compared with that of the best check Hachalu at Girar Jarso in 2018, Degem in 2018, and Degem in 2019, respectively. Similarly, at Girar Jarso in 2019, the high yielding accession 29531 had a yield advantage of 4.17% as compared with the best check Moti.

Table 6. Mean and ranges of the nineteen traits 96 for faba bean accessions evaluated in the study

Trait	Girar Jarso 2018			Girar Jarso 2019			Degem 2018			Degem 2019		
	Min	Mean	Max	Min	Mean	Max	Min	Mean	Max	Min	Mean	Max
LL	3.14	4.68	6.82	3	5.47	8.57	4.45	6.79	9.33	4.55	6.82	9.30
LW	1.34	2.34	3.37	1.15	2.28	4.74	1.79	3.02	4.52	1.80	3.03	4.50
LA	4.20	7.99	14.92	3.84	9.71	20.19	5.83	13.91	24.54	5.88	13.94	24
DTF	46	49.07	53	46	58.69	63	55	59.66	64.61	55	59.65	64.61
NPPN	1	1.35	2.25	1	1.37	2.21	1	1.52	2.33	0.81	1.64	2.57
IL	1.5	2.81	6	2.04	3.95	9	2.25	5.21	7.50	1.68	5.77	9.15
LPH	15	22.14	37.19	14.50	35.03	59	19.50	33.04	53	18.68	39.87	65.50
PH	32	50.50	104.50	38	97.55	142	63.50	90.47	118	51.48	105.48	141.50
NPPPL	5	8.50	21	5	13.62	35	6	13.71	25.50	5.76	15.92	30.60
NSPP	1	2.03	4	1.51	2.20	3.74	1.53	2.20	3.09	1.25	2.26	3.06
NBPPL	0	31	1.5	0	0.48	2	0	0.84	2	0	0.93	2
PL	3.30	4.85	6.90	2.82	5.58	8.82	3.50	5.82	9	2.57	5.91	9.22
PW	2.95	3.84	4.80	1.10	2.71	3.65	1.90	3.97	5.50	1.05	3.07	5
NSPPL	13	21.18	47.11	13	31.32	83	14	30.05	60.50	15.44	34.62	65.15
DM	109	122.66	139	121	141.88	153	138.20	153.81	161	138	153.74	161
SFP	58	73.22	88	60	82.66	95	73.83	94.16	104	73.83	94.08	103.80
SYPP	26	72.83	193	45	134.11	235	53	141.27	258	58	141.30	250
TSW	273.50	462.30	715.50	320	462.61	719	354	543.66	873	354	545.04	896.57
GY	0.29	1.09	2.50	0.66	1.79	3.00	0.64	1.69	3.00	0.64	1.71	3.00

LL: leaf length (cm), LW: leaf width (cm), LA: leaf area (cm²), DTF: days to flowering, NPPN: number of pods per node, IL: internode length (cm), LPH: lowest pod height (cm), PH: plant height (cm), NPPPL: number of pods per plant NSPP: number of pods per pod, NBPPL: number of branches per plant, PL: pod length (cm), PW: pod width (cm), NSPPL: number of seeds per plant, DM: days to maturity, SFP: seed filling period, SYPP: seed yield per plot (g), TSW: thousand seed weight (g), GY: grain yield (t/ha)

4.1.2.2 Estimates of genetic parameters

4.1.2.2.1 Estimates of variance components

Estimates of phenotypic and genotypic variances, phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), broad-sense heritability (h_b^2), genetic advance (GA), and genetic advance as percent of the mean (GAM) at Girar Jarso and Degem districts during 2018 and 2019 main cropping season are presented in tables 7 and 8, respectively. The high genotypic and phenotypic variance at Girar Jarso in 2018 was observed for thousand seed weight followed by seed yield per plot and plant height. At Girar Jarso in 2019, the high genotypic and phenotypic variance was shown by plant height, the number of seeds per plant, days to maturity, seed filling period, seed yield per plot, and thousand seed weight. Plant height, number of seeds per plant, seed yield per plot, and thousand seed weight has exhibited high genotypic and phenotypic variances at Degem during the 2018 and 2019 main cropping season. The estimates of phenotypic and genotypic variances were the highest for thousand seed weight followed by seed yield per plot and the lowest for the number of pods per node followed by the number of seeds per pod at all environments.

At Girar Jarso in 2018, the genotypic variance was greater than its corresponding environmental variance for the traits plant height, the number of seeds per pod, days to maturity, thousand seed weight, and grain yield. On the other hand, the magnitude of genotypic variance was smaller than that of environmental variance at the same location for leaf length, leaf area, number of pods per node, internode length, the lowest pod height, number of pods per plant, pod length, pod width, and seed yield per plot. This signifies the effect of environmental factors on the phenotypic expression of these traits was high. At Girar Jarso in 2019, the genotypic variance was greater than environmental variances for most of the traits except pod width, seed yield per plot, and grain yield. On the other hand, the magnitude of genotypic variance was smaller than that of environmental variance at the same location for pod width, seed yield per plot, and grain yield.

At Degem in 2018, the genotypic variance is smaller than that of environmental variance except for leaf length, leaf width, leaf area, days to flowering, days to maturity, seed filling period, and thousand seed weight. At Degem in 2019, the genotypic variance was greater than that of environmental variance for most of the traits except pod width.

At Girar Jarso in 2018, the PCV and GCV ranged from the low value for days to maturity (6.59%, 5.46%) to the high value for the number of branches per plant (195.56%, 105.91%). At Girar Jarso in 2019, the PCV and GCV ranged from the low value for days to flowering (4.77%, 4.65%) to the high value for the number of branches per plant (110.96%, 88.63%). At Degem in 2018, the PCV and GCV ranged from the low value for days to maturity (3.79%, 3.62%) to the high value for the number of branches per plant (85.18%, 33.12%). Similarly, at Degem in 2019, the PCV and GCV ranged from the low value for days to maturity (3.79%, 3.62%) to the high value for the number of branches per plant (68.74%, 55.99%).

Generally, the GCV values were lower than that of PCV for all environments. The PCV values for leaf length, leaf area, number of pods per node, internode length, lowest pod height, plant height, number of pods per plant, number of branches per plant, pod width, number of seeds per plant, seed yield per plot, thousand seed weight, and grain yield was higher than that of GCV values of these traits at Girar Jarso in both years. However, the difference was lower for days to maturity in the same environments. The difference between PCV and GCV values was high for the number of pods per node, internode length, lowest pod height, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, pod length, pod width, number of seeds per plant, seed yield per plot, and grain yield; low for leaf length, leaf width, leaf area, days to flowering, days to maturity, seed filling period and thousand seed weight at Degem during 2018 and 2019 main cropping season, respectively.

The highest PCV at Girar Jarso in 2018 was observed for the number of branches per plant (195.56%) followed by seed yield per pot (63.99%), and grain yield (62.12%). The highest GCV

values were observed for the number of branches per plant (105.91%) followed by grain yield (51.25%), and seed yield per plot (44.93%). The lowest PCV and GCV values were observed for days to maturity (6.59%, 5.46%).

At Girar Jarso in 2019, the highest PCV and GCV values were observed for the number of branches per plant (110.96%, 88.63%) followed by the number of seeds per plant (55.96%, 52.22%), and the number of pods per plant (55.90%, 51.55%). The lowest PCV and GCV values were recorded by days to flowering (4.77%, 4.65%) followed by days to maturity (8.14%, 8.13%).

Similarly, at Degem in 2018, the highest PCV and GCV values were observed for the number of branches per plant (85.18%, 33.12%) followed by the number of seeds per plant (41.94%, 29.27%). The lowest PCV and GCV values were also observed by days to maturity (3.79%, 3.62%) followed by days to flowering (4.31%, 4.10%), and seed filling period (6.74%, 6.57%).

At Degem in 2019, the highest PCV and GCV values were recorded for the number of branches per plant (68.74%, 55.99%) followed by the number of pods per plant (38.79%, 34.49%), and the number of seeds per plant (38.13%, 34.33%). The lowest PCV and GCV values were recorded by days to maturity (3.79%, 3.62%) followed by days to flowering (4.32%, 4.09%), and seed filling period (6.74%, 6.57%).

4.1.2.2.2 Estimation of broad-sense heritability and genetic advance

In this study estimate of heritability in a broad sense ranged from 19.81% for leaf area to 68.73% for days to maturity at Girar Jarso in 2018. On the other hand, at Girar Jarso in 2019, broad-sense heritability was ranged from 23.20% for pod width to 99.70% for the seed filling period (Table 7). At Degem in 2018, an estimate of heritability in a broad sense ranged from 13.72% for internode length to 99.99% for leaf area. At Degem in 2019, the heritability values ranged from 48.07 % for pod width to 99.99% for leaf area (Table 8).

At Girar Jarso in 2018, heritability estimates were high for days to maturity (68.73%) followed by grain yield (68.06%) and thousand seed weight (65.18%), while the medium heritability estimates were obtained for the number of seeds per plant (58.87%) followed by seed yield per plot (49.31 %) and pod width (47.79%). The heritability was low for the traits leaf area (19.81%) followed by the number of pods per node (23.10%) and the number of branches per plant (29.33%). Days to maturity (99.66%) followed by seed filling period (99.70%) and days to flowering (95.11%) are traits with a high heritability value at Girar Jarso in 2019. On the other hand, seed yield per plot (48.24%) and pod width (23.20%) exhibited medium and low heritability, respectively. Leaf area (99.99%), leaf width (99.25%), and leaf length (99.08%) exhibited high heritability at Degem in 2018. Traits number of seeds per plant (48.70%) followed by seed yield per plot (44.11%) and the number of pods per plant (41.36%) exhibited medium heritability values in the same environment. Traits number of branches per plant (15.11%) followed by the number of seeds per pod (20.17%) and the lowest pod height (20.22%) were found to have low heritability. At Degem in 2019, traits leaf area (99.99%), leaf length (98.77%), and leaf width (97.86%) had relatively high heritability values. Pod width (48.07%) was found to have a medium heritability value.

Estimates of GA for grain yield was 0.95 t/ha at Girar Jarso in 2018 indicating that whenever we select the best 5% high yielding genotypes as parents, the mean grain yield of progenies could be improved by 0.95 t/ha for the first cycle, that is, mean genotypic value of the new population for grain yield was improved from 1.09 t/ha to 2.04 t/ha. In the same way, the GA value will be 0.61 t/ha, 1.69 t/ha, and 1.71 t/ha at Girar Jarso in 2019, Degem in 2018, and Degem in 2019, respectively (Tables 7 and 8).

Maximum GAM at 5% selection intensity was recorded for the number of branches per plant (118.16%) followed by grain yield (87.09%) and seed yield per plot (64.99%) at Girar Jarso in 2018. It was minimum for days to maturity (9.33%) followed by leaf area (13.19%) and leaf

length (13.72%). At Girar Jarso in 2019, GAM at 5% selection intensity was high for the number of branches per plant (145.83%) followed by the number of seeds per plant (100.36%) and the number of pods per plant (97.95%). The minimum GAM observed for days to flowering (9.34%) followed by pod width (11.34%) and days to maturity (16.71%). At Degem in 2018, leaf width (97.23%), grain yield (54.03%), and the number of branches per plant (53.63%) exhibited high genetic advance as a percent of the mean. The minimum genetic advance as percent of mean was observed for thousand seed weight (0.49%), plant height (0.69%), and seed yield per plot (0.93%). At Degem in 2019, the number of branches per plant (93.97%), leaf area (65.78%), and the number of seeds per plant (63.68%) exhibited high genetic advance as a percent of the mean. At this location, days to maturity (7.12%), days to flowering (7.99%), and seed filling period (13.19%) exhibited minimum genetic advance as percent of the mean (tables 7 and 8).

The present study showed that plant height, thousand seed weight and grain yield revealed high heritability coupled with high GAM at Girar Jarso in 2018. In the same environment, internode length, lowest pod height, number of pods per plant, number of seeds per plant, and seed yield per plant exhibited medium heritability and high GAM. At Girar Jarso in 2019, most of the traits exhibited high heritability and high GAM. On the other hand, seed yield per plot, thousand seed weight, and grain yield exhibited medium heritability and high GAM. At Degem in 2018, leaf length, leaf width, and leaf area revealed high heritability coupled with high GAM. The trait grain yield exhibited medium heritability and high GAM. At Degem in 2019, most of the traits showed high heritability and high GAM except for the traits days to flowering, pod width, days to maturity, and seed filling period.

Table 7. Phenotypic variance, genotypic variance, environmental variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad-sense, genetic advance and genetic advance as percent of mean of 96 Ethiopian faba bean accessions at Girar Jarso during 2018 and 2019 main cropping season

Traits	Girar Jarso 2018								Girar Jarso 2019							
	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h_b^2 (%)	GA	GAM %	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h_b^2 (%)	GA	GAM %
LL	1.00	0.31	0.69	21.48	11.96	31.01	0.64	13.72	1.10	0.87	0.23	19.17	17.08	79.42	1.72	31.36
LW	-	-	-	-	-	-	-	-	0.39	0.30	0.09	27.54	24.33	78.05	0.99	44.29
LA	6.53	1.29	5.24	32.32	14.39	19.81	1.04	13.19	12.93	10.03	2.9	37.01	32.61	77.61	5.75	59.18
DTF	-	-	-	-	-	-	-	-	7.82	7.44	0.38	4.77	4.65	95.11	5.48	9.34
NPPN	0.17	0.04	0.13	30.91	14.85	23.10	0.20	14.70	0.07	0.05	0.02	19.10	16.69	76.34	0.41	30.04
IL	1.31	0.52	0.79	41.08	25.92	39.81	0.94	33.69	1.36	1.09	0.27	29.61	26.51	80.14	1.93	48.89
LPH	38.39	17.09	21.30	28.14	18.77	44.51	5.68	25.80	58.98	47.97	11.01	21.93	19.77	81.33	12.87	36.73
PH	289.56	183.89	105.67	34.04	27.13	63.51	22.26	44.53	448.41	376.10	72.31	21.71	19.88	83.87	36.59	37.51
NPPPL	15.75	7.19	8.56	46.78	31.60	45.65	3.73	43.99	57.96	49.30	8.66	55.90	51.55	85.06	13.34	97.95
NSPP	-	-	-	-	-	-	-	-	0.13	0.10	0.03	15.55	13.53	75.69	0.56	24.25
NBPPL	0.36	0.11	0.25	195.56	105.91	29.33	0.36	118.16	0.29	0.18	0.11	110.96	88.63	63.80	0.71	145.83
PL	1.47	0.45	1.02	25.11	13.83	30.32	0.76	15.69	0.78	0.64	0.14	15.80	14.37	82.69	1.50	26.91
PW	0.45	0.22	0.23	17.45	12.07	47.79	0.66	17.18	0.41	0.10	0.31	23.72	11.42	23.20	0.31	11.34
NSPPL	75.95	44.71	31.24	41.20	31.61	58.87	10.57	49.97	307.18	267.42	39.76	55.96	52.22	87.06	31.43	100.36
DM	65.13	44.76	20.37	6.59	5.46	68.73	11.43	9.33	133.38	132.92	0.46	8.14	8.13	99.66	23.71	16.71
SFP	-	-	-	-	-	-	-	-	128.60	128.22	0.38	13.72	13.70	99.70	23.29	28.18
SYPP	2182.73	1076.23	1106.5	63.99	44.93	49.31	47.45	64.99	2108.29	654.30	1453.99	34.24	19.07	31.03	29.35	21.89
TSW	9427.53	6145.10	3282.43	21.02	16.97	65.18	130.38	28.22	9371.03	6040.40	3330.63	20.93	17.08	64.46	128.54	27.79
GY	0.46	0.31	0.15	62.12	51.25	68.06	0.95	87.09	0.38	0.18	0.2	34.15	24.33	48.24	0.61	33.94

Table 8. Phenotypic variance, genotypic variance, environmental variance, phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad-sense, genetic advance and genetic advance as percent of mean of 96 Ethiopian faba bean accessions at Degem during 2018 and 2019 main cropping season

Traits	Degem 2018								Degem 2019							
	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h_b^2 (%)	GA	GAM %	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	h_b^2 (%)	GA	GAM %
LL	1.31	1.29	0.02	16.80	16.73	99.08	2.93	43.07	1.30	1.29	0.01	16.75	16.65	98.77	2.32	34.08
LW	0.38	0.37	0.01	20.36	20.28	99.25	2.93	97.23	0.38	0.37	0.01	20.37	20.15	97.86	1.24	41.06
LA	19.83	19.83	0.00	31.98	31.98	99.99	2.96	21.23	19.77	19.76	0.01	31.93	31.93	99.99	9.16	65.78
DTF	6.61	5.97	0.64	4.31	4.10	90.42	2.67	4.48	6.63	5.96	0.67	4.32	4.09	89.87	4.77	7.99
NPPN	0.12	0.03	0.09	22.47	11.09	24.35	0.72	47.51	0.13	0.10	0.03	21.72	19.03	76.83	0.56	34.37
IL	1.82	0.25	1.57	25.90	9.59	13.72	0.41	7.78	1.61	1.11	0.5	22.03	18.25	68.62	1.80	31.14
LPH	83.99	16.98	67.01	27.82	12.51	20.22	0.60	1.81	102.80	83.13	19.7	25.43	22.87	80.87	16.89	42.37
PH	241.24	50.72	235.5	17.22	7.89	21.03	0.62	0.69	310.91	239.93	71	16.72	14.69	77.17	28.03	26.58
NPPPL	30.16	12.48	17.68	40.25	25.88	41.36	1.22	8.96	38.14	30.15	8	38.79	34.49	79.06	10.06	63.18
NSPP	0.18	0.04	0.14	19.28	8.66	20.17	0.60	27.14	0.19	0.12	0.07	19.22	15.30	63.37	0.57	25.09
NBPPL	0.50	0.08	0.42	85.18	33.12	15.11	0.45	53.63	0.41	0.27	0.14	68.74	55.99	66.36	0.88	93.97
PL	1.65	0.59	1.06	22.02	13.16	35.74	1.06	18.14	1.50	1.17	0.33	20.73	18.30	77.93	1.97	33.27
PW	0.50	0.12	0.38	17.84	8.83	24.49	0.72	18.19	0.37	0.18	0.19	19.78	13.71	48.07	0.60	19.59
NSPPL	156.81	76.37	80.44	41.94	29.27	48.70	1.44	4.82	174.26	141.27	33	38.13	34.33	81.07	22.04	63.68
DM	33.97	30.98	2.99	3.79	3.62	91.17	2.70	1.75	33.97	30.96	3.01	3.79	3.62	91.14	10.94	7.12
SFP	40.24	38.25	1.99	6.74	6.57	95.05	2.81	2.99	40.17	38.18	2	6.74	6.57	95.03	12.41	13.19
SYPP	2754.90	1215.21	1540	37.25	24.74	44.11	1.30	0.93	1845.88	1273.86	572	30.41	25.26	69.01	61.08	43.23
TSW	13306.88	11935.81	1371	21.24	20.12	89.70	2.65	0.49	14405.54	13399.54	1006	22.02	21.24	93.02	229.98	42.20
GY	0.30	0.09	0.21	32.41	17.98	30.77	0.91	54.03	0.20	0.13	0.07	26.02	21.30	66.99	0.61	35.91

4.1.3 Association among traits

4.1.3.1 Estimates of correlation coefficients at phenotypic and genotypic levels

Estimates of phenotypic and genotypic correlation coefficients of the studied traits for the Girar Jarso 2018, Girar Jarso 2019, Degem 2018 and Degem 2019 are shown in Tables 9, 10, 11, and 12, respectively. The magnitudes of genotypic correlation coefficients for most of the traits were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the presence of inherent association among various traits.

4.1.3.2 Correlation of grain yield with other traits

Grain yield showed positive and significant genotypic and phenotypic association with most of the studied traits. Significant positive phenotypic and genotypic correlation coefficients were detected between grain yield and number of pods per plant, number of branches per plant, number of seeds per plant, and seed yield per plot at Girar Jarso in 2018. While, at Girar Jarso in 2019, grain yield revealed significant positive correlation coefficients with leaf length, leaf width, leaf area, lowest pod height, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, pod length, number of seeds per plant, and seed yield per plot at both genotypic and phenotypic level. Phenotypic and genotypic correlation coefficients revealed a positive and significant association of grain yield with leaf length, plant height, seed yield per plot, and thousand seed weight at Degem in 2018. Whereas, at Degem in 2019, grain yield showed a positive and significant association with seed yield per plot and thousand seed weight at both genotypic and phenotypic levels.

On the other hand, grain yield showed negative and significant correlations with days to flowering ($r_g = -0.21^*$) and number of pods per node ($r_g = -0.23^*$) at Degem in 2018 at a genotypic level. In addition, grain yield showed non-significant genotypic and phenotypic correlation with days to maturity in all environments.

4.1.3.2 Correlations among other traits

At Girar Jarso in 2018, thousand seed weight showed positive and significant association with most of the traits under study except for the traits number of pods per node, pod width, days to maturity, and seed yield per plot at the genotypic level and it had positive and significant phenotypic correlation with leaf length, leaf width, leaf area, internode length, lowest pod height, plant height, number of branches per plant, and pod length. Thousand seed weight revealed a positive and significant association with leaf length, leaf width, leaf area, pod length, pod width, days to maturity, and seed filling period at both genotypic and phenotypic levels at Girar Jarso in 2019. At Degem in 2018, thousand seed weight showed positive and significant genotypic correlation coefficients with internode length, lowest pod height, plant height, number of seeds per pod, pod length, pod width, days to maturity, seed filling period, and seed yield per plot, while it was associated negatively and significantly with the number of pods per node, number of pods per plant, and number of seeds per plant. It was also associated positively and significantly with leaf length, leaf area, plant height, number of seeds per plant, seed yield per plot at the phenotypic level. At Degem in 2019, thousand seed weight revealed positive and significant genotypic and phenotypic correlation coefficients with internode length, pod length, pod width, days to maturity, seed filling period, and seed yield per plot, while it showed negative and significant genotypic and phenotypic correlation coefficients with a number of pods per node and number of seeds per plant.

At genotypic and phenotypic levels positive and significant correlation coefficients of seed yield per plot with internode length, lowest pod height, plant height, number of pods per plant, number of seeds per plant, and days to maturity were obtained at Girar Jarso in 2018. At Girar Jarso in 2019, seed yield per plot showed positive and significant correlation coefficients with most of the traits under study except the traits days to flowering, days to maturity, and seed filling period at the genotypic level. While it was also associated positively and significantly with most of the traits except days to flowering, internode length, number of seeds per pod, pod width, days to

maturity, and seed filling period at the phenotypic level. At the genotypic level, seed yield per plot showed positive and significant correlation coefficients with most of the traits except days to maturity, and number of pods per node at Degerm in 2018. While, at the phenotypic level seed yield per plot exhibited positive and significant correlation coefficients with leaf length, leaf area, plant height, number of pods per plant, number of branches per plant, and number of seeds per plant. On the other hand, seed yield per plot associated negatively and significantly with days to flowering at the genotypic level. At Degerm in 2019, positive and significant correlation coefficients of seed yield per plot with leaf length, leaf area, plant height, number of pods per plant, and number of seeds per plant were revealed at both genotypic and phenotypic level, while seed yield per plot was negative and significantly associated with days to flowering at both genotypic and phenotypic level.

At Girar Jarso in 2018 and 2019, the seed filling period showed positive and significant correlation coefficients with leaf length, leaf width, leaf area, internode length, lowest pod height, plant height, pod length, and days to maturity at both genotypic and phenotypic level. At Girar Jarso in 2018, the seed filling period correlated negatively and significantly with the number of seeds per pod and pod width at the genotypic level. Genotypic and phenotypic correlation coefficients of seed filling period with days to maturity were positive and significant at Degerm in 2018 and 2019. While at Degerm during the two years the seed filling period was negatively and significantly correlated with days to flowering at both genotypic and phenotypic levels.

Days to maturity associated positively and significantly with leaf length, leaf width, leaf area, days to maturity, internode length, lowest pod height, plant height, and pod length at both genotypic and phenotypic level at Girar Jarso in 2018 and 2019. At Degerm in 2018, days to maturity was associated positively and significantly with lowest pod height, and plant height at

both genotypic and phenotypic level, and also similar results obtained at Degem in 2019 at the genotypic level.

The number of seeds per plant was positively and significantly associated with leaf area, the number of pods per node, plant height, and the number of branches per plant at the genotypic and phenotypic levels at all environments. At Girar Jarso in 2018, pod width was negatively and significantly correlated with leaf length, leaf area, days to flowering, internode length, and plant height at a genotypic level, while positively and significantly correlated with the number of branches per plant, and pod length at the phenotypic level. Pod width was correlated positively and significantly with leaf length, leaf width, leaf area, number of seeds per pod, and pod length at both genotypic and phenotypic levels at Girar Jarso in 2019. Whereas, pod width was correlated positively and significantly with pod length at the genotypic and phenotypic levels in all environments. At the genotypic and phenotypic level, pod length correlated positively and significantly with internode length, and the number of seeds per pod in all environments. The number of branches per plant was correlated positively and significantly with the number of pods per plant both at the genotypic and phenotypic levels in all environments.

At Girar Jarso in 2018, the number of seeds per pod was correlated positively and significantly with plant height both at the genotypic and phenotypic levels. On the other hand, the number of seeds per pod correlated negatively and significantly with leaf width, number of pods per node, and number of pods per plant both at the genotypic and phenotypic level at Degem during 2018 and 2019 main cropping season. Number of pods per plant-associated positively and significantly with leaf length, leaf area, number of pods per node, and plant height both at the genotypic and phenotypic level at all environments. Plant height was correlated positively and significantly with the lowest pod height both at the genotypic and phenotypic levels in all environments. Whereas, the lowest pod height was correlated positively and significantly with the number of pods per node both at the genotypic and phenotypic levels in all environments.

At the genotypic and phenotypic level, internode length was correlated positively and significantly with leaf length, leaf width, and leaf area at Girar Jarso in 2018 and 2019. The number of pods per nod correlated positively and significantly with leaf length, leaf width, and leaf area both at the genotypic and phenotypic level at Girar Jarso in 2019, while it was correlated negatively and significantly with leaf width at Girar Jarso in 2018 at the genotypic level. Days to flowering were correlated positively and significantly with leaf length and leaf area at the genotypic level at Girar Jarso in 2018. Leaf area associated positively and significantly with leaf length, and leaf width at the genotypic and phenotypic levels in all environments. Leaf width associated positively and significantly with leaf length both at the genotypic and phenotypic levels in all environments.

Table 9. Estimates of correlation coefficients at genotypic (below diagonal) and phenotypic (above diagonal) levels among 19 traits of 96 faba bean accessions at Girar Jarso during 2018 main cropping season

Trait	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	DM	SFP	SYPP	TSW	GY
LL		0.70**	0.91**	0.18	0.17	0.42**	0.54**	0.68**	0.34**	0.17	0.32**	0.49**	-0.12	0.39**	0.48**	0.53**	0.19	0.29**	0.07
LW	0.97**		0.82**	0.12	0.1	0.23*	0.42**	0.39**	0.258	0.04	0.24*	0.30**	0.13	0.28**	0.32**	0.35**	0.09	0.24*	0.03
LA	1.00**	1.00**		0.19	0.15	0.36**	0.48**	0.58**	0.34**	0.1	0.29**	0.36**	-0.08	0.35**	0.41**	0.43**	0.14	0.22*	0.04
DTF	0.55**	0.15	0.49**		0.21	0.46**	0.37**	0.44**	0.18	-0.17	0.21*	0.04	-0.18	0.19	0.41**	0.17	0.12	0.03	0.07
NPPN	0.07	-0.38**	-0.1	0.1		0.09	0.38**	0.29**	0.36**	-0.03	0.19	0.05	-0.02	0.34**	0.1	0.14	0.08	0.02	0.02
IL	0.66**	0.65**	0.80**	1.00**	0.08		0.51**	0.68**	0.35**	0.16	0.27**	0.41**	-0.04	0.38**	0.49**	0.34**	0.22*	0.24*	0.15
LPH	0.69**	0.83**	0.71**	0.90**	0.41**	0.71**		0.75**	0.39**	0.12	0.34**	0.45**	0.05	0.34**	0.49**	0.53**	0.25*	0.28**	0.19
PH	0.82**	0.65**	0.79**	1.00**	0.22*	0.88**	0.90**		0.56**	0.24*	0.49**	0.55**	-0.1	0.55**	0.51**	0.49**	0.32**	0.35**	0.18
NPPPL	0.25*	0.22*	0.23*	0.60**	0.32**	0.57**	0.53**	0.57**		0.03	0.44**	0.28**	-0.02	0.79**	0.20*	0.20*	0.25*	0.13	0.20*
NSPP	0.94**	-0.23*	0.44**	-	-	0.34**	0.39**	0.60**	0.28**		0.05	0.47**	0.04	0.14	-0.06	0.03	0.12	0.19	0.11
NBPPL	0.59**	0.46**	0.61**	1.00**	0.51**	0.34**	0.58**	0.72**	0.74**	-0.25*		0.32**	0.22*	0.52**	0.16	0.15	0.18	0.21*	0.21*
PL	0.86**	0.81**	0.80**	0.20*	-0.06	0.48**	0.75**	0.69**	0.34**	1.00**	0.56**		0.26*	0.35**	0.35**	0.32**	0.17	0.56**	0.14
PW	-0.32**	0.21*	-0.20*	-	-	0.28**	0.02	-0.23*	-0.06	-0.16	0.2	0.19		-0.03	-0.1	-0.08	0.01	0.06	0.08
NSPPL	0.35**	0.30**	0.30**	0.60**	0.32**	0.43**	0.44**	0.54**	0.82**	0.09	0.77**	0.37**	-0.11		0.14	0.13	0.29**	0.18	0.24*
DM	0.80**	0.85**	0.81**	1.00**	0.26*	0.66**	0.64**	0.60**	0.28**	-0.68**	0.11	0.49**	-0.19	0.09		0.79**	0.22*	0.17	0.13
SFP	1.00**	1.00**	1.00**	1.00**	0.89**	0.85**	1.00**	1.00**	0.77**	-0.44**	0.32**	0.87**	-0.34**	0.26**	1.00**		0.19	0.168	0.079
SYPP	0.16	0.11	0.17	0.40**	-0.06	0.31**	0.39**	0.32**	0.30**	0.20*	0.24*	0.2	0.03	0.26*	0.26*	0.47**		0.07	0.74**
TSW	0.39**	0.42**	0.26*	0.20*	-0.09	0.34**	0.37**	0.47**	0.20*	1.00**	0.30**	0.99**	0.13	0.24*	0.19	0.32**	0.08		0.07
GY	0.03	-0.02	0	0.20*	-0.06	0.23*	0.30**	0.16	0.23*	0.23*	0.30**	0.14	0.11	0.20*	0.14	0.15	0.69**	0.09	

Table 10. Estimates of correlation coefficients at genotypic (below diagonal) and phenotypic (above diagonal) levels among 19 traits of 96 faba bean accessions at Girar Jarso during 2019 main cropping season

Trait	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	DM	SFP	SYPP	TSW	GY
LL		0.63**	0.88**	0.15	0.28**	0.49**	0.46**	0.64**	0.42**	0.09	0.34**	0.50**	0.26*	0.42**	0.42**	0.42**	0.45**	0.30**	0.38**
LW	0.63**		0.90**	-0.03	0.37**	0.28**	0.37**	0.39**	0.33**	0.05	0.21	0.37*	0.28**	0.33**	0.33**	0.38**	0.31**	0.33**	0.28**
LA	0.89**	0.90**		0.06	0.36**	0.41**	0.47**	0.55**	0.40**	0.03	0.32**	0.46**	0.26*	0.41**	0.40**	0.43**	0.42**	0.35**	0.37**
DTF	0.17	-0.03	0.07		-0.06	0.004	0.12	0.22*	0.15	-0.13	0.04	-0.03	-0.17	0.14	0.22*	0.11	-0.07	-0.11	0.04
NPPN	0.27**	0.36**	0.35**	-0.05		0.24*	0.24*	0.35**	0.45**	0.09	0.05	0.06	0.09	0.45**	0.13	0.16	0.28**	-0.01	0.13
IL	0.51**	0.29**	0.44**	0.02	0.21*		0.56**	0.56**	0.38**	0.04	0.42**	0.24*	0.1	0.42**	0.27**	0.31**	0.17	0.14	0.13
LPH	0.44**	0.36**	0.46**	0.13	0.21*	0.57**		0.64**	0.41**	0.01	0.27**	0.27**	0.14	0.43**	0.24*	0.22*	0.29**	0.17	0.23*
PH	0.65**	0.36**	0.55**	0.26*	0.30**	0.55**	0.63**		0.73**	0.1	0.46**	0.26*	-0.07	0.75**	0.29**	0.28**	0.49**	0.01	0.40**
NPPPL	0.43**	0.28**	0.38**	0.15	0.41**	0.35**	0.41**	0.78**		0.08	0.55**	0.11	-0.11	0.89**	0.1	0.11	0.45**	-0.03	0.37**
NSPP	0.11	0.07	0.05	-0.12	0.13	0.03	0	0.11	0.14		0.03	0.27**	0.28**	0.17	0.05	0.05	0.16	0.01	0.22*
NBPPL	0.38**	0.21*	0.34**	0.1	-0.01	0.46**	0.25*	0.48**	0.54**	0.09		0.14	-0.25*	0.53**	-0.05	-0.01	0.38**	0.09	0.37**
PL	0.54**	0.39**	0.50**	-0.03	0.04	0.23*	0.25*	0.24*	0.1	0.27**	0.19		0.38**	0.19	0.44**	0.44**	0.24*	0.47**	0.27**
PW	0.47**	0.54**	0.51**	0.27**	0.14	0.19	0.22*	-0.08	-0.16	0.45**	-0.42**	0.60**		-0.1	0.40**	0.40**	-0.05	0.35**	-0.01
NSPPL	0.39**	0.27**	0.36**	0.17	0.42**	0.38**	0.42**	0.77**	0.91**	0.21*	0.55**	0.18	-0.16		0.14	0.14	0.43**	-0.04	0.39**
DM	0.46**	0.38**	0.46**	0.23*	0.16	0.32**	0.27**	0.34**	0.13	0.07	0.03	0.47**	0.62**	0.17		0.97**	0.02	0.33**	0.05
SFP	0.47**	0.43**	0.49**	0.12	0.19	0.35**	0.25*	0.32**	0.14	0.06	0.07	0.46**	0.61**	0.18	0.97**		0.04	0.36**	0.05
SYPP	0.69**	0.49**	0.64**	-0.08	0.44**	0.30**	0.44**	0.66**	0.45**	0.45**	0.49**	0.41**	0.47**	0.50**	0.1	0.11		0.07	0.77**
TSW	0.42**	0.41**	0.47**	-0.12	0.03	0.19	0.28**	0.07	0	-0.05	0.17	0.53**	0.58**	-0.02	0.37**	0.40**	0.22*		0.05
GY	0.52**	0.35**	0.48**	0.06	0.2	0.18	0.31**	0.49**	0.34**	0.44**	0.34**	0.39**	0.34**	0.42**	0.12	0.11	0.82**	0.14	

Table 11. Estimates of correlation coefficients at genotypic (below diagonal) and phenotypic (above diagonal) levels among 19 traits of 96 faba bean accessions at Degem during 2018 main cropping season

Trait	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	DM	SFP	SYPP	TSW	GY
LL		0.79**	0.93**	-0.09	0.07	0.13	-0.06	0.12	0.32**	-0.07	0.12	-0.06	-0.1	0.18	0.05	0.09	0.25*	-0.01	0.25*
LW	0.79**		0.95**	-0.01	0.08	0.01	-0.09	0.06	0.34**	-0.22*	0.10	-0.1	-0.05	0.24*	0.06	0.08	0.18	-0.06	0.14
LA	0.93**	0.95**		-0.03	0.11	0.07	-0.08	0.11	0.38**	-0.16	0.10	-0.09	-0.13	0.25*	0.05	0.07	0.23*	-0.07	0.21*
DTF	-0.10	-0.01	-0.04		0.06	-0.09	0.07	0.09	-0.02	-0.14	-0.11	0.09	-0.01	-0.14	-0.03	-0.41**	-0.19	0.01	-0.09
NPPN	0.08	0.12	0.15	0.08		-0.03	0.24*	0.17	0.54**	-0.38**	-0.02	-0.31**	-0.17	0.37**	-0.01	-0.04	0.04	-0.37**	-0.01
IL	0.26*	0.01	0.17	-0.15	0.01		-0.10	0.15	0.10	0.04	0.18	0.31**	0.15	-0.03	-0.05	-0.02	0.20	0.20	0.15
LPH	-0.13	-0.16	-0.16	0.17	0.21*	-0.001		0.48**	0.08	-0.01	-0.23*	0.06	0.31**	0.01	0.23*	0.17	0.15	0.16	0.03
PH	0.20*	0.10	0.19	0.21*	0.13	0.12	0.52**		0.36**	0.03	-0.05	0.28**	0.22*	0.31**	0.26*	0.19	0.43**	0.25*	0.36**
NPPPL	0.41**	0.45**	0.48**	-0.03	0.80**	0.09	0.30**	0.42**		-0.27**	0.29**	-0.17	-0.09	0.77**	0.07	0.07	0.28**	-0.25*	0.18
NSPP	-0.06	-	-0.23*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
		0.35**		0.31**	0.43**	0.62**	-0.08	-0.16	-0.26*		0.17	0.34**	0.03	0.17	0.01	0.08	0.17	0.10	0.14
NBPPL	0.23*	0.22*	0.24*	-0.13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
					0.30**	0.45**	-0.20*	-0.20*	0.28**	0.99**		0.18	0.01	0.35**	0.07	0.10	0.22*	0.09	0.11
PL	-0.07	-0.11	-0.11	0.06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
					0.83**	0.91**	0.07	0.27**	-0.45**	0.78**	0.58**		0.26**	-0.07	0.10	0.07	0.18	0.58**	0.15
PW	-0.14	-0.04	-0.19	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
					0.76**	0.43**	0.50**	-0.06	-0.36**	0.34**	-0.31**	0.39**		-0.17	0.17	0.18	0.17	0.47**	0.08
NSPPL	0.21*	0.29**	0.29**	-0.11	0.53**	-0.09	0.06	0.27**	0.85	0.04**	0.62**	-0.37**	-0.42**		0.05	0.09	0.37**	-0.26**	0.20*
DM	0.06	0.07	0.05	-0.08	-0.03	0.04	0.42**	0.49**	0.12	-0.04	0.19	0.10	0.28**	0.07		0.91**	0.11	0.27**	0.01
SFP	0.10	0.09	0.08	-	-0.08	0.11	0.28**	0.32**	0.11**	0.11	0.21*	0.07	0.26**	0.11	0.92**		0.18	0.25*	0.06
					0.46**														
SYPP	0.32**	0.23*	0.30*	-	-0.02	0.90**	0.36**	0.82**	0.37**	0.29**	0.46**	0.20*	0.36**	0.33**	0.13	0.25*		0.26**	0.82**
					0.29**														
TSW	-0.01	-0.06	-0.06	0.003	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
					0.63**	0.40**	0.33**	0.34**	-0.36**	0.26*	0.20	0.86**	0.79**	-0.37**	0.31**	0.29**	0.35**		0.22*
GY	0.36**	0.20	0.31	-0.21*	-0.23*	0.93**	0.09	0.76**	0.23*	0.34**	0.18	0.17	0.23*	0.06	0.00	0.12	0.77**	0.34**	

