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GENOTYPE BY ENVIRONMENT INTERACTION AND STABILITY ON YIELD, YIELD COMPONENTS AND PROTEIN CONTENT OF FABA BEAN (Vicia faba L.) ACROSS FABA BEAN GROWING AREA OF ETHIOPIA

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M.Sc. THESIS

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THESIS APPROVAL SHEET

As member of the board of Examiners of Master of Science (M.Sc.) thesis open defense examination, we have read and evaluated this thesis prepared by Mr. **Gebeyaw Achenef** entitled **Genotype by Environment Interaction and Stability on Yield, Yield Components and Protein Content of Faba bean (*Vicia faba* L.) Across Faba bean Growing Area of Ethiopia**. We here by certify that, the thesis is accepted for fulfilling the requirements for the award of the degree of Master of Sciences (M.Sc.) in **Plant Breeding**.

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DECLARATION

This is to certify that this thesis entitled **Genotype by Environment Interaction and Stability on Yield, Yield Components and Protein Content of Faba bean (*Vicia faba* L.) Across Faba bean Growing Area of Ethiopia** submitted in partial fulfillment of the requirements for the award of the degree of Master of Science in **Plant Breeding** to the Graduate Program of College of Agriculture and Environmental Sciences, Bahir Dar University by Mr. **Gebeyaw Achenef** (ID. No. BDU1018508PR) is an authentic work carried out by him under our guidance. The matter embodied in this project work has not been submitted earlier for award of any degree or diploma to the best of our knowledge and belief.

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2) Muluken Bantayehu (Ass.Prof.) Co-advisor)

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GENOTYPE BY ENVIRONMENT INTERACTION AND STABILITY ON YIELD, YIELD COMPONENTS AND PROTEIN CONTENT OF FABA BEAN (*Vicia faba* L.) ACROSS FABA BEAN GROWING AREA OF ETHIOPIA

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ABSTRACT

Faba bean (*Vicia faba* L.) is an important cool season food legume belongs to fabaceae family. Twelve faba bean genotypes were evaluated in 2018/2019 cropping season across seven environments in Ethiopia using randomized complete block design with four replications. The objectives were to determine magnitude of genotype, environment and genotype by environment interaction and yield stability, identifying stable faba bean genotypes across the target environments. The Combined analysis of variance across locations was done using mixed model and the result showed that grain yield was highly significant difference ($p<0.01$) among genotypes, environments and G x E interaction. Environment explained 88.4% of the treatment variation whereas; G and G x E accounted 1.1% and 2.7% respectively. The mean grain yield of environments ranged from 950.5 kg ha^{-1} at Adet to 4509.3 kg ha^{-1} at Holetta. The highest yield was obtained from standard check Tumsa (3171.8 kg ha^{-1}) followed by G8 (EH 09017-5) and G6 (EH 010058-2) with mean grain yield 3125.3 kg ha^{-1} and 3081.4 kg ha^{-1}, respectively whereas, the lowest yield was obtained from G7 (2653.3 kg ha^{-1}). Eight stability parameters (ωi, σ^2, S^2di, bi, Pi, ASV, AMMI and GGE biplot) were employed to identify stable genotypes with high protein content and large seed size. The Pearson correlation showed highly significant positive rank correlation Pi ($r = 0.978$) between cultivar mean performance and mean grain yield and Shukula stability variance (σ^2) showed perfect ($r=1$) significant positive rank correlation with (ωi) hence, the two stability parameters were similar for ranking purposes. The application of AMMI and GGE biplot facilitate the visual comparison and identification of superior genotypes for supporting decision on variety selection and recommendation in different environments. AMMI model selected best genotypes that suit for a specific environment. Accordingly, G11, G8, G4 and G3 genotypes were selected as best for Assasa; G11, G3, G8 and G12 for Kulumsa; G12, G5 G1 and G8 for Bekoji; G12, G3, G8 and G5 for Adet and G12, G1, G4 and G5 for Debark. The stability parameters identified G8, G6 and G12 were stable and high yielder by most stability measures coupled with high protein content and large seed size. The polygon view of GGE biplot identified two mega environments E1 and E2 as one mega environment and G11 (EH 09046-3) was the vertex genotype. The second mega environment comprises E3, E4, E5, E6 and E7 and G12 (Tumsa) was the winning genotype. This indicated no single genotypes showed superior performance across all environments. Since the experiment was done only one year at seven environments, it has to be repeated in multi locations to provide more reliable results and make recommendations for wide or specific adaptable genotypes.