Table 12. Estimates of correlation coefficients at genotypic (below diagonal) and phenotypic (above diagonal) levels among 19 traits of 96 faba bean accessions at Degem during 2019 main cropping season

Trait	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	DM	SFP	SYPP	TSW	GY
LL		0.79**	0.93**	-0.09	0.06	0.06	-0.02	0.14	0.31**	-0.12	0.04	-0.09	0.01	0.17	0.05	0.09	0.20*	-0.01	0.18
LW	0.80**		0.95**	-0.02	0.1	-0.07	-0.03	0.1	0.35**	-0.21*	0.04	-0.08	0.05	0.25*	0.06	0.07	0.16	-0.07	0.1
LA	0.93**	0.95**		-0.03	0.12	0	-0.02	0.16	0.38**	-0.18	0.03	-0.09	0.01	0.26*	0.05	0.07	0.22*	-0.07	0.16
DTF	-0.1	-0.01	-0.04		0.11	-0.07	0.11	0.14	-0.01	-0.15	-0.08	0.12	0.05	-0.11	-0.02	-0.41**	-0.23*	0.02	-0.14
NPPN	0.06	0.11	0.12	0.12		0.06	0.27**	0.30**	0.52**	-0.37**	0.03	-0.17	0.06	0.37**	0.01	-0.04	0.01	-0.27**	-0.03
IL	0.06	-0.09	0.01	-0.06	0.06		0.02	0.26*	0.1	0.04	0.09	0.37**	0.35**	-0.03	-0.04	-0.01	0.18	0.22*	0.11
LPH	-0.03	-0.04	-0.03	0.17	0.28**	0.03		0.43**	0.1	-0.11	-0.2	0.03	0.31**	-0.02**	0.26	0.18	0.01*	0.11	-0.12
PH	0.15	0.11	0.17	0.16	0.31**	0.31**	0.41**		0.40**	-0.07	-0.04	0.2	0.33**	0.29**	0.2	0.11	0.26*	0.14	0.16
NPPPL	0.33**	0.38**	0.41**	-0.01	0.56**	0.09	0.1	0.42**		-0.31**	0.27**	-0.1	0.09	0.78**	0.11	0.09	0.25*	-0.24*	0.12
NSPP	-0.09	-0.22*	-0.18	-0.18	-0.38**	0.15	-0.14	-0.09	-0.33**		0.2	0.31**	-0.08	0.15	-0.03	0.05	0.14	0.11	0.13
NBPPL	0.04	0.05	0.05	-0.08	0.01	0.11	-0.23*	-0.04	0.29**	0.30**		0.17	0.07	0.30**	0.14	0.17	0.2	0.11	0.08
PL	-0.08	-0.07	-0.08	0.08	-0.2	0.46**	0.02	0.21	-0.12	0.36**	0.21*		0.32**	-0.05	0.07	0.03	0.12	0.50**	0.12
PW	0.03	0.09	0.02	0.04	0.04	0.47**	0.34**	0.42**	0.14	-0.15	0.09	0.38**		-0.09	0.17	0.14	0.17	0.43**	0.13
NSPPL	0.17	0.26*	0.26**	-0.08	0.39**	-0.06	-0.01	0.25*	0.79**	0.13	0.31**	-0.11	-0.09		0.07	0.1	0.32**	-0.29**	0.15
DM	0.06	0.07	0.05	-0.08	0.02	0.01	0.29**	0.25*	0.15	-0.05	0.18	0.08	0.22*	0.09		0.92**	0.04	0.25*	-0.04
SFP	0.1	0.08	0.08	-0.46**	-0.03	0.04	0.18	0.15	0.12	0.06	0.2	0.04	0.19	0.1	0.92**		0.15	0.24*	0.05
SYPP	0.23*	0.19	0.24*	-0.29**	-0.01	0.29**	-0.01	0.31**	0.29**	0.18	0.23*	0.14	0.26*	0.34**	0.05	0.17		0.26**	0.82**
TSW	-0.01	-0.07	-0.06	0.01	-0.28**	0.25*	0.1	0.14	-0.26*	0.17	0.14	0.55**	0.58**	-0.32**	0.28**	0.27**	0.30**		0.22*
GY	0.20*	0.11	0.19	-0.19	-0.06	0.22*	-0.16	0.19	0.14	0.17	0.06	0.14	0.21*	0.14	-0.05	0.06	0.82**	0.25*	

4.1.4 Path coefficient analysis

Path coefficient analysis provides a more realistic picture of the relationship among the traits and reveals whether the association of each individual trait with yield is due to its direct effect on yield or due to indirect effects via other component traits. In the present study, path coefficient analysis was done on the basis of genotypic correlation coefficients and the results are presented in tables 13, 14, 15, and 16, respectively.

4.1.4.1 Genotypic path analysis of grain yield with other traits

At Girar Jarso in 2018, days to flowering, and the number of branches per plant exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield. Internode length, lowest pod height, and the number of pods per plant also exerted negative direct effects but exhibited a positive correlation with grain yield. The number of seeds per pod also showed negative direct effects and a positive correlation with grain yield. On the other hand, the number of seeds per plant, and seed yield per plot exerted a positive direct effect and also had a positive association with grain yield.

At Girar Jerso in 2019, leaf length, leaf area, plant height, number of pods per plant, pod length, and seed yield per plot exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield. Whereas, leaf width, lowest pod height, number of seeds per pod, number of branches per plant, pod width, and number of seeds per plant exerted a positive direct effect and also had a positive association with grain yield. Leaf width exerted the highest positive direct effects followed by the number of seeds per plant and both traits also exhibited a positive correlation with grain yield.

At Dagem in 2018, internode length exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield. The number of pods per plant also exerted negative direct effects on grain yield and also had a positive association with grain yield. Pod width exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield. Seed

yield per plot also exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield. Even though the number of pods per node associated negatively and significantly with grain yield, this trait exerted positive direct effects on grain yield. The negative association of the number of pods per node with grain yield attributed to the negative indirect effects of this trait through internode length, number of pods per plant, number of seeds per pod, and thousand seed weight. Leaf length, plant height, number of seeds per pod, and thousand seed weight exerted positive direct effects on grain yield and also had a positive association with grain yield.

At Degem in 2019, seed yield per plot exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield due to its positive indirect effects through leaf length, internode length, and pod width. Thousand seed weight also exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield due to its positive indirect effects through internode length and pod width. On the other hand, leaf length, internode length, and pod width exerted a positive direct effect and also had a positive association with grain yield.

Table 13. Path analysis of the direct (bold) and indirect effects of eighteen traits on grain yield in faba bean accessions at Girar Jarso during 2018 main cropping season

Trait	DTF	IL	LPH	NPPPL	NSPP	NBPPL	NSPPL	SYPP	rg
DTF	-13.98	-17.51	-35.77	-4.79	7.99	-10.31	2.85	1.80	0.20*
IL	-13.98	-17.51	-28.05	-4.76	-2.74	-3.51	2.18	1.49	0.23*
LPH	-12.59	-12.36	-39.74	-4.39	-3.13	-5.96	2.24	1.88	0.30**
NPPPL	-8.02	-9.97	-20.88	-8.35	-2.23	-7.66	4.19	1.45	0.23*
NSPP	13.98	-5.99	-15.57	-2.33	-7.99	2.54	0.48	0.96	0.23*
NBPPL	-13.98	-5.96	-22.97	-6.21	1.97	-10.31	3.95	1.16	0.30*
NSPPL	-7.79	-7.46	-17.38	-6.84	-0.75	-7.95	5.12	1.23	0.20*
SYPP	-5.29	-5.48	-15.64	-2.54	-1.62	-2.52	1.31	4.77	0.69**

Table 14. Path analysis of the direct (bold) and indirect effects of eighteen traits on grain yield in faba bean accessions at Girar Jarso during 2019 main cropping season

Trait	LL	LW	LA	LPH	PH	NPPPL	NSPP	NBPPL	PL	PW	NSPPL	SYPP	rg
LL	-2.31	11.08	-12.91	0.93	-0.17	-0.64	0.15	0.12	-0.09	-0.59	0.94	-4.29	0.52**
LW	-1.44	17.69	-13.07	0.77	-0.10	-0.42	0.09	0.06	-0.10	-0.41	0.66	-3.00	0.35**
LA	-2.04	15.85	-14.59	0.97	-0.14	-0.57	0.07	0.11	-0.10	-0.56	0.88	-3.97	0.48**
LPH	-1.01	6.37	-6.68	2.13	-0.17	-0.62	-0.01	0.08	-0.04	-0.65	1.03	-2.74	0.31**
PH	-1.50	6.42	-7.99	1.33	-0.26	-1.17	0.15	0.15	0.02	-1.19	1.88	-4.06	0.49**
NPPPL	-0.98	4.96	-5.49	0.88	-0.21	-1.50	0.20	0.18	0.03	-1.41	2.23	-2.75	0.34**
NSPP	-0.24	1.16	-0.75	-0.01	-0.03	-0.21	1.43	0.03	-0.09	-0.32	0.50	-2.80	0.44**
NBPPL	-0.87	3.62	-5.01	0.54	-0.13	-0.81	0.13	0.31	0.08	-0.85	1.35	-3.00	0.34**
PL	-1.24	6.86	-7.24	0.53	-0.06	-0.14	0.38	0.06	-0.12	-0.27	0.44	-2.52	0.39**
PW	-1.09	9.49	-7.40	0.47	0.02	0.233	0.64	-0.13	-0.19	0.25	-0.40	-2.88	0.34**
NSPPL	-0.89	4.74	-5.26	0.90	-0.20	-1.37	0.30	0.17	0.03	-1.54	2.44	-3.10	0.42**
SYPP	-1.60	8.58	-9.37	0.94	-0.17	-0.67	0.65	0.15	-0.09	-0.77	1.23	6.18	0.82**

Table 15. Path analysis of the direct (bold) and indirect effects of eighteen traits on grain yield in faba bean accessions at Degem during 2018 main cropping season

Trait	LL	DTF	NPPN	IL	PH	NPPPL	NSPP	PW	SYPP	TSW	rg
LL	0.07	0.51	4.30	-0.81	2.80	-8.35	-0.89	0.23	-2.16	-0.01	0.36**
DTF	-0.01	-4.90	4.04	0.46	2.93	0.52	-4.70	-0.08	1.95	0.01	-0.20*
NPPN	0.01	-0.38	51.93	-0.03	1.74	-16.37	-6.54	1.32	0.13	-0.98	-0.20*
IL	0.02	0.72	0.51	-3.12	1.85	-1.87	9.46	-0.74	-6.08	0.62	0.93**
PH	0.02	-1.05	6.61	-0.42	13.68	-8.81	-2.52	0.10	-5.57	0.54	0.76**
NPPPL	0.03	0.13	41.35	-0.29	5.86	-20.55	-3.96	0.63	-2.54	-0.56	0.23*
NSPP	-0.00	1.50	-22.09	-1.92	-2.24	5.30	15.37	-0.59	-1.94	0.40	0.34*
PW	-0.01	-0.24	-39.68	-1.34	-0.81	7.50	5.28	-1.72	-2.41	1.23	0.23*
SYPP	0.02	1.41	-1.03	-2.81	11.26	-7.70	4.40	-0.6	-6.77	0.54	0.77**
TSW	-0.00	-0.02	-32.60	-1.24	4.77	7.33	3.98	-1.36	-2.35	1.56	0.34**

Table 16. Path analysis of the direct (bold) and indirect effects of eighteen traits on grain yield in faba bean accessions at Degem during 2019 main cropping season

Trait	LL	IL	PW	SYPP	TSW	rg
LL	6.08	0.92	-1.76	-0.04	0.04	0.20*
IL	0.39	14.55	10.14	-0.06	-1.42	0.22*
PW	0.17	6.88	8.56	-0.05	-3.26	0.21*
SYPP	1.39	4.27	3.08	-0.19	-1.70	0.82**
TSW	-0.04	3.64	12.33	-0.06	-5.66	0.25*

4.1.5 Multivariate analysis

4.1.5.1 Cluster analysis

The D^2 values based on the mean of each trait of accessions resulted in classifying the 96 faba bean accessions into five distinct clusters (Figure 2 and Table 17) at Girar Jarso in 2018. The number of accessions in each of five clusters ranged from five to forty-four in the smallest and largest cluster, respectively. Cluster I (45.8%) was the largest cluster containing 44 accessions

which comprised of 41 landrace accessions from 13 administrative zones and 3 released varieties (Bulga-70, Dagim, and Hachalu). Cluster II and V (34.4%) had 18 and 15 accessions respectively, and cluster III (14.6%) had 13 landrace accessions and one released variety. Cluster IV (5.2%) was the least with only five landrace accessions from 3 administrative zones.

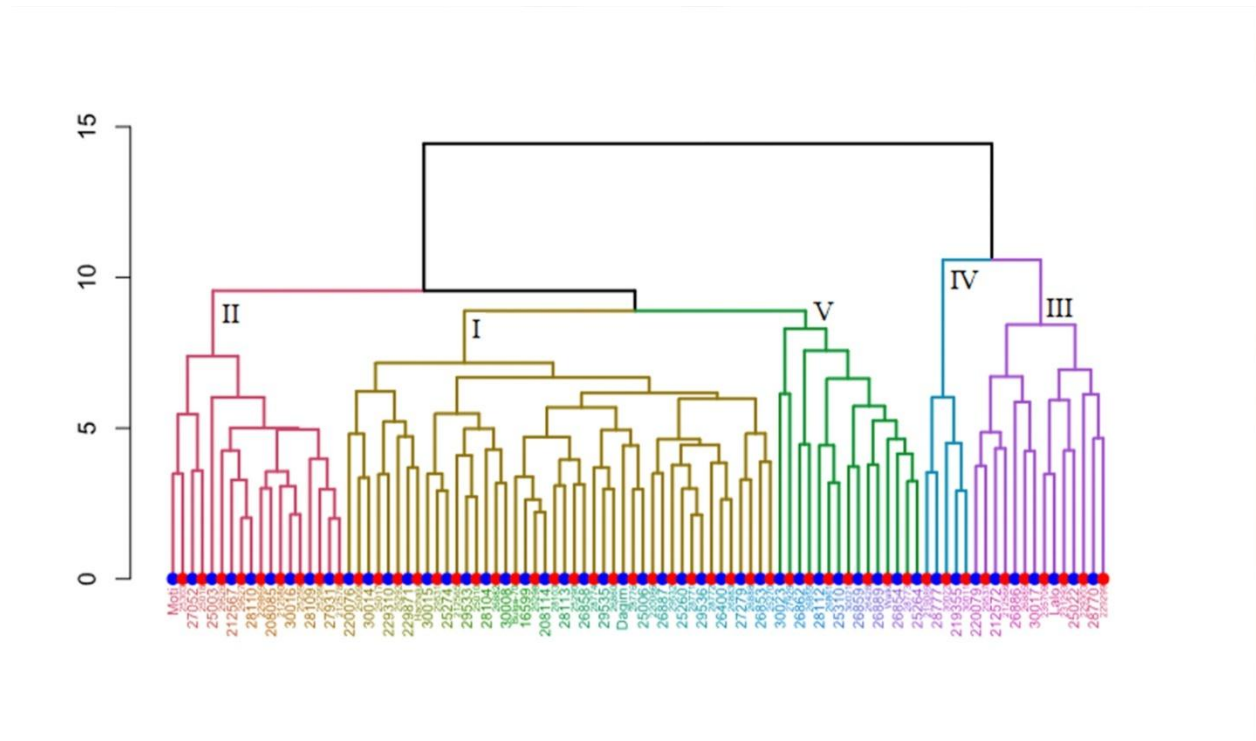


Figure 2. Dendrogram based on 19 morphological traits of 90 landrace accessions and 6 released varieties evaluated at Girar Jarso in 2018

Table 17. Grouping of the 96 Ethiopian faba bean accessions into different diversity clusters at Girar Jarso in 2018

Cluster	Number & % of accessions	Grouped accessions	Origins
I	44 (45.8%)	25009, 28774, 28771, 28776, 28772, 220086, 220076, 16599, 27279, 229871, Hachalu, 25006, 26400, 25017, 29531, 29532, 29535, 29533, 29536, 26882, 26883, 26887, 28103, 26860, 28104, Bulga-70, Dagim, 25298, 25292, 25290, 208114, 229310, 212565, 25010, 26888, 26858, 26853, 28113, 3008, 30014, 3005, 25260, 25270, 25274	Arsi, Bale (4), , Central Tigray (3), East Gojam (5), East Hararghe (5), Gedeo (6), Kembata (3), North Shewa A. (3), North Shewa O. , Segen (3), Sidama, West Arsi (3), West Shewa (3)
II	18 (18.8%)	27052, 27931, 229869, 29526, 29527, Moti, 25303, 25299, 212580, 212580, 212578, 208085, 25003, 25018, 28109, 28110, 30016, 25259	Arsi, Bench Maji, East Gojam, East Hararghe (2), Kembata (2), North Shewa A. (4), North Shewa O. (2), Sidama (2), West Arsi, West Shewa
III	14 (14.6%)	231293, 28770, 235709, 220079, 29537, 26886, 26885, Lalo, 212572, 229299, 212566, 229303, 25022, 30017	Arsi, Bale, Bench Maji, Central Tigray, East Hararghe., Gedeo (2), Lalo, North Shewa Amhara (2), North Shewa Oromia (3), West Arsi
IV	5 (5.2%)	219089, 219355, 28777, 30022, 30011	Arsi (2), Bale (2), West Arsi
V	15 (15.6%)	30023, 30021, 28773, 27929, 26428, 26861, 26859, 26862, Walki, 25310, 26855, 26854, 26889, 28112, 25264	Bale (3), Bench Maji, East Gojam, Gedeo (3), Kembata, Segen (3), Sidama, West Shewa

At Girar Jarso in 2019, cluster analysis grouped the 90 landrace accessions and 6 released varieties into five distinct groups (Figure 3 and Table 18). The number of accessions per cluster varied from 36 in cluster I to 10 in clusters III and V. So, the first cluster consisted of accessions 36, and the second cluster consisted of 19 landraces and five released varieties (Walki, Lalo, Bulga-70, Moti, and Hachalu). The third and the fourth cluster consisted of 10 and 16 landrace accessions, respectively. On the other hand, the fifth cluster consisted of 9 landrace accessions and one released variety (Dagim) (Figure 3 and Table 18).

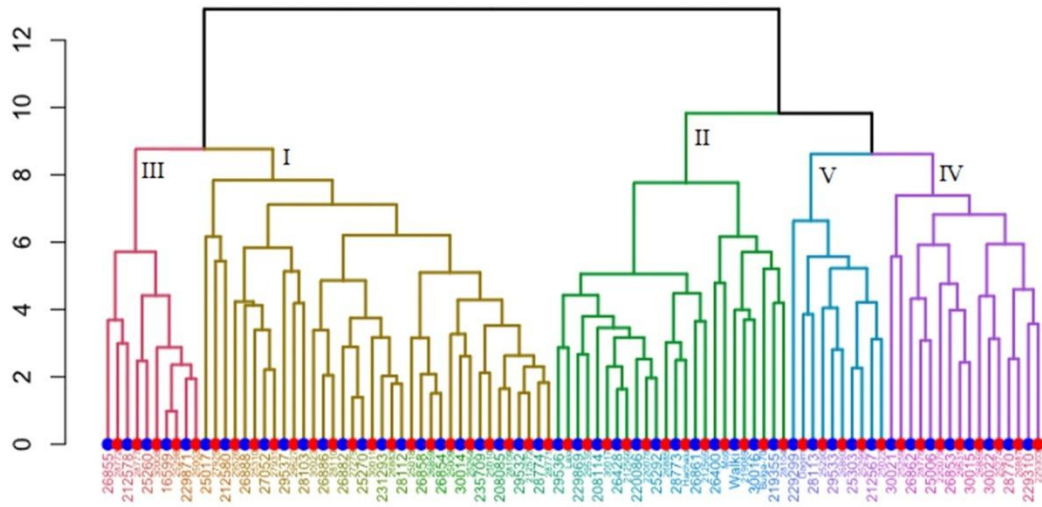


Figure 3. Dendrogram based on 19 morphological traits of 90 landrace accessions and 6 released varieties evaluated at Girar Jarso in 2019

Table 18. Grouping of the 96 Ethiopian faba bean accessions into different diversity clusters at Girar Jarso in 2019

Cluster	Number & % of accessions	Grouped accessions	Origins
I	36 (37.5%)	25009, 27931, 29526, 26882, 212580, 26888, 28112, 27052, 235709, 29527, 26883, 212572, 26854, 30011, 231293, 27929, 29532, 26886, 208085, 26858, 30014, 30023, 27279, 29537, 28103, 25010, 28109, 25264, 28774, 25017, 26859, 25310, 25018, 28110, 25270, 28771	Arsi (4), Bench Maji (3), , East Hararghe (4), Gedeo (5), North Shewa A. (3), Segen (3), Sidama (3), West Arsi (2), Bale (2), East Gojam (2), North Shewa O. (2), West Shewa (2), Kembata
II	24 (25%)	219089, 219355, 28773, 220086, 220076, 26428, 229869, 26400, 29535, 29536, 26861, 26885, 28104, Walki, Lalo, Bulga-70, Moti, Hachalu, 25292, 208114, 212565, 212566, 30016, 30017	Arsi (2), Bale, Central Tigray (2), East Gojam (4), East Hararghe, Gedeo (3), Kembata , North Shewa A. (2), North Shewa O., West Arsi (2)
III	10 (10.4%)	28777, 28772, 16599, 229871, 25298, 212578, 25003, 26855, 30008, 25260	Bale (2), Central Tigray, East Gojam, Kembata (2)., Segen, North Shewa Amhara, West Arsi, West Shewa
IV	16 (16.7%)	30022, 28776, 30021, 28770, 220079, 25006, 29531, 26862, 26887, 229310, 229303, 26889, 26853, 30015, 25259, 25274	Bale (4), Central Tigray, East Gojam, East Hararghe, Gedeo (2), North Shewa A. North Shewa O., Segen (2), West Arsi, West Shewa (2)
V	10 (10.4%)	29533, 26860, Dagim, 25303, 25299, 225290, 212567, 229299, 25022, 28113	East Hararghe, Gedeo, North Shewa O.(2), Kembata (2), North Shewa A. (2), Sidama

At Degem in 2018, cluster I was the largest of all clusters containing 41 landraces and 2 released varieties (Dagim and Walki). Cluster III comprised the second largest group with all members are landraces. Cluster II, the third-largest group, contained 16 landraces and 2 released varieties (Lalo and Bulga-70). Cluster V comprised seven landraces. Cluster IV was the least only with one landrace and two released varieties (Moti and Hachalu) (Figure 4 and Table 19).

Table 19. Grouping of the 96 Ethiopian faba bean accessions into different diversity clusters at Degem in 2018

Cluster	Number & % of accessions	Grouped accessions	Origins
I	43 (44.8%)	25009, 30022, 28774, 28771, 28776, 30021, 28770, 220079, 220076, 16599, 229871, 26428, 26400, 29531, 29535, 29533, 29536, 29537, 26859, 26862, 26885, 26887, 26886, 26860, 28104, Dagim, Walki, 25310, 25303, 25299, 25298, 25290, 212567, 212578, 25010, 26854, 26853, 28112, 30008, 25264, 25260, 25259, 25274	Arsi, Bale (6), Central Tigray (3), East Gojam (3), East Hararghe (5), Gedeo (7), Kembata (5), North Shewa A. (2), North Shewa O., Segen (2), Sidama, West Arsi, West Shewa (4)
II	18 (18.8%)	27052, 231293, 28777, 25006, 229869, 25017, Lalo, Bulga-70, 25292, 212572, 208114, 229310, 212566, 25022, 25018, 26858, 28113, 25270	Arsi (2), Bale, East Gojam (3), Kembata, North Shewa A. (3), North Shewa O. (3), Segen, Sidama, West Shewa
III	25 (26%)	219089, 219355, 30023, 28772, 27931, 27929, 220086, 27279, 29526, 29527, 29532, 26861, 26882, 26883, 28103, 229303, 25003, 26855, 28109, 28110, 30011, 30014, 30016, 30017, 30015	Arsi (2), Bale (2), Bench Maji (2), Central Tigray, East Gojam, East Hararghe (3), Gedeo (4), North Shewa O. (2), Segen, Sidama (2), West Arsi (5)
IV	3 (3.1%)	28773, Moti, Hachalu	Bale
V	7 (7.3%)	235709, 212580, 229299, 208085, 212565, 26888, 26889	Bench Maji, North Shewa A. (4), Segen (2)

As indicated at Degem in 2019 the number of released varieties and landrace accessions in each of five clusters ranged from three to forty-one in the smallest and largest group, respectively (Figure 5 and Table 20). Cluster II was the largest one and is comprised of forty landrace accessions and one released variety (Lalo). Cluster I comprised 40 accessions, with 37 landraces and 3 released varieties (Dagim, Walki, and Bulga-70). On the other hand, clusters III and V each consisted of nine and three landraces, respectively. Cluster IV consisted of one landrace accession and two released varieties (Moti and Hachalu).

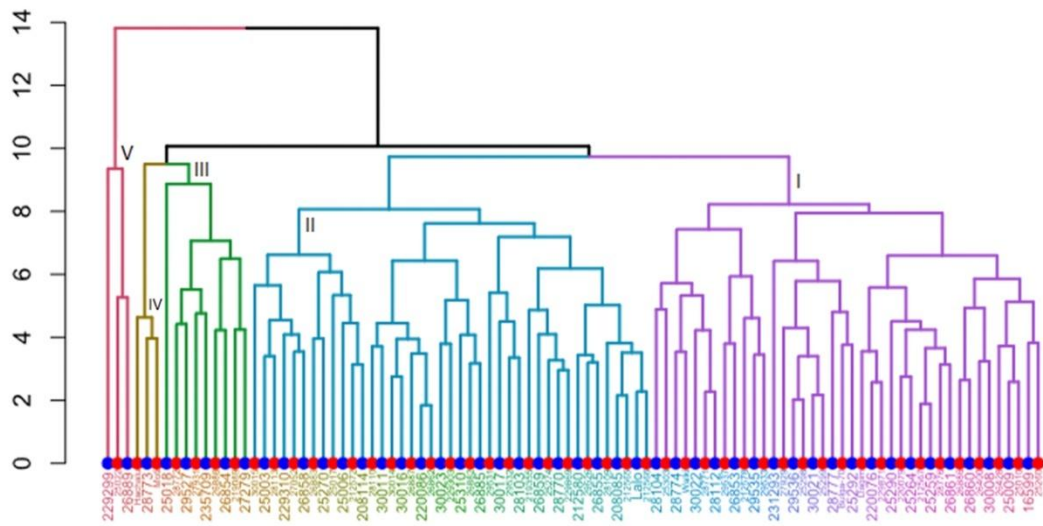


Figure 5. Dendrogram based on 19 morphological traits of 90 landrace accessions and 6 released varieties evaluated at Degem in 2019

Table 20. Grouping of the 96 Ethiopian faba bean accessions into different diversity clusters at Degem in 2019

Cluster	Number & % of accessions	Grouped accessions	Origins
I	40 (41.7%)	25009, 231293, 28777, 30022, 28774, 28771, 28776, 30021, 27929, 220079, 220076, 16599, 229871, 26428, 26400, 29535, 29533, 29536, 29537, 26861, 26886, 26860, 28104, Dagim, Walki, Bulga-70, 25303, 25299, 25298, 25292, 25290, 212567, 212578, 25010, 26853, 28112, 30008, 25264, 25260, 25259	Arsi (2), Bale (6), Bench Maji, Central Tigray (3), East Gojam (3), East Hararghe (4), Gedeo (4), Kembata (5), North Shewa A. (2), North Shewa O., Segen, Sidama, west Arsi, West Shewa (3)
II	41 (42.7%)	27052, 219355, 30023, 28770, 220086, 25006, 229868, 25017, 29531, 29526, 29532, 26859, 26882, 26862, 26885, 26883, 26887, 28103, Lalo, 25310, 212580, 212572, 204114, 208085, 229310, 212565, 212566, 229303, 25003, 26855, 26858, 28109, 28110, 28113, 30011, 30014, 30016, 30017, 30015, 25270, 25274	Arsi (3), Bale, Central Tigray, East Gojam (3), East Hararghe (3), Gedeo (7), Kembata, North Shewa A. (6), North Shewa O. (3), Segen (2), Sidama (3), West Arsi (5), West Shewa (2)
III	9 (9.4%)	219089, 28772, 27931, 235709, 27929, 29527, 25018, 26888, 26854,	Arsi, Bale, Bench Maji (2), East Gojam, East Hararghe, North Shewa O., Segen (2)
IV	3 (3.1%)	28773, Moti, Hachalu	Bale
V	3 (3.1%)	229299, 25022, 26889	North Shewa A., North Shewa O., Segen,

At Girar Jarso in 2018, landrace collections from most of the administrative zones were distributed in most of the clusters than any other (Table 21). The landrace collections from all of the AZs except Bench Maji grouped in the first cluster. The landrace collections from 13, 10, 9, 3, and 8 AZs were grouped into clusters I, II, III, IV, and V, respectively. Besides, released varieties also distributed in most of the clusters. Similarly, at Girar Jarso in 2019, landrace accessions from most of the AZs were distributed in most of the clusters except the AZs of Arsi, Sidama, and Bench Maji (Table 22). On the other hand, at Degem in 2018, landrace accessions from North Shewa Amhara, East Gojam, Arsi, Bale, North Shewa Oromia, Sidama, and Segen were distributed in most of the clusters (Table 23). At Degem in 2019 also landrace accessions from North Shewa Amhara, East Gojam, Arsi, Bale, North Shewa Oromia, East Hararghe, and Segen were distributed in most of the clusters (Table 24).

Table 21. Clustering pattern of Ethiopian faba bean accessions from different AZs over 5 clusters at Girar Jarso in 2018

Subpopulation	Number of accessions	Number of accessions in each cluster				
		I	II	III	IV	V
North Shewa A	9	3	4	2	-	-
East Gojam	7	5	1	-	-	1
West Arsi	6	3	1	1	1	-
Arsi	5	1	1	1	2	-
Bale	10	4	-	1	2	3
North Shewa O	6	1	2	3	-	-
East Hararghe	8	5	2	1	-	-
West Shewa	5	3	1	-	-	1
Sidama	4	1	2	-	-	1
Gedeo	11	6	-	2	-	3
Segen	6	3	-	-	-	3
Kembata	6	3	2	-	-	1
Bench Maji	3	-	1	1	-	1
Central Tigray	4	3	-	1	-	-
Released	6	3	1	1	-	1
Total	96	44	18	14	5	15

Table 22. Clustering pattern of Ethiopian faba bean accessions from different AZs over 5 clusters at Girar Jarso in 2019

Subpopulation	Number of accessions	Number of accessions in each cluster				
		I	II	III	IV	V
North Shewa A	9	3	2	1	1	2
East Gojam	7	2	3	1	1	-
West Arsi	6	2	2	1	1	-
Arsi	5	3	2	-	-	-
Bale	10	3	1	2	4	-
North Shewa O	6	2	1	-	1	2
East Hararghe	8	4	2	-	1	1
West Shewa	5	2	-	1	2	-
Sidama	4	3	-	-	-	1
Gedeo	11	5	3	-	2	1
Segen	6	3	-	1	2	-
Kembata	6	1	1	2	-	2
Bench Maji	3	3	-	-	-	-
Central Tigray	4	-	2	1	1	-
Released	6	-	5	-	-	1
Total	96	36	24	10	16	10

Table 23. Clustering pattern of Ethiopian faba bean accessions from different AZs over 5 clusters at Degem in 2018

Subpopulation	Number of accessions	Number of accessions in each cluster				
		I	II	III	IV	V
North Shewa A	9	2	3	-	-	4
East Gojam	7	3	3	1	-	-
West Arsi	6	1	-	5	-	-
Arsi	5	1	2	2	-	-
Bale	10	6	1	2	1	-
North Shewa O	6	1	3	2	-	-
East Hararghe	8	5	-	3	-	-
West Shewa	5	4	1	-	-	-
Sidama	4	1	1	2	-	-
Gedeo	11	7	-	4	-	-
Segen	6	2	1	1	-	2
Kembata	6	5	1	-	-	-
Bench Maji	3	-	-	2	-	1
Central Tigray	4	3	-	1	-	-
Released	6	2	2	-	2	-
Total	96	43	18	25	3	7

Table 24. Clustering pattern of Ethiopian faba bean accessions from different AZs over 5 clusters at Degem in 2019

Subpopulation	Number of accessions	Number of accessions in each cluster				
		I	II	III	IV	V
North Shewa A	9	2	6	-	-	1
East Gojam	7	3	3	1	-	-
West Arsi	6	1	5	-	-	-
Arsi	5	2	2	1	-	-
Bale	10	6	2	1	1	-
North Shewa O	6	1	3	1	-	1
East Hararghe	8	4	3	1	-	-
West Shewa	5	3	2	-	-	-
Sidama	4	1	3	-	-	-
Gedeo	11	4	7	-	-	-
Segen	6	1	2	2	-	1
Kembata	6	5	1	-	-	-
Bench Maji	3	1	-	2	-	-
Central Tigray	4	3	1	-	-	-
Released	6	3	1	-	2	-
Total	96	40	41	9	3	3

4.1.5.2 Cluster mean analysis

The mean value of the 19 traits in each cluster is presented in Table 25 at Girar Jarso in 2018 and the characteristic feature of each cluster is described below. Cluster I consisted of 44 accessions among which three are released varieties (Bulga-70, Dagim, and Hachalu) having the characteristic of intermediate for most of the traits except number of seeds per pod with low value. Cluster II had 18 accessions possessing one released variety (Moti), with a feature of intermediate days to flowering, number of pods per node, internode length, number of seeds per

pod, pod width, and grain yield. Fifteen accessions made cluster V, among which one is released variety (Walki). This cluster could be characterized by low number of days to flowering, number of pods per node, internode length, and grain yield. Fourteen accessions that formed cluster III is characterized by intermediate feature for most of the traits except number of pods per plant, pod width, number of seeds per plant, seed yield per plot, and grain yield with high mean value. Cluster IV consisted of 5 accessions with high mean value for most of the traits.

At Girar Jarso in 2019, cluster trait mean performance is presented in Table 25. Cluster I had relatively higher pod width but low days to flowering, a number of branches per plant, seed yield per plot, and grain yield. High leaf length, leaf width, leaf area, pod length, days to maturity, seed filling period, and thousand seed weight were characteristics of cluster II. Cluster III was characterized by a low character for most of the traits, except for the traits days to flowering and number of branches per plant with an intermediate character. Cluster IV had a relatively intermediate mean value for all the traits. Cluster V had a high mean value for days to flowering, number of pods per node, internode length, lowest pod height, plant height, number of pods per plant, number of seeds per plant, number of branches per plant, and number of seeds per plant while intermediate for the other traits.

At Degem in 2018, the cluster means of different traits were compared and are presented in Table 26. Most of the trait mean values in cluster I are relatively intermediate except the low mean values for the traits leaf length, leaf width, leaf area, number of pods per node, number of pods per plant, seed yield per plot, and grain yield. Cluster II had high mean values for the traits leaf length, leaf width, leaf area, and a number of pods per node while low mean values for the traits number of seeds per pod and number of branches per plant. Cluster III was characterized by a high mean value for the trait number of seeds per pod, days to maturity, and seed filling period but exhibited low mean value for days to flowering. Cluster IV relatively had higher mean values for the traits internode length, lowest pod height, plant height, pod length, pod width, seed

yield per plot, thousand seed weight, and grain yield. Cluster V revealed relatively higher mean values for the traits number of pods per plant, number of branches per plant, and number of seeds per plant. This cluster revealed low mean values for the traits internode length, lowest pod height, plant height, pod length, pod width, days to maturity, seed filling period, and thousand seed weight.