Keywords: AMMI, GGE Biplot, Environment, Rank correlation, Stability

ABBREVATIONS AND ACRONYMS

AEC	Average Environment Coordinate
AMMI	Additive Main effect and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	Additive Main effect and Multiplicative Interaction Stability Value
Bi	Regression coefficient
CSA	Central Statistical Agency
CV	Coefficient of Variability
FAO	Food and Agriculture Organization
GGE	Genotype plus Genotype by Environment interaction
GEI	Genotype by Environment Interaction
IBPGR	International Board of Plant Genetic Resources
ICARDA	International Center of Agricultural Research in the Dray Areas
IPCA	Interaction Principal Component Axis
MET	Multi-Environment Trial
MoA	Ministry of Agriculture
PCA	Principal Component Axis
Pi	Cultivar superiority performance measure
RCBD	Randomized Complete Block Design
SVD	Singular Value Decomposition
S^2di	Mean deviation from regression
Wi	Wricke's ecovalence
$\sigma 2$	Shukula stability variance

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CHAPTER1. INTRODUCTION

Faba bean (*Vicia faba* L.) belongs to the fabaceae family is an important cool season food legume. It ranks fourth in terms of total world grain legumes after pea (*Pisum sativum*), chickpea (*Cicer arietinum*) and lentil (*Lens culinaris*) (Kumar and Baum, 2018). Faba bean is commonly known as broad bean, horse bean and sometimes field bean. The crop is originated in Near Eastern but there are also evidences showed that for its multiple domestication and secondary centers of diversity are postulated to Afghanistan and Ethiopia (Veloso, 2016).

Currently, faba bean is a global legume grain crop concentrated in nine major agro-ecological regions with 4.7 million tons produced annually over 3.4 million hectares. The largest producers in the world are; China (1.4 Mt), Ethiopia (0.8 Mt), European countries (0.7 Mt; mainly France, U.K, Germany and Italy), Australia (0.3 Mt) and Morocco (0.2 Mt) (Puspitasari, 2017 and Yang *et al.,* 2017). The FAOSTAT (2016) report reveals, the productivity of improved varieties is very high (3.5 t/ha) compared to the country's national average yield (1.8 ton/ha).

In Ethiopia, faba bean is grown in almost all regions occupying 3.45% (437,106.04 hectares) from the total area (12.61%) allotted for pulse with 3.01% (9,217,615.35 quintals) out of the total annual pulse production in the country (CSA, 2018). It is manly cultivated by subsistence farmers on smallholdings in highland and mid-highland altitude areas of the country with altitude ranging from 1800-3000 m.a.s.l and receiving an annual rainfall of 700–1100 mm (Tekle Edossa *et al.,* 2016).

Faba bean is indispensible in every Ethiopian life due to its utilization in the principal dish of the peoples in the country. It is also an important protein complement in the cereal-based Ethiopian food, especially for people who have low level of income and cannot afford animal protein. Additionally, it also plays a great role in sustainable farming system of the country as low input "break" crop in cereals helps to ameliorate soil fertility relative to mono-culture of cereals (Tamene Temesgen *et al.,* 2015).

Genotype by Environment interaction refers to different ranking of genotypes across environments (Gauch, 2006). Crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of

environmental conditions. Evaluating genotypes under diverse environmental conditions to recommend new varieties for release as cultivars is fundamental and it has direct role on the adoption of a variety, productivity and total production of the crop (Eyeberu Abere, 2017). Genotypes grown in different environments would frequently encounter significant fluctuations in yield performance, especially when the growing environments are absolutely different among them, and the test genotypes differentially respond to changes in the growing environments (Alghamdi *et al.*, 2012).

Under the occurrences of frequent global climate change, besides the distribution and intensity of annual precipitation differs from one environment to another that makes the genotype x environment interaction effect became prominent in the world agriculture and in particular in Ethiopia (Eyeberu Abere, 2017). This condition triggers high incidence of biotic and abiotic stresses such as the incidence of disease or insect pests, variation on soil fertility, moisture stress etc. which are the main contributors of genotype by environment interaction and yield instability which is a common features in Ethiopia. This incidence also caused high yield penalty at household level especially in those areas where faba bean production prominently occur (Eyeberu Abere, 2017).