At Dagem in 2019, the mean values of the traits for each cluster are presented in Table 26. Cluster I was characterized by intermediate character for all the traits except low value for leaf length, leaf width, leaf area, number of pods per node, number of pods per plant, and number of seeds per plant. Similarly, cluster II also had an intermediate character for most traits except a low mean value for the trait days to flowering and a high mean value for the trait days to maturity and seed filling period. Cluster III had a high mean value for the traits number of pods per node, number of pods per plant, number of seeds per pod, number of branches per plant, number of seeds per plant, and grain yield and intermediate for the other traits. Cluster IV exhibited superior internode length, lowest pod height, plant height, pod length, pod width, seed yield per plot, and thousand seed weight. This cluster exhibited low number of seeds per pod and the number of seeds per plant. Cluster V was characterized by superior leaf length, leaf width, leaf area, and days to flowering. On the other hand, it was inferior for the traits internode length, lowest pod height, plant height, number of seeds per pod, number of branches per plant, pod length, pod width, days to maturity, seed filling period, seed yield per plot, thousand seed weight and grain yield.

Table 25. Cluster mean for 19 traits in 96 Ethiopian faba bean accessions at Girar Jarso during 2018 and 2019 main cropping season

Trait	Cluster at Girar Jarso 2018					Cluster at Girar Jarso 2019				
	I	II	III	IV	V	I	II	III	IV	V
LL	4.54	3.89	5.10	6.49	5.07	4.87	6.54	4.07	5.56	6.32
LW	2.36	1.75	2.62	2.83	2.59	2.05	2.84	1.51	2.17	2.52
LA	7.66	5.67	9.28	12.03	9.17	7.78	13.79	5.26	9.37	11.92
DTF	49.19	48.81	48.64	52.20	48.37	57.83	58.96	59.10	58.88	60.40
NPPN	1.42	1.18	1.48	1.51	1.16	1.27	1.48	1.17	1.44	1.56
IL	2.72	2.64	3.02	4.74	2.42	3.26	4.55	3.01	4.57	4.89
LPH	21.89	18.83	23.08	33.93	22.05	31.51	38.16	28.84	39.04	39.94
PH	46.6	42.4	56.64	96.75	50.48	77.29	112.09	72.48	116.58	130.18
NPPPL	8.02	6.86	12.93	10.78	7	8.45	15.73	6.77	19.38	24.83
NSPP	1.90	2.01	2.11	2.23	2.30	2.31	2.36	1.99	2.14	2.62
NBPPL	0.18	0.17	0.64	0.70	0.43	0.18	0.63	0.35	0.66	1.10
PL	4.63	4.39	5.19	6.07	5.33	5.53	6.25	4.74	5.13	5.74
PW	3.94	3.59	3.99	3.16	3.92	3.01	2.90	1.97	2.37	2.50
NSPPL	19.48	17.61	32.31	26.25	18.4	18.96	37.72	14.70	41.51	60.78
DM	122.40	120.30	120.40	137.80	123.20	143.14	150.33	125.8	133.81	146
SFP	73.42	69.94	70.25	85.60	75.23	84.22	91.21	66.4	74.63	85.60
SYPP	68.76	55.75	93.29	90.60	80.27	91.13	167.44	114.6	151.88	200
TSW	469	420.80	471.90	538	458.40	468.52	510.58	417.55	420.88	438
GY	1.15	0.93	1.43	1.07	0.80	1.38	2.13	1.45	1.98	2.50

Table 26. Cluster mean for 19 traits in 96 Ethiopian faba bean accessions at Degem during 2018 and 2019 main cropping season

Trait	Cluster at Degem 2018					Cluster at Degem 2019				
	I	II	III	IV	V	I	II	III	IV	V
LL	6.11	7.89	7.15	6.26	7.16	6.16	7.52	6.33	6.26	7.90
LW	2.62	3.70	3.16	2.80	3.33	2.65	3.38	2.93	2.8	3.80
LA	10.96	18.85	15.21	11.76	15.70	11.09	16.70	12.91	11.63	19.50
DTF	60.46	59.33	58.39	60.23	59.91	60.41	58.83	59.45	60.21	60.57
NPPN	1.47	1.66	1.49	1.59	1.56	1.57	1.63	1.94	1.67	1.59
IL	4.86	5.36	5.70	6.50	4.57	5.68	5.80	6.06	7.53	3.89
LPH	34	32.81	31.57	42.33	29.04	40.86	39.71	37.78	47.85	27.23
PH	88.78	91.44	94.48	100.67	79.64	100.60	109.70	112.90	118.47	77.49
NPPPL	10.99	16.47	15.83	11.50	16.71	12.74	17.30	24.44	14.43	15.42
NSPP	2.23	1.96	2.36	2.13	2.18	2.23	2.30	2.45	2.03	1.67
NBPPL	0.62	0.50	1.26	1.17	1.43	0.76	1	1.5	1.17	0.33
PL	5.82	5.00	6.41	8.17	4.82	5.81	5.84	6.30	8.62	4.19
PW	3.98	3.98	3.93	5.17	3.54	3.04	3.17	2.76	4.37	1.72
NSPPL	24.10	30.81	36.97	23.33	42.83	26.90	37.13	58.24	28.25	38.61
DM	152.84	153.56	156.76	155.89	149.06	152.50	155.91	150.70	155.88	148.13
SFP	92.35	94.15	98.54	95.59	89.12	91.99	97.12	91.15	95.59	87.60
SYPP	127.09	131.44	169.76	183	134	124.5	153.28	160.8	164.5	118.95
TSW	546.97	481.24	590.06	781.07	416.37	552.70	546.29	463.40	802.25	412.90
GY	1.58	1.61	1.88	2.07	1.68	1.544	1.83	1.90	1.86	1.49

4.1.5.3 Estimation of intra and inter-cluster squared distances (D^2)

The average intra and inter-cluster D^2 values are presented in Table 27 at Girar Jarso in 2018. The distance analysis showed that both intra and inter-cluster distances were highly significant ($P < 0.01$). There were 10 possible pair-wise genetic distances between clusters. Maximum average intra cluster D^2 was obtained in cluster I ($D^2=233.47$) followed by cluster V ($D^2 = 131.62$) and

cluster III ($D^2=121.52$). The lowest intra D^2 was recorded in cluster II ($D^2=77.69$) and cluster IV ($D^2 = 82.34$). The maximum inter-cluster distances were found between cluster I and cluster V ($D^2 = 444.19$) followed by cluster I and cluster IV ($D^2 = 318.36$) and cluster I and cluster II ($D^2 = 314.87$). The minimum squared distance was between cluster II and cluster IV ($D^2 = 115.72$) followed by cluster III and cluster IV ($D^2 = 161.77$).

Table 27. Intra (bolded diagonal) and inter-cluster distance between Ethiopian faba bean accessions categorized into 5 clusters at Girar Jarso in 2018

Cluster	Distance Between Clusters				
	I	II	III	IV	V
I	233.47	314.87	254.93	318.36	444.19
II		77.69	186.65	115.72	206.33
III			121.52	161.77	292.16
IV				82.34	210.84
V					131.62

Similarly, at Girar Jarso in 2019, both intra and inter-cluster distances were highly significant ($P < 0.01$) (Table 28). The highest inter-cluster distance was observed between clusters I and III ($D^2 = 434.59$) followed by clusters III and IV ($D^2 = 399.59$) and clusters III and V ($D^2 = 343.95$). The lowest inter-cluster distance was recorded between clusters I and IV ($D^2 = 206.21$) followed by clusters IV and V ($D^2 = 216.15$) and clusters I and V ($D^2 = 249.81$) showing narrow genetic divergence between these clusters. The high intra cluster D^2 was obtained in cluster III ($D^2 = 213.27$) followed by cluster II ($D^2 = 180.80$), and cluster I ($D^2 = 157.36$). The minimum intra cluster D^2 was obtained in cluster V ($D^2 = 125.24$) followed by cluster IV ($D^2 = 145.92$).

Table 28. Intra (bolded diagonals) and inter-cluster distance between Ethiopian faba bean accessions categorized into 5 clusters at Girar Jarso in 2019

Cluster	Distance Between Clusters				
	I	II	III	IV	V
I	157.36	291.82	434.59	206.21	249.81
II		180.80	314.47	307.29	277.25
III			213.27	399.59	343.95
IV				145.92	216.15
V					125.24

The highly significant ($P < 0.01$) inter and intra cluster D^2 values are presented in Table 29 at Degem in 2018. The largest inter-cluster distance was recorded between cluster II and cluster V ($D^2 = 527.97$) followed by cluster I and cluster V ($D^2 = 437.32$), and cluster IV and cluster V ($D^2 = 380.66$). The lowest inter-cluster distance was revealed between cluster I and cluster II ($D^2 = 194.27$) followed by cluster I and cluster IV ($D^2 = 205.73$), and cluster I and cluster III ($D^2 = 225.17$). The highest intra cluster distance was obtained in cluster V ($D^2 = 185.53$) followed by cluster II ($D^2 = 160.32$), and cluster III ($D^2 = 146.51$). The minimum intra cluster distance was obtained in cluster I ($D^2 = 116.87$) followed by cluster IV ($D^2 = 145.43$).

Table 29. Intra (bolded diagonals) and inter-cluster distance between Ethiopian faba bean accessions categorized into 5 clusters at Degem in 2018

Cluster	Distance Between Clusters				
	I	II	III	IV	V
I	116.87	194.27	225.17	205.73	437.32
II		160.32	316.77	288.51	527.97
III			146.51	244.20	338.40
IV				145.43	380.66
V					185.53

At Degem in 2019, the average intra and inter-cluster D^2 values are presented in Table 30. The χ^2 -test for the five clusters indicated that there was a statistically highly significant difference among all the clusters ($P < 0.01$). Similarly, there was a highly significant difference ($P < 0.01$) between intra cluster distances. The highest average inter-cluster distance was recorded between cluster II and cluster V ($D^2 = 548.57$) followed by cluster IV and cluster V ($D^2 = 449.80$), and cluster I and cluster V ($D^2 = 422.63$). The minimum inter-cluster distance was observed between cluster I and cluster IV ($D^2 = 166.77$) followed by cluster II and cluster IV ($D^2 = 195.42$). Maximum average intra cluster D^2 was obtained in cluster III ($D^2 = 218.19$) followed by cluster I ($D^2 = 171.98$), and cluster II ($D^2 = 133.43$) while the lowest D^2 was recorded in cluster V ($D^2 = 96.55$) followed by cluster IV ($D^2 = 110.61$).

Table 30. Intra (bolded diagonal) and inter-cluster distance between Ethiopian faba bean accessions categorized into 5 clusters at Degem in 2019

Cluster	Distance Between Clusters				
	I	II	III	IV	V
I	171.98	264.23	276.45	166.77	422.63
II		133.43	414.36	195.42	548.57
III			218.19	318.34	316.91
IV				110.61	449.80
V					96.55

4.1.5.4 Principal component analysis

Principal component analysis (PCA) was computed for 90 landrace accessions and 6 released varieties from 14 administrative zones of the collection as shown in Tables 31 and 32. At Girar Jarso in 2018, the first six principal components having Eigen value between 1.06 and 5.55 were found to be significant and accounted for about 68.23% of the total variance (Table 31).

Table 31. Eigen vector, Eigen values, total variance, and cumulative variance of the significant principal components for 19 traits of 96 Ethiopian faba bean accessions at Girar Jarso during 2018 and 2019 main cropping season

Trait	Girar Jarso-2018						Girar Jarso-2019				
	Eigen Vector						Eigen Vector				
	PC1	PC2	PC3	PC4	PC5	PC6	PC1	PC2	PC3	PC4	PC5
LL	0.33	-0.15	-0.22	-0.01	0.25	-0.15	0.32	0.12	0.06	0.05	-0.17
LW	0.26	-0.15	-0.33	-0.01	0.38	0.04	0.27	0.17	0.13	-0.16	-0.41
LA	0.30	-0.15	-0.33	-0.08	0.33	-0.08	0.32	0.14	0.10	-0.06	-0.36
DTF	0.14	-0.22	0.08	-0.23	-0.41	0.10	0.06	0.02	-0.53	0.37	0.06
NPPN	0.16	0.10	-0.23	-0.26	-0.28	0.08	0.21	-0.07	-0.09	-0.54	-0.06
IL	0.25	-0.05	0.17	0.15	-0.31	-0.03	0.27	-0.04	-0.08	-0.07	0.09
LPH	0.30	-0.14	0.05	0.001	-0.21	0.05	0.26	0.001	-0.10	-0.07	-0.04
PH	0.37	0.02	0.02	0.03	-0.17	-0.11	0.34	-0.15	-0.13	0.002	0.08
NPPPL	0.25	0.34	-0.22	-0.17	-0.15	0.03	0.27	-0.23	-0.21	-0.15	0.12
NSPP	0.10	0.22	0.16	0.39	0.04	-0.52	0.06	0.03	0.35	-0.17	0.66
NBPPL	0.19	0.24	-0.002	0.12	-0.04	0.45	0.22	-0.23	0.05	0.26	0.07
PL	0.24	0.17	0.14	0.47	-0.01	-0.12	0.19	0.27	0.29	0.15	0.20
PW	0.04	0.17	0.03	0.36	0.19	0.65	0.01	0.28	0.15	-0.34	0.16
NSPPL	0.25	0.42	-0.15	-0.07	-0.15	-0.07	0.29	-0.21	-0.16	-0.16	0.20
DM	0.24	-0.39	0.29	-0.04	-0.07	0.10	0.15	0.45	-0.29	0.13	0.20
SFP	0.20	-0.36	0.24	0.06	0.09	0.05	0.15	0.46	-0.23	0.08	0.17
SYPP	0.18	0.21	0.43	-0.36	0.28	-0.04	0.26	-0.23	0.25	0.24	-0.01
TSW	0.17	-0.10	0.08	0.22	0.05	0.06	0.08	0.33	0.26	0.19	-0.12
GY	0.13	0.26	0.44	-0.34	0.31	0.04	0.23	-0.19	0.28	0.36	0.07
Eigen values	5.55	1.90	1.75	1.50	1.33	1.06	6.74	2.73	1.43	1.14	1.11
Proportion	29.21	9.82	9.19	7.90	6.98	5.59	35.46	14.16	7.53	5.98	5.83
Cumulative	29.21	38.57	47.76	55.66	62.64	68.23	35.85	50.01	57.54	63.52	69.36

A variance of 29.21%, 9.82%, 9.19%, 7.90%, 6.98%, and 5.59% were extracted from the first to the sixth components, respectively. The relative contribution of the two PCs was plotted and presented in Figure 6.

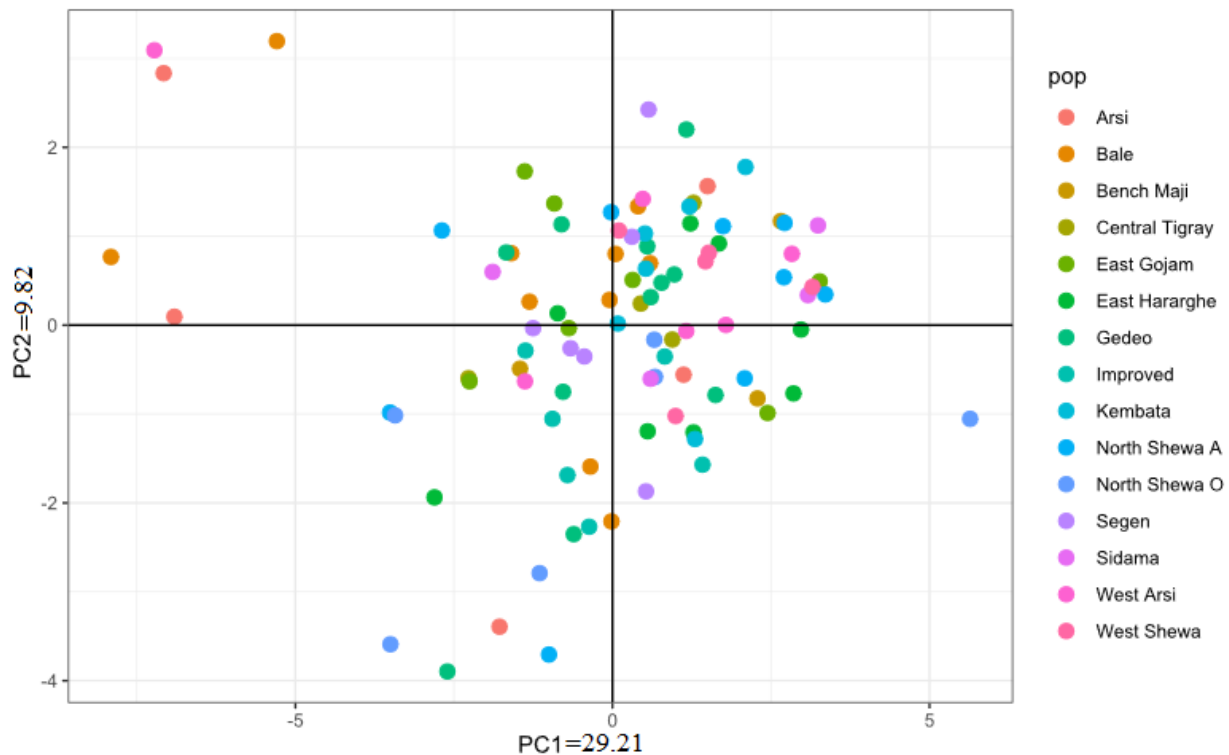


Figure 6. The relative position of 90 landrace accessions and 6 released varieties on the first and second principal axis at Girar Jarso in 2018

The first principal component (PC1) had 5.55 of the original variables and contributed 29.21% to the total observed variability; PC2 had 1.90 and contributed 9.82% of the total variation. The first principal component was largely determined by the traits like leaf length, leaf width, leaf area, internode length, lowest pod height, plant height, number of pods per plant, and number of seeds per plant. The variation in the second PCA was mainly due to days to flowering, number of pods per plant, number of seeds per pod, number of branch per plant, number of seeds per plant, days to maturity, seed filling period, seed yield per plot, and grain yield had a significant contribution. Likewise, the third PCA explained mainly from the traits leaf length, leaf width, leaf area, number of pods per plant, days to maturity, seed filling period, seed yield per plot, and grain yield. The number of pods per node, number of seeds per pod, pod length, pod width, seed

yield per plot, and grain yield were among the main contributors to the variation observed in the fourth component. The major traits contributing to the fifth principal component were leaf length, leaf width, leaf area, days to flowering, number of pods per node, internode length, seed yield per plot, and grain yield. The variability in the sixth component was attributed mainly due to the number of seeds per pod, the number of branches per plant, and pod width.

At Girar Jarso in 2019, the first 5 principal components having eigenvalues above 1 with a value of 69.36% cumulative variance among the accessions for the 19 traits of which 50.01% was contributed by the first two PCs (Table 31). The relative contribution of the two PCs was plotted and presented in Figure 7.

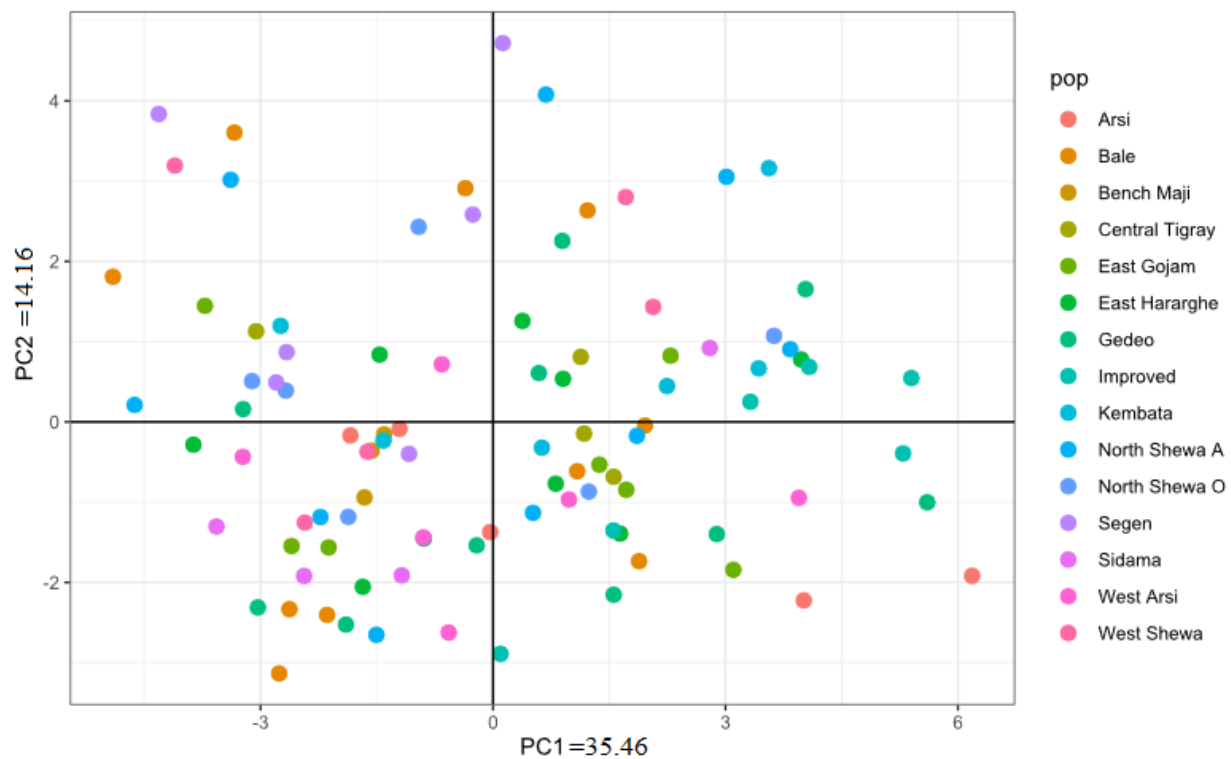


Figure 7. The relative position of 90 landrace accessions and 6 released varieties on the first and second principal axis at Girar Jarso in 2019

The first component (PC1) had 6.74 of the original variables and contributed 35.46% to the total observed variability; PC2 had 2.73 and contributed 14.16% of the total variation. In PC1, there were 9 most important contributing traits to the total variability, 5 traits in PC2, 7 traits in PC3, 5 traits in PC4, and 3 traits in PC5. Traits like leaf length, leaf width, leaf area, internode length,

plant height, lowest pod height, number of seeds per plant, number of pods per plant, and seed yield per plot contributed a lot for principal component (PC1); pod length, pod width, days to maturity, seed filling period, and thousand seed weight had contributed in the second principal component (PC2); days to flowering, number of seeds per pod, pod length, days to maturity, seed yield per plot, thousand seed weight, and grain yield in the third principal component (PC3) were the major contributors to each principal components (PC). In addition, days to flowering, number of pods per node, number of branches per plant, pod width, and grain yield contributed largely to the fifth principal component (PC5).

At Dagem in 2018, the first PC accounted for 22.20% of the total variation, whereas the corresponding values for the second to the seventh PCs were 14.43%, 11.23%, 9.52%, 8.17%, 6.87%, and 5.44%, respectively (Table 32). The first seven principal components with eigenvalues greater than one combined explained about 77.86% of the total variation. The relative contribution of the two PCs was plotted and presented in Figure 8. The first principal component (PC1) had 4.22 of the original variables and contributed 22.2% to the total observed variability; PC2 had 2.74 and contributed 14.43% of the total variation. Traits having relatively higher value in the first principal component (PC1) were days to maturity, seed yield per plot and thousand seed weight, having more contribution to the total diversity and they were responsible for the differentiation of the five clusters. The variation in the second PC was mainly due to the number of seeds per plant, seed yield per plot, and thousand seed weight. Likewise, leaf width, lowest pod height, plant height, number of pods per plant, number of seeds per plant, and seed yield per plot were among the major contributors to the variation in the third component. Days to flowering, number of pods per plant, number of seeds per plant, days to maturity, and seed filling period were the major contributors to the variation observed in the fourth component. The variability in the fifth component was attributed mainly to the lowest pod height, plant height, number of pods per plant, number of seeds per plant, days to maturity, and seed filling period. PC6, on the other hand, accounted for about 6.87% of the total variation among the accessions.

The variation in this component is mainly due to traits such as lowest pod height, plant height, number of seeds per plant, and days to maturity. Furthermore, PC7 contributed 5.44% of the total variation in the accessions which was mainly resulted from leaf area, days to maturity, and seed filling period.

At Degem in 2019, the principal component analysis showed that the first seven principal components with eigenvalues greater than unity altogether explain about 77.89% of the entire diversity among the accessions for all the 19 traits (Table 32). The relative contribution of the two PCs was plotted and presented in Figure 9. The first principal component (PC1) had 3.79 of the original variables and contributed 19.97% to the total observed variability; PC2 had 3.00 and contributed 15.81% of the total variation. Among the 19 traits studied, 6 of them had a high contribution effect to the first PC, and these traits were leaf length, leaf width, leaf area, number of pods per plant, number of seeds per plant, and seed yield per plot. The second component accounting for 15.81% of the total variation predominantly illustrates the variation in the number of seeds per pod, pod length, pod width, and thousand seed weight. The third principal component accounted for 11.08% of the total variation and it was chiefly accounted by variation in leaf length, leaf area, number of pods per node, lowest pod height, plant height, number of pods per plant, number of seeds per plant and grain yield. The fourth principal component accounted for 9.70% of the total variation and was indicated with high variation in days to maturity and seed filling period. The fifth principal component that accounted for about 8.66% of the total variation was due mainly to high variation in lowest pod height, number of seeds per pod, number of branches per plant, pod width, number of seeds per plant, and seed yield per plot. The sixth principal components also accounted for about 7.17% of the total variation, and its major contributors are variations in days to flowering, internode length, number of branches per plant, seed yield per plot, and grain yield. PC7 accounted for 5.50% of the total variation that mainly resulted from the traits such as days to flowering, number of branches per plant, and pod length.

Table 32. Eigen vector, Eigen values, total variance, and cumulative variance of the significant principal components for 19 traits of 96 Ethiopian faba bean accessions at Degem during 2018 and 2019 main cropping season

Trait	Degem-2018							Degem-2019						
	Eigen vector							Eigen vector						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC1	PC2	PC3	PC4	PC5	PC6	PC7
LL	0.00	0.01	-0.00	0.02	-0.00	-0.03	-0.04	0.39	-0.15	-0.27	-0.06	0.22	-0.02	-0.01
LW	0.00	0.00	0.5	0.01	-0.01	-0.01	-0.02	0.38	-0.19	-0.23	-0.08	0.24	-0.02	0.08
LA	-0.00	0.02	0.02	0.04	-0.05	-0.08	-0.23	0.41	-0.19	-0.25	-0.06	0.23	0.01	0.07
DTF	0.02	-0.01	-0.04	0.23	0.11	-0.07	0.75	-0.09	-0.05	0.11	0.14	0.23	0.33	0.75
NPPN	-0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.16	-0.12	0.47	0.11	0.05	0.005	-0.07
IL	0.00	0.00	0.01	-0.01	-0.01	-0.04	-0.01	0.11	0.18	-0.00	0.22	0.21	-0.49	-0.20
LPH	0.00	0.01	0.32	-0.05	0.41	0.85	0.03	0.07	0.20	0.34	-0.06	0.27	0.24	-0.20
PH	0.02	0.09	0.89	-0.06	0.15	-0.40	0.01	0.24	0.22	0.32	0.10	0.13	0.18	0.02
NPPPL	-0.00	0.04	0.12	0.18	-0.22	-0.01	0.01	0.36	-0.12	0.33	0.07	-0.12	-0.12	0.05
NSPP	0.00	0.00	0.00	-0.00	-0.00	0.00	-0.01	-0.04	0.25	-0.14	0.15	-0.38	-0.07	0.17
NBPPL	0.00	0.00	-0.00	0.01	-0.02	-0.01	-0.01	0.19	0.09	-0.05	0.03	-0.26	-0.41	0.34
PL	0.00	0.00	0.01	-0.01	-0.01	-0.01	0.00	0.04	0.42	-0.07	0.19	0.12	-0.18	0.29
PW	0.00	0.00	0.01	-0.01	0.01	0.01	-0.00	0.06	0.4	0.11	0.10	0.25	-0.09	-0.06
NSPPL	-0.01	0.12	0.25	0.48	-0.72	0.30	0.00	0.32	-0.08	0.29	0.11	-0.38	-0.09	0.09
DM	0.05	0.01	-0.09	0.68	0.39	-0.12	0.16	0.10	0.23	0.09	-0.59	-0.07	0.09	0.24
SFP	0.03	0.01	-0.04	0.45	0.28	-0.06	-0.60	0.14	0.24	0.02	-0.60	-0.16	-0.05	-0.08
SYPP	0.14	0.98	-0.11	-0.08	0.06	-0.00	0.01	0.28	0.20	-0.14	0.19	-0.28	0.36	-0.17
TSW	0.99	-0.14	0.01	-0.04	-0.05	0.02	-0.01	0.04	0.42	-0.19	0.01	0.21	0.02	-0.02
GY	0.00	0.01	-0.00	-0.00	0.00	-0.01	0.01	0.20	0.15	-0.25	0.23	-0.24	0.43	-0.12
Eigen values	4.22	2.74	2.13	1.81	1.55	1.30	1.03	3.79	3.00	2.10	1.84	1.65	1.36	1.04
Proportion	22.20	14.43	11.23	9.52	8.17	6.87	5.44	19.97	15.81	11.08	9.70	8.66	7.17	5.50
Cumulative	22.20	36.63	47.86	57.38	65.55	72.42	77.86	19.97	35.78	46.86	56.56	65.22	72.39	77.89

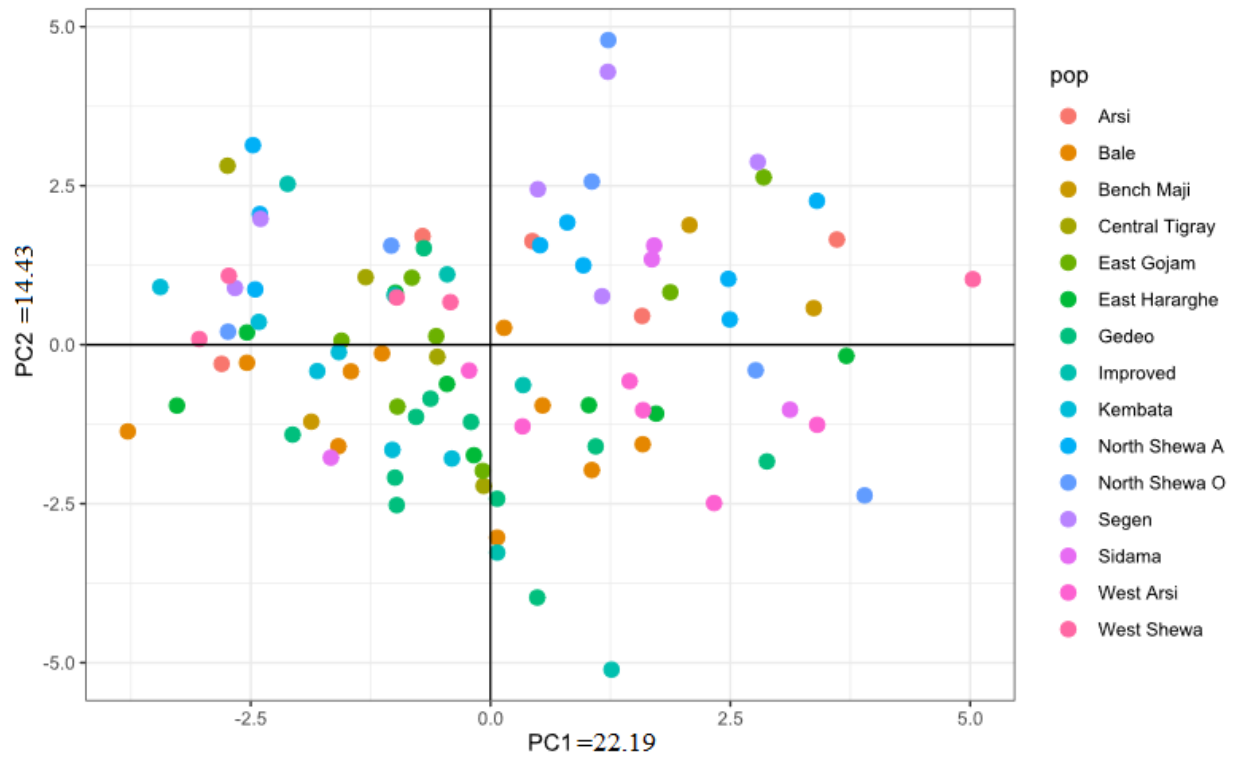


Figure 8. The relative position of 90 landrace accessions and 6 released varieties on the first and second principal axis at Degem in 2018

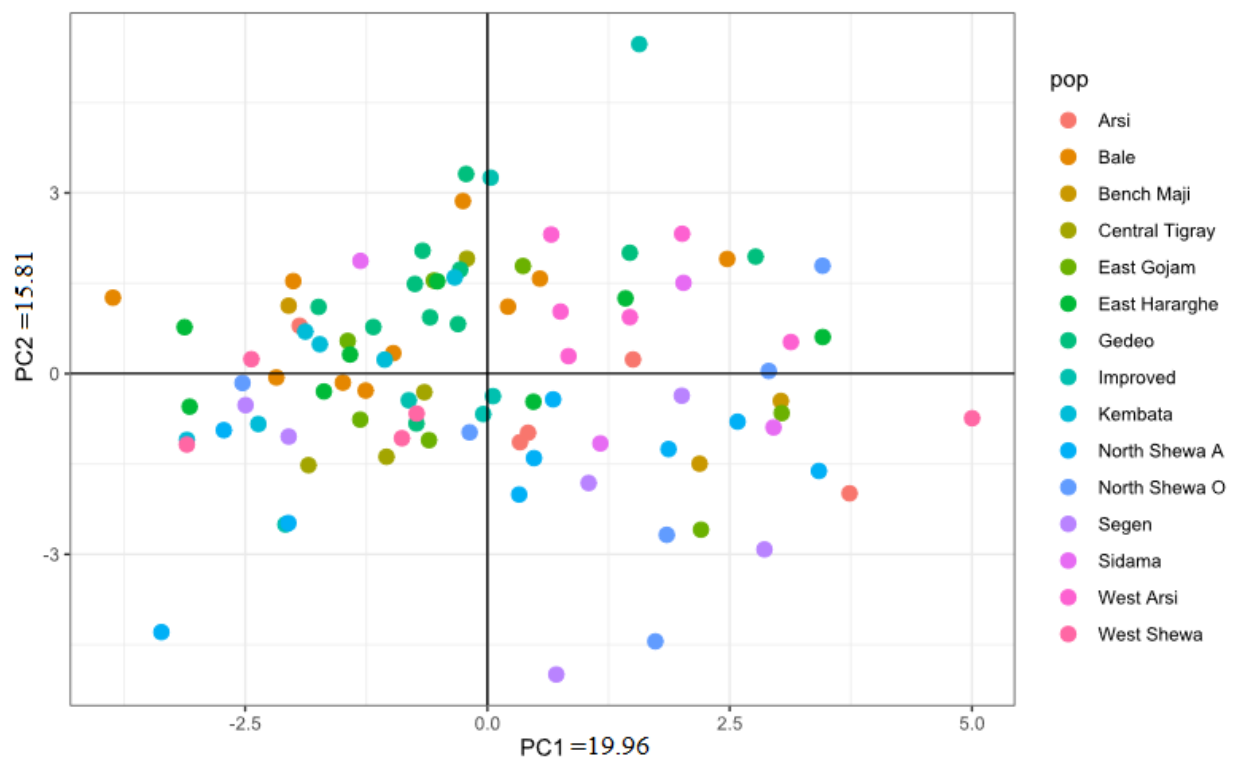


Figure 9. The relative position of 90 landrace accessions and 6 released varieties on the first and second principal axis at Degem in 2019

4.2 Genetic diversity analysis based on ISSR markers

4.2.1 ISSR primers banding patterns and diversity

Among the seventeen screened primers, nine of them (six di-nucleotide, one tetra-nucleotide, and two penta-nucleotide) gave clear, reproducible, and polymorphic bands selected as informative markers. The names, annealing temperature, repeat motif, number of scored bands, number of polymorphic bands, percentage of polymorphism, the number of private bands, number of rare bands, number of abundant bands, and fragment size amplified are shown in Table 33. The nine ISSR primers generated a total of 167 bands ranging from 133 bp to 3000 bp with all primers 100% polymorphic. The highest variation in fragment size was observed for primer UBC815 (333 bp-3000 bp) and the lowest for primer UBC873 (133 bp-800 bp). The average of the total bands per primer was 18.56, ranging from 14 to 25 bands. The maximum number of bands was amplified with di-nucleotide primer UBC815 followed by UBC841 and UBC812, with 25, 24, and 23 bands, respectively, while the minimum number was also amplified with di-nucleotide primer UBC824 with band number 14. Three primers UBC835, UBC873, and UBC881 revealed, 17 bands and primers UBC840 and UBC880 also showed 15 bands. The mean of the private allele is 1.4, ranging from 0 to 4. Rare bands are polymorphic bands that were reported in less than 5% of the accessions under study. The mean of the rare band is 3.2 per primer, with its total of 29 across the accessions. Both the largest private bands and the largest rare bands of 4 and 7, respectively, were generated by the primer UBC873. Common bands are polymorphic bands that were reported in 5 - 50% of the accessions. The mean of the common band is 13.9 per primer, with its total of 125 across the accessions. Both primer UBC812 and UBC841 amplified the maximum number of common bands with the value of 21. On the other hand, primer UBC880 and UBC881 amplified the minimum common bands with a value of 9. Abundant bands are polymorphic bands that were reported in more than 50% of the accessions. The mean of the abundant band is 1.4 per primer, with its total of 13 across accession. The primer UBC881 showed the highest abundant bands of 6.