Knowledge on G x E interaction leads to successful evaluation of stable genotypes that could be used for wide verses specific adaptation. Moreover, to select a cultivar with high yielding ability and stability, high attention should be given to the importance of stability in performance for genotypes under different environments and their interaction (Ghazy *et al.*, 2012). Yield is a complex quantitative character and is greatly influenced by environmental variation therefore, selections based on yield *per se* at a single location in a year may not be effective (Eyeberu Abere, 2017). Hence, evaluating of genotypes across different range of environments and years helps to select either consistently yielding genotypes across environment and year (wide adaptation) or specifically best performing cultivars at few environments (specific adaptation).

Multi-environment trials (MET) also helps to identify locations that best represent the target environments (Yan *et al.*, 2000 and Fekadu Gurmu *et al.*, 2012). In plant breeding program yield stability is an important feature to measure consistence relative performance of genotypes across a wide range of environments. The relative performances of genotypes for quantitative traits i.e. yield and other characters were influence from one environment

to another (Fasahat P. *et al.,* 2015). The procedure of selection and recommendation of varieties for target set of environments became difficult when it is a "crossover" type of G x E interaction that makes the breeder job more complicated due to the differential genotypic responses that result in rank changes of genotypes across environments.

Despite many studies have been carried out on faba bean to evaluate effects of genotype by environment interactions on agronomic traits (Torres *et al.*, 2012; Zhou *et al.*, 2011; Tamene Temesgen, *et al.*, 2015; Temesgen Alene, 2015; Abdalla *et al.*, 2015), the information regarding the quality characteristics such as seed protein content and seed size is lacking. The purpose of this research activity was to understand how the grain protein and seed size vary across environments in order to provide information for the breeding program and the agricultural research in the faba bean production value chain. Therefore, this project was designed to evaluate the advanced faba bean genotypes for its stability of performance under diverse environmental conditions.

1.2 Objectives

1.2.1 General objective:-

To determine the magnitude of genotype by environment interaction, yield stability and their effect on grain yield and quality parameters so as to increase productivity of faba bean in Ethiopia.

1.2.2. Specific objectives**:-**

- To identify high yielding and stable faba bean genotype/s used to cultivate over wide range of environments.
- To identify faba bean genotypes with better grain quality characters to serve as parents in the future breeding program.
- To classify environments in to homogenous group based on the genotypes performance across environments.
- To identify ideal and desirable environments for variety evaluation.

CHAPTER 2. LITERATURE REVIEW

2.1. Origin and Domestication of Faba bean

Faba bean is an ancient crop and several studies have been investigated on its origin and domestication. According to Veloso, (2016), the best known species of the genus are V. faba (faba bean) and V. sativa and it's center of origin is Near Eastern with four different radiations; for Europe along the North African coast, to Spain; along the Nile, to Ethiopia; along from Mesopotamia to India. Secondary centers of diversity are postulated to have occurred in Afghanistan and Ethiopia (Veloso, 2016)

Surhan *et al.,* (2017) reported faba bean was domesticated in the Levant where archaeological evidence of its cultivation dates to the 10th millennium B.P. and its cultivation spread to Anatolia and then Europe via, the Mediterranean coast and China via Mesopotamia. Due to the high protein and starch content of its seeds, this legume has a vital role in the human diet especially in the Mediterranean region, the Middle East, North Africa, much of Asia, and Latin America (Surhan *et al.,* 2017). Although as several authors reported that the high rainfall regions of Central Asia and Mediterranean region have proposed as possible origin, the exact geographical origin of V. faba is still debated (Singh *et al.,* 2015).

2.2. Taxonomy and Reproduction of the Crop

Faba bean is grouped under Fabaceae family and it is an auto diploid plant with huge genome size (13000 Mega base pair) and fewer chromosome numbers (2n = 2x = 12) than other Vicia species (Hou *et al.,* 2015). The botanical classification of faba bean are; "major" (large-seeded or "broad" bean), "equine" (mid-sized or "horse" bean), and "minor" (small, rounded seed) types (Sullivan and Angra, 2016).

According to Singh *et al.,*(2015) the wild progenitor has not been found and major differences exist between V. faba and other species belonging to the Narbonensis complex (V. *narbonensis,*V. *galilea,* V. *johannis* and V. *hyaeniscyamus*) is with the chromosome number where *Vicia faba* has 2n = 12 and 2n = 14 for species of the Narbonensis complex. That is why all attempts at inter-specific hybridization between *Vicia faba* and these other species have been failed due to ovules that stopped to develop or due to aborted embryos (Puspitasari, 2017).

Vicia faba paucijuga is a subspecies, presently found from Afghanistan to India, is a primitive form. The main description of this ancestor are short stem, small leaves, very small seed (1000 seed weight lower than 250g) and partially autogamy, large seeded types (*Vicia faba* major) with 1000 seed weight greater than 1 kg have developed in South Mediterranean countries and China (Singh *et al.,* 2015).

The large seeded type expanded in the 16th century toward Mexico and South America. The small seeded types with 1000 seed weight less than 500g (*Vicia faba* minor) are found in Ethiopian and have been favored by North European agriculture. Medium seeded types (*Vicia faba* equina) have developed throughout Middle-East and North Africa with major concentration in Egypt. Therefore, Singh *et al.,* (2015), argued there are four equivalent subspecies of *Vicia faba,* those are paucijuga, minor, equina and major.

Faba bean is an entomophilous plant and the flowers are usually visited by pollinating insects, such as honey bees (*Apis mellifera*), bumble bees (*Bombus* sp.) and solitary bees (Puspitasari, 2017). Both self and cross fertilization can occur in the same plant. Cross-fertilization fully depends on pollinator activity while self-fertilization occurs by pollinators or by spontaneous selfing. The rate of cross-fertilization is varying from about 45–60% and depends on genetic and environmental factors. Self-fertilization happening without pollinators or without external mechanic stimulus in faba bean referred as auto-fertility (Puspitasari, 2017).

2.3. Ecological Adaptation of the crop in Ethiopia

The faba bean crop is grown in Ethiopia in the high and mid altitude areas of the country. The high altitude area is characterized with an altitude range above 2200 m.a.s.l that received an average annual rainfall of 900 mm with the mean daily temperature of 10-18ºC whereas the mid-altitude (Weyna dega zones) characterized with altitude range of 1800-2200 m.a.s.l and received 740 mm of rainfall annually with mean daily temperature of 18-22 ºC (Asfaw Tilay *et al.,* 1994). According to Belachew *et al.,* (2017) faba bean grows best in soil with the pH ranged from 6.5 to 9 during June to December in rotation with the cereals and help as a break crop in the agriculture system of the country. The crop is mainly cultivated under the rain fed condition by the farmers.

2.4. Production, productivity and Economic Importance of Faba bean

Faba bean ranks fourth in terms of total world grain production after pea (*Pisum sativum*), chickpea (*Cicer arietinum*) and lentil (*Lens culinaris*) (Kumar and Baum, 2018). The largest producers in the world are; China (1.4 Mt), Ethiopia (0.8 Mt), European countries (0.7 Mt; mainly France, U.K, Germany and Italy), Australia (0.3 Mt) and Morocco (0.2 Mt) (Puspitasari, 2017). According to FAOSTAT (2014) report the productivity of faba bean in major producing countries ranged from 2.8 to 4.3 tons ha^{-1} where Germany (4.3 tons ha^{-1}), France (3.7 tons ha^{-1}) and Australia (2.8 tons ha^{-1}) reached the climax. The same report also showed Ethiopia is the leading producer of faba bean in Africa and covers about 56% of the production in Africa. Among the pulses grown in Ethiopia, faba bean accounted for 3.45% area of production (about 437,106.04 hectares) (CSA, 2018). The productivity of the crop under smallholder farmers is not more than 1.89 tons ha^{-1} (CSA, 2015), despite the potential of the productivity of high yielding varieties (> 2.0 tons ha^{-1}) (MOA, 2011).