The effective multiplex ratio, polymorphic information content, marker index, resolving power, number of observed alleles, the number of effective alleles, Shannon information index, gene diversity, allelic evenness, and number of accessions identified per primer are shown in Table 34. Each accession genetic profile was evaluated through the ISSR marker performances of PIC, MI, RP, and EMR parameters. The highest and the lowest PIC values of 0.44 and 0.19 were exhibited by the primer UBC881 and UBC873, respectively, with the mean value of PIC 0.32. MI indicated the general usefulness of the markers. The highest and the lowest MI values of 7.44 and 3.18 were exhibited by the primer UBC815 and UBC873, respectively, with the mean value of MI 5.87. Resolving power is the discriminatory potential of the markers. Similar to PIC, the highest (12.13) and the lowest (2.96) RP values were exhibited by the primer UBC881 and UBC 873, respectively, with a mean of 7.14. The highest and the lowest EMR values of 25.00 and 14.00 were exhibited by the primer UBC815 and UBC824, respectively, with a mean of 18.34 per primer. The number of observed alleles (N_a) was 2. The mean value of the number of effective alleles (N_e) is 1.40, ranging from 1.99 to 1.60. The highest Shannon information index (I) of 0.53 and gene diversity (GD) of 0.36 was observed from primer UBC881 followed by UBC824 with Shannon information index of 0.50 and gene diversity of 0.33. The least Shannon information index of 0.25 and gene diversity of 0.15 were obtained from primer UBC873 followed by UBC835 with Shannon information index of 0.32 and gene diversity of 0.20. Allelic evenness ranged from 0.52 to 0.79, with a mean of 0.66. The number of effective alleles and allelic evenness for primer UBC881 is slightly higher than the other primers. The overall Shannon information index (I) by the nine primers was 0.40, while gene diversity (GD) and allelic evenness were 0.26 and 0.66, respectively. Hence, the results showed that primer UBC881 revealed a high level of genetic variation. The data obtained from each primer allowed the differentiation of a mean of 72.67 accessions per primer, ranging from 62 to 83 accessions identified.

Table 33. Number of scored bands, polymorphic bands, private bands, rare bands, common bands, abundant bands and fragment size amplified by nine ISSR primers in faba bean accessions

Primer	Repeat Motif	T (°C)	NSB	NPB	NPvB	NRB	NCB	NAB	FS
UBC812	(GA)8A	45	23	23	2	2	21	0	200-2000
UBC815	(CT)8G	42	25	25	2	3	20	2	333-3000
UBC824	(TC)8G	48	14	14	0	0	13	1	400-1500
UBC835	(AG)8YC	48	17	17	2	6	10	1	150-1000
UBC840	(GA)8YT	42	15	15	2	1	12	2	300-1500
UBC841	(GA)8YC	43	24	24	0	2	21	1	350-1500
UBC873	(GACA)4	45	17	17	4	7	10	0	133-800
UBC880	(GGAGA)3	45	15	15	2	6	9	0	200-1500
UBC881	(GGGTG)3	47	17	17	0	2	9	6	350-1400
Total			167	167	13	29	125	13	-
Average					1.4	3.2	13.9	1.4	-

T (°C): annealing temperature; NSB: number of scored band; NPB: number of polymorphic band; NPvB: number of private bands; NRB: number of rare bands; NCB: number of common bands; NAB: number of abundant band; FS: fragment size amplified

Table 34. Marker parameters statistics calculated across nine ISSR primers in 96 faba bean accessions

Locus	EMR	PIC	MI	RP	Na	Ne	I	GD	Evenness	NG
UBC812	21.04	0.41	6.35	6.73	2	1.36	0.39	0.24	0.64	66
UBC815	25.00	0.36	8.96	11.50	2	1.47	0.45	0.30	0.71	78
UBC824	14.00	0.42	5.85	6.79	2	1.54	0.50	0.33	0.75	66
UBC835	17.00	0.25	4.22	4.65	2	1.30	0.32	0.20	0.59	67
UBC840	15.00	0.33	4.97	6.38	2	1.44	0.43	0.28	0.69	79
UBC841	24.00	0.32	7.60	8.85	2	1.38	0.41	0.26	0.66	74
UBC873	17.00	0.19	3.18	2.96	2	1.20	0.25	0.15	0.52	62
UBC880	15.00	0.28	4.22	4.27	2	1.33	0.34	0.21	0.61	79
UBC881	17.00	0.44	7.46	12.13	2	1.60	0.53	0.36	0.79	83
Total	-	-	-	-	-	-	-	-	-	654
Mean	18.34	0.32	5.87	7.14	2	1.40	0.40	0.26	0.66	72.67

EMR: effective multiplex ratio; PIC: polymorphic information content; MI: marker index; RP: resolving power; Na: Number of observed alleles; Ne: Number of effective alleles; I: Shannon's index; GD: Nei's gene diversity and NG: number of genotypes identified per primer

4.2.2 Population genetic diversity

The population, number of samples, percent of polymorphism, number of observed alleles, effective number of allele, Shannon diversity index, gene diversity, and unbiased gene diversity are shown in Table 35. Based on the geographic origin or AZs, the population from East Hararghe showed the highest percentage of polymorphism followed by North Shewa Amhara with 72.46% and 68.86%, respectively. While the least percentage of polymorphism was detected from the Sidama population, followed by Bench Maji with 44.91% and 46.11%, respectively. The average percentage of polymorphism was 57.27%, indicating a high level of polymorphism and variation within geographical populations. Both accessions from North Shewa Amhara and East Hararghe populations revealed the highest number of observed alleles. On the other hand, accessions from West Shewa and North Shewa Amhara populations revealed the highest effective number of alleles. The highest Shannon information index ($I = 0.31$), gene diversity ($h = 0.20$), and unbiased gene diversity ($uh = 0.23$) were obtained from the West Shewa population, followed by North Shewa Amhara ($I = 0.31$, $h = 0.19$, and $uh = 0.21$). While the least Shannon information index ($I = 0.19$), gene diversity ($h = 0.11$), and unbiased gene diversity ($uh = 0.11$) were detected by the Bale population. Based on breeding status, the landrace population showed a higher percentage of polymorphism with 98.20%, while the released variety population showed a 65.27% percentage of polymorphism, but Shannon information index, gene diversity, and unbiased gene diversity are higher in released varieties than the landrace population. Regarding geographical origin, the overall Shannon information index and gene diversity were 0.25 and 0.16, respectively. While average Shannon information index and gene diversity relative to the breeding status were 0.29 and 0.18, respectively.

Table 35. Genetic parameter estimates based on ISSR markers among faba bean subpopulations

Based on Geographical Origin (AZs)							
Pop	N	%P	Na	Ne	I	h	uh
North Shewa A	9.00	68.86	1.38	1.31	0.31	0.19	0.21
East Gojam	7.00	57.49	1.15	1.21	0.23	0.14	0.15
West Arsi	6.00	57.49	1.15	1.23	0.24	0.15	0.17
Arsi	5.00	50.90	1.04	1.25	0.24	0.16	0.17
Bale	10.00	55.69	1.11	1.15	0.19	0.11	0.11
North Shewa O	6.00	54.49	1.09	1.23	0.24	0.15	0.17
East Hararghe	8.00	72.46	1.45	1.29	0.30	0.19	0.20
West Shewa	5.00	64.07	1.29	1.33	0.31	0.20	0.23
Sidama	4.00	44.91	0.90	1.20	0.21	0.13	0.15
Gedeo	11.00	65.27	1.31	1.20	0.23	0.14	0.15
Segen	6.00	62.87	1.28	1.27	0.28	0.18	0.19
Kembata	6.00	47.31	0.96	1.20	0.20	0.13	0.14
Bench Maji	3.00	46.11	0.92	1.24	0.24	0.15	0.19
Central Tigray	4.00	53.89	1.09	1.27	0.26	0.17	0.20
Total	6.43	57.27	1.15	1.24	0.25	0.16	0.17
Based on Breeding Status							
Landraces	90.00	98.20	1.96	1.24	0.29	0.17	0.17
Improved	6.00	65.27	1.33	1.31	0.30	0.20	0.21
Total	48.00	81.74	1.65	1.27	0.29	0.18	0.19

N: number of sample, %P: Percentage of polymorphic loci; Na: Number of observed alleles; Ne: Number of effective alleles; I: Shannon's information index; h: Diversity (expected heterozygosity), uh: unbiased diversity (Unbiased expected heterozygosity);

Figure 10 shows the number of bands, number of bands with frequencies greater than or equal to 5%, the number of private bands, number of less common bands with frequencies less than or equal to 25% and 50%, and expected heterozygosity. Table 36 also supports the patterns depicted in figure 10. According to table 36, accessions from East Hararghe had the highest number of bands and number of bands with frequencies greater than or equal to 5% by 121 values for both followed by accessions from North Shewa Amhara which also had a value of 115 for both numbers of bands and number of bands with frequencies greater than or equal to 5%.

Among the fifteen pre-defined populations, private bands were found in seven populations with East Hararghe possessing the highest number of private bands of 5, suggesting that there are potential sources of alleles and traits of agronomic importance, whereas North Shewa Amhara, West Arsi, Gedeo, and Segen had the lowest number of private band of one. Using primer

UBC812, a private band was observed in accession 26855 from the Segen population with a molecular size of 200 bp. In primer UBC815, two private bands were observed in accession 30014 from the West Arsi population and accession 29527 from the East Hararghe population with band sizes of 633 bp and 733 bp, respectively. Primer UBC835 had two private bands with band sizes of 310 bp and 566 bp that were observed in released variety Dagim and accession 26859 from the Gedeo population, respectively. Primer UBC840 had only one private band in accession 29527 from the East Hararghe population. Primer UBC873 had four private bands 133 bp, 466 bp, 533 bp, and 650 bp were observed in accession 212572 from North Shewa Amhara, released variety Moti, accession 29532 from East Hararghe population, and accession 25260 from West Shewa population. While accession 29536 from East Hararghe population had two private bands with band sizes 533 bp and 566 bp in primer UBC880.

The highest number of less common alleles with frequencies less than or equal to 25% was revealed by East Hararghe and Gedeo populations with a value of four. Both accessions from North Shewa Amhara and East Hararghe populations also revealed the highest less common alleles with frequencies less than or equal to 50% with values of 30 for both administrative zones. Accessions from East Hararghe had the highest expected heterozygosity (0.26) followed by released variety (0.26) and West Arsi (0.25). The highest unbiased expected heterozygosity was exhibited by West Arsi (0.32) followed by released varieties (0.31) and the Central Tigray (0.30). So, having the highest number of alleles, the number of alleles with frequencies greater than or equal to 5%, and the number of less common alleles with frequencies less than or equal to 50%; East Hararghe and North Shewa Amhara could be the most important populations. East Hararghe and North Shewa Amhara had also the highest percent of polymorphism (72.46%, 68.86%), Shannon diversity index (0.39, 0.37), and expected gene diversity (0.26, 0.25), respectively.

Table 36. Important allelic pattern for each pre-defined population

Pop	No. alleles	No. alleles freq. $\geq 5\%$	No. of private alleles	No. LComm alleles freq. $\leq 25\%$	No. LComm alleles freq. $\leq 50\%$	h \pm SD	uh \pm SD
North Shewa A	115	115	1	2	30	0.25 \pm 0.02	0.28 \pm 0.02
East Gojam	96	96	0	2	15	0.20 \pm 0.02	0.24 \pm 0.02
West Arsi	96	96	1	2	16	0.21 \pm 0.02	0.25 \pm 0.02
Arsi	89	89	0	0	15	0.20 \pm 0.02	0.25 \pm 0.02
Bale	93	93	0	1	17	0.17 \pm 0.01	0.19 \pm 0.02
North Shewa O	91	91	0	1	15	0.20 \pm 0.02	0.24 \pm 0.02
East Hararghe	121	121	5	4	30	0.26 \pm 0.01	0.29 \pm 0.02
West Shewa	108	108	2	3	22	0.25 \pm 0.02	0.32 \pm 0.02
Sidama	75	75	0	1	13	0.19 \pm 0.02	0.25 \pm 0.02
Gedeo	109	109	1	4	26	0.21 \pm 0.01	0.23 \pm 0.02
Segen	109	109	1	2	26	0.23 \pm 0.02	0.28 \pm 0.02
Kembata	81	81	0	1	10	0.17 \pm 0.02	0.20 \pm 0.02
Bench Maji	77	77	0	2	11	0.21 \pm 0.02	0.31 \pm 0.03
Central Tigray	92	92	0	3	17	0.22 \pm 0.02	0.30 \pm 0.02
Improved	113	113	2	2	27	0.26 \pm 0.02	0.31 \pm 0.02

Number of alleles, number of alleles with frequencies greater than or equal to 5%, number of private alleles, number of less common alleles with frequencies less than or equal to 25%, number of less common alleles with frequencies less than or equal to 50%, h: expected heterozygosity, uh: unbiased expected heterozygosity, SD: standard deviation

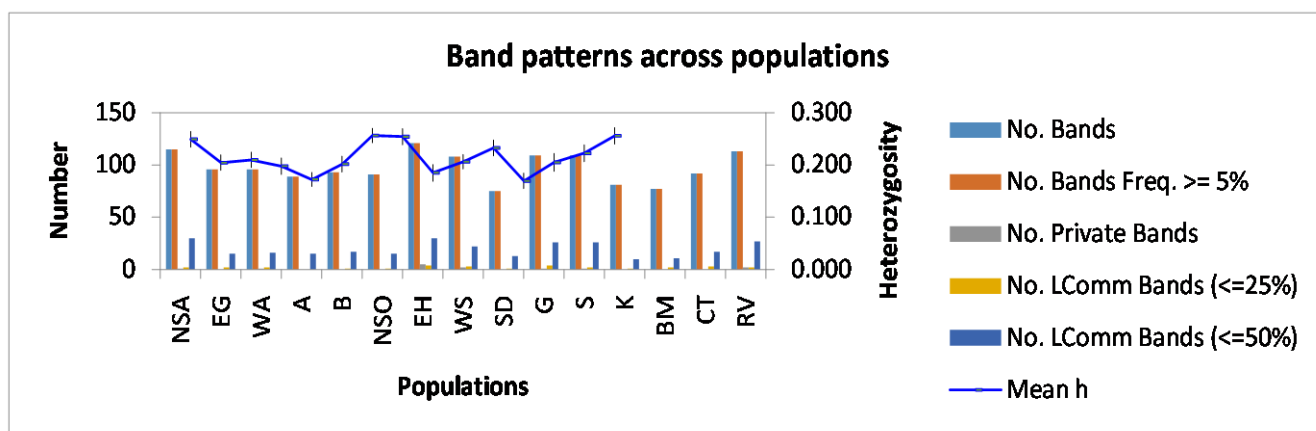


Figure 10. Band patterns across populations for ISSR marker

4.2.3 Analysis of molecular variance

AMOVA based on fourteen AZs that are the geographic origin of 90 landrace accessions revealed that the highest percentage of variation is attributed to variation within populations (99%), while 1% is due to the among-population variation. AMOVA based on breeding status indicated that the higher percentage of variation is also attributed to the variation within populations (97%), while 3% is due to the among populations variation that is among landraces and released varieties. Generally, the result of AMOVA in both cases revealed that the larger genetic diversity was found within the population but very low genetic diversity was found among populations (Table 37).

Table 37. Analysis of molecular variance among and within faba bean subpopulations

Based on Geographical Origin						
Source of variation	df	SS	MS	EV	PV	P value
Among Region	3	47.51	15.84	0.00	0%	0.93
Among populations	10	225.31	22.53	0.25	1%	0.25
Within populations	76	1593.80	20.97	20.97	99%	0.58
Total variations	89	1866.62		21.22	100%	
Based on Breeding Status						
Among populations	1	27.67	27.67	0.57	3%	0.14
Within populations	94	1994.62	21.22	21.22	97%	0.17
Total variations	95	2022.29		21.79	100%	

df: degrees of freedom; SS: sum of squares; EV: estimated variance, PV: percentage variance

4.2.4 Cluster analysis

Neighbor-joining (NJ) clustering algorithm was used to construct a dendrogram for 96 individuals based on 167 bands obtained with 9 ISSR primers. The accessions were categorized on their geographic origin into fourteen populations consisting of landraces and one population derived from released variety to be used as a control. All the accessions in the study grouped into 7 clusters (Figure 11 and Table 38). However, the cluster analysis generated using ISSR markers has not agreed with the pre-defined population structure based on administrative zones. The number of accessions in each of seven clusters ranged from a minimum of five to a maximum of twenty-four. According to the result, C3 contained 24 accessions (25%) followed by C5, C1, C4, C6, C7 and C2 containing 18 (18.8%), 14 (14.6%), 13 (13.5%), 12 (12.5%), 10 (10.5%) and 5 (5.2%) proportions, respectively. C1 was the third-largest cluster containing 14 accessions derived from North Shewa Amhara (7.1%), East Gojam (14.3%), West Arsi (7.1%), Arsi (7.1%), Bale (14.3%), East Hararghe (7.1%), West Shewa (7.1%), Segen (7.1%), Kembata (7.1%), Central Tigray (7.1%) and released varieties (14.3%) in the respective proportions, which may imply the presence of gene flow between and within populations or no clear grouping based on geographic origin. So, C1 comprised 12 landraces from ten different administrative zones and two released varieties (Walki and Bulga-70). While C2 was the smallest cluster consisting of 5 accessions only from three administrative zones:

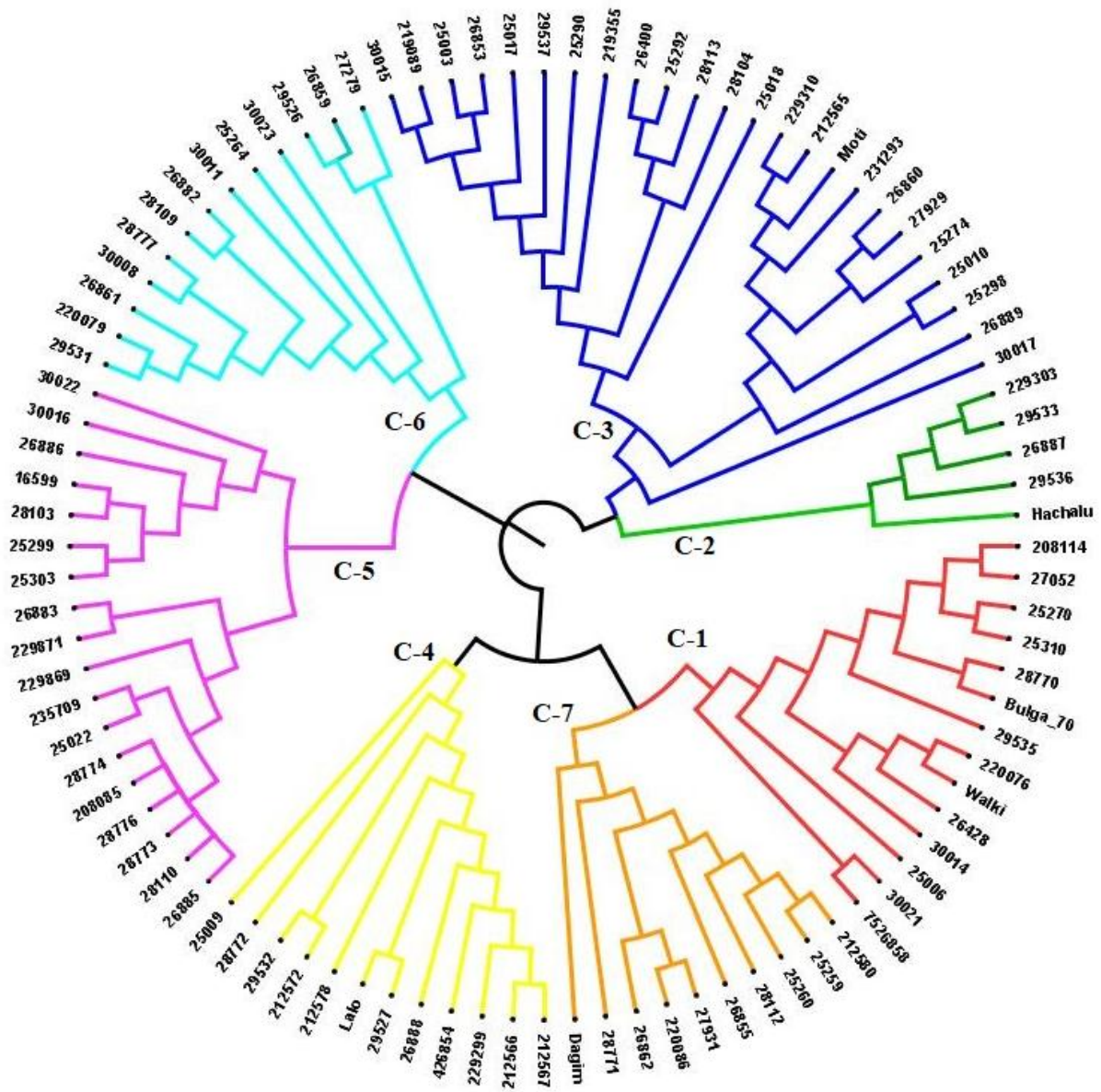


Figure 11. Dendrogram for 90 faba bean landrace accessions and 6 released varieties based on NJ analysis of amplified bands by nine ISSR primers

Table 38. Clustering 96 faba bean accessions into seven clusters using 167 bands of 9 ISSR primers.

Cluster	Number of accessions	Accessions
C1	14	30021, 26858, 25006, 30014, 26428, 220076, Lalo, 29535, 208114, 27052, 28770, Bulga-70, 25270, 25310
C2	5	29536, Moti, 26887, 229303, 29533
C3	24	25292, 26400, 28104, 28113, 25290, 29537, 26853, 25003, 219089, 30015, 219355, 25017, 25018, 27929, 26860, 25274, 212565, 229310, Hachalu, 231293, 25298, 25010, 26889, 30017
C4	12	Walki, 29527, 29532, 212572, 212566, 212567, 229299, 26854, 26888, 212578, 28772, 25009
C5	18	26886, 30016, 30022, 229871, 26883, 229869, 26885, 28110, 28773, 28776, 208085, 28774, 25022, 235709, 25303, 25299, 28103, 16599
C6	13	26861, 29531, 220079, 28777, 3008, 28109, 30011, 30023, 25264, 26859, 29526, 26882, 27279
C7	10	28771, Dagim, 26862, 27931, 220086, 26855, 28112, 25260, 212580, 25259

4.2.5 The geographical pattern of genetic diversity

The landraces collected from different administrative zones and released varieties were dispersed over clusters C1 to C7, indicating that there was no definite association between sources of origin and clustering pattern. Accessions from fourteen administrative zones were distributed over most of the clusters exhibiting high genetic diversity in most of the administrative zones. Accessions from five origins, namely North Shewa Amhara, Bale, East Hararghe, Gedeo, and released varieties were distributed in five of the total clusters, indicating accessions resulting from these sources were comparatively dispersed in most clusters. While accessions from East Gojam, West Arsi, North Shewa Oromia, West Shewa, Sidama, Segen, and Central Tigray were dispersed over four of the seven clusters. Finally, accessions from Arsi, Kembata, and Bench Maji were distributed over three of the seven clusters (Table 39). These results indicated that

there was no clear interrelationship observed between the origin of accessions and the pattern of diversity, as there were a number of accessions from the same source of origin which fell into different clusters and accessions from different origins overlapped in the same clusters (Table 39).

Table 39. Clustering pattern of 96 Ethiopian faba bean accessions from different origin over seven clusters using 167 bands of 9 ISSR primers

Origin	Number of accession	Number of accessions in each cluster						
		C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇
North Shewa A	9	1	-	2	4	1	-	1
East Gojam	7	2	-	2	-	2	1	-
West Arsi	6	1	-	2	-	1	2	-
Arsi	5	1	-	3	1	-	-	-
Bale	10	2	-	-	1	4	2	1
North Shewa O	6	-	1	3	1	1	-	-
East Hararghe	8	1	2	1	2	-	2	-
West Shewa	5	1	-	1	-	-	1	2
Sidama	4	-	-	1	-	1	1	1
Gedeo	11	-	1	2	-	4	3	1
Segen	6	1	-	2	2	-	-	1
Kembata	6	1	-	3	-	2	-	-
Bench Maji	3	-	-	1	-	1	-	1
Central Tigray	4	1	-	-	-	1	1	1
Released	6	2	1	1	1	-	-	1
Total	96	14	5	24	12	18	13	10

From the NJ dendrogram (Figure 12), it was apparent that the populations from Bale and Arsi were the most distantly related and clustered separately from each other, showing a level of genetic variation between them. Populations from fourteen administrative zones and one released variety group of *Vicia faba* were grouped into four clusters; cluster I (Segen and released variety), cluster II (Arsi and Kembata), cluster III (Bale, Gedeo, Sidama, West Arsi and East Gojam) and cluster IV (West Shewa, Central Tigray, East Hararghe, Bench Maji, North Shewa Oromia, and North Shewa Amhara) which contained 2, 2, 5, 6 populations, respectively.

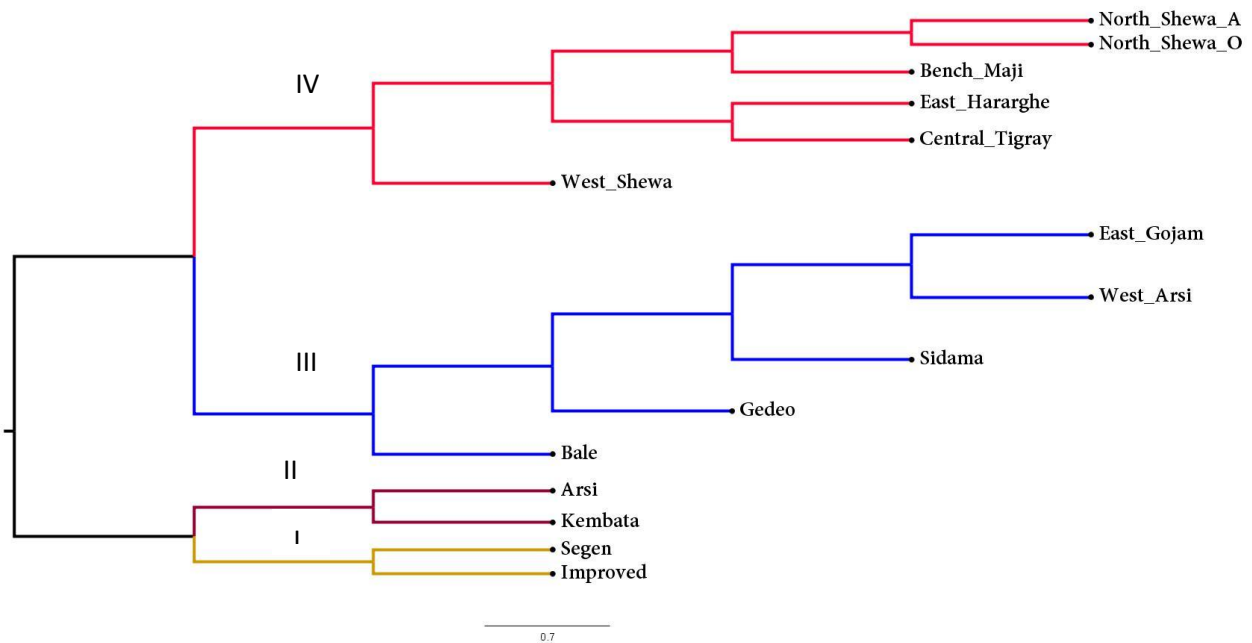


Figure 12. NJ based dendrogram for 15 faba bean pre-defined populations using 9 ISSR primers and Nei's (1972) genetic similarity coefficients

4.2.6 Principal coordinate analysis

Principal coordinate analysis (PCoA) results using two and three coordinates are indicated in figures 13 and 14, respectively, using GenAlEx v. 6.5 software (Peakall and Smouse, 2012). PCoA in the two-dimensional coordinates revealed 39.04% of the total variation, with 20.8% and 18.15% explained by PC1 and PC2, respectively (Figure 13). The first three coordinates of the

PCoA accounted together 51.23% of the total variation, with 20.8%, 18.15%, and 12.28% explained by PC1, PC2, and PC3, respectively. The patterns of distribution of accessions in the PCoA plot revealed seven clusters in the two-dimensional and three-dimensional coordinates. The clusters identified through PCoA analysis were also similar to those identified in the NJ cluster analysis and also from the STRUCTURE analysis, thereby illustrating the conformity of results obtained from the study.

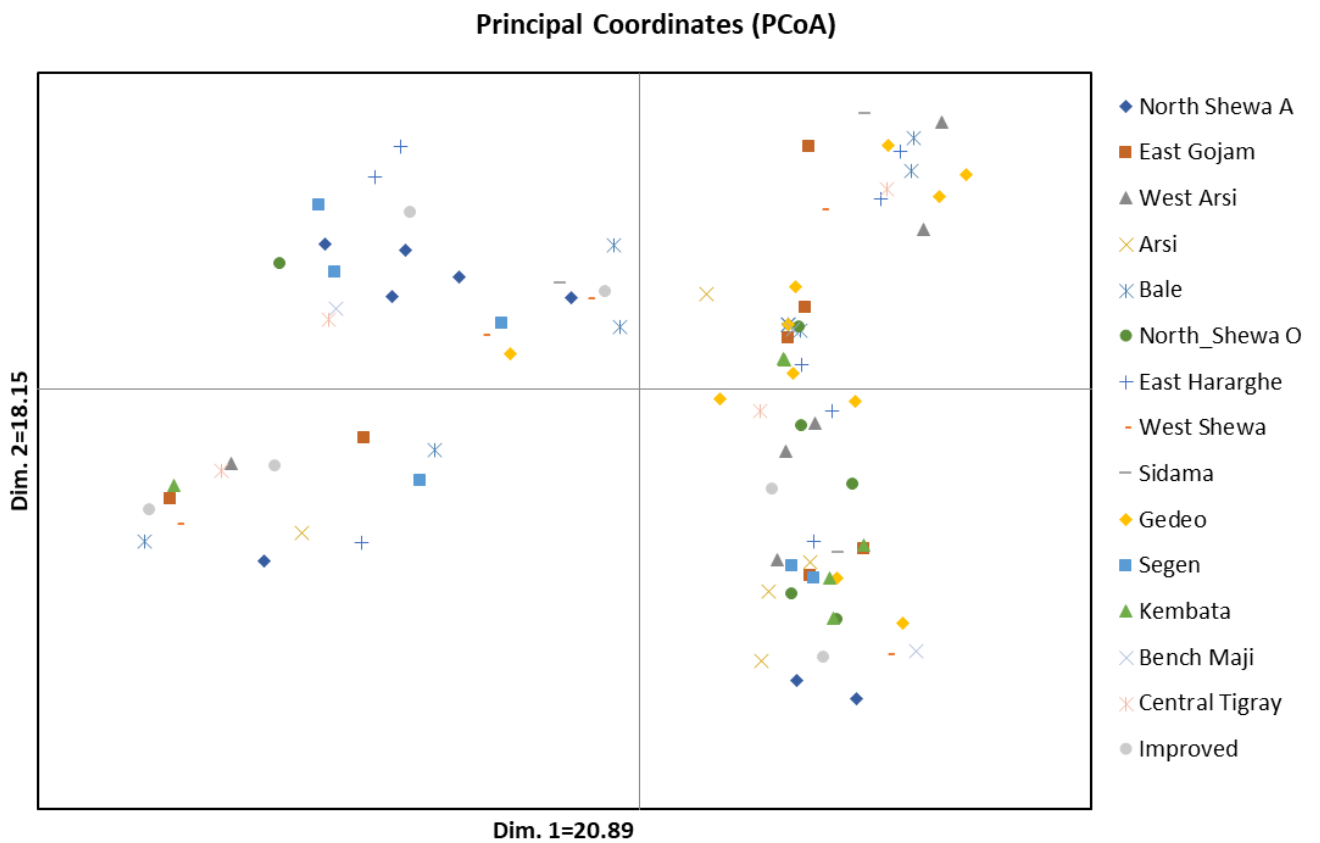


Figure 13. Two-dimensional representation of principal coordinate analysis of genetic relationships among 96 Ethiopian faba bean accessions of 15 populations using ISSR data

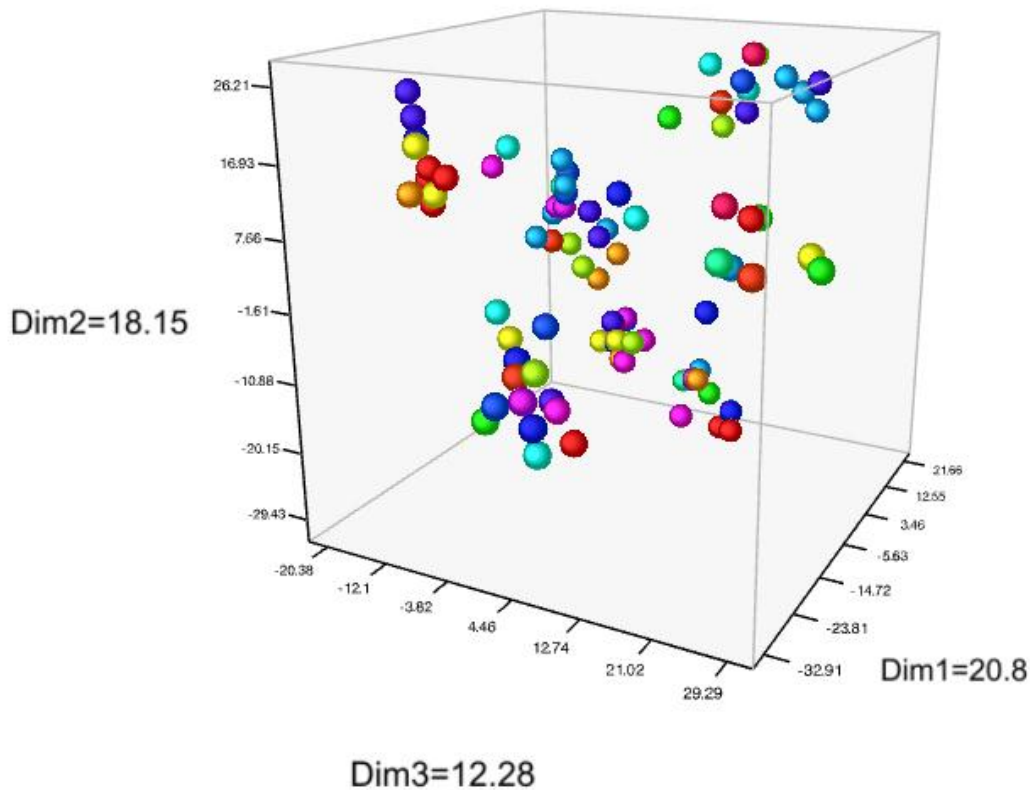


Figure 14. Three-dimensional representation of principal coordinate analysis of genetic relationships among 96 Ethiopian faba bean accessions of 15 populations using ISSR data

4.2.7 Distance-based population differentiation

4.2.7.1 Genetic distance and identity

The genetic distance among the fifteen pre-defined populations ranged from 0.01 to 0.04 (Table 40). Accessions from Bale were distantly related to accessions of Arsi (0.04) followed by accessions from Segen that were distantly related to accessions of Gedeo (0.04) and Bench Maji (0.04). The least genetic distance was revealed between accessions from Gedeo and Sidama populations (0.01) followed by accessions from Bale and East Gojam populations (0.01). Genetic identity coefficients ranged from 0.96 to 0.99. Based on the estimated genetic identity coefficient, the highest genetic identity value was observed between Sidama and Gedeo (0.99) followed by

East Gojam and Bale (0.99), and between West Arsi and Gedeo (0.99). The least genetic identity value was observed between accessions of Arsi and Bale (0.96) followed by Gedeo and Segen (0.96).

4.2.7.2 Genetic differentiation and gene flow

Genetic differentiation on faba bean landraces collected from AZs of Ethiopia revealed that PhiPT values among pairs of the population ranged from 0.00 to 0.27, with an overall mean of 0.07 (Table 41). There was little population differentiation among East Gojam and East Hararghe (PhiPT = 0.00), Arsi and West Shewa (PhiPT = 0.00), Bale and Gedeo (PhiPT=0.00), North Shewa Oromia and Gedeo (PhiPT=0.00), East Hararghe and Gedeo (PhiPT=0.00), North Shewa Oromia and Central Tigray (PhiPT=0.00). Very high population differentiation was observed between Central Tigray and Bench Maji (PhiPT=0.27). A large degree of population differentiation was observed among Bench Maji and Sidama (PhiPT=0.21), Bench Maji and West Shewa (PhiPT=0.20), Central Tigray and West Shewa (PhiPT=0.18), Sidama and West Arsi (PhiPT = 0.17), and Bale and Arsi (PhiPT=0.17). Moderate genetic differentiation was observed between Central Tigray and Sidama (PhiPT = 0.14). Among 105 pair wise PhiPT values 52 of them ranged from 0.00 -0.05, 46 of them ranged from 0.05 - 0.15, 6 of them ranged from 0.15-0.25, and 1 pair above 0.25; showed little, moderate, large, and very large genetic differentiation, respectively. A high level of gene flow (Nm), ranging from 0.68-24.75, was detected among the pre-defined populations from fourteen administrative zones and one released variety group. The lowest level of genetic differentiation and high level of gene flow were observed among those from West Shewa and North Shewa Amhara, released varieties and East Gojam, released varieties and West Arsi, released varieties and Arsi, Central Tigray and Bale, released varieties and East Hararghe, Segen and East Hararghe, West Shewa and East Hararghe, Segen and West Shewa, Segen and Sidama, Central Tigray and Kembata.

Table 40. Nei's genetic identity (above diagonal) and genetic distance (below diagonal) among faba bean populations.

	NSA	EG	WA	A	B	NSO	EH	WS	SD	G	S	K	BM	CT	RV
NSA	****	0.98	0.98	0.98	0.98	0.99	0.98	0.98	0.98	0.98	0.98	0.98	0.98	0.99	0.98
EG	0.02	****	0.99	0.97	0.99	0.99	0.98	0.97	0.99	0.99	0.97	0.99	0.98	0.98	0.97
WA	0.02	0.01	****	0.97	0.99	0.99	0.99	0.98	0.99	0.99	0.97	0.98	0.98	0.98	0.97
A	0.02	0.03	0.03	****	0.96	0.98	0.97	0.97	0.96	0.96	0.98	0.98	0.97	0.97	0.97
B	0.02	0.01	0.01	0.04	****	0.98	0.98	0.97	0.99	0.99	0.96	0.98	0.98	0.98	0.96
NSO	0.01	0.01	0.02	0.02	0.02	****	0.99	0.97	0.98	0.99	0.98	0.99	0.98	0.97	0.97
EH	0.02	0.02	0.01	0.03	0.02	0.02	****	0.97	0.98	0.99	0.97	0.98	0.97	0.98	0.97
WS	0.02	0.04	0.02	0.03	0.03	0.03	0.03	****	0.98	0.97	0.96	0.97	0.98	0.98	0.97
SD	0.03	0.01	0.01	0.04	0.01	0.02	0.02	0.02	****	0.99	0.96	0.98	0.98	0.98	0.96
G	0.02	0.01	0.01	0.04	0.01	0.01	0.01	0.03	0.01	****	0.96	0.98	0.99	0.98	0.96
S	0.02	0.04	0.03	0.03	0.04	0.02	0.03	0.04	0.04	0.04	****	0.97	0.96	0.97	0.98
K	0.02	0.02	0.02	0.02	0.03	0.01	0.02	0.03	0.02	0.02	0.03	****	0.98	0.98	0.97
BM	0.02	0.02	0.02	0.04	0.02	0.02	0.03	0.03	0.02	0.02	0.04	0.02	****	0.98	0.97
CT	0.02	0.02	0.02	0.04	0.02	0.03	0.02	0.02	0.02	0.02	0.03	0.02	0.02	****	0.98
RV	0.02	0.03	0.03	0.03	0.04	0.03	0.03	0.03	0.04	0.04	0.02	0.03	0.03	0.02	***

*

NSA: North Shewa Amhara, EG: East Gojam, WA: West Arsi, A: Arsi, B: Bale, NSO: North Shewa Oromia, EH: East Hararghe, WS: West Shewa, SD: Sidama, G: Gedeo, S: Segen, K: Kembata, BM: Benchi Maji, CT: Central Tigray, RV: Released Variety

Table 41. PhiPT values (above diagonal) and Gene flow (Nm, below diagonal)

	NSA	EG	WA	A	B	NSO	EH	WS	SD	G	S	K	BM	CT	RV
NSA	0	0.07	0.05	0.02	0.13	0.03	0.02	0.01	0.04	0.14	0.1	0.08	0.07	0.03	0.06
EG	3.32	0	0.11	0.04	0.04	0.04	0	0.03	0.11	0.02	0.03	0.07	0.12	0.08	0.01
WA	4.75	2.02	0	0.03	0.02	0.05	0.06	0.02	0.17	0.08	0.02	0.06	0.13	0.13	0.01
A	12.25	6.00	8.08	0	0.17	0.09	0.05	0	0.02	0.11	0.05	0.1	0.1	0.02	0.01
B	1.67	6.00	12.25	1.22	0	0.09	0.05	0.11	0.09	0	0.14	0.1	0	0.01	0.12
NSO	8.08	6.00	4.75	2.53	2.53	0	0.03	0.04	0.06	0	0.06	0.08	0.17	0	0.02
EH	12.25	****	3.92	4.75	4.75	8.08	0	0.01	0.06	0	0.01	0.05	0.04	0.08	0.01
WS	24.75	8.08	12.25	****	2.02	6.00	24.75	0	0.12	0.06	0.01	0.06	0.2	0.18	0.04
SD	6.00	2.02	1.22	12.25	2.53	3.92	3.92	1.83	0	0.13	0.01	0.03	0.21	0.14	0.04
G	1.54	12.25	2.88	2.02	****	****	****	3.92	1.67	0	0.12	0.03	0.1	0.02	0.12
S	2.25	8.08	12.25	4.75	1.54	3.92	24.75	24.75	24.75	1.83	0	0.02	0.09	0.08	0.06
K	2.88	3.32	3.92	2.25	2.25	2.88	4.75	3.92	8.08	8.08	12.25	0	0.09	0.01	0.05
BM	3.32	1.83	1.67	2.25	****	1.22	6.00	1.00	0.94	2.25	2.53	2.53	0	0.27	0.11
CT	8.08	2.88	1.67	12.25	24.75	****	2.88	1.14	1.54	12.25	2.88	24.75	0.68	0	0.13
RV	3.92	24.75	24.75	24.75	1.83	12.25	24.75	6.00	6.00	1.83	3.92	4.75	2.02	1.67	0

4.2.8 Model-based population structure

According to the results, K was determined as 7 subpopulations (Figure 15) because of the relatively high ΔK value of K = 7 based on a method described by Evanno *et al.* (2005). The standard deviation (SD) for each value of K is also important when deciding the correct number of subpopulations: SD values are shown in Table 42 and support the choice of K = 7 since the lowest SD was obtained at highest $\Delta K = 12$. The analysis for K = 7 populations showed individual landrace accessions from the fourteen collection sites distributed between the seven populations is demonstrated by a bar plot (Figure 16). Each accession in the graph was represented by a single vertical line broken into K colored segments, with lengths proportional to each of the K inferred clusters. Each color represents the proportion of the membership of each accession, represented by a vertical line, to the 7 clusters. Different colors represent different subpopulations. On the graph, the x-axis shows the individuals in the populations and the y-axis demonstrates the percentage identity to the group to which it belongs. A genotype was considered to belong to a cluster if its membership coefficient was ≥ 0.80 . Genotypes with membership coefficients lower than 0.80 at each assigned K were regarded as admixed (Table 43). Among the fifteen pre-defined populations, ten of them have admixed individuals with the proportion ranged from 9.09 (Gedeo population) to 40.00 (Bale population). The average proportions of admixed individuals are 13.9.

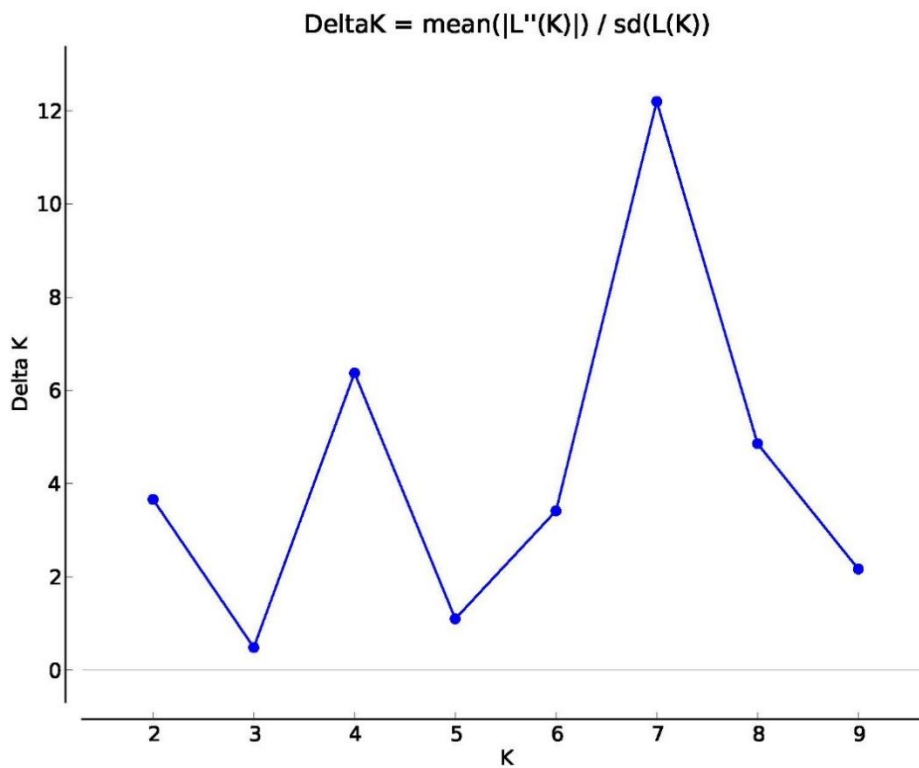


Figure 15. ΔK was used to determine the most appropriate K value for population structure in faba bean population.

Table 42. The standard deviation (SD) and ΔK for each value of k to determine the most appropriate k value.

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	3	-6528.000000	0.458258	—	—	—
2	3	-5680.533333	36.443975	847.466667	133.466667	3.662242
3	3	-4966.533333	190.850264	714.000000	92.866667	0.486594
4	3	-4345.400000	32.736371	621.133333	208.666667	6.374154
5	3	-3932.933333	108.062451	412.466667	119.000000	1.101215
6	3	-3401.466667	106.582941	531.466667	364.300000	3.417995
7	3	-3234.300000	11.583177	167.166667	141.300000	12.198725
8	3	-3208.433333	37.538558	25.866667	182.466667	4.860780
9	3	-3365.033333	79.832345	-156.600000	173.200000	2.169547
10	3	-3348.433333	280.153964	16.600000	—	—

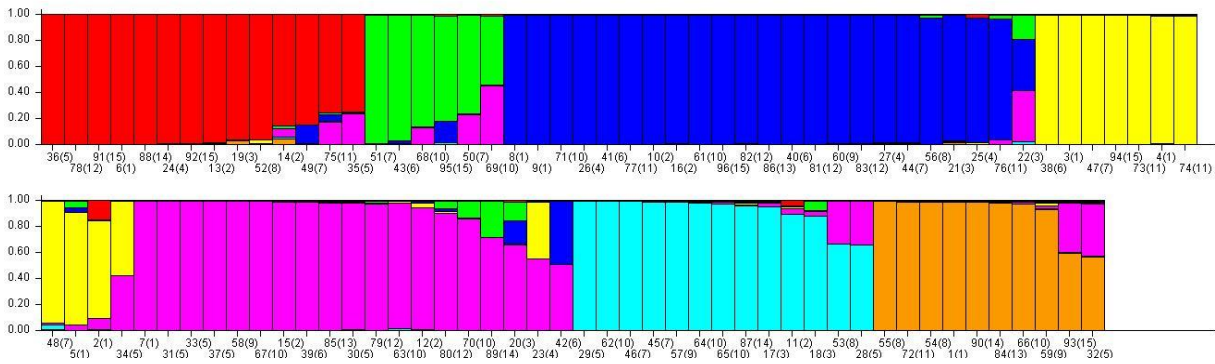
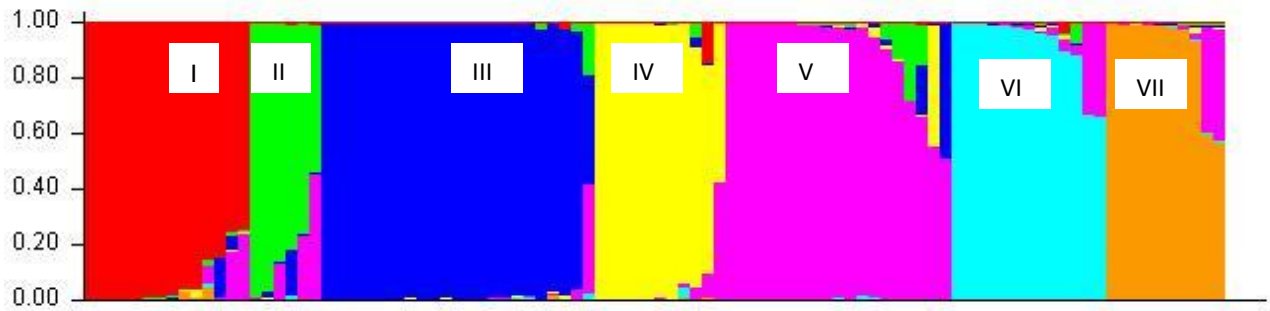
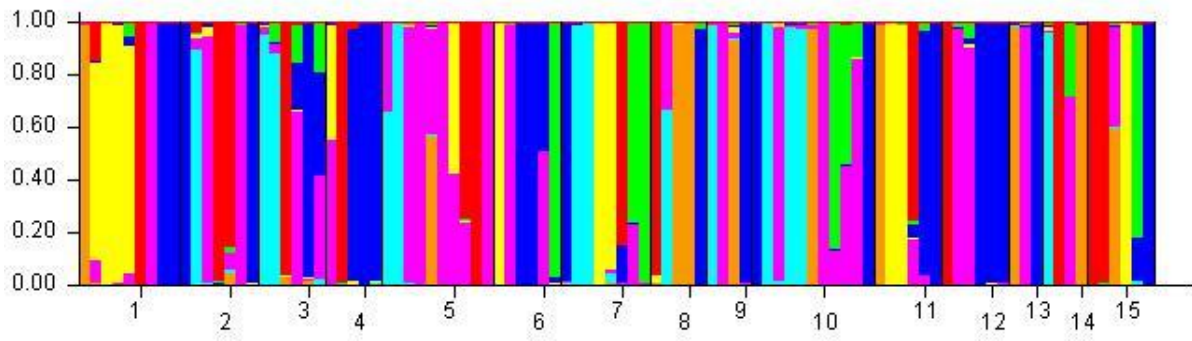


Figure 16. The bar plot for $K=7$. Red, Green, Blue, Yellow, Pink, Light blue and Orange represent cluster 1, cluster 2, cluster 3, cluster 4, cluster 5, cluster 6 and cluster 7, respectively.

Table 43. Proportion of membership of each pre-defined population in each of the clusters obtained at the best K (K=7)

Population	Number of accessions	Admixed individual	Proportion of membership in each cluster (%)						
			Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
North Shewa A	9	11.11	11.11	0.00	22.22	33.33	11.11	0.00	11.11
East Gojam	7	0.00	28.57	0.00	28.57	0.00	42.86	14.29	0.00
West Arsi	6	33.33	16.67	0.00	16.67	0.00	0.00	33.33	0.00
Arsi	5	20.00	60.00	0.00	20.00	0.00	0.00	0.00	0.00
Bale	10	40.00	10.00	0.00	0.00	0.00	40.00	10.00	10.00
North Shewa O	6	16.67	0.00	16.67	33.33	16.67	16.67	0.00	0.00
East Hararghe	8	0.00	12.50	12.50	12.50	25.00	0.00	25.00	0.00
West Shewa	5	20.00	20.00	0.00	20.00	0.00	0.00	0.00	40.00
Sidama	4	0.00	0.00	0.00	25.00	0.00	25.00	25.00	25.00
Gedeo	11	9.09	0.00	9.09	18.18	0.00	27.27	27.27	9.09
Segen	6	16.67	0.00	0.00	33.33	33.33	0.00	0.00	16.67
Kembata	6	0.00	16.67	0.00	50.00	0.00	33.33	0.00	0.00
Bench Maji	3	0.00	0.00	0.00	33.33	0.00	33.33	0.00	33.33
Central Tigray	4	25.00	25.00	0.00	0.00	0.00	0.00	25.00	25.00
Released	6	16.67	33.33	16.67	16.67	16.67	0.00	0.00	0.00

Genetic divergence (among clusters), expected heterozygosity (within the cluster), and proportion of the membership of the samples in each of the clusters are presented in Table 44. The maximum net nucleotide distance among the seven clusters was detected between C1 and C4 (0.24), indicating the hybridization between the accessions in C1 and C4 provided higher hybrid vigor as compared to the other clusters. While a minimum distance was detected between C2 and C3 (0.10) followed by C2 and C5 (0.11). Similarly, the second and third most genetic divergent clusters were C4 and C6 (0.21) and C3 and C4 (0.20), respectively. The maximum expected heterozygosity within the seven clusters was observed within C2 (0.19) followed by C7 (0.16), while the minimum expected heterozygosity was observed within C5 (0.02) followed by C6 (0.12). Based on the membership coefficient, the proportion of the clusters ranged from 3.66 to 21.99. Cluster III and cluster I are the first and second-largest proportions with values 21.99

and 15.59, respectively, while, the smallest proportion in cluster II (3.66) followed by cluster IV (8.33).

Table 44. Genetic divergence among (net nucleotide distance) and within (expected heterozygosity) cluster, and the proportion of membership of the samples in each of the clusters obtained at the best K (K=7)

	Net nucleotide distance							Expected heterozygosity	Proportion of membership	DAPC
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII			
Cluster I	-	0.17	0.18	0.19	0.20	0.24	0.18	0.12	15.59	0.12
Cluster II		-	0.10	0.17	0.11	0.14	0.16	0.19	3.66	0.05
Cluster III			-	0.20	0.14	0.19	0.17	0.14	21.99	0.14
Cluster IV				-	0.20	0.21	0.19	0.12	8.33	0.10
Cluster V					-	0.16	0.18	0.02	15.31	0.22
Cluster VI						-	0.18	0.12	10.66	0.23
Cluster VII							-	0.16	11.35	0.15

DAPC: Discriminant analysis of principal components.

4.2.10 Discriminant analysis of principal components

A discriminant analysis of principal components (DAPC) was also model-based used to infer the population structure of faba bean accessions. The results of the scatterplot of faba bean accessions using discriminant analysis of principal components (DAPC) are exhibited in figure 17. The obtained figure represents the individuals as dots and the clusters as inertia ellipses. The 96 accessions were grouped into seven clusters based on DAPC. The DAPC results in table 44 also indicated C6 (0.23) and C5 (0.22) showed the largest proportion of discriminant analysis of principal components (DAPC), while C2 (0.05) and C4 (0.10) showed the smallest proportion of discriminant analysis of principal components among the seven clusters. So, C1 and C3 contained 12 accessions each. C2 and C4 also contained 9 accessions each. C6, C5, and C7 contained 15, 13, and 11 accessions, respectively. Both the cluster analysis and the discriminant analysis of principal components classified the 96 faba bean accessions into seven clusters even

though the number of accessions in each cluster is not similar since DAPC based on the retained discriminant functions. The attained clusters were not in agreement with the geographical location of the accessions. Besides the scatter plots of discriminant functions, group membership's probability of DAPC is illustrated in figure 18 below. DAPC also provides membership probabilities of 96 faba bean accessions for the different clusters based on the retained discriminant functions.

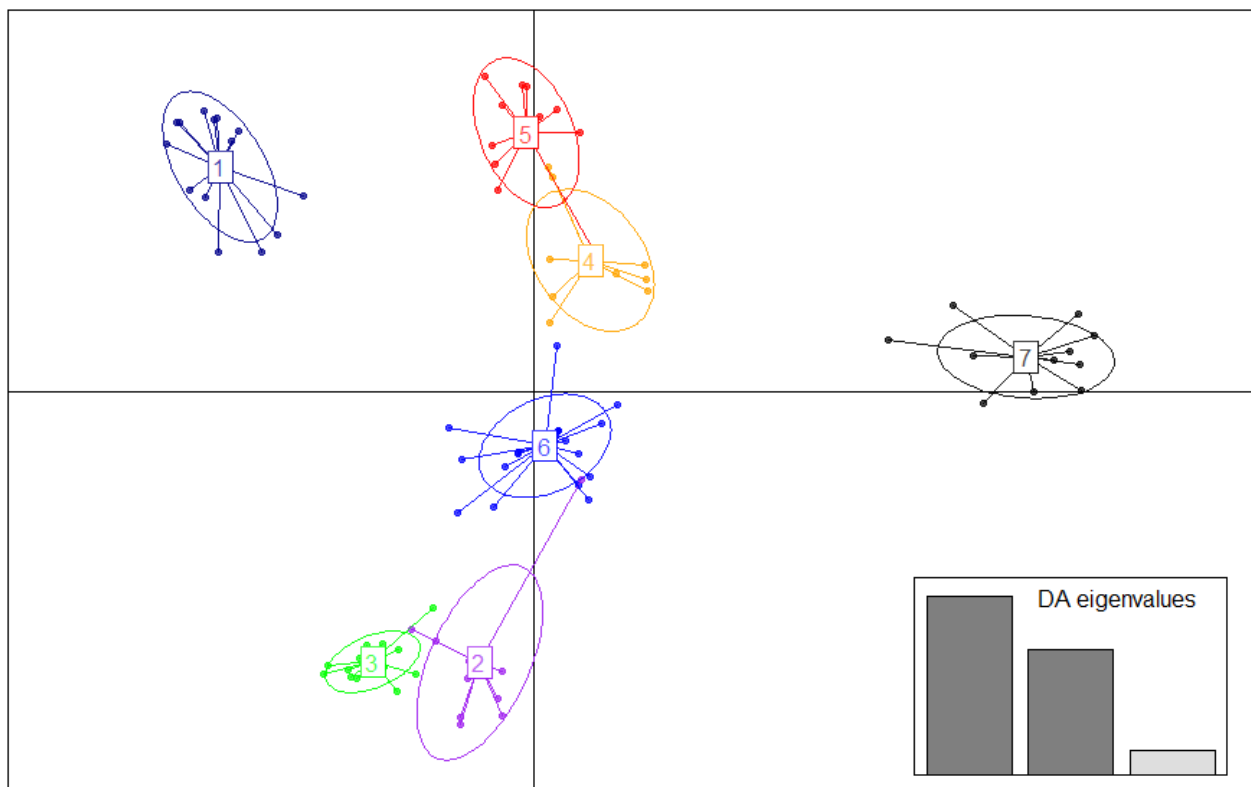


Figure 17. Scattered plot of faba bean accessions using DAPC based on ISSR data

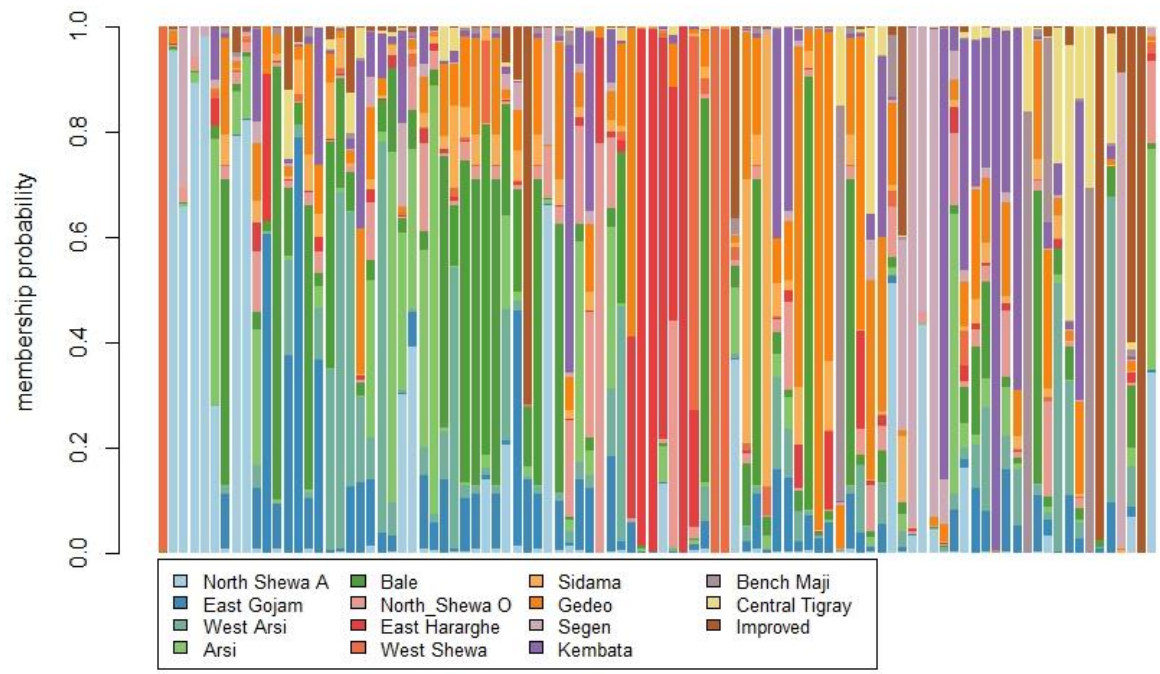


Figure 18. Membership coefficients of faba bean accessions using DAPC based on ISSR data

5 DISCUSSION

5.1 Genetic diversity, association and morphological diversity study

5.1.1 Analysis of variance

Ethiopian faba bean landrace accessions are contributing desirable genes for adaptability parameters in faba bean improvement program. In crop genetic improvement, breeding gain requires heritable variation in important agronomic traits of the crop. Therefore, the available genetic variation, heritability and expected genetic gain in important agronomic traits are useful to design better effective breeding strategies in faba bean landrace accessions.

The analysis of variance due to faba bean accessions exhibited significant to highly significant differences for most of the traits, suggesting an adequate amount of genetic variability among accessions and can provide further chances for improvement in the future breeding program. This revealed that there is sufficient possibility for the improvement of promising accessions from the present gene pool for yield and its components. Alghamdi (2007) also observed a highly significant difference between faba bean genotypes on traits such as flowering date, maturity date, number of branches per plant, number of seeds per plant, number of pods per plant, and thousand seed weight. Peyman (2014) reported a highly significant difference between faba bean genotypes for seed yield per plot, number of seeds per pod, number of pods per plant, thousand seeds weight, and pod length. Peyman (2015) reported a highly significant difference with pod length, days to maturity, thousand seed weights, and the number of seeds per plant. Ammar *et al.* (2015) similarly observed a highly significant difference between faba bean genotypes with traits: days to flowering and maturity, plant height, number of branches per plant, number of pods per plant, and number of seeds per plant. These results are similar to the findings of other

scholars like Fikiresilassei and Soboka (2012), and Fatih *et al.* (2017) with faba bean for most of the traits.

5.1.2 Mean performance

The mean and ranges of the traits revealed that there is a wider range of variability for most of the studied traits. Hence, the result of the range of traits suggested that there were considerable differences in all of the traits in all environments. This is primarily attributed to differences in the accessions evaluated and the test environment due to the differences in their climatic and agro-ecological parameters such as rainfall, temperature, and edaphic conditions. These results reflect the selection prospects for these traits to improve the performance through a breeding program. In agreement with this study, Sheelamary and Shivani (2015) reported a wider range of variability on plant height, number of pods per plant, and seed yield per plot.

5.1.3 Genetic parameters

Crop improvement is mainly based on the existence of sufficient genetic variability in accessions (Makanda *et al.*, 2009). The amount of genotypic and phenotypic variability existing in a species is the most important point to be considered in crop selection criteria. The wide ranges of phenotypic and genotypic variances in the current study indicated the existence of variability in the tested faba bean accessions for improvement. In order to improve grain yield and its related traits, knowledge of the extent of genetic variability that is measured by GCV and PCV (Jiang *et al.* 2014) is crucial for any breeding program. Genotypic and phenotypic coefficients of variation were reported as the major tools used to measure the variability that exists in a given population (Burton and Devane, 1953). As compared to PCV, the magnitude of genetic variation of GCV is better assessed, so breeders commonly focus on traits with high GCV estimates (Assefa *et al.*, 2015). The current study revealed that the phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficients of variation (GCV) for all traits, indicating high

genetic and environmental effects on the traits. High (30% & above) to moderate (15-30%) GCV values for most of the traits in this study also suggested the possibility of improving these traits through selection since these traits played a great role in the contribution of the total variation. Moreover, the difference between PCV and GCV was very narrow which indicated the importance of genetic variance in the inheritance of the studied traits. The closeness of PCV and GCV values also showed a little environmental effect on the expression of these traits. The minimum differences between PCV and GCV values imply additive gene effects, indicating that genotypes can be improved and selected for these traits. In agreement with the results of this work, Fikiresilassei and Soboka (2012) reported high GCV and PCV for the number of pods per plant and grain yield. Fatih *et al.* (2017) also reported high GCV and PCV for thousand seed weight and grain yield that agree with this study.

5.1.4 Broad-sense heritability and genetic advance

As a guiding factor to breeders for developing a successful breeding program, understanding the heritability of economically important traits (Jiang *et al.* 2014) and the genetic advance as percent of mean (Elangovan *et al.* 2014) is very crucial. In this study, moderate to high broad-sense heritability for most of the traits was observed. Hence, a high estimate of heritability indicates that selection based on mean would be successful in improving these traits since it can be mainly determined by the genetic constitution. The low heritability value indicates a limited possibility of improvement for these traits through selection because the environmental effect is more evident than the genetic effect. In agreement with the results of this work, Peyman (2015) reported high heritability for the number of seeds per plant and thousand seed weights. The results of this research are also similar to the results of Bakhiet *et al.* (2015), Sheelamary (2015), Muluaem *et al.* (2013), Toker (2004), Alghamdi (2007), and Abo El-zahab *et al.* (1980). Abdulaziz *et al.* (2015) also reported moderately high heritability for leaf length, leaf width, leaf area,

lowest pod height, plant height, number of pods per plant, number of seeds per plant, number of seeds per pod, and thousand seed weight, indicating the possibility of improvement via selection for these traits.

In this study, a medium to high heritability and GCV was associated with a medium to high genetic advance as a percent of the mean for most of the traits. This result agrees with the work of Dixit *et al.* (1970) who reported high heritability and GCV that associated with high genetic advance as percent of the mean. Both heritability and GCV also gave the best picture for the expected genetic advance as a percent of the mean as reported by Swamp and Changle (1962). Traits that showed high and moderate heritability are found to have high GCV values than traits that showed low heritability. Since most of the variation is genetic as compared to the environment, selection for these traits is relatively easy. On the other hand, traits such as leaf area, number of pods per node, and number of branches per plant at Girar Jarso in 2018; pod width at Girar Jarso in 2019; and traits such as number of pods per node, internode length, lowest pod height, and number of branches per plant at Degem in 2018 with high PCV values have less heritability which means variation for these traits is more of the environment than genetic and it is not advisable to select for these traits. In the current study, plant height, thousand seed weight, and grain yield with high heritability were followed by a high genetic advance at Girar Jarso in 2018, while at Girar Jarso in 2019 high heritability and high genetic advance obtained for most of the traits except days to flowering, pod width, days to maturity, seed yield per plot, and grain yield. At Degem in 2018, leaf length, leaf width, and leaf area exhibited high heritability followed by high genetic advance, whereas most of the traits under study revealed high heritability and high genetic advance except for days to flowering, pod width, days to maturity, and seed filling period at Degem in 2019. Similarly, Bora *et al.* (1998) stated that a high heritability was followed by a high genetic advance for a number of pods per plant, which

indicates high additive gene action and the possibility of trait improvement through selection. Therefore, mass selection and/or other breeding methods based on progeny testing could result in a high possibility of improvement in this trait. However, days to maturity and days to flowering possessed high heritability with low genetic advance as percent of the mean, at Girar Jarso in 2018, and Girar Jarso in 2019, respectively. While days to flowering and days to maturity also possessed high heritability with low genetic advance as percent of mean at Degem during 2018 and 2019 main cropping season, indicating the large number of non-additive gene action that could be exploited through heterosis. Hence, though heritability assessments offer the basis for selection on phenotypic performance, the estimates of heritability and genetic advance should always be considered concurrently, as high heritability is not always related to high genetic advance (Johnson *et al.*, 1955). In addition to this, they also indicated that high heritability along with high genetic advance as a percentage of mean implies the role of additive genes for the expression of the traits, and thus it could be very effective in crop improvement programs upon selection. Therefore, selection based on these traits with a relatively high genetic advance as a percent of the mean would result in the improvement of the performance of the genotypes for that trait.

5.1.5 Correlation coefficient

Grain yield is the result of many traits which are interdependent. Breeders always look for genetic variation among traits to select desirable types. Some of these traits are highly associated among themselves and with grain yield. The analysis of the relationship among these traits and their association with grain yield is essential to establish selection criteria (Singh *et al.* 1990). Therefore, improvement in yield can only be effective when other components of traits influencing it directly or indirectly are taken into consideration in the selection process. A selection pressure employed for the improvement of any traits greatly correlated with grain yield

concurrently affects a number of other correlated traits (Tiwari and Lavanya, 2012). Hence, knowledge of the association of grain yield with its component traits is believed to provide a guideline to the plant breeders for making improvements through selection. Results from the analysis of correlation coefficients revealed that genotypic correlation coefficients are greater than their corresponding phenotypic coefficients. This shows that selection based on phenotypic mean performance may improve the genotypic performance because the effect of environments on the expression of most of the traits is relatively lower.

In the present study, grain yield showed significant to highly significant positive genotypic and phenotypic correlation with most of the traits considered and therefore, breeding for improvement of these traits will improve the grain yield of faba bean and breeder can use these traits as a selection criteria. Hence, indirect selection based on these traits will improve grain yield. On the contrary, grain yield revealed a negative and positive non-significant genotypic and phenotypic correlation with some traits so selection based on these traits will not improve the grain yield of faba bean. In line with the current study, Tadese *et al.* (2011) reported a positive and significant correlation of grain yield with the number of seeds per pod at the genotypic level at Sinana, Ethiopia. The authors also reported a positive and significant correlation of grain yield with days to flowering, days to maturity, number of pods per plant, number of seeds per pod at the genotypic level at Sinja, Ethiopia. On the other hand, the authors reported a positive and significant correlation of grain yield with plant height, number of seeds per plant, and thousand seed weight at the phenotypic level at Sinja. Yassin (1973) also reported a positive and significant correlation of grain yield with the number of pods per plant at the genotypic level. Peyman (2014) also reported positive and significant correlations between grain yield and number of pods per plant, number of seeds per pod, and pod length. Alghamdi (2007); Azarpou *et al.* (2012); Mulualem *et al.* (2013); and Abdella *et al.* (2015) reported a positive and

significant association between grain yield and thousand seed weight. Keneni and Jarso (2002) also observed a positive and significant association between grain yield and the number of pods per plant. Ulukan (2003); Abdelmula *et al.* (2007); Tadese *et al.* (2011); and Ouji *et al.* (2011) reported a positive and significant phenotypic relationship between the number of pods per plant and trait; plant height, seed yield per plot, number of seeds per plant and thousand seed weight. Hence, the positive correlation of the aforementioned traits with grain yield showed that these traits are the most significant ones to be considered for indirect selection to improve grain yield since grain yield can be concurrently improved with a trait for which it exhibited a strong correlation. Days to flowering and the number of pods per node revealed a negative and significant genotypic correlation with grain yield. This indicated a reverse association between days to flowering and the number of pods per node with grain yield and improvement for these traits decreases grain yield at Degem in 2018. On the other hand, the non-significant association of grain yield with days to maturity at the genotypic and phenotypic level revealed that selection for an increased level of these traits may not bring significant change in grain yield. In contrast to this study, Fatih and Hamza (2017) observed negative and significant phenotypic relationships for grain yield and days to maturity.

For most studied traits, the phenotypic correlation coefficients were less than the genotypic correlation coefficients and the ratios of the two correlations (genotypic correlation to phenotypic correlation) were greater than the corresponding environmental correlation coefficients (phenotypic correlation – genotypic correlation). This suggests that the apparent associations might be largely due to genetic causes and the environment played a minimum role in the associations among the traits. The substantial positive correlations between grain yield and yield-related traits indicate that enhancement of these traits can pay positively towards improved grain yield; and hence, can be considered when indirectly selecting for high grain yield in the process

of faba bean breeding. Thus, correlation helps breeders to identify the traits that could be used as selection criteria in a breeding program. These results suggest that improvement of grain yield in faba bean linked with these traits and the selection of these traits might have an impact on grain yield. These results are in agreement with those obtained by Sheelamary and Shivani (2015), and Muluaem *et al.* (2013).

5.1.6 Genotypic path coefficient

Breeders frequently determine the relationships of grain yield and its component using a simple correlation coefficient. But this does not provide an exact picture of the relative importance of the direct and indirect influence of each of the traits towards grain yield (Tefera, 1988). The genotypic correlations were further subjected to path coefficient analysis, which involves the partitioning of the correlation coefficients into direct and indirect effects via alternative traits. The benefit of path analysis is that it permits the apportioning of the correlation coefficient into its components. One component is the indirect effect (s) of a predictor variable on the response variable through the predictor variables. The second component is the direct effect of a predictor variable upon its response variable (Dewey and Lu, 1959). Grain yield is the final product of various traits and here it was considered to be the resultant variable while the rest of the variables were causal variables. Each trait does influence grain yield by its direct and indirect contributions with other traits.

At Girar Jarso in 2018 number of seeds per plant and seed yield per plot, and at Girar Jarso in 2019 the trait leaf width exerted a positive direct effect and also had a positive association with grain yield. While at Degem in 2018 also leaf width, plant height, number of seeds per pod, and thousand seed weight, and at Degem in 2019 internode length, and pod width exerted a positive direct effect and also had a positive association with grain yield. Since their direct effect and correlation with grain yield were positive; these traits could be used as a reliable in indirect

selection for higher grain yield. This indicated that selection based on these traits will improve the grain yield at this particular location for the particular crop. It also implies that those traits are the most important component of grain yield. This result also agrees with Tadesse *et al.* (2011) reported the number of pods per plant, the number of seeds per pod, thousand seed weight, and pod length had high positive direct effects on grain yield.

At Degem in 2018, the number of pods per node exerted positive direct effects on grain yield but associated negatively and significantly with grain yield due to the negative indirect effects of this trait through internode length, number of pods per plant, number of seeds per pod, and thousand seed weight. Under these conditions, a restricted concurrent selection model is to be followed, i.e. restrictions are to be imposed to nullify the undesirable indirect effects through internode length, number of pods per plant, number of seeds per pod, thousand seed weight to use direct effects (Singh and Kakar, 1977).