In terms of agricultural importance, a legume crop comes second to cereals as a source of human food and animal feed. Among food legume crops faba bean represent an important component of agricultural food crops consumed in developing countries and it is considered as essential crop to attain food and nutritional security for both poor producers and consumers. As a result, in dietary terms, food legumes complement cereal crops as a source of protein and minerals whereas, in agricultural production, it serve as rotational crop with cereals that helps to reduce soil pathogens and supply nitrogen to the following crops (Dyke and Prew, 1983).

According to Gowda *et al.,* (1997) faba bean serve as a feed crop in many farming systems and achieve higher prices compared to cereals and it's increasingly grown to supplement farmers' income. The important and diverse role played by faba bean in the farming systems and in foods of poor people, makes it an ideal crop for reducing poverty and hunger, improving human well-being, nutrition and enhancing ecosystem recover. Its' importance as food crop lies primarily high in its protein content. Faba beans' grain protein is the natural supplements to cereal grain protein. It also provides fat, carbohydrate, bone building minerals and vitamins essential for good health.

Faba bean is indispensible in every Ethiopian life. It is mainly used as an alternative with pea to prepare flour called *"shiro"* which is used to make *"shiro wot"* (mainly available

almost in all Ethiopian dishes). Faba bean has several important contributions including high nutritional value, long storage times and relatively least cost in comparison to animal products. It plays an important role in protein, energy and micronutrient provision to populations in the developing world (Dilis and Trichopoulou, 2009).

It also serves as source income for farmers and earning foreign currency to the country. It reduces cost of fertilizer for the following cereal crop production for smallholder farmers by adding nitrogen. Currently biological nitrogen fixation of faba bean becomes more important, because of the depletion of fossil fuel and increasing environmental deterioration in the world, it is renewable, clean and environment friendly compared with industrially produced nitrogen fertilizer (Jensen and Hauggaard, 2003).

2.5. Genotype by Environment Interactions

Genotype-by-Environment interaction (GEI) refers to the change or modification of genetic factors by environmental factors and to the role of genetic factors in describing the performance of genotypes in different environments (Dia *et al.*, 2016). The association between the environment and the phenotypic expression of a genotype constitute the G X E interaction. The G X E interaction determines if a genotype is widely adapted for an entire range of environmental conditions or separate genotypes must be selected for different sub- environments. When G X E interaction occurs, factors present in the environment (temperature, rainfall, etc.) as well as the genetic constitution of an individual (genotype), influence the phenotypic expression of a trait. The impact of an environmental factor on different genotypes may vary implying that the productivity of an animal or plant may also vary from one environment to the next. Therefore, the breeding plans may focus on the G X E interaction to select the best genotype for a target population of environments (Bondari, 2015).

Breeders and genetists developed continually endeavor to enhance the genetic base of crop species and prevent problems related with genetic vulnerability. With emphasis on enhancing the genetic base and unpredictable climatic factors encountered at different sites and/or years, differential responses are expected of improved cultivars-strains in different environments. These differential genotypic responses to different environments are collectively called genotype-by-environment (GE) interaction (Kang, 1998).

Genotype-environment interaction is one of the major crucial issues to the plant breeder in developing improved varieties (Eberhart and Russell, 1966). When varieties are compared over a series of environments, the relative rankings usually differ. This causes difficulty in demonstrating the significant superiority of any variety. This interaction is usually present whether the varieties are pure lines, single-cross or double-cross hybrids, top crosses, lines, or any other material with which the breeder may be working (Kang, 1998).

The above reports showed how the genetic x environment interaction is important and essential in any breeding program. Since the G X E interaction effect is complicated, to study the effect requires the integrated approaches of various scientific fields including agriculture, biology, statistics, computer and genetics (Zelalem Tazu, 2011 and Bondari, 2015).

2.6. Effects of Genotype and Environment on Yield

Cultivar performance is a function of genotype, and the nature of the production environment (Abel Moges, 2017). Environment factors have a larger effect on quantitative traits, as a result of which performance tests of potential cultivars are conducted in multiple year and locations. In addition to genotype and environment main effects on the performance of genotypes are also determined with G x E interaction, which is differential response of genotypes to environmental changes (Crossa *et al*., 1990). High seasonal variability influence on yield is common in pulse crops due to pollination deficiency, water stress, competition from vegetative sinks, and losses due to diseases. The occurrence of such variability makes it difficult to predict ideal genotypes for both maximal yields in favorable seasons and stable yield under environmental stress conditions (Abel Moges, 2017).