The negative direct effect of days to flowering, number of branches per plant, internode length, lowest pod height, number of pods per plant, and number of seeds per pod was compensated by their indirect positive effect via other traits at Girar Jarso in 2018. At Girar Jarso in 2019 the negative direct effect of leaf length, leaf area, plant height, number of pods per plant, pod length, and seed yield per plot was compensated by its indirect positive effects through leaf width, lowest pod height, number of seed per pod, number of branches per plant, and number of seeds per plant. Internode length, number of pods per plant, pod width, seed yield per plot exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield due to its positive indirect effects through other traits at Degem in 2018. At Degem in 2019 seed yield per plot, and thousand seed weight exerted negative direct effects on grain yield but exhibited a positive correlation with grain yield due to its positive indirect effects through other traits. According to Singh and Chaudhary (1977), when a trait had a positive correlation and high

positive indirect effects on the other hand it had negative direct effects, so emphasis must be given to the indirect effects and consequently, indirect causal factors are to be considered concurrently for selection in this situation.

5.1.7 Cluster analysis

In the current study, cluster analysis distinguished five different groups of faba bean accessions in all environments. This indicated the presence of wide diversity or variability among the accessions. In concurrent with the present study, Sarparast *et al.* (2011) and Chaubey *et al.* (2012) used cluster analysis to study genetic divergence of 70 faba bean accessions and to investigate the genotypic structure of nine faba bean genotypes, respectively using morphological traits. Al-barri and Shtaya (2013) used cluster analysis to further investigate the interrelationships of Palestine faba bean germplasms using six agronomic traits. Another investigation also indicated that the hierarchical cluster analysis was used for the classification of 14 faba bean genotypes according to some morphological traits (Chaieb *et al.* 2011). Polignano *et al.* (1993) used cluster analysis for the classification of 106 faba bean accessions from Ethiopia and Afghanistan using eight morphological traits. Yahia *et al.* (2012) also clustered 42 faba bean populations based on phenotypic traits. Keneni *et.al.* (2005) used cluster analysis to classify faba bean landraces in the study of the extent and pattern of generic existence of Ethiopian faba bean landraces using 160 accessions and 11 phenotypic traits and the report revealed the existence of high genetic diversity in Ethiopian faba bean landraces.

In all environments landrace accessions from most of the administrative zones were distributed in most of the clusters indicating the existence of more genetic diversity in these AZs as compared to the others. This also revealed accession from the same AZs might have different genetic backgrounds. There was no definite clustering pattern of the landraces based on AZs of the collection. Clustering of accessions based on the agronomic traits under study revealed no

distinct administrative zone grouping patterns that means accessions from the same or adjacent regions appeared in different clusters. On the other hand, accessions from different administrative zones might have been grouped into similar cluster due to the introduction of accessions from the same source, exchange of seeds among farmers, and a tendency of resource-poor farmers in marginal areas, of selection for the same traits.

5.1.8 Cluster mean analysis

According to Singh (1990) based on the specific objectives of hybridization, it is, therefore, advisable that the selection of parents should consider not only the distance between clusters but also the distinct advantages of each cluster and each accession within a cluster. So, the cluster mean performances showed the existence of significant variation among the different clusters for individual traits considered.

5.1.9 Intra and inter-cluster D^2 values

In the present study, both intra and inter-cluster distances showed highly significant ($P < 0.01$) differences. The average inter-cluster distances were higher than the average intra-cluster distances, which indicates the presence of wide genetic diversity among the accessions of different clusters than those of the same cluster. So, accessions grouped in the same clusters (intra-cluster) are expected to be genetically more similar than accessions grouped in different clusters (inter-clusters). This result revealed that the maximum inter-cluster distances were between cluster I and cluster V ($D^2 = 444.19$) and cluster I and cluster III ($D^2 = 434.59$) at Girar Jarso in 2018 and 2019 main cropping season, respectively. On the other hand, the highest inter-cluster distances were obtained between cluster II and cluster V ($D^2 = 527.97$) and cluster II and cluster V ($D^2 = 548.57$) at Degem in 2018 and 2019 main cropping season, respectively. These high values of inter-cluster distances may result due to the differences in the genetic background of the materials, indicating the presence of wider genetic divergence between these clusters. The

maximum intra cluster distances were in cluster I ($D^2 = 233.47$) and cluster III ($D^2 = 213.27$) at Girar Jarso in 2018 and 2019 main cropping season, respectively. Whereas, the maximum intra cluster distances were in cluster V ($D^2 = 185.53$) and cluster III ($D^2 = 219.19$) at Degem in 2018 and 2019 main cropping season, respectively, indicating the possibility of selecting better genetic divergent parents within these clusters.

According to Ghaderi *et al.* (1984) increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. The hybridization between parents of most divergent clusters would be expected to reveal maximum heterosis and wide variability in genetic architecture (Singh *et al.*, 1987). At Degem in 2019, cluster II followed by cluster IV, and I were the most divergent clusters from cluster V. However, the chance of getting segregants with a high grain yield level is quite limited when one of the clusters has a very low grain yield level (Samal *et al.*, 1989). Cluster V had the lowest mean performance in grain yield. This indicates that the chance of getting segregants with high grain yield is limited between crosses of cluster V with the other clusters. The advantages of each cluster and each accession within a cluster should be considered during the selection of parents, depending on specific objectives of hybridization (Singh, 2001). Thus, at Degem in 2019 crosses involving cluster II with cluster III, cluster III with cluster IV, and cluster I with cluster III are suggested to exhibit high heterosis and could result in segregants with higher grain yield.

The minimum inter-cluster distances were obtained between cluster II and cluster IV ($D^2 = 115.72$) and cluster I and cluster IV ($D^2 = 206.21$) at Girar Jarso in 2018 and 2019 main cropping season, respectively. While the minimum inter-cluster distances were obtained between cluster I and cluster II ($D^2 = 194.27$) and cluster I and cluster IV ($D^2 = 166.77$) at Degem in 2018 and

2019 main cropping season, respectively. This indicates that accessions in these clusters were not genetically diverse or there was little genetic diversity between these clusters. The accessions belonging to these clusters were relatively cluster to each other in comparison to accessions grouped in other clusters. Thus crossing of accessions from these clusters may not produce a higher amount of heterotic expression in the F_1 's and a wide range of variability in the subsequent segregating F_2 populations. Parents selected from divergent cluster groups are expected to produce maximum genetic recombination. Therefore, the present study revealed the presence of significant genetic variability among the tested accessions. Thus, there is an opportunity to improve grain yield through the hybridization of accessions from different clusters and subsequent selection from segregating advanced generations.

5.1.10 Principal component

According to Sharma (1998), the principal component analysis reveals the significance of the major provider to the total variation for differentiation. Generally, the principal component analysis exhibited diversity since the entire variation cannot be explained in terms of a few PCs. This also showed the contribution of a number of traits towards the overall observed diversity. Traits with the major absolute values closer to unity in the first principal component impact the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). Accordingly, most of the traits individually contributed small effects to the total variation and, therefore, the differentiation of the accessions into different clusters was rather dictated by the cumulative effects of a number of traits. Owing to being the largest portion of the total variation presented in PCs in all environments, the traits that brought about significant variation in all PCs were selected to be the most important ones in their application vis-à-vis improvement of faba bean. The present study confirmed that the Ethiopian faba bean accessions showed variation for the traits studied. This trait diversity among the accession suggests the presence of opportunities

for genetic improvement through selection directly from the accessions and/or selection of diverse parents for hybridization programs and conservation of the accessions for further utilization. The result from principal components (PCs) with an Eigen value greater than one contributed more than 60% of the total variation in all environments. In this study, the PCA separated variability among the accessions based on grain yield and its component traits. This suggests that the traits with high Eigen vectors are the most important for use in future faba bean breeding and conservation studies. This finding agrees with the results reported by Mulugeta (2016), Keneni *et al.* (2005), and Yahia *et al.* (2012).

5.2 Genetic diversity analysis based on ISSR markers

5.2.1 ISSR primers banding patterns and diversity

Assessment of genetic diversity in the faba bean germplasm is required to exploit these genetic resources in crop breeding programs and designing future conservation practices. Because of the difficulties to achieve interspecific crosses with *Vicia faba*, only natural variability or mutation is available to breeders (Duc *et al.*, 2010). ISSR molecular markers have been used successfully in germplasm characterization (Terzopoulos and Bebeli, 2008) and the potential of ISSR markers to generate genetic information through polymorphic fragments depends on the microsatellite frequency and their distribution in the genome-wide scale of the species (Morgante *et al.*, 1993). The present study was designed to see the genetic diversity existing among 96 faba bean accessions using 9 ISSR primers. All nine ISSR primers were 100% polymorphic with an average of 18.6 polymorphic bands per primer. Such considerable differences in the number of bands detected may arise from differences in the diversity of the test accessions used, the number of accessions examined and the genotyping method used. In this study, the ISSR markers were able to detect a considerable level of genetic diversity in faba bean accession and it would also be recommended for use in future studies on faba bean. In disagreement to this study,

Terzopoulou and Bebeli (2008) reported percent of polymorphism ranging from 37.5% to 84.62% with an average of 67.48% by using 11 ISSR primers in studying the genetic diversity of the Greek faba bean population and Abdel-razzak *et al.* (2012) also found a range of percent of polymorphisms which varied from 52.08% to 92.31% with an average 69.10% within 10 faba bean genotypes from Egypt using nine ISSR primers. The present study detected a higher percent of polymorphism as compared to other studies based on faba bean using ISSR primers and also different markers on other legume crops. In agreement with this study, Merji *et al.* (2012) found 97.3% of average polymorphism in the analysis of the effect of gamma radiation on various characters of 22 faba bean genotypes grown in Tunisia using 15 ISSR primers. Salazar-Laureles *et al.* (2015) also reported percent of polymorphism ranging from 71.4% to 100% with an average of 91.3% in the analysis of genetic variability within a Chilean faba bean accession using ISSR markers. Wang *et al.* (2012) also reported the percentage of polymorphisms ranging from 91% to 100% with an average of 93% in the study of genetic diversity and the relationship of global faba bean germplasms.

In the present study, the PIC values ranged from 0.19 to 0.44 with a mean of 0.33. In this study, 78% of the primers had moderate informative PIC values and the rest of them had slightly informative PIC values. In disagreement with this study, Terzopoulos and Bebeli (2008) reported a PIC value of 0.30 - 0.50 and an average of 0.21 using the inter-simple sequence repeat (ISSR) markers. Similar to this study, Gong *et al.* (2011) reported PIC values varied from 0.06 to 0.43 with an average of 0.30 in their study in order to investigate the genetic variation of 29 faba bean cultivars from China and Europe using 11 EST-SSR markers. In agreement with this study, the PIC of 0.06-0.43 with an average of 0.29 was reported in Chinese and European collections (Ya-Ming *et al.*, 2011), but a high PIC of 0.96 was reported by Alghamdi *et al.* (2012) using Sequence Related Amplified Polymorphism (SRAP) markers. Therefore, all of the markers used

are recommended in other future evaluations of faba bean accession. Similar to the current study Abdollah *et al.* (2011) reported moderate values of PIC ranged from 0.13 to 0.42 with an average of 0.22. In contrast to the current study, Abdollah *et al.* (2011) indicated that MI values ranged from 0.41 to 3.36 with an average of 1.34 and EMR varied from 1.8 to 12 with a mean value of 5.69. While the estimates of RP ranged from 7.2 to 16.5 with an average of 12 per primer. Genetic diversity of expected heterozygosity often indicates genetic diversity in a population (Nassiry *et al.*, 2009). In contrast to this study, Backouchi *et al.* (2015) reported a number of effective alleles (N_e) ranged from 1.17 to 1.45 with a mean of 1.26 in genetic diversity in Tunisian populations of faba bean (*Vicia faba* L.) based on RAPD molecular markers. In contrast to this study, Ma *et al.* (2011) also reported a number of observed alleles between 2 and 9 and gene diversity between 0.05 and 0.83 in the study employing 32 accessions of faba bean and 21 microsatellite markers. Gong *et al.* (2010) reported a higher number of alleles ranging from 1 to 3 and gene diversity from 0 to 0.64 in the study comprising 29 faba bean genotypes and 11 microsatellite markers.

5.2.2 Population genetic diversity

The degree of polymorphism among the breeding status of faba bean accessions ranged from 65.27 for the released varieties to 98.20 for the landrace accessions. The highest polymorphism observed in the landrace accessions as compared to the released varieties could be explained by the broader spectrum of landrace accessions as a reservoir of different alleles. Using 9 ISSR primers, the population of West Shewa revealed the highest Shannon information index and gene diversity, whereas the population from Bale showed the least Shannon information index and gene diversity. Shannon information index and gene diversity ranged from 0.19 to 0.31 and 0.11 to 0.20 with a mean value of 0.25 and 0.16, respectively. This result is in contrast with Abdel-Razak *et al.*, (2012) who studied faba bean by using ISSR markers showing higher Shannon

information index and gene diversity values of 0.53 and 0.35, respectively. The mean Nei's (1973) gene diversity (0.16) and mean of an effective number of alleles (1.24) in the faba bean accessions were lower than that reported by Yahia *et al.* (2014), who reported a mean value of gene diversity and an effective number of alleles, 0.43 and 1.26, respectively, using 16 Tunisian faba bean populations and 16 polymorphic SSR markers. In contrast to the current study, Wang *et al.* (2012) who studied genetic diversity and relatedness of 802 faba bean genotypes using 11 inter-simple sequence repeat (ISSR) primers, reported a 1.38 mean effective number of alleles. This may be different due to the faba bean genotypes used in the study. Zong *et al.* (2009), who studied molecular variations of 243 faba bean germplasm originated from different geographical areas using 10 AFLP primer pairs, reported a higher range of Nei's (1973) gene diversity (0.04 - 0.17) and Shannon information index (0.06-0.25) than ours, which might be explained by the different DNA markers used. Contrary to this study, Wang *et al.* (2012) signified Shannon information index and gene diversity ranging from 0.27 to 0.39 and 0.18 to 0.26, respectively using 11 ISSR primers. Accessions from West Shewa followed by North Shewa Amhara and East Hararghe were found to be of high diversity as opposed to those from the other AZs. Hence, further collection, conservation, and utilization programs would be carried out from AZs with high genetic diversity. The study of genetic distance between fifteen pre-defined populations would also be important for accessions improvement. The present study showed the highest inter-population genetic distance between Bale and Arsi populations as compared to the other pair-wise distance values. As a result, hybridization between accessions from distantly related populations of Bale and Arsi is supposed to yield higher hybrids as compared to less distantly related populations.

5.2.3 Analysis of molecular variance

In the current study, AMOVA results attributed 99% of genetic diversity within fourteen landrace populations and 1% among faba bean populations based on geographical origin. Similarly, the study by Oliviera *et al.* (2006) showed the highest proportion of 81% within genetic variation and 19% among genetic variation in genetic diversity and structure analysis using 26 nuclear SSRs. Kwon *et al.* (2010) also reported a large amount of variation within faba bean landraces. Similarly, Ramakrishnan *et al.* (2016) reported 76.48% polymorphism within populations on 128 genotypes using the RAPD marker. Babu *et al.* (2007) analyzed 32 genotypes using RAPD markers and found 9% polymorphism. Ouji *et al.* (2012) reported 74.3% genetic diversity within nine populations of Tunisian faba bean than that of among population which is also congruent with findings from the current study. Similar results were found in 12 genotypes of cherry plum (Wo'hrmann *et al.*, 2011) in which 96.8% of the total variance was identified and attributed to divergence within populations and only 3.2% was attributed to divergence among populations and Tsehay (2012) reported high variation (90.59%) attributed to the within species component, while the remaining variation (9.41%) was due to among species variation. By using 11 ISSR markers, Mulugeta (2016) reported 91% of the within group variation and 9% among group variation. Gichuki *et al.* (2003) also found that in 74 genotypes of sweet potato, 93.4% of the total variance was within populations and 6.6% of the variance was among the various geographical regions which may imply high genetic exchange or gene flows among populations by the dispersal of the seeds and seed exchange via market channels. A previous study by Terzopoulos and Bebeli (2008) also indicated a high level of genetic diversity within the populations of Mediterranean-type faba beans. This study revealed that the variation within populations is large in faba bean. This has also been reported in Soybean (Jin *et al.*, 2006) and *Lathyrus sativa* populations (Belaid *et al.*, 2006). The partially allogamous nature of faba bean could also be the other possible factor for high genetic variation within groups. The pollen of

faba bean can easily move by insect pollinators like bees and bee beetles causing out crossing of the varieties (Ellwood *et al.*, 2008). The small differentiation, low percentage of variation partitioned among populations of faba bean from different locations observed in this study could be the transfer of seeds among AZs by a farmer to farmer seed exchange, and exchange of seeds through relief agencies like NGOs. Ethiopian faba bean growers get their seed mostly by an informal seed exchange system. In this line, there has been a lot of genetic exchange among farmers' landrace for seed (Alemu *et al.*, 2010). Therefore, the AMOVA analysis showed high genetic variation within populations which indicates the existence of high gene flow or genetic exchange and low genetic differentiation among populations.

5.2.4 Cluster analysis

The current study indicated seven clusters using ISSR primers based on NJ which had the potential to detect genetic variability in faba bean accessions. The present study is similar to Abdel-Razzak *et al.* (2012) who studied genetic diversity in 10 faba bean genotypes from Egypt using ISSR clustered the individuals depending on their genetic similarity rather than their geographical origin. Wang *et al.* (2012) and Salazar-laurels *et al.* (2014) also reported clustering of genotypes from different groups into the same cluster without showing a clear-cut category. Accessions from the same administrative zones were often in different clusters and likewise, accessions from different administrative zones were clustered together, indicating the existence of accession diversity within the population of origin. Therefore, the analysis of the NJ tree showed no clear cut pattern in relation to geographical origin, which could be due to higher gene flow between pre-defined populations. On the other hand, accessions from non-neighboring AZs clustered together in particular groups as also observed through a study on local field pea and faba bean accessions in Ethiopia (Keneni *et al.*, 2005). The PCoA results revealed that the first two and three axes represent 39.04% and 51.23%, respectively, of the total variability. The result

of PCoA in both two-dimensional and three-dimensional coordinates was similar to NJ result indicating the conformity of the results obtained from the study.

5.2.5 Genetic differentiation and gene flow

In the current study, the values of most of the pair-wise comparisons among the fifteen pre-defined populations were ranging from 0.00 to 0.15 PhiPT. The low value of PhiPT implies that there is a high level of gene flow, which leads to genetic homogeneity (Beyene *et al.* 2014). So, in this study, the relatively little to moderate PhiPT and high level of Nm strongly indicate that the exchange of genetic materials between 15 pre-defined populations is sufficient to counter the genetic composition of the population. Hence, based on the administrative zones, there was no population structure observed due to high degree of gene flow between faba bean accessions or it may be explained by the partially allogamous habit of faba bean associated with the frequent seed exchange.

5.2.6 Population structure

In this study, STRUCTURE and DAPC used to analyze the population structure of 96 accessions appeared to provide complementary information. Results of both STRUCTURE and DAPC divided 96 accessions into seven clusters. The difference between DAPC and NJ in the assignment of accessions to clusters could be explained by the fact that the DAPC is based on k-means which is a non-hierarchical clustering method, whereas NJ method is an agglomerative hierarchical method of clustering (Campoy *et al.* 2016). The STRUCTURE analysis also agreed with the dendrogram analysis in that seven clusters were found in the population. Thus, both analyses gave similar clustering in the faba bean population, although they are based on different methods which are model-based and distance-based, respectively. The complementarity of this result indicates the representative nature of the used markers. These results agree with Wang *et al.* (2012), who witnessed congruency between both analyses, and Maria *et al.* (2015) who also

showed the agreement between dendrogram and PCA results. The current study is also in agreement with Mulugeta (2016) and Salazar-laureles *et al.* (2015) in their studies of faba bean genetic diversity using ISSR markers.

6.0 CONCLUSION AND RECOMMENDATION

6.1 Conclusion

Faba bean plays a significant role in both the human diet and animal feed since it has high protein and starch content in its seeds. It can also contribute to the ecological role serving as the fixation of nitrogen, break disease cycles in the cereal-based rotations and also control weeds. In the current study, genetic diversity based on morphological and ISSR markers revealed levels of variation important for future improvement programs.

The present study revealed that the faba bean landrace accessions had significant variability for most of the traits. These indicated promising genetic diversity in faba bean landrace accessions, which can be exploited in future improvement attempts in Ethiopia. Moderate to high phenotypic coefficient of variation, genotypic coefficient of variation, broad sense heritability and genetic advance as percent of mean revealed for most of the traits in all environments, indicating the possibility of improving these traits through selection. Grain yield showed positive and significant genotypic and phenotypic correlation with most of the studied traits, suggesting that improvement of grain yield in faba bean linked with these traits and the selection of these traits might have an impact on grain yield. Traits that exerted a positive direct effect on yield and correlated positively with yield are used as a selection criterion in indirect selection.

Besides, evaluation of Eigen vectors from principal component analysis indicated that leaf length, leaf width, leaf area, number of pods per plant, and number of seeds per plant were the most important traits in explaining the genetic variability in the first principal components at three environments. It was also noted that differentiation of the accessions into different clusters was because of a cumulative effect of a number of traits rather than the small contribution of each trait. This study generally implied that the presence of significant genetic variability or divergence among the accessions. Thus, there is an enormous opportunity to bring about

improvement through direct selection and hybridization which involves crossing of accessions from different clusters. In the present study crosses involving parents from maximum inter-cluster distances are suggested to exhibit high heterosis and could result in segregating with higher grain yield.

The present study detected a higher percent of polymorphism with 100% polymorphism as compared to other studies based on faba bean using ISSR primers and also different markers on other legume crops. In addition, it also showed that based on different diversity indices faba bean landraces possess a wide range of genetic diversity which mostly resides within accessions, and this indicated that the different geographic origins harbor high levels of genetic diversity important for improvement and conservation programs. The AMOVA also indicated that high genetic variation within populations than among populations that reveals the presence of high gene flow and low genetic differentiation among populations. Landrace accessions from fourteen administrative zones of the country were distributed over the majority of the clusters, exhibiting high genetic diversity in most of the collection sites and accessions from the same administrative zones might have different genetic background.

6. 2 Recommendation

The estimates of heritability and genetic advance ought to always be considered at the same time as high heritability is not always related to high genetic advances. From a breeding point of view, those traits having a genetically positive direct effect on grain yield should be given due attention when the collection, conservation, and selection of landraces targeted for yield improvement will have been planned. Further collection, conservation, and utilization programs would be recommended from administrative zones with high genetic diversity. In this study, the ISSR markers were able to detect a considerable level of genetic diversity in faba bean accession and it would be also recommended for use in future studies on faba bean.

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APPENDIXES

Appendix I: Monthly and Annual Rainfall (mm) of Girar Jarso from (2002-2018)

Year	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec	Annual RF
2002	41.50	16.80	138.80	41.90	23.60	70.30	230.80	313.00	141.20	0.00	0.00	42.40	1060.30
2003	23.40	51.10	50.80	112.60	2.10	121.90	360.00	311.00	124.10	2.80	1.80	15.00	1176.60
2004	0.90	11.70	55.40	123.50	27.20	151.50	296.60	299.20	119.40	14.20	3.70	0.00	1103.30
2005	49.00	1.00	73.00	69.00	81.60	76.40	285.50	212.50	119.50	10.70	4.40	0.00	982.60
2006	77.30	29.70	69.80	83.00	45.70	75.20	486.50	357.80	96.10	8.00	5.90	14.30	1349.30
2007	21.30	46.40	24.00	41.20	58.70	120.30	375.30	314.60	125.60	8.80	2.40	0.00	1138.60
2008	1.80	1.00	0.00	30.30	62.90	66.80	293.00	414.70	98.20	19.20	58.60	0.00	1046.50
2009	16.60	2.70	39.70	52.70	16.40	47.30	463.10	440.30	79.80	62.90	0.00	0.00	1221.50
2010	11.50	32.60	71.20	72.80	112.80	64.50	449.20	336.60	86.00	1.70	16.20	28.40	1283.50
2011	15.60	0.00	55.30	45.10	96.00	135.70	246.50	421.80	179.00	0.00	42.60	0.00	1237.60
2012	21.70	0.00	22.60	75.90	29.00	112.40	410.10	408.90	136.50	3.00	0.00	11.70	1231.80
2013	0.00	0.00	10.30	32.00	31.30	155.70	425.60	395.30	99.80	56.10	2.10	0.00	1208.20
2014	3.70	23.70	61.90	78.10	50.90	39.50	380.90	342.60	109.30	17.80	0.80	11.30	1120.50
2015	0.40	3.10	20.90	4.70	71.10	116.60	223.70	230.90	102.00	36.40	5.60	66.30	881.70
2016	0.00	32.00	31.60	0.00	189.60	145.20	443.30	294.10	100.30	0.00	0.00	0.00	1236.10
2017	0.00	0.00	36.80	10.10	129.10	31.90	354.80	323.60	0.00	0.00	3.20	0.00	889.50
2018	0.00	40.80	0.00	0.00	0.00	122.90	395.70	357.60	68.50	0.00	0.00	0.00	985.50

Appendix II: Monthly and Annual Rainfall (mm) of Degem from (2002-2018)

Year	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec	Annual RF
2002	0.00	0.00	0.00	0.00	0.00	0.00	228.40	289.30	127.90	0.60	91.20	0.00	737.40
2003	33.00	61.90	81.90	82.80	13.70	103.20	484.40	335.40	145.40	0.00	2.70	0.00	1344.40
2004	26.80	9.10	60.40	59.90	20.40	0.00	209.80	350.40	57.40	10.30	0.00	17.90	822.40
2005	29.90	1.10	85.60	112.40	40.40	113.50	279.80	261.60	130.80	19.90	0.80	6.20	1082.00
2006	39.10	15.50	113.20	108.80	52.40	68.50	428.30	452.80	123.90	7.90	19.00	11.70	1441.10
2007	50.70	67.10	0.00	42.90	62.20	161.50	0.00	355.30	131.60	11.90	1.10	0.00	884.30
2008	14.30	1.20	0.00	40.10	90.10	144.70	390.50	322.90	65.80	60.70	115.50	0.00	1245.80
2009	8.70	3.40	36.40	45.20	15.20	23.30	0.00	0.00	0.00	0.00	0.00	0.00	132.20
2010	4.50	58.60	119.20	78.00	78.10	70.60	262.00	363.40	127.80	0.00	24.20	19.00	1205.40
2011	6.00	0.00	59.20	47.50	56.10	97.40	248.90	375.80	98.60	0.00	32.50	0.00	1022.00
2012	0.00	0.00	0.00	59.00	12.50	112.00	396.50	324.60	105.90	14.40	0.00	20.80	1045.70
2013	0.00	5.40	19.00	41.80	17.70	139.00	365.20	259.30	153.40	104.10	0.00	0.00	1104.90
2014	5.20	38.00	57.40	68.90	59.70	85.30	372.20	370.00	114.50	21.90	21.90	0.00	1215.00
2015	9.20	0.00	0.00	6.60	104.10	154.00	173.50	229.40	116.20	0.00	0.00	0.00	793.00
2016	0.00	13.60	14.60	40.30	154.80	235.80	355.40	0.00	0.00	24.60	21.30	0.00	860.40
2017	0.00	0.00	0.00	0.00	71.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.20
2018	0.00	0.00	0.00	0.00	6.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.80

Appendix III. Mean Monthly Maximum Temperature (°C) of Girar Jarso from (2002-2018)

Year	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec	Mean Tmax
2002	19.76	21.75	21.17	22.52	24.35	22.60	20.31	18.21	18.75	19.82	20.37	20.09	20.81
2003	20.52	21.91	22.35	22.25	24.09	21.46	17.87	17.58	18.64	19.65	19.60	0.00	18.83
2004	0.00	21.83	22.45	21.62	23.60	21.54	18.79	18.64	19.01	19.37	20.38	20.65	20.72
2005	20.40	23.31	22.85	22.75	21.54	22.45	18.41	18.67	19.14	19.71	19.96	20.46	20.80
2006	21.33	22.44	21.61	21.37	22.43	22.28	18.39	17.74	18.49	20.23	20.05	19.65	20.50
2007	19.65	21.08	23.07	22.74	23.75	21.19	17.89	18.10	18.63	19.02	19.69	19.61	20.37
2008	20.72	21.59	23.43	22.60	22.89	22.05	19.32	18.36	19.63	19.90	19.39	19.73	20.80
2009	20.12	21.55	23.22	23.12	24.07	24.31	17.88	18.26	19.74	19.23	19.91	19.25	20.89
2010	20.28	21.01	21.77	22.11	22.70	22.63	18.64	17.63	18.81	19.97	19.61	19.57	20.39
2011	20.54	22.02	21.31	23.23	22.93	22.27	18.69	18.27	19.01	19.91	19.86	20.23	20.69
2012	21.05	22.60	23.41	22.76	24.64	23.21	18.41	18.52	19.35	19.91	20.97	20.31	21.26
2013	21.26	23.04	23.68	24.70	23.37	22.05	17.85	16.71	19.07	18.79	19.96	19.62	20.84
2014	20.64	21.16	22.33	22.33	22.40	23.14	19.58	17.85	18.72	19.37	19.98	19.47	20.58
2015	20.56	22.98	23.16	23.96	22.94	22.43	21.10	18.75	19.66	20.74	20.77	20.22	21.44
2016	20.88	22.70	24.27	0.00	21.55	21.88	18.77	18.26	19.47	0.00	20.03	19.69	17.29
2017	20.84	0.00	23.43	23.56	22.46	23.39	18.85	18.21	0.00	0.00	19.94	0.00	21.34
2018	0.00	21.73	0.00	0.00	0.00	20.44	18.46	18.03	19.70	0.00	0.00	0.00	19.67
Mean	18.15	20.75	21.38	20.1	21.75	22.43	18.80	18.11	17.88	16.213	18.85	16.39	20.47

Appendix IV: Mean Monthly Minimum Temperature (°C) of Girar Jarso from (2002-2018)

Year	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec	Mean Tmin
2002	7.17	8.11	9.37	8.88	10.50	9.33	9.65	9.20	8.57	6.11	5.77	8.18	8.40
2003	7.49	8.31	8.97	10.20	10.50	8.92	9.42	9.95	9.07	5.65	6.26	5.55	8.36
2004	8.00	7.40	9.05	9.72	9.11	9.29	9.07	9.20	8.41	5.21	5.58	6.78	8.07
2005	6.80	8.19	9.38	9.74	10.00	9.45	9.29	9.56	9.26	5.73	4.89	4.01	8.03
2006	6.62	7.93	9.06	9.35	9.18	9.06	9.15	8.71	8.62	7.33	5.89	6.69	8.13
2007	7.68	8.55	8.67	9.43	10.10	9.21	9.65	9.16	8.86	5.31	5.48	4.17	8.02
2008	6.44	6.93	8.04	9.05	10.10	9.66	9.18	8.91	8.51	6.21	5.52	5.42	7.83
2009	6.55	8.40	9.08	9.52	9.45	9.91	9.20	9.51	8.76	6.96	5.01	7.86	8.35
2010	7.17	10.40	9.82	10.60	11.20	10.10	9.83	9.79	9.23	6.73	6.24	6.75	8.99
2011	7.78	6.45	8.49	9.63	10.20	9.84	9.40	9.42	9.14	5.77	7.42	4.82	8.20
2012	5.82	5.82	8.42	10.50	10.60	9.76	9.55	9.15	8.79	5.37	6.13	5.95	7.99
2013	6.50	7.81	10.30	9.43	10.80	10.10	10.00	9.35	9.07	7.11	6.52	4.96	8.50
2014	7.30	8.91	9.48	9.91	10.10	10.30	10.20	9.25	8.98	7.04	6.16	6.16	8.65
2015	5.87	8.02	8.21	9.45	10.50	10.50	10.10	10.00	9.21	7.74	7.81	7.96	8.78
2016	9.20	9.53	10.90	0.00	0.00	10.00	10.00	9.83	9.76	0.00	5.77	5.43	6.70
2017	5.24	9.15	10.00	9.76	10.80	10.30	10.20	9.95	0.00	0.00	6.08	0.00	6.79
2018	0.00	0.00	0.00	0.00	0.00	10.00	9.54	9.51	8.91	0.00	0.00	0.00	9.49
Mean	6.57	7.64	8.66	8.54	9.01	9.73	9.62	9.43	8.39	5.19	5.68	5.33	8.11

Appendix V: Mean Monthly Temperature (°C) of Girar Jarso from (2002-2018)

Year	Jan	Feb	Mar	Apr	May	June	July	Aug	Sept	Oct	Nov	Dec	Mean
2002	13.47	14.93	15.27	15.7	17.43	15.97	14.98	13.71	13.66	12.97	13.07	14.14	14.61
2003	14.01	15.11	15.66	16.23	10.5	15.19	13.65	13.77	9.07	12.65	12.93	2.78	13.60
2004	4.00	14.62	15.75	15.67	16.36	15.42	13.93	13.92	13.71	12.29	12.98	13.72	20.72
2005	13.6	15.75	16.12	16.25	15.77	15.95	13.85	14.12	14.2	12.72	12.43	12.24	20.80
2006	13.98	15.19	15.34	15.36	15.81	15.67	13.77	13.23	13.56	13.78	12.97	13.17	20.50
2007	13.67	14.82	15.87	16.09	16.93	15.2	13.77	13.63	13.75	12.17	12.59	11.89	20.37
2008	13.58	14.26	15.74	15.83	16.5	15.86	14.25	13.64	19.63	13.06	12.46	12.58	14.32
2009	13.335	14.98	16.15	16.32	16.76	17.11	9.20	9.51	14.25	6.96	5.01	7.86	14.62
2010	13.73	15.71	15.80	16.36	16.95	16.37	14.24	13.71	18.81	13.35	12.93	13.16	14.69
2011	14.16	14.24	14.90	16.43	16.56	16.06	14.05	13.85	19.01	12.84	13.64	12.53	14.45
2012	13.44	14.21	15.92	16.63	17.62	16.49	13.98	13.84	14.07	12.64	13.55	13.13	14.63
2013	13.88	15.43	16.99	17.07	17.09	16.08	13.93	13.03	14.07	12.95	13.24	12.29	14.67
2014	13.97	15.04	15.91	16.12	16.25	16.72	14.89	13.55	13.85	13.21	13.07	12.82	14.62
2015	13.22	15.5	15.69	16.71	16.72	16.47	15.60	14.38	14.44	14.24	14.29	14.09	15.11
2016	15.04	16.12	17.59	0.00	10.78	15.94	14.39	14.05	14.62	0.00	12.90	12.56	12.00
2017	13.04	4.58	16.72	16.66	16.63	16.85	14.53	14.08	0.00	0.00	13.01	0.00	14.07
2018	6.52	2.29	8.36	8.33	8.32	13.42	12.03	11.80	4.46	0.00	6.51	0.00	11.78
Mean	12.36	14.2	15.02	14.32	15.38	16.08	14.21	13.77	13.14	10.7	12.27	10.86	14.29

Appendix VI. Mean performance analysis of nineteen traits of faba bean accession tested at Girar Jarso during 2018 main cropping season

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
1	30011	4.25	2.08	7.3	46	1	2	19.5	47.5	4	2.65	0.5	6.5	3.75	11	118	72	70	490	0.88
2	30023	5.15	2.67	8.97	47.5	1	4	19.5	54.75	4.5	2.65	0	6.25	4.1	11.5	121	73.5	33	707.5	0.42
3	30008	5.15	2.77	8.82	51	1.59	2.55	27.25	54.75	5.5	1.85	0.5	5.15	4.35	10	127	76	55	557	0.69
4	28109	4.05	2.12	6.44	51	1.25	1.75	17.5	30.25	4.5	1.1	0.5	3.25	3.5	5	127	76	50	488	0.63
5	25264	3.73	1.83	6.29	49	1	4	13.5	22.5	2.5	1.42	0	4	3.65	3.5	127	69	50	441.5	0.6
6	29531	4.37	2.47	7.46	51	1.25	2.1	20	41	8.5	2.2	0.5	4.25	3.55	17	121	70	300	520	3.75
7	220079	4	2.1	6.38	49	1	1	18	27	2	1.5	0	2.5	2.5	3	127	78	50	430	0.6
8	28777	4.73	2.23	7.52	49	1.25	3.3	22.75	53.75	4.5	1.5	0.5	4.25	4.35	6.5	127	78	26	440	0.3
9	30022	4.3	2.23	6.76	51	1.65	3	22	45.75	3.5	1.75	0	3.85	3.8	6	114.5	63.5	67	415	0.8
10	26861	4.93	2.28	8.42	49.5	1	2.5	19.25	38.5	5	1.5	1.5	4.75	4.05	6.5	127	74.5	42	471	0.5
11	29526	5.12	2.1	7.23	46	1	2.5	11.5	36.5	3	1.7	0	4.5	3.25	4.5	121	69	25	486.5	0.3
12	27279	3.63	1.37	4.6	46	1.92	2.5	15.75	41.5	5	2.64	0	4.5	3.5	13	112	69	38	411	0.5
13	26859	5.22	2.43	8.18	47.5	1	2.15	25.25	48.75	2.5	2.84	0	5	4	6.5	127	79.5	28	405.5	0.4
14	26882	5.4	2.32	8.66	46	1	2.42	13.25	50.75	5	1.4	1	7	4.9	7	127	72	100	520	1.3
15	27931	5.05	2.3	8.01	46	1.17	2.25	19.75	43	3	2.63	0	4.85	4.15	7.5	112	72	45	455	0.6
16	220086	4.07	2.22	6.12	49.5	1.5	5	30.25	47.75	2.5	2.09	1	4.75	4.4	5	127	77.5	42	480	0.5
17	26862	5.75	3.17	10.8	46	1	1.95	26.25	40.25	2.5	1.75	0	4.25	3.8	4	127	81	22	385	0.28
18	25260	4.67	1.98	6.72	51	2.05	2.2	26.25	45	4	1.65	0.5	4.75	4.15	7	127	76	37	352	0.5
19	212580	4.47	2.1	6.49	47.5	1.22	2.75	16.5	44.5	7	2.13	0	4.6	3.7	13.5	127	79.5	24	342	0.31
20	25259	3.47	1.37	4.42	46	1.25	1.75	16.75	37	5.5	1.68	0	4	3.05	9.5	112	63	33	382	0.4
21	28110	3.65	1.65	5.21	49.5	1	2.3	17.25	32.6	2	2.25	0	4.75	3.4	4.5	127	68.5	42	465	0.5
22	28774	4.98	2.93	9.96	47.5	1	3	22.75	48.5	7.5	2.57	0	6.15	3.9	16.5	127	73.5	33	540	0.4
23	28771	4.83	2.33	8.06	47.5	1.17	2.75	17.75	46.5	11.5	1.78	0	5.25	4.75	17	127	79.5	125	465	1.6
24	28112	4.68	2.25	8.22	49	1	2.65	28.5	59	2.5	2.17	1	5.1	4.4	5.5	127	78	45	527.5	0.57

App. VI. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
25	26885	4.33	2.33	7.46	49	1.12	3.75	24.5	63.5	14	2.13	1	5.75	4.4	29.5	115	66	100	510	1.25
26	28776	4.32	2.73	7.68	49	1.17	4	18	46.75	5	2.24	0.5	5.25	4.15	13	121	78	63	433	0.79
27	26855	4.58	2.65	9.16	47.5	1	2	16.6	25	1	1	0	2.95	3.2	1	105.5	67	35	402.5	0.4
28	Dagim	4	2.1	6.52	51	1.25	2.25	22	60.5	12	2.65	0.5	5.75	3.95	32	109	67	70	422	0.9
29	Walki	6.03	3.07	10.9	49	1	3.35	25.45	78.5	7	2.63	1.5	5.35	4.75	18	105.5	60	75	544	0.9
30	29527	4.65	2.33	8	46	1.13	2.5	16.5	41.75	3.5	2.75	0	5	3.7	9.5	121	66	49	447.5	0.62
31	29532	4.48	2.68	7.57	49.5	1	3	18	38.5	3.5	1.4	0	5.25	3.9	5	127	77.5	38	525.5	0.48
32	28772	4.87	2.57	8.16	46	1.8	2.7	25.75	49.5	6.5	2.46	0	5.5	4.3	16.5	127	81	65	286.5	0.8
33	212572	5.12	2.48	10.6	49.5	1.85	3.1	22.25	49.5	12	1.39	0.5	3.7	3.95	19.5	127	77.5	75	544	0.9
34	26883	4.5	2.53	7.72	49.5	1.06	2.3	13.25	38.5	5.5	2.5	0.5	3.75	3.65	14	118	68.5	88	501	1.1
35	26888	4.33	2.02	7.02	46	1.38	2	12.5	31.5	3.5	2.63	0	3.5	3.1	8.5	105.5	68.5	34	393	0.4
36	212566	5.57	2.65	10.7	49.5	1.57	2.75	23.75	55.5	8.5	2.32	0.5	5.25	3.75	18.5	127	68.5	92	376	1.16
37	212567	4.05	1.83	5.9	49.5	1.45	2.75	27	57.5	6.5	2.4	0	5.25	4	15.5	127	77.5	133	399	1.67
38	229299	4.87	2.45	8.91	47.5	1.13	3.75	15.5	46.75	8.5	1.75	0.5	4.85	3.85	16.5	127	70.5	44	419	0.6
39	229871	4.73	2.4	8.6	49.5	2.35	2	24.25	53.75	10.5	2.1	0	4.75	4.25	22.5	127	77.5	50	411	0.63
40	212578	4.07	2.27	6.2	51	1.25	2.5	22.1	36.75	2	1.84	0.5	3.75	4.1	3.5	121	73	58	333	0.7
41	25009	4.03	1.9	6.69	51	1.67	2	27	46.5	7	1.68	0	4	3.75	14.5	112	64	42	438.5	0.53
42	26854	5.75	3	10.9	49	1.4	2.5	13.5	48.5	8	1.7	1.5	5.55	3.9	13	121	75	50	376	0.6
43	30014	5.3	3	10.1	51	1.5	2.5	27.75	49	5	1.5	0	5	4.7	7.5	127	76	50	470	0.6
44	Lalo	4.82	2.47	9.93	51	1.35	2.05	20.25	52.25	10	2.31	1.5	5	4.5	24	118	70	50	430	0.63
45	220076	5.47	2.48	9.89	49.5	2.13	2.25	19.75	46.5	7.5	1.58	0	4.5	3.1	9.5	127	77.5	34	453	0.4
46	26428	5.23	3.22	11.8	51	1.43	2.75	24.5	60	8.5	2.1	0	4.5	3.75	18.5	127	76	120	387.5	1.5
47	30021	5.17	2.7	9.57	51	1.34	3	23	43.5	3.5	2.5	0	6.5	3.85	9.5	118	67	38	530	0.5
48	28770	4.68	2.48	8.1	47.5	1.4	3	19.5	55.5	14.5	1.7	0.5	5	3.85	22.5	127	65	89	424	1.1

App. VI. Cont...

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	
49	Bulga-70	4.72	2.3	7.38	46	1	2.5	20.5	43.25	4.5	1.6	0	4.5	3.5	7	127	75	42	453	0.53
50	25006	4.07	1.88	6.85	49.5	1.25	2.3	21.25	37.6	4.5	1.42	0	3.3	3	6	115	74.5	53	367	0.7
51	25270	6	2.38	10.1	47.5	1.21	2	16.25	37.65	6.5	1.97	0	4.25	3.65	15	112	73.5	46	410	0.58
52	25310	4.45	2.25	6.94	49.5	1.17	2.5	21.45	45	7	2	0.5	4.65	3.8	13	115	71.5	42	451.5	0.53
53	26858	4.28	2.63	8.11	49	1.5	2.5	20.25	39.75	7	1.43	0	4	4	10.5	127	72	50	332	0.6
54	27052	3.35	1.67	5.01	51	1.55	3.5	23.5	63.5	14	1.64	0	4	4	23	127	73	50	400	0.6
55	208114	4.12	2.1	6.72	46	1.38	2.5	24.85	39.75	4	2.29	0	4	3.7	7	118	78	31	420	0.4
56	29535	4.7	2.37	7.86	51	1.34	5.5	19.85	47	3.5	2.8	0.5	6.15	4.65	9.5	127	70	67	500	0.8
57	29533	4.3	2.2	7.18	51	1.34	2.75	18	43.75	6	2.6	0	4.75	4.15	14	127	70	113	480	1.42
58	26887	4.52	2.15	6.78	49	1	4	23.75	56.5	5.5	2.13	0	5	4	12	124	75	100	450	1.3
59	229303	4.88	2.55	8.26	49.5	1.9	2.25	22.5	64	24	1.9	1.5	5.5	3.85	48	109	68.5	88	475	1.1
60	229869	3.65	1.67	5.47	49	1.47	3.5	23.25	54.25	9	2.24	0	4.1	3.85	20.5	109	69	75	360	0.9
61	235709	5.35	3.08	12.3	51	1.34	4	22	47	8	1.75	0	3.75	3.9	16.5	124	73	50	320	0.6
62	26886	4.62	2.2	6.9	49	1.5	4.25	21.25	58	15	2.18	0.5	6.5	4.75	34	124	75	200	602.5	2.5
63	16599	4.47	2.05	6.62	47.5	1.29	1.75	21.75	49	9	2.23	0	4.75	3.35	18.5	127	79.5	42	443.5	0.5
64	28103	5.37	2.25	9.04	46	1	1	19	41.5	2	3	0	7.5	3.9	5	118	72	63	565	0.8
65	29536	5.2	2.58	9	49	1.11	2.5	20.25	50.25	7.5	2.08	0	4.25	4.35	18.5	127	78	133	460	1.7
66	25303	3.15	1.62	4.5	53	1.67	2.75	14.5	42	4.5	2.1	0	4.35	3	9.5	112	59	70	470	0.9
67	25299	4.67	2.42	7.62	51	1.5	2.5	18.25	40.25	2.5	2.09	0	5	4.25	5.5	121	70	33	490	0.4
68	25022	4.47	2.48	8.75	53	1.25	2.5	15.5	44.75	6.5	2.38	1	4.65	3.45	17.5	127	74	75	390	0.9
69	Moti	3.93	2.2	5.83	49	1.5	2.5	30.25	47.75	2.5	1.84	0	7	4	5	127	78	50	719	0.6
70	208085	4.4	1.92	6.22	51	1.13	3.2	14.15	42	5.5	1.72	0	4.25	3	9.5	124	73	67	480	0.8
71	25010	3.19	1.57	4.89	49.5	1.34	2	9.5	26	3	1.4	0	3.25	3.1	5	111.5	62	58.5	399	0.7
72	25298	5.37	2.97	8.99	47.5	1.25	2.5	22.5	36.6	2	1.5	0	4.35	3.6	3.5	127	79.5	23	468	0.3

App. VI. Cont...

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
73	27929	3.87	1.72	5.83	47.5	1	2	14	30.5	2	3	0	4.5	3.5	5	112	64.5	30	475	0.4
74	28773	4.57	2.53	8.39	47.5	1.17	2	25.75	46.5	4	1.77	0	5.5	4.05	7.5	121	73.5	75	600	0.9
75	30016	4.45	2	6.3	47.5	2.04	2.33	23.5	55.75	9	1.82	1.5	4.5	4	18	127	79.5	30	580	0.4
76	26860	4.23	2.25	7.38	49	1.38	3.25	21	50	6.5	2.61	0	5.75	4.5	17	127	78	67	420	0.8
77	25274	3.43	2.3	5.73	53	1	2.5	22	26	1	1	0	4	4	1	127	74	50	380	0.63
78	26889	4.69	2.17	9.67	47.5	1.25	3.5	18.5	36.5	5	1.78	0	3.5	3.3	12	108.5	61	41.5	360	0.5
79	229310	5.12	2.63	9.54	51	1.44	3.55	22.5	50.5	8.5	1.52	0	4.35	4.1	13	127	76	63	380	0.79
80	212565	4.88	2.1	7.77	51	1.8	2.7	22.85	47	6	1.75	0	4.25	3.65	11	127	76	75	430	0.9
81	Hachalu	4.98	2.8	8.84	47.5	1.87	2.75	34.45	62	9	2.67	0	5.85	4.95	24.5	115	67.5	100	625	1.3
82	231293	5.8	3.12	11.2	47.5	2.63	2.75	33.5	68	17	1.9	3	5.75	3.9	52	121	73.5	140	480	1.8
83	30017	4.12	2.25	7.88	49	1.13	3.25	29.5	68	10	2.29	2.5	5.25	5.6	16	127	78	100	391.5	1.3
84	25292	4.2	3.8	8.65	49	1.42	2	22	36	5	1.88	0	3.6	3.6	8.5	115	66	50	434	0.6
85	28113	4.6	2.23	7.52	49	1.42	2.5	24	54.25	7.5	1.75	0	4.75	4.45	15	115	66	65	450	0.8
86	25290	4.78	2.7	7.99	47.5	1.15	2.7	18.5	34	7.5	2.33	0	5.5	4.35	14	127	79.5	26	400	0.3
87	28104	4.82	2.43	8.76	49.5	1.15	2.25	19.25	53.25	8.5	2.04	1	5.25	3.5	17.5	127	77.5	38	580	0.5
88	26400	4.67	1.83	7.03	47.5	1.44	2.75	19	50.25	7.5	1.91	0.5	4.75	4.15	16.5	127	79.5	115	580	1.4
89	25017	4.35	2.62	8.54	47.5	1.67	2.75	19.5	48.25	8	2.25	0	4.75	3.4	18	121	73.5	59	626	0.7
90	25003	3.22	1.19	4.15	47.5	1	2	16.75	33	2.5	1	0	4.25	4.2	2.5	112	64.5	38	443	0.5
91	26853	4.2	1.37	5.99	46	1.2	2.5	14.75	35.25	4	3.29	0	4.25	2.65	11	118	72	43	380	0.5
92	29537	5.2	2.67	8.57	46	1.1	2.5	20.75	51.25	4.5	2.6	0	5.5	3.9	12	127	81	160	569.5	2
93	25018	3.98	1.4	4.92	53	1	2.75	22	40	4.5	1.73	0	4.5	3.5	7.5	121	68	108	320.5	1.4
94	30015	4.97	2.38	6.81	51	1.44	3.5	21.5	73.75	11	2.37	1.5	5.5	3.95	29	127	76	138	438	1.73
95	219089	7.85	3.15	14.4	56	1.49	6.25	46.38	135.1	22.75	2.69	1	8.13	2.09	54.75	151	95	125	605	1.56
96	219355	8.63	3.3	11.9	56	1.95	6	43.5	132.8	9.75	2.15	0.75	6.63	1.9	21	151	95	140	660	1.75

App. VI. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
Mean		4.66	2.33	7.93	49.1	1.34	2.77	21.33	48.21	6.5	2.09	0.34	4.83	3.85	13.5	122.2	73.1	67.1	460.2	0.84
CV		18.1	26	29.9	5.1	27.92	32.5	24.9	26.05	62.62	45.7	176.4	20.9	12.7	70.3	4.08	10.3	54.21	12.75	53.9
SE		0.85	0.61	2.38	2.5	0.37	0.9	5.31	12.56	4.07	0.95	0.6	1.01	0.49	9.5	4.99	7.55	36.4	58.67	0.45

Appendix VII. Mean performance analysis of nineteen traits of faba bean accession tested at Girar Jarso during 2019 main cropping season

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
1	30011	5.25	2.42	9.57	56	1.67	3.32	35.14	79.32	9.7	2.62	0.17	3.24	3.17	25.18	152.5	95	80	490	1.01
2	30023	4.8	1.75	6.67	58	1	2.76	27.63	68.28	5.45	2.1	0.15	5.47	3.33	11.8	152	93	69	707.5	0.87
3	30008	4.94	1.87	7.27	61	1	2.95	32.13	66.48	5.6	1.85	0	5.05	2.83	11.53	132	70	83	557	1.04
4	28109	4.93	1.98	7.56	61	1.17	2.88	26.65	84.68	7.95	2.05	0	5.53	2.98	16.5	153	90	62.5	488	0.79
5	25264	4.88	2.08	7.98	59	1.62	3.63	23.78	86.33	17.3	1.76	0	4.3	2.67	30	150	92	83.5	441.5	1.05
6	29531	5.59	2.12	9.1	61	1.58	3.25	30.75	102.4	17.1	2.57	0.19	5.68	2.98	50.98	128	65	145.5	520	1.82
7	220079	6.38	2.73	13.4	58	1.43	3.78	55.83	121.9	16	2.12	0.19	5.1	3.23	35.45	127	68	245	385	3.05
8	28777	3.3	1.3	3.84	59	1.5	3.1	24	49.9	2.8	2.2	0	5.02	1.7	6.8	123	62	66	440	0.83
9	30022	4.25	1.48	5.21	61	1.12	5.88	38.18	115.6	15	2.61	0.75	4.83	2	52	132	70	119.5	415	2.05
10	26861	7.25	3.15	17.6	60.5	1.42	3.35	37.54	113.3	14	2.25	0.83	7.25	2.59	32	153	90.5	129	471	1.62
11	29526	4.23	1.55	5.41	56	1.13	2.53	24.4	61.94	5.53	3.05	0.37	5.65	2.87	16.88	128	70	82.5	486.5	1.04
12	27279	4.94	2.02	7.69	56	1.23	2.9	27.39	68.88	7.75	2.62	0	5.3	2.48	20.2	151.5	95	60	411	0.75
13	26859	5.1	1.77	7.13	58	1.31	3.08	30.88	74.95	8	2.15	0	4.85	2.65	17.75	132	73	52.5	405.5	0.66
14	26882	4.92	1.89	7.27	56	1.03	2.77	40.19	88.13	4.5	2.6	0	5.88	3.2	10.75	150.5	95	80	520	1
15	27931	5.1	1.93	7.62	56	1.16	3.29	38.42	98.99	6.63	2.54	0	6.05	2.98	16.88	133	75	122.5	455	1.54
16	220086	5.94	2.72	12.2	60	1.6	3.22	32.75	106.6	21.5	2.4	0	5.63	2.85	50.63	153	91	172	480	2.15
17	26862	4.9	1.93	7.37	56	1.58	6.59	43.82	115.6	18.38	2.14	0.19	4.89	2.01	37.38	151.5	95	154	385	1.93
18	25260	3.85	1.3	4.2	61	1.33	2.75	28.6	70	8	1.88	0	4.5	1.5	15	121	60	125	352	1.57
19	212580	3.9	1.7	5.44	49	1.33	2.5	14.5	38	4	2.25	0	4	3.6	9	128	77	122.5	342	1.54
20	25259	6	2.5	11.2	56	1.2	9	58	124	14	2.14	1	4.5	3	30	131	75	140	382	1.76
21	28110	3.9	1.47	4.92	61	1.07	2.61	30.59	61.75	3.75	2	0	5.07	2.91	7.5	151	90	52	465	0.66
22	28774	4.93	1.68	6.57	58	1.08	2.83	27.09	71.09	6.5	2.27	0	5.79	3.15	14.75	151	93	47.5	540	0.6
23	28771	5.62	2.09	8.92	58	1	3.25	29.69	79.75	6.25	2.05	0	6.15	2.95	12.63	151	93	61.5	465	0.77
24	28112	5.1	2.07	8.72	59	1.26	3.13	38.44	85.34	7.63	2.32	0.38	5.57	3.12	17.63	151	92	88	527.5	1.1

App. VII. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
25	26885	6.1	2.54	11.6	59	1.21	4.06	43.04	108	14.75	2.55	0.38	6.25	2.91	38	151	92	128.5	510	1.61
26	28776	5.17	2.89	11.1	59	1.75	3.89	39.98	111.7	25.25	1.51	0.19	5.88	2.77	32.38	151	92	178.5	433	2.24
27	26855	3	1.15	3.43	58	1.26	2.04	28.44	90.25	7.75	1.89	0.38	2.82	1.1	13.38	126	68	135.5	402.5	1.7
28	Dagim	6.99	2.75	14.3	61	1.73	5.95	40.07	131.9	53	2.85	1.13	5.88	2.34	115	151	90	204.5	422	2.56
29	Walki	6.57	3.53	17.1	59	1.89	4.44	44.13	139.5	56	2.18	0.88	6.53	3.02	77	151	92	169	544	2.11
30	29527	4.6	1.45	5.51	56	1.41	4.27	26.95	58.88	15.63	2.17	0.75	5.32	3.54	33.63	131	75	146.5	447.5	1.83
31	29532	4.87	2.04	7.72	60	1.18	2.77	30.24	70.82	6.25	2.59	0	6	3.11	15.88	151	91	61.5	525.5	0.77
32	28772	3.85	1.4	4.46	56	1	3.1	34.3	74.3	5	1.8	0.5	4.25	1.7	9	121	65	62.5	286.5	0.78
33	212572	5.12	2.27	8.81	60	1.4	3.25	32.38	79.49	6.38	2.32	0.13	6.17	3.23	14.38	151	91	74	544	0.93
34	26883	4.93	1.8	7.01	60	1.38	4.42	39.49	92.12	7.25	2.285	0	5.88	2.94	16.63	151	91	87.5	501	1.1
35	26888	5.34	2.32	9.11	56	1.15	4.15	24.13	85.5	4.325	2.53	0.38	7.59	3.04	38.63	129	73	108	393	1.35
36	212566	6.82	2.84	14.5	60	1.58	4.03	36.38	106.3	13.5	2.44	0	5.28	2.72	33.38	151	91	124	376	1.55
37	212567	6.27	2.87	13.1	61	1.89	3.65	46.79	136.3	34.5	2.385	0.63	5.52	2.69	83	151	90	161	399	2.02
38	229299	6.35	2.39	11.3	58	1.51	4.13	29.32	131.1	35	3.74	1.13	5	2.92	145.5	126	68	234.5	419	2.94
39	229871	4.1	1.8	5.81	60	1	3.25	23.75	70.5	7	1.93	0	5.25	2.1	13.5	126	66	118.5	411	1.49
40	212578	4.5	1.4	5.06	61	1.18	2.7	24.6	73	6.5	2.15	0.5	5	1.4	14	126	65	127	333	1.59
41	25009	4.37	2.38	7.73	61	1.33	3.4	34.57	88.88	11.88	2.15	0.5	4.82	2.29	25.75	151	90	82	438.5	1.03
42	26854	4.33	2.39	8	59	1.36	2.8	32.82	75.38	6.25	2.17	0.125	5.09	2.47	13	131	72	60.5	376	0.76
43	30014	5.6	2.39	10	61	1.28	3.13	30.72	95	14.25	1.82	0	5.09	3.22	25.88	151	90	95	470	1.19
44	Lalo	6.2	2.65	12.2	61	2.04	3.4	36.32	91.44	11.88	2.23	0.25	6.75	3.25	24.5	151	90	163.5	430	2.05
45	220076	5.88	2.38	10.4	60	1.31	4.25	35.13	110	18.88	2.5	0.44	5.48	2.6	47	151	91	142.5	453	1.78
46	26428	6.43	2.85	13.4	61	1.5	4.07	37.44	116	18	2.39	0.32	5.64	3.16	43.75	151	90	115	387.5	1.44
47	30021	7.15	2.13	11.2	61	1.14	6.94	37.44	117.3	25.5	1.54	1.13	5.19	2.63	36.88	151	90	92	530	1.15

App. VII. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
48	28770	6.6	2.7	12.9	54	1.31	3.05	32.75	108	19	2.05	0.5	4.85	2	39	126	72	220	424	2.75
49	Bulga-70	8.02	3.47	20.9	56	1.58	6.25	38.57	140.8	40	1.67	1.13	5.44	2.3	64.63	151	95	216	453	2.7
50	25006	5.98	2.6	11.6	61	2.12	4.87	39	136	21.63	1.82	0.13	4.63	2.65	38.75	151	90	173	367	2.16
51	25270	4.68	2	7.57	58	1.06	2.74	27.69	64.44	6	2.41	0.13	5.34	2.74	14.5	151	93	81	410	1.02
52	25310	4.47	3.47	11	58	1.14	2.83	31.69	67.2	4.63	2.47	0	5.54	2.7	11.13	131	73	115	451.5	1.44
53	26858	5.09	2	8.23	59	1.39	4.29	27.53	82.88	8.63	2.11	0.13	4.95	2.86	18.63	126	67	73	332	0.92
54	27052	5.37	2.12	8.67	61	1.09	3.44	37.49	87.22	5.5	2.4	0	5.95	3.05	12.75	131	70	100	396	1.26
55	208114	6.13	2.27	10.4	56	1.37	4.19	38.15	121.4	15.63	2.48	0.5	6.17	2.68	38.25	151	95	175	420	2.19
56	29535	6.7	2.54	12.6	61	1.23	4.08	34.69	105.6	10.25	2.48	0	6.24	3.2	25.38	151	90	218	500	2.73
57	29533	6.2	2.78	12.8	61	1.39	4.23	42	127	31	2.46	1	6.63	2.05	74.25	151	90	185	520	2.31
58	26887	6.15	2.8	12.5	59	1.25	3.5	28	112	12.5	2.16	0.5	5.6	2	27	126	67	117.1	450	2.8
59	229303	5.05	1.8	7.12	60	1.1	3.35	33	107	11	1.91	0.5	5.85	1.8	21	126	66	179	475	2.24
60	229869	6.07	2.38	11.2	59	1.34	5.07	34	124.6	8.13	2.88	0	5.82	2.95	22.13	151	92	208	360	2.6
61	235709	4.69	2.12	7.7	61	1.15	3.24	31.07	73.57	7.63	2.2	0.25	5.24	2.82	17.63	151	90	117.5	320	1.47
62	26886	4.13	1.58	5.45	61	1.05	2.65	37.37	73.88	3.38	1.94	0.13	5.32	3.25	6.875	151	90	45	602.5	0.57
63	16599	4.12	1.87	6.12	58	1.23	3.44	30.63	80.25	5.13	2.27	0.25	4.88	2.44	11.25	126	68	90	443.5	1.13
64	28103	4.73	1.7	6.4	56	1.02	3.9	34.88	88.13	10.75	2.26	1.25	6.75	3.37	23.5	151	95	152	565	1.9
65	29536	5.52	1.93	8.15	59	1.74	4.44	36.69	103.9	10.5	2.35	0.13	6.63	2.75	23.5	151	92	189	460	2.36
66	25303	6.4	2.68	12.6	63	1.22	3.91	36.94	117.5	19	2.28	0.82	4.95	2.64	43.63	151	88	217.5	470	2.72
67	25299	7.32	2.43	13.1	61	1.31	5.37	36.57	130.7	20.63	2.23	0.8	5.57	2.37	46	151	90	217.5	490	2.72
68	25022	5.77	2.3	10.1	63	1.8	4.75	45.9	137.1	21.13	2.63	0.63	5.44	3.28	53.75	151	88	235	390	2.94
69	Moti	7.23	3.3	17.3	59	1.57	4	46.13	100	17.5	1.85	0.5	5.45	2.72	31.25	131	72	229	719	2.86
70	208085	5.4	1.83	8.24	61	1.27	3.25	24	69.9	6.63	2.11	0	5.4	2.39	12.75	151	90	92.5	480	1.16

App. VII. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
71	25010	4.89	1.59	6.34	61	1.22	3.28	35.13	72.1	4.25	2.5	0	5.69	3.1	10.63	151	90	107	399	1.34
72	25298	4.53	1.69	6.26	58	1.11	3.79	31.38	83.8	6.75	2.16	0.25	5.03	2.37	14.38	126	68	110	468	1.38
73	27929	4.6	1.8	6.41	46	1.29	3.1	39	87	4.5	2.67	0	6.25	3.7	12	115	69	158	475	1.97
74	28773	6.53	2.69	12.9	58	1.27	4.89	33	106.1	12	2.34	0.75	6.63	2.9	28	151	93	158	600	1.98
75	30016	6.58	2.54	12.3	58	1.7	5.63	37.07	123.4	21.63	2.43	0.57	7	3.23	52.63	151	93	225	580	2.82
76	26860	5.44	2.17	9.09	59	1.6	5.38	46.88	132.3	28	2.59	1	6.43	2.3	72.25	151	92	235	420	2.94
77	25274	5.04	1.77	7.26	60	1.43	5.13	45.38	138.8	26.13	2.61	1.37	5.32	2.61	68.25	131	71	250	410	3.13
78	26889	4.1	1.6	5.39	58	1.57	3.4	41	111	33	2.15	1	4	1.8	71	126	68	277.5	360	3.47
79	229310	5	1.9	7.4	61	1.21	3.8	30.75	128	25.5	2.02	1.5	5.6	1.8	51.5	126	65	165	380	2.06
80	212565	6.4	2.94	13.8	61	1.34	4	33.08	71.6	7.75	2.77	0.75	5.49	2.6	18.88	151	90	120	430	1.51
81	Hachalu	5.89	2.37	10.9	58	1.13	3.84	29.82	87.7	6.38	2.58	0.39	7.02	3.28	16.5	151	93	124	625	1.56
82	231293	5.68	2.1	9.37	58	1.28	4.19	45.32	101.3	10	2.25	0.38	6	2.69	20.88	151	93	104.5	480	1.06
83	30017	5.95	2.78	12.2	59	1.24	3.82	36.68	109.1	11.38	2.49	0.25	5.87	2.97	28.88	151	92	113	391.5	1.41
84	25292	5.85	2.23	9.81	59	1.42	3.93	23.13	121.8	18.5	2.51	0.82	5.29	2.97	46.88	151	92	129	434	1.61
85	28113	5.44	2.33	9.84	59	1.83	7	33.88	123.9	26	2.88	1.13	5.44	2.37	72	151	92	100	450	1.25
86	25290	7	2.5	12.9	58	1.36	4.5	41	142	30	2.3	1	6.5	2	69	126	68	210	400	2.63
87	28104	7.28	3.15	17.1	61.5	1.63	7.75	59	134.8	20.25	2.35	0.63	6.75	2.94	48.25	151	89.5	170	580	2.13
88	26400	5.38	4.74	17.7	58	1.14	4.13	42.25	107.3	16.25	2.04	0.88	6	3.01	32.88	151	93	262.5	580	3.29
89	25017	4	3.6	10.7	49	2	3.5	25	53	6	2.5	0	4.5	3.2	15	127	78	76	625.8	0.95
90	25003	4.57	1.48	5.59	59	1.15	2.97	30.57	66.4	6	1.81	0.13	5.59	2.66	12.13	131	72	119	443	1.49
91	26853	5.5	2	8.42	56	1.82	3.2	33.5	122	20	2.2	0	5	1.9	44	126	70	265	380	3.31
92	29537	5.72	2.35	10.2	56	1.74	4.13	37.5	88.4	9.13	2.73	0.63	5.94	3.13	25.88	126	70	225	569.5	2.82
93	25018	5.38	2.04	8.38	63	1.38	3.19	34.74	79.8	9.75	2.27	0.32	3.99	3.5	21.13	131	68	50.5	320.5	0.64
94	30015	6.19	1.88	8.92	61	1.45	3.5	37.19	97.1	10.13	2.76	0	5.13	2.79	28.63	131	70	137.5	438	1.72

App. VII. Cont....

S/N	Acc	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPP	NSPPL	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
95	219089	7.68	3.18	17.5	56	1.57	5.88	47.69	126.6	27.88	2.38	0.75	8.82	3.3	61.38	151	95	208	605	2.6
96	219355	8.57	2.9	17.9	56	1.64	6.5	43.25	126.9	8.88	2.14	0.88	6.57	2.7	19	151	95	175	660	2.19
Mean		5.46	2.25	9.66	58.68	1.37	3.93	35.01	97.63	14.07	2.3	0.39	5.55	2.72	32.02	141.6	82.7	137.9	459.6	1.74
CV		9.35	13.3	18.54	1.07	10.27	15.9	10.35	13.55	32.71	7.64	60.29	10.2	21.7	23.49	0.61	0.76	45.79	12.83	44.1
SE		0.51	0.3	1.79	0.63	0.14	0.62	3.62	13.23	4.6	0.18	0.24	0.57	0.59	7.52	0.87	0.63	63.18	58.98	0.77

Appendix VIII. Mean performance analysis of nineteen traits of faba bean accession tested at Degem during 2018 main cropping season

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
1	30011	6.83	2.91	13.16	57.00	1.57	5.00	29.25	83.0	14.00	2.25	1.50	6.50	4.60	33.50	161.0	104.0	110.0	631.0	1.38
2	30023	7.63	3.99	19.56	60.23	1.48	5.00	28.00	85.00	11.00	2.59	0.50	7.00	4.75	28.50	153.0	100.0	183.0	660.8	2.29
3	30008	6.47	2.63	11.40	60.23	1.95	4.50	30.50	83.50	14.50	1.71	1.00	6.50	4.15	24.50	161.0	101.0	135.0	613.6	1.69
4	28109	8.34	4.10	21.99	60.23	1.65	4.75	31.50	75.50	13.50	2.00	2.00	5.50	3.65	26.00	153.0	93.1	137.0	613.6	1.72
5	25264	4.95	1.86	6.61	60.23	1.49	4.50	25.00	81.50	11.00	2.44	1.00	5.05	4.00	26.50	153.0	93.1	108.0	495.6	1.36
6	29531	7.32	3.05	14.67	60.23	1.20	4.25	25.00	85.50	9.00	2.56	0.00	7.00	4.30	22.00	153.0	93.1	269.0	637.2	3.36
7	220079	5.91	2.52	10.11	60.23	1.51	4.00	22.00	87.00	14.50	1.97	1.00	5.50	3.75	26.50	153.0	93.1	120.0	401.2	1.50
8	28777	6.89	3.23	14.63	60.23	1.37	6.50	35.50	80.50	14.50	1.90	1.00	5.50	3.70	27.50	153.0	93.1	144.0	566.4	1.81
9	30022	4.45	1.79	5.83	60.23	1.40	4.35	40.00	93.50	7.00	2.46	0.50	5.50	3.8	16.5	153.0	93.1	100.0	641.0	1.30
10	26861	6.08	2.34	9.70	56.94	1.22	5.00	26.00	81.00	15.00	2.30	1.00	5.75	4.05	35.00	161.0	104.0	128.0	566.0	1.60
11	29526	7.63	2.97	14.92	56.94	1.16	6.00	27.50	84.50	14.50	2.18	1.00	6.50	3.95	31.00	153.0	96.3	141.0	496.0	1.80
12	27279	6.075	2.20	9.07	56.94	1.56	7.00	29.50	92.50	14.00	2.47	1.00	8.00	3.75	35.00	153.0	96.3	110.0	448.0	1.40
13	26859	7.03	3.08	14.26	56.94	1.69	4.00	34.00	80.50	12.50	1.71	0.50	5.50	3.10	20.50	161.0	104.0	94.0	425.0	1.20
14	26882	7.74	2.73	13.95	56.94	1.00	6.00	37.00	85.00	10.00	2.96	1.50	7.75	4.10	14.50	161.0	104.0	170.0	755.0	2.10
15	27931	7.135	3.02	14.18	56.94	2.09	4.75	41.00	110.0	24.00	2.01	1.50	4.50	3.75	48.00	153.0	96.3	194.0	566.0	2.40
16	220086	6.15	2.87	11.80	56.94	1.44	6.50	32.50	88.00	10.00	2.45	1.00	5.50	4.75	24.50	161.0	104.0	166.0	590.0	2.10
17	26862	6.125	3.08	12.73	56.94	1.50	5.25	38.00	95.00	8.00	2.69	0.50	5.25	3.85	21.50	161.0	104.0	150.0	543.0	1.90
18	25260	5.80	2.34	9.30	60.23	2.33	4.60	40.00	90.00	14.00	2.55	0.50	5.10	4.00	37.00	153.0	93.1	175.0	448.0	2.20
19	212580	6.60	3.26	14.18	60.23	1.45	4.50	26.50	86.50	18.50	2.60	2.00	5.50	4.15	46.50	153.0	93.1	142.0	425.0	1.80
20	25259	4.95	2.31	7.98	56.94	1.45	3.50	30.00	69.50	13.00	2.40	1.00	5.25	3.35	28.00	153.0	96.3	96.0	425.0	1.20
22	28774	7.21	3.26	15.4	60.23	1.25	4.50	45.00	109.0	12.00	2.62	1.00	6.00	4.00	31.00	153.0	93.1	205.4	732.0	2.60
23	28771	5.94	2.42	9.77	60.23	1.21	4.50	41.00	89.00	10.50	2.58	1.00	7.00	4.35	27.50	153.0	93.1	127.0	543.0	1.60
24	28112	6.22	2.81	11.69	60.23	1.18	5.25	35.00	90.00	10.00	2.50	0.50	7.50	4.25	25.00	153.0	93.1	108.0	661.0	1.40

App. VIII. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
25	26885	7.21	2.87	13.67	60.23	1.07	4.50	28.50	90.00	9.00	2.99	0.50	6.25	3.80	26.50	161.0	101.0	180.0	856.0	2.30
26	28776	5.44	2.7	9.975	60.23	1.29	4.50	36.50	82.00	10.00	2.13	0.50	5.00	3.75	20.50	161.0	101.0	58.0	598.0	0.70
27	26855	7.63	3.65	18.08	60.23	1.39	4.25	22.00	79.50	14.00	2.44	1.50	5.75	3.25	35.00	161.0	101.0	140.0	496.0	1.80
28	Dagim	5.97	2.76	11.09	64.61	1.46	4.50	38.00	78.00	10.50	1.79	0.50	4.25	3.75	17.00	153.0	88.8	81.0	398.0	1.00
29	Walki	7.98	3.18	16.53	60.23	1.29	3.90	44.00	101.0	10.50	2.02	0.50	5.50	4.00	21.50	153.0	93.1	150.0	661.0	1.90
30	29527	6.92	3.57	16.17	56.94	1.70	4.00	30.00	102.0	25.00	2.70	2.00	7.00	3.65	60.50	153.0	96.3	271.2	520.0	3.40
31	29532	6.86	3.50	15.71	56.94	1.30	4.75	25.00	85.50	15.00	2.75	1.00	6.25	3.75	39.50	153.0	96.3	280.0	708.0	3.50
32	28772	5.195	2.24	8.09	56.94	1.53	6.00	24.50	103.0	18.50	2.84	1.50	6.00	3.25	52.00	153.0	96.3	277.0	519.0	3.50
33	212572	8.34	3.47	18.75	56.94	1.74	5.00	36.50	96.00	20.00	2.20	0.50	4.10	3.90	32.50	153.0	96.3	170.0	543.0	2.10
34	26883	7.85	3.18	16.32	56.94	1.34	7.5	39.5	107	18.5	2.39	1	6	4.75	44	153	96.3	222	590	2.8
35	26888	6.45	3.33	14.13	56.94	1.65	6	27	71.5	20.5	2.43	2	5.25	4	49.5	138	81.3	138	425	1.7
36	212566	7.49	3.33	16.29	56.94	1.42	5	27.5	65.5	10.5	2.22	1	4.75	4.45	24	153	96.3	90	401	1.1
37	212567	5.65	1.97	7.77	56.94	1.49	4	34	75.5	11.5	2.5	0.5	4.25	3.5	29	153	96.3	119	401	1.5
38	229299	6.47	2.97	12.77	56.94	1.2	2.25	23.25	66	6	2.38	0	3.75	2.5	14.25	153	96.3	75	413	0.9
39	229871	6.01	2.63	10.66	64.61	1.71	4	42	92.5	17.5	2.1	1	5.75	4.5	34	153	88.8	135	561	1.7
40	212578	6.75	3.18	14.17	60.23	1.22	3.5	35.5	85	9.5	2.24	0.5	5	4.25	20.5	138	78.1	105	425	1.3
41	25009	5.12	2.34	8.32	64.61	1.56	5.5	34.5	91	9	2.71	0	5.5	3.9	24	153	88.8	117	519	1.5
42	26854	4.63	2.18	7.14	60.23	1.8	5.5	19	90	15	2.42	1	5.5	3.4	36.5	138	78.1	128	425	1.6
43	30014	6.92	3.29	14.96	56.94	1.49	6.5	34.5	109	16.5	2.39	1.5	5.75	4.5	40	161	104	111	519	1.4
44	Lalo	7.74	3.02	15.07	60.23	1.38	5.5	35.5	84	11	2.25	1	5.25	4.15	24	153	93.1	83	496	1
45	220076	6.08	2.42	9.98	64.61	1.8	4	32.5	75	14.5	1.74	1.5	4.75	3.5	23	153	88.8	55	448	0.7
46	26428	4.85	2.1	7.2	64.61	1.47	7	34	99	15.5	1.66	1	4.25	4.35	25	153	88.8	150	472	1.9
47	30021	7.56	3.29	16.25	60.23	1.21	5.5	21	90	6	2.59	1.5	7	3.85	15.5	153	93.1	75	596	0.9