High genotype x environment interaction mean the lack of stability in quantitatively inherited traits, and this is a challenging problem especially in areas with unpredictable environmental factors. The genotypes differ both in their yield potentials and in the degree of environmental elasticity. Therefore, testing a range of genotypes under representative multiple environments enables identify genotypes with relatively high mean yields and minimal environmental variances. Tekalgn Afeta (2017) conducted multi location trial of faba bean genotypes to determine GEI for grain yield. The result showed GEI effect was

significant and the difference in performance of genotypes in different environments indicated the effect of significant GEI for the expression of the character.

2.7. Effects of G X E Interaction on Protein Content

Protein content in grain legumes is strongly influenced by the environment (Burstin *et al.,* 2007). In pea, Mathews and Arthur (1985) underlined the importance of the environmental effects on protein content than genetic effects in 255 genotypes. Gueguen and Barbot (1988) found protein content varying from 18.1 to 27.8% for cultivar Amino depending on the environment.

Environmental variability is probably caused by several factors. Karjalainen and Kortet (1987) showed that protein content was positively associated with the sum of temperature from sowing to maturity and especially during flowering and beginning of seed filling. Larmure *et al.,* (2005) further specified the effect of temperature during seed-filling on seed protein content through its effect on N/C ratio. All environmental factors that impact nitrogen nutrition, such as drought stress, soil compacting, root diseases and pests may also influence seed protein content through their impact on nitrogen availability (Biarnès *et al.,* 2000).

Genotype-by-environment effects are also usually significant even though often of lower magnitude (Burstin *et al.,* 2007). As a result seed protein content heritability values are very variable across experiments depending on the extent of genetic variability analyzed, unpredictable environment variation and experimental design. Despite significant influence of environment and the presence of frequent genotype-by-environment interactions, seed protein content heritability is generally moderate to high this suggesting that, selection of cultivars for protein can be successful by considering the effect of genotype environment and their interactions.

An average range given for world faba bean protein content from various sources is close to each other: 22-37% (Monti and Grillo, 1983), 26-41% (Picard, 1977), and 23-39% (Hulse, 1994). In Ethiopia, figures for protein contents are much lower than those give elsewhere it is generally between 22 and 29%. Here, protein content seems to vary with altitude, being higher at mid-altitude than at high altitude areas (Youhans Degago, 2000). Food legumes in general and faba bean in particular are nutritionally complementary to the cereal food system in that the essential amino acids that are deficient in one may be

provided by the other. Faba bean contains relatively large amount of lysine and cereals have great amount of Sulphur containing amino acids i.e. methionine and cysteine.

2.8. Concept of Stability

The plant breeder is always interested in the stability performance for the characters, which are of economically important. The desirable genotype should have low G x E interactions for important characters to get the desirable performance of genotypes over wide range of environmental conditions. Genotype x environment interactions are of common occurrence and often creates manifold difficulties in interpreting results and thus hamper the progress of breeding programs (Zakir, 2018).

Tewodros Mulualem and Zelalem Bekeko (2017) explained that, stability usually refers to a genotype's ability to perform consistently whether at high or low yield levels across a wide range of environments. Therefore, stability analysis provides a general summary of the response patterns of genotypes to change environments or the interaction of genotypes with locations and other agro-ecological conditions that help in getting information on adaptability and stability of performance of genotypes (Abuali *et al.*, 2014). Although the terms of phenotypic stability, yield stability and adaptation are often used in quite different senses, an ideal genotype should have both high mean yield performance and high stability across environments (Zakir, 2018).

Most stability measures relate to either of two contrasting concepts of stability: "static" (Type-1) and "dynamic" (Type 2) (Becker and Léon, 1988; Lin *et al.*, 1986). Similarly Alberts (2004) describe stability as static or biological and dynamic or agronomical stability. In terms of static or biological stability; a genotype is considered to be stable if it's among environment variance is small. A stable genotype possesses consistence performance regardless of any environmental variations. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness. The parameters used to measure this type of stability are coefficient of variability (CVi) and the genotypic variances across environments (Si^2).