App. VIII. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
48	28770	6.01	2.84	11.44	60.23	1.48	4.5	39	98	11	2.5	0.5	5.5	3.95	27.5	153	93.1	124	484	1.6
49	Bulga-70	7.6	3.05	15.2	56.94	1.32	7.25	25.5	87	9.5	1.75	0.5	4.5	3.75	17.5	153	96.3	88	568	1.1
50	25006	8.69	3.36	18.93	56.94	2	3.75	38	98	22.5	1.64	0	3.5	3.9	37	153	96.3	174	425	2.2
51	25270	8.59	4.28	23.55	56.94	1.81	6.5	37.5	103	24	2.12	0.5	5	4	51	153	96.3	275	496	3.4
52	25310	7.56	2.81	13.99	56.94	1	5.5	34	96.5	5.5	2.98	1	5.25	4	17.5	153	96.3	161	537	2
53	26858	9.04	4.52	26.1	60.23	1.6	5.5	26	98.5	20	1.91	0.5	5.5	3.9	36.5	153	93.1	119	354	1.5
54	27052	9.33	3.75	22.49	60.23	2	4.5	43	109	19	2.5	0.5	5.5	3.9	49	153	93.1	153	425	1.9
55	208114	8.41	3.86	20.91	56.94	1.52	4.5	44	111	13.5	2.59	0	5.5	3.75	35	153	96.3	169	401	2.1
56	29535	6.57	2.34	10.42	64.61	1.38	4.5	32.5	92.5	10	3.24	0	6.5	4.6	29.5	138	73.8	139	543	1.7
57	29533	5.69	2.7	10.4	60.23	1.17	4.5	39	94.5	5.5	3.54	0.5	8	4.5	19.5	138	78.1	100	609	1.3
58	26887	5.16	2.39	8.52	60.23	1.34	5.5	35	99	13.5	1.98	0.5	7	4.5	27.5	161	101	107	653	1.3
59	229303	9.33	3.57	21.46	56.94	1.51	7	37	88	12	3.09	1.5	6.5	4.15	37.5	161	104	258	590	3.2
60	229869	6.44	3.36	14.26	60.23	1.41	4	24.5	89	10.5	2.15	0	5.25	4	22.5	153	93.1	150	378	1.9
61	235709	7.53	3.26	16.04	64.61	1.6	5.75	28	87	20.5	2.6	1.5	4.75	3.5	53.5	153	88.8	180	354	2.3
62	26886	5.41	2.73	10.03	60.23	1.22	4	40	106	11	2.15	0	6	4.25	23.5	161	101	147	614	1.8
63	16599	5.3	2.42	8.82	60.23	2.2	6	45	103	16.5	1.82	0	6	4.75	30	153	93.1	133	496	1.7
64	28103	7.21	3.08	14.61	56.94	1.44	6	19.5	84	16.5	2.41	1.5	6.5	4.4	40	153	96.3	150	828	1.9
65	29536	6.75	3.12	13.91	60.23	1.44	6.5	23.5	77	8	2.29	1.5	6.5	3.5	17.5	153	93.1	167	566	2.1
66	25303	6.36	3.71	15.46	64.61	1	4	22.5	76	6	2.1	1	6.5	4	12.5	153	88.8	93	590	1.2
67	25299	6.82	3.02	13.59	60.23	1.18	5	31	88	8	3.01	1	7.5	3.85	23.5	153	93.1	131	620	1.6
68	25022	8.48	4.52	24.54	64.61	1.88	5	30	81	18.5	1.59	0.5	4	3.5	29	153	88.8	78	401	1
69	Moti	6.39	3.05	12.94	60.23	1.55	5.5	38.5	102	11.5	1.84	1	9	5	21	153	93.1	150	833	1.9
70	208085	6.92	3.26	14.82	60.23	1.56	4	40.5	90	18	2.16	1.5	5	4.05	39	153	93.1	114	401	1.4

App. VIII. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
71	25010	4.85	2.28	7.73	64.61	1.52	6.5	30	83.5	10	1.78	0	5.5	3.65	18	153	88.8	320	496	4
72	25298	6.75	2.66	11.99	60.23	1.22	7	17.5	78	11	2.44	1	6.5	3.75	20.5	153	93.1	106	555	1.3
73	27929	6.68	2.63	11.74	56.94	1.3	7.5	27	76.5	6.5	3.05	0.5	6.75	4.15	20	153	96.3	113	496	1.4
74	28773	6.22	2.97	12.33	60.23	1.72	7.5	45.5	86	8	2.47	1	7.5	5	19	153	93.1	188	637	2.4
75	30016	6.68	3.15	13.9	60.23	1.59	6	29	109	20	1.93	1	6	3.75	38	161	101	155	543	1.9
76	26860	5.86	2.24	9.01	60.23	1.88	4	53	118	15	2.05	0	6	3.95	31	161	101	129	566	1.6
77	25274	6.08	2.84	11.55	56.94	1.8	4	36.5	83	11	1.91	0	5	3.75	21	153	96.3	138	472	1.7
78	26889	8.73	3.86	21.66	60.23	1.68	5.5	22	78	17	1.65	1	5	2.85	29.5	138	78.1	142	425	1.8
79	229310	8.66	3.5	19.6	60.23	2.14	6	20	104	21	1.96	1	5.15	3.15	41	153	93.1	179	472	2.2
80	212565	7.42	3.36	16.31	60.23	1.75	4	34.5	78.5	15.5	2.07	2	4.5	3.75	34	153	93.1	133	472	1.7
81	Hachalu	6.18	2.39	10.01	60.23	1.5	6.5	43	114	15	2.1	1.5	8	5.5	30	161	101	211	873	2.6
82	231293	7.44	4.01	17.49	66.45	1.59	6.5	37	65	14	1.62	0.5	5	4.5	22	175	108	53	631	0.7
83	30017	7.07	3.39	15.71	60.23	1.18	6	32.5	118	17	1.89	1	7	4.5	34	153	93.1	258	755	3.2
84	25292	5.8	3.05	11.82	60.23	1.34	4.5	28	83.5	7	1.75	0.5	4.25	4.5	11.5	153	93.1	157	590	2
85	28113	8.38	4.31	23.16	60.23	1.7	6	29.5	112	16.5	1.7	0	6.3	4	29.5	153	93.1	58	590	0.7
86	25290	5.44	2.03	7.72	56.94	1.75	4	33	63.5	10.5	1.99	0	5	4	20	153	96.3	88	519	1.1
87	28104	7.32	2.63	12.76	64.61	1.5	6	33.5	88	7.5	2.09	0	6.5	4.65	15.5	153	88.8	100	833	1.3
88	26400	6.36	2.87	12.17	60.23	1.5	4.5	49	98	9	1.96	0.5	5.5	4.35	16.5	161	101	150	618	1.9
89	25017	8.2	4.38	23.05	60.23	1.5	5.5	30	79.5	10.5	1.53	0.5	5	4.5	15	153	93.1	193	543	2.4
90	25003	8.2	3.86	20.4	60.23	1.53	5	35	102	17.5	1.91	0.5	6.25	4.5	33.5	161	101	200	552	2.5
91	26853	6.01	1.79	7.54	56.94	1.53	7.5	31.5	89	10.5	1.81	0.5	5.5	3.75	19	138	81.3	118	425	1.5
92	29537	6.65	2.6	11.56	56.94	1.56	6	22.5	83	13.5	1.89	1	6	3.75	19.5	138	81.3	166	543	2.1
93	25018	6.57	3.6	15.52	64.61	2.16	5	42.5	99.5	25.5	1.9	0.5	6	4.1	46.5	161	96.3	34	384	0.4

App. VIII. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
94	30015	9.15	3.39	20.06	64.61	1.41	5.75	35.5	109	26	2.19	1.5	7	4.5	32.2	161	96.3	169	637	2.1
95	219089	6.20	3.09	15.86	61.32	1.49	6.25	36.38	92	22.75	2.6	1	8.13	2.09	54.75	152.3	90.95	150	531	1.9
96	219355	8.09	3.05	17.51	61.32	1.95	6	33.5	98	9.75	2.08	0.75	6.63	1.9	21	152.3	90.95	130	495.6	1.6
Mean		6.8	3.02	13.95	59.78	1.52	5.4	32.84	90.2	13.6	2.26	0.83	5.83	3.98	29.19	154	94.27	145	544.6	1.81
CV		1.65	1.77	0.32	1.6	19.92	51.3	25.7	15.7	36.4	20.16	85.71	17.7	15.7	38.6	1.4	1.71	40.45	5.67	42.9
SE		0.11	0.05	0.05	0.95	0.3	2.77	8.44	14.1	4.95	0.45	0.71	1.03	0.63	11.25	2.16	1.61	58.7	30.91	0.78

Appendix IX. Mean performance analysis of nineteen traits of faba bean accession tested at Degerm during 2019 main cropping season

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
1	30011	6.72	2.8	13.1	56.5	1.57	4.5	29.15	82.5	13.5	2.24	1	6	4.1	33	157	103.5	109.5	630.5	1.37
2	30023	7.58	3.9	19.5	59.7	1.47	4.5	27.5	84.5	10.5	2.58	0.45	6.5	4.7	28	152.5	100.5	182.5	660.3	2.29
3	30008	6.42	2.6	11.4	59.7	1.94	4	30	83	14	1.71	0.95	6	4.1	24	160.4	100.1	134.8	613.1	1.69
4	28109	8.34	4	22	59.7	1.64	4.25	31	75	13	1.99	1.95	5	3.15	25.5	152.9	92.59	133	614.1	1.67
5	25264	4.95	1.9	6.6	59.7	1.49	4	24.5	81	10.5	2.43	0.95	5	3.5	26	153.9	93.59	108.6	496.1	1.36
6	29531	7.27	3	14.7	59.7	1.15	4.2	24.5	86	9.5	2.57	0	7.5	4.35	22.5	154.4	94.09	269	637.2	3.36
7	220079	5.9	2.5	10.1	59.7	1.5	3.45	21.45	87	13.5	1.96	0.95	4.9	3.65	25.5	154.5	94	124.4	401.5	1.56
8	28777	6.94	3.2	14.6	59.7	1.32	6.95	36.5	81.5	14.5	5.95	0.9	5.25	3.65	27.5	155	93.5	145.2	566.5	1.82
9	30022	4.45	1.8	5.83	60.2	1.45	4.4	40.5	94	7.5	2.46	0.5	6	3.3	17	153	93.5	100.8	641	1.26
10	26861	6.08	2.3	9.7	56.9	1.22	4.5	25.5	81.5	14.5	2.3	0.95	5.25	4	35.5	160.5	104.5	128.4	566	1.61
11	29526	7.63	3	14.9	56.9	1.16	6	27.5	84.5	14.5	2.18	1	6.5	3.95	31	153.4	96.3	141	495.6	1.77
12	27279	6.08	2.2	9.07	56.9	1.56	7	29.5	92.5	14	2.47	1	8	3.75	35	153.4	96.3	110	448.4	1.38
13	26859	7.03	3.1	14.3	56.9	1.69	4	34	80.5	12.5	1.71	0.5	5.5	3.1	20.5	160.9	103.8	94	424.8	1.18
14	26882	7.74	2.7	14	56.9	1	6	37	85	10	2.96	1.5	7.75	4.1	14.5	160.9	103.8	170	755.2	2.13
15	27931	7.14	3	14.2	56.9	2.09	4.75	41	110	24	2.01	1.5	4.5	3.75	48	153.4	96.3	194	566.4	2.43
16	220086	6.2	2.9	11.8	57.4	1.49	7	33	88.5	10.5	2.45	0.95	5	4.7	25	161.4	104.3	170	590.5	2.13
17	26862	6.13	3.1	12.7	57.4	1.4	5.25	38	95	8.45	2.69	0.45	5.25	3.9	21.95	161	104.5	153.4	543.5	1.98
18	25260	5.8	2.3	9.3	60.2	2.34	4.35	39.5	89.5	13.5	2.45	0.5	4.6	3.75	36.5	153.5	93	175.6	448	2.2
19	212580	6.6	3.3	14.2	60.2	1.44	4.4	27	86	18	2.58	1.95	5	4.05	46	153	93.5	146	424.5	1.83
20	25259	4.95	2.3	7.98	56.9	1.46	3.45	29.5	69	12.5	2.4	0.95	4.75	3.3	27.5	153	95	95.6	424.5	1.2
21	28110	5.94	3.2	12.5	56.9	1.64	5	37	96.5	20.5	2.71	1.5	6	4.85	48	160.9	103.8	200	590	2.51
22	28774	7.21	3.3	15.4	60.2	1.25	4.5	45	109	12	2.62	1	6	4	31	153.4	93.09	205.4	731.6	2.57
23	28771	5.94	2.4	9.77	60.2	1.21	4.5	41	89	10.5	2.58	1	7	4.35	27.5	153.4	93.09	127	542.8	1.59
24	28112	6.22	2.8	11.7	60.2	1.18	5.25	35	90	10	2.5	0.5	7.5	4.25	25	153.4	93.09	108	660.8	1.35

App. IX. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
25	26885	7.21	2.9	13.7	60.2	1.07	4.5	28.5	90	9	2.99	0.5	6.25	3.8	26.5	160.9	100.6	180	855.5	2.25
26	28776	5.44	2.7	9.98	60.2	1.24	4.45	36	81.5	9.9	2.13	0.5	4.9	4.2	20	160.5	100.5	57.6	598	0.72
27	26855	7.63	3.6	18.1	60.2	1.39	4.2	21.95	79	13.95	2.44	1.4	5.7	3.2	34.95	160.5	100.5	140.6	495.5	1.76
28	Dagim	5.97	2.8	11.1	64.6	1.46	4	37.5	77.5	10	1.79	0.45	3.75	3.7	16.5	153	88.5	80.8	397.5	1.01
29	Walki	7.98	3.2	16.5	60.2	1.3	3.8	44.5	102	11	2.04	0.45	5	4.5	22	153	93.5	154	660.5	1.93
30	29527	6.92	3.6	16.2	56.9	1.68	3.95	29.5	101	24.5	2.68	1.95	6.5	3.7	60	153.5	95.5	271.2	519.5	3.39
31	29532	6.86	3.5	15.7	56.9	1.3	4.75	25	85.5	15	2.75	1	6.25	3.75	39.5	153.4	96.3	280	708	3.51
32	28772	5.2	2.2	8.09	56.9	1.53	6	24.5	103	18.5	2.84	1.5	6	3.25	52	153.4	96.3	277	519.2	3.47
33	212572	8.34	3.5	18.8	56.9	1.74	5	36.5	96	20	2.2	0.5	4.1	3.9	32.5	153.4	96.3	170	542.8	2.13
34	26883	7.85	3.2	16.3	56.9	1.34	7.5	39.5	107	18.5	2.39	1	6	4.75	44	153.4	96.3	222	590	2.78
35	26888	6.45	3.3	14.1	56.9	1.65	6	27	71.5	20.5	2.43	2	5.25	4	49.5	138.2	81.32	138	424.8	1.73
36	212566	7.49	3.3	16.3	56.9	1.42	4.95	27	65	10.45	2.17	0.95	4.7	4.4	23.5	153	96	90.4	401	1.13
37	212567	5.65	2	7.77	56.9	1.48	3.95	33.5	75	11	2.49	0.5	4.2	3.5	28.5	153	96	119.8	401	1.5
38	229299	6.47	3	12.8	56.9	1.3	2.25	23.25	67	6	2.37	0	3.75	2.5	15.25	154	97	76	414	0.95
39	229871	6.01	2.6	10.7	64.6	1.71	3.95	42.25	92	17	2.09	0.95	5.25	4	33.5	153	88.5	135.6	560.5	1.7
40	212578	6.75	3.2	14.2	60.2	1.23	3.45	36	85.5	9.45	2.25	0.5	4.5	4.15	20	138	78	108	424.5	1.35
41	25009	5.12	2.3	8.32	64.6	1.56	5.5	34.5	91	9	2.71	0	5.5	3.9	24	153.4	88.81	117	519.2	1.47
42	26854	4.63	2.2	7.14	60.2	1.8	5.5	19	90	15	2.42	1	5.5	3.4	36.5	138.2	78.11	128	424.8	1.61
43	30014	6.92	3.3	15	56.9	1.49	6.5	34.5	109	16.5	2.39	1.5	5.75	4.5	40	160.9	103.8	111	519.2	1.39
44	Lalo	7.74	3	15.1	60.2	1.38	5.5	35.5	84	11	2.25	1	5.25	4.15	24	153.4	93.09	83	495.6	1.04
45	220076	6.08	2.4	9.98	64.6	1.8	4	32.5	75	14.5	1.74	1.5	4.75	3.5	23	153.4	88.81	55	448.4	0.69
46	26428	4.85	2.1	7.2	64.6	1.42	6.95	33.9	98.5	15	1.65	0.95	4.2	4.3	24.5	153	88.5	149.8	472	1.88
47	30021	7.56	3.3	16.2	60.2	1.21	5.4	21.5	89.5	5.5	2.54	1.45	6.5	3.8	15	153	93	74.6	595.5	0.94

App. IX. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
48	28770	6.01	2.8	11.4	60.2	1.49	4.45	40	99	12.5	2.55	0.5	5.5	4.4	28.5	153.5	94	124.8	484.5	1.56
49	Bulga-70	7.6	3	15.2	56.9	1.37	7.75	25	87.5	9	1.8	0.5	4.45	3.7	18	153	95	88.6	567.5	1.11
50	25006	8.69	3.4	18.9	56.9	2.05	3.7	38.5	98.5	23	1.65	0	3.45	3.95	37.5	153	96	175	424.5	2.19
51	25270	8.59	4.3	23.6	56.9	1.81	6.5	37.5	103	24	2.12	0.5	5	4	51	153.4	96.3	275	495.6	3.44
52	25310	7.56	2.8	14	56.9	1	5.5	34	96.5	5.5	2.98	1	5.25	4	17.5	153.4	96.3	161	536.9	2.02
53	26858	9.04	4.5	26.1	60.2	1.6	5.5	26	98.5	20	1.91	0.5	5.5	3.9	36.5	153.4	93.09	119	354	1.49
54	27052	9.33	3.8	22.5	60.2	2	4.5	43	109	19	2.5	0.5	5.5	3.9	49	153.4	93.09	153	424.8	1.92
55	208114	8.41	3.9	20.9	56.9	1.52	4.5	44	111	13.5	2.59	0	5.5	3.75	35	153.4	96.3	169	401.2	2.12
56	29535	6.57	2.3	10.4	64.6	1.33	4.4	32.45	92	9.5	3.23	0	6.45	4.55	29	138	73.5	139.6	542.5	1.75
57	29533	5.69	2.7	10.4	60.2	1.16	4.45	38.5	94	5.4	3.49	0.5	8.5	4	19	138	78	100.4	608	1.26
58	26887	5.16	2.4	8.52	60.2	1.34	5.4	36	99	14.5	1.99	0.5	7	3.95	28.5	161	100.5	108	653.5	1.35
59	229303	9.33	3.6	21.5	56.9	1.51	7.5	37.5	88.5	12.5	3.14	1.45	7	4.65	38	160.5	103.5	258.6	590.5	3.24
60	229869	6.44	3.4	14.3	60.2	1.42	4.05	25	89.5	11	2.14	0	4.75	3.9	23	153	93.25	150.6	377.5	1.89
61	235709	7.53	3.3	16	64.6	1.6	5.75	28	87	20.5	2.6	1.5	4.75	3.5	53.5	153.4	88.81	180	354	2.25
62	26886	5.41	2.7	10	60.2	1.22	4	40	106	11	2.15	0	6	4.25	23.5	160.9	100.6	147	613.6	1.84
63	16599	5.3	2.4	8.82	60.2	2.2	6	45	103	16.5	1.82	0	6	4.75	30	153.4	93.09	133	495.6	1.67
64	28103	7.21	3.1	14.6	56.9	1.44	6	19.5	84	16.5	2.41	1.5	6.5	4.4	40	153.4	96.3	150	828.4	1.88
65	29536	6.75	3.1	13.9	60.2	1.44	6.5	23.5	77	8	2.29	1.5	6.5	3.5	17.5	153.4	93.09	167	566.4	2.09
66	25303	6.36	3.7	15.5	64.6	1	4	22.5	76	6	2.1	1	6.5	4	12.5	153.4	88.81	93	590	1.17
67	25299	6.82	3	13.6	60.2	1.13	4.5	30.5	87.5	7.5	3	0.95	7	3.8	23	153	93	127	620	1.59
68	25022	8.48	4.5	24.5	64.6	1.88	5.5	30.5	81.5	19	1.59	0.45	3.95	3.4	29.5	153.5	89	82	401	1.03
69	Moti	6.39	3	12.9	60.2	1.54	4.5	39	103	12	1.84	0.95	9.5	4.5	21.5	153	93.5	154	833	1.93
70	208085	6.92	3.3	14.8	60.2	1.56	4	40.5	90	18	2.16	1.5	5	4.05	39	153.4	93.09	114	401.2	1.43

App. IX. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
71	25010	4.85	2.3	7.73	64.6	1.52	6.5	30	83.5	10	1.78	0	5.5	3.65	18	153.4	88.81	320	495.6	4
72	25298	6.75	2.7	12	60.2	1.22	7	17.5	78	11	2.44	1	6.5	3.75	20.5	153.4	93.09	106	554.6	1.33
73	27929	6.68	2.6	11.7	56.9	1.3	7.5	27	76.5	6.5	3.05	0.5	6.75	4.15	20	153.4	96.3	113	495.6	1.42
74	28773	6.22	3	12.3	60.2	1.72	7.5	45.5	86	8	2.47	1	7.5	5	19	153.4	93.09	188	637.2	2.36
75	30016	6.68	3.2	13.9	60.2	1.58	5.95	28.95	108	20.5	1.92	0.95	5.95	3.7	37.5	160.5	100.5	154.6	542.5	1.94
76	26860	5.86	2.2	9.01	60.2	1.9	3.95	52.5	118	15.5	2.04	0	5.5	3.9	31.5	161	100.5	129.6	566.4	1.62
77	25274	6.08	2.8	11.5	56.9	1.85	3.95	43.5	83.5	11.5	1.92	0	4.5	3.8	21.5	153	96.5	138.4	472.5	1.73
78	26889	8.73	3.9	21.7	60.2	1.69	6	22.5	78.5	17.5	1.65	1.05	5.5	2.9	30	138	78.5	146	425	1.83
79	229310	8.66	3.5	19.6	60.2	2.14	5.5	19.5	104	21.5	1.91	1.05	5.1	3.2	41.5	153	92.5	178.6	472.5	2.24
80	212565	7.42	3.4	16.3	60.2	1.75	4	34.5	78.5	15.5	2.07	2	4.5	3.75	34	153.4	93.09	133	472	1.67
81	Hachalu	6.18	2.4	10	60.2	1.5	6.5	43	114	15	2.1	1.5	8	5.5	30	160.9	100.6	211	873.2	2.64
82	231293	7.44	4	17.5	66.4	1.59	6.5	37	65	14	1.62	0.5	5	4.5	22	174.7	108.1	53	631.2	0.67
83	30017	7.07	3.4	15.7	60.2	1.18	6	32.5	118	17	1.89	1	7	4.5	34	153.4	93.09	258	755.2	3.23
84	25292	5.8	3	11.8	60.2	1.34	4.5	28	83.5	7	1.75	0.5	4.25	4.5	11.5	153.4	93.09	157	590	1.97
85	28113	8.38	4.3	23.2	60.2	1.71	5.5	29	113	16	1.7	0	5.8	3.9	29	153.5	93	60	590.5	0.75
86	25290	5.44	2	7.72	56.9	1.8	3.8	32.5	63	11	1.96	0	4.5	3.5	19.5	153	95	88.4	519.5	1.11
87	28104	7.32	2.6	12.8	64.6	1.45	6.5	34	88.5	8	2.59	0	6.95	4.7	16	153.5	89	99.6	833.1	1.25
88	26400	6.36	2.9	12.2	60.2	1.45	4.45	48.5	97.5	8.5	1.95	0.5	5	4.3	16	160.9	100.5	150.4	618	1.88
89	25017	8.2	4.4	23.1	60.2	1.5	5.5	30	79.5	10.5	1.53	0.5	5	4.5	15	153.4	93.09	193	542.8	2.42
90	25003	8.2	3.9	20.4	60.2	1.53	5	35	102	17.5	1.91	0.5	6.25	4.5	33.5	160.9	100.6	200	552.2	2.51
91	26853	6.01	1.8	7.54	56.9	1.53	7.5	31.5	89	10.5	1.81	0.5	5.5	3.75	19	138.2	81.32	118	424.8	1.48
92	29537	6.65	2.6	11.6	56.9	1.56	6	22.5	83	13.5	1.89	1	6	3.75	19.5	138.2	81.32	166	542.8	2.08
93	25018	6.57	3.6	15.5	64.6	2.16	5	42.5	99.5	25.5	1.9	0.5	6	4.1	46.5	160.9	96.3	34	383.5	0.43
94	30015	9.15	3.4	20.1	64.6	1.4	5.7	35	109	25.5	2.19	1.45	6.95	4.45	32.15	160.5	96	169.4	637	2.12

App. IX. Cont....

S/N	Accession	LL	LW	LA	DTF	NPPN	IL	LPH	PH	NPPL	NSP	NBPPL	PL	PW	NSPP	DM	SFP	SYPP	TSW	GY
95	219089	6.2	3.09	15.86	61.32	1.5	6.26	36.39	91.5	22.78	2.6	0.95	8.07	2.05	54.73	152	91	151	531.5	1.89
96	219355	8.09	3.05	17.51	61.32	1.96	6.5	33.55	98.5	9.78	2.1	0.76	6.57	1.95	20.5	152	91.5	130.6	495.6	1.64
Mean		6.8	3.01	13.94	59.75	1.52	5.38	32.86	90.27	13.64	2.3	0.81	6.18	3.94	29.22	153.3	94.29	145.4	544.6	1.82
CV		1.7	1.97	0.33	1.64	20.04	52.1	25.77	15.65	36.29	32.1	84.34	99.4	16.1	38.48	7.1	1.75	39.32	5.67	39.2
SE		0.12	0.06	0.05	0.98	0.3	2.81	8.47	14.13	4.95	0.74	0.68	6.14	0.64	11.24	10.89	1.65	57.17	30.9	0.71

Appendix X. Duncan's Multiple Range Test for the trait grain yield

Means with the same letter are not significantly different														
Duncan Grouping											Mean	Accession		
								A				2.88	29531	
								B				2.41	30017	
			C					B		D		2.24	29532	
			C					B		D		2.23	29527	
			C					B		D		2.21	229303	
			C					B		D		2.20	29537	
			C		E			B		D		2.18	26400	
F			C		E			B		D		2.15	28772	
F			C		E			B		D	G	2.05	219089	
F			C		E			B	H	D	G	2.00	25270	
F			C		E	I		B	H	D	G	1.98	29536	
F			C		E	I		B	H	D	G	1.98	26883	
F			C		E	I			H	D	G	1.97	Hachalu	
F			C		E	I	J		H	D	G	1.95	26889	
F			C	K	E	I	J		H	D	G	1.92	235709	
F	L		C	K	E	I	J		H	D	G	1.90	229310	
M	F	L	C	K	E	I	J		H	D	G	1.89	25274	
M	F	L	C	K	E	I	J		H	D	G	1.88	28773	
M	F	L	C	K	E	I	J		H	D	G	1.88	25010	
M	F	L	C	K	E	I	J		H	D	G N	1.88	26886	
M	F	L	C	K	E	I	J		H	D O	G N	1.86	219355	
M	F	L	C	K	E	I	J		H P	D O	G N	1.85	Walki	
M	F	L	C	K	E	I	J	Q	H P	D O	G N	1.82	25310	
M	F	L	C	K	E	I	J	Q	H P	D O	G N	1.81	30015	
M	F	L	C	K	E	I	J	Q	H P	D O	G N	1.81	28770	
M	F	L	C	K	E	I	J	Q	H P	D O	G N	1.81	26885	
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.80	Moti
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.80	25006
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.79	26860
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.79	29535
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.78	30016
M	F	L	C	K	E	I	R	J	Q	H P	D O	G N	1.78	229869
M	F	L		K	E	I	R	J	Q	H P	D O	G N	1.77	220086
M	F	L		K	E	I	R	J	Q	H P	D O	G N	1.77	208114
M	F	L	S	K	E	I	R	J	Q	H P	O	G N	1.73	26887

App. X. Cont....

Means with the same letter are not significantly different																						
Duncan Grouping															Mean	Accession						
M	F	L	S	K	E	I	R	J	Q	H	P	T	O	G	N	1.73	25017					
M	F	L	S	K	E	I	R	J	Q	H	P	T	O	G	N	1.73	28103					
M	F	L	S	K	U	I	R	J	Q	H	P	T	O	G	N	1.70	27931					
M	F	L	S	K	U	I	R	J	Q	H	P	T	O	G	N	1.70	220079					
M	F	L	S	K	U	I	R	J	Q	H	P	T	O	G	N	1.69	26853					
M	V	L	S	K	U	I	R	J	Q	H	P	T	O	G	N	1.67	26882					
M	V	L	S	K	U	I	R	J	Q	H	P	T	O	G	N	1.67	28774					
M	V	L	S	K	U	W	I	R	J	Q	H	P	T	O	G	N	1.66	26428				
M	V	L	S	K	U	W	I	R	J	Q	H	P	T	O	G	N	1.65	212567				
M	V	L	S	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.63	25299			
M	V	L	S	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.62	25003			
M	V	L	S	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.61	30023			
M	V	L	S	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.61	25260			
M	V	L	S	Y	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.60	29533		
M	V	L	Z	S	Y	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.59	25292	
M	V	L	Z	S	Y	K	X	U	W	I	R	J	Q	H	P	T	O	G	N	1.58	28110	
M	V	L	Z	S	Y	K	X	U	W	I	R	J	Q	H	P	T	O	A	N	1.56	25022	
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q	H	P	T	O	A	N	1.55	25303
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q		P	T	O	A	N	1.53	26855
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q		P	T	O	A	N	1.53	26861
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q		P	T	O	A	N	1.52	212565
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q		P	T	O	A	N	1.52	26862
M	V	B	L	Z	S	Y	K	X	U	W	I	R	J	Q		P	T	O	A	N	1.52	212572
M	V	B	L	Z	S	Y	K	X	U	W		R	J	Q		P	T	O	A	N	1.49	27052
M	V	B	L	Z	S	Y	K	X	U	W		R		Q		P	T	O	A	N	1.48	30022
M	V	B	L	Z	S	Y	K	X	U	W		R		Q		P	T	O	A	N	1.47	Dagim
M	V	B	L	Z	S	Y	K	X	U	W		R		Q		P	T	O	A	N	1.47	229299
M	V	B	L	Z	S	Y		X	U	W		R		Q		P	T	O	A	N	1.44	26888
M	V	B	L	Z	S	Y		X	U	W		R	C	Q		P	T	O	A	N	1.43	30008
M	V	B		Z	S	Y		X	U	W		R	C	Q		P	T	O	A	N	1.42	26854
	V	B		Z	S	Y		X	U	W		R	C	Q		P	T	O	A	N	1.41	25290
	V	B		Z	S	Y		X	U	W		R	C	Q		P	T	O	A		1.40	212580
	V	B		Z	S	Y		X	U	W		R	C	Q		P	T	O	A		1.39	28104
	V	B		Z	S	Y		X	U	W		R	C	Q	D	P	T	O	A		1.38	Bulga-70
	V	B		Z	S	Y		X	U	W		R	C	Q	D	P	T		A		1.38	28771
	V	B		Z	S	Y		X	U	W		R	C	Q	D		T		A		1.38	Lalo
	V	B		Z	S	Y		X	U	W		R	C	Q	D		T		A		1.36	229871

App. X. Cont....

Means with the same letter are not significantly different														Mean	Accession
Duncan Grouping															
V	B	Z	S	Y	X	U	W	R	C	Q	D	T	A	1.36	208085
V	B	Z	S	Y	X	U	W	R	C	Q	D	T	A	1.35	27929
V	B	Z	S	Y	X	U	W	R	C		D	T	A	1.33	25009
V	B	Z	S	Y	X	U	W		C		D	T	A	1.29	212566
V	B	Z	S	Y	X	U	W		C		D	T	A	1.29	212578
V	B	Z	S	Y	X	U	W	E	C		D	T	A	1.28	28113
V	B	Z	S	Y	X	U	W	E	C		D	T	A	1.27	30011
V	B	Z	S	Y	X	U	W	E	C		D	T	A	1.27	25259
V	B	Z	S	Y	X	U	W	E	C		D	T	A	1.26	29526
V	B	Z		Y	X	U	W	E	C		D	T	A	1.26	28777
V	B	Z		Y	X	U	W	E	C		D		A	1.25	28109
V	B	Z		Y	X	U	W	E	C		D		A	1.24	28112
V	B	Z		Y	X		W	E	C		D		A	1.21	16599
	B	Z		Y	X		W	E	C		D		A	1.19	28776
	B	Z		Y	X		W	E	C		D		A	1.19	30014
	B	Z		Y	X			E	C		D		A	1.16	25264
	B	Z		Y				E	C		D		A	1.14	220076
	B	Z						E	C		D		A	1.13	26858
	B	Z						E	C		D		A	1.12	27279
	B							E	C		D		A	1.10	231293
	B							E	C		D			1.09	25298
								E	C		D			0.96	30021
								E			D			0.93	26859
								E						0.83	25018

Appendix XI: Quantity and quality of genomic DNA extracted from faba bean accession

No.	Nucleic acid concentration (ng/ μ L)	260/280	Accession	No.	Nucleic acid concentration (ng/ μ L)	260/280	Accession
1	228.3	2.06	30011	49	216.1	2.07	Bulga-70
2	1564.7	2.09	30023	50	134.7	2.07	25006
3	275.2	2.05	30008	51	314.1	1.97	25270
4	782.7	1.95	28109	52	216.2	2.04	25310
5	379	2.06	25264	53	269.9	2.1	26858
6	1130.3	2.02	29531	54	284.9	2.08	27052
7	600.8	2.01	220079	55	375.7	2.07	208114
8	237	1.99	28777	56	476.2	2.01	29535
9	3504.4	2.1	30022	57	674.7	1.87	29533
10	260.2	2.08	26861	58	264.2	2.05	26887
11	998.5	1.93	29526	59	924.4	2.02	229303
12	671.6	1.98	27279	60	343.8	1.98	229869
13	553.8	1.99	26859	61	720.8	1.96	235709
14	693.4	2.01	26882	62	414.4	1.98	26886
15	972.9	1.99	27931	63	933.3	2.03	16599
16	838.4	2.04	220086	64	563.4	1.91	28103
17	578	1.9	26862	65	354.5	2.04	29536
18	764.6	1.87	25260	66	327.6	2.02	25303
19	428.6	1.76	212580	67	413.3	2.01	25299
20	1282.2	2.04	25259	68	416.7	1.98	25022
21	1023.8	2.07	28110	69	479.4	1.97	Moti
22	673.4	2.01	28774	70	321.3	2.06	208085
23	1260.3	2.1	28771	71	435.8	1.9	25010
24	1010.3	2.09	28112	72	568.5	2	25298
25	127.3	2.01	26885	73	1071.5	2.04	27929
26	848.2	2.07	28776	74	1157.9	2.05	28773
27	1536.9	2.09	26855	75	743	1.93	30016
28	1193.6	2.12	Dagim	76	1684.7	2.08	26860
29	2041.7	2.12	Walki	77	676	2.09	25274

App. XI. Cont....

No.	Nucleic acid concentration (ng/ μ L)	260/280	Accession	No.	Nucleic acid concentration (ng/ μ L)	260/280	Accession
30	1128.4	2.1	29527	78	213.9	2.02	26889
31	838.3	2.12	29532	79	1650.2	2.02	229310
32	1430.4	2.08	28772	80	1454.3	2.03	212565
33	1091.3	2.08	212572	81	882.7	2.04	Hachalu
34	1147.4	2.01	26883	82	866.2	2.05	231293
35	837.9	2.09	26888	83	1417.4	2.04	30017
36	890.7	2.09	212566	84	1788.3	2	25292
37	1406.2	2.15	212567	85	242.7	1.94	28113
38	1276.3	2.1	229299	86	1073	2.08	25290
39	613.6	2.02	229871	87	210.2	1.98	28104
40	494.3	2.03	212578	88	2163.6	2.1	26400
41	608.5	2.04	25009	89	327.7	1.84	25017
42	348.8	2.03	26854	90	152.5	2.02	25003
43	206	2.07	30014	91	1481.1	1.92	26853
44	503.2	2.04	Lalo	92	561.3	2.02	29537
45	351.3	2	220076	93	1204.4	2	25018
46	112.9	2.07	26428	94	1537.5	2	30015
47	406.9	2.03	30021	95	301	1.93	219089
48	438.5	2.05	28770	96	1794.2	2	219355