A genotype is considered to be stable if its response to environments is parallel to the mean response of all genotypes in the trial. Albert called this stability the dynamic or agronomic concept of stability. A stable genotype has no deviations from the general response to environments and thus permits a predictable response to environments. A

regression coefficient (bi) (Finlay and Wilkinson, 1963) and Shukla's (1972) stability variance (σ^2_i) can be used to measure type 2 stability. The other stability definition, if the residual mean square (MS) from the regression model on the environmental index is small. The environmental index implicates the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. This is also part of the dynamic or agronomic stability concept (Alberts, 2004).

2.9. Statistical Methods to measure G X E Interaction and Stability

Genotype-by-Environment (G × E) interaction analysis is an important prerequisite for recommendation of novel selections for large-scale production. It enables assessment of the relative performance and stability of genotypes for yield and yield-related traits since, the performance of tested genotypes is influenced by the genotype, the environment, and G × E interaction (Horn *et al.*, 2017).

Yield trial, typically testing a number of varieties in a number of environments, is one of the most common activities in agricultural research. Accordingly, statistical analysis of yield trials can help agronomists, breeders, and other agricultural researchers to make faster progress (Gauch, 2006). Since the most stable genotype(s) may not be the highest yielding, the use of methods that integrate yield performance and stability to select superior genotypes becomes important. Many stability statistics have been used to determine whether or not cultivars evaluated in MET are stable (Tekelign Afeta, 2018). Those different statistical methods that have been proposed for the estimation and partitioning of G x E interactions can be broadly categorized into four groups: the analysis of components of variance, stability analysis, multivariate methods and qualitative methods.

If relative performances of cultivars grown in different range of environments are different, the G X E interaction becomes a major challenging factor to crop breeding programs. Several statistical methods have been widely adapted to analyze and interpret G × E data to reveal patterns of GEI, such as joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966;), sum of squared deviations from regression (Eberhart and Russel, 1966), stability variance (Shukla, 1972), stability ecovalence (Wi^2) proposed by (Wricke, 1962); combined analysis of variance (ANOVA) to quantify G X E interactions that describe the main effects Genotype (G) and environment (E) but this did not provide enough information to explain the interaction effect (Dagnachew *et al.*, 2014).

2.9.1. Analysis of variance (ANOVA)

The classical method of summarizing the variation in response of a number of varieties grown in different environments by partitioning the sum of squares into components due to varieties, environments and variety-environment interaction convey little information on the individual patterns of response. Further partition of the interaction sum of squares by grouping varieties or environments may help to identify major sources of interaction in the data, but when such groupings are achieved they are often difficult to interpret biologically and not repeated in subsequent years (Kempton, 1984).

In a conventional cultivar evaluation trial in which the yield of genotypes (G) is measured in environments (E) over replicates (R), the classic model to analyze the total yield variation contained in a GER observation is the analysis of variance (Crossa, 1990). The within environment residual mean square measures the error in estimating the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another. After replicate effects are removed when combining the data, the G x E observations are partitioned into two sources: additive main effects for genotype and the non-additive effect due to G x E interaction (Agegnehu Mekonen, 2017). The analysis of variance of the combined data expresses the observed (Yij) mean yield of the i^{th} genotype at the j^{th} environments as:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$$

Where, **μ** is the general mean, $\mathbf{G_i}$, $\mathbf{E_j}$, and $\mathbf{GE_{ij}}$ are the effect of the genotype, environment, and genotype by environment interaction, respectively and **eij** is the average of the random errors associated with the r^{th} plot that receives the i^{th} genotype in the j^{th} environment. The non-additive interaction (GE_{ij}) as defined in the above equation implies that an expected value (Y_{ij}) depends not only on the level of G and E separately, but also on the particular combination of levels of G and E (Crossa, 1990).

2.9.2. Wricke's Stability

Wricke's stability measure assumes the contribution of each genotype to the G X E interaction sum square as a stability measures. Castelo *et al.*, (2016) discussed and supported the idea of Wricke, (1962). To evaluate the stability by using the dynamic concept based only on ANOVA components, the Wricke (1962) methodology where popularly known as "Ecovalence" (Wi) is the important one. The parameter is estimated

by the decomposition of the sum of squares of the G x E interaction (quite similar to the model of Plaisted and Peterson, which in turn proposes the decomposition of variance of the G x E interaction) in parts related to genotypes in an isolated manner and this method is proposed to use the sum of square of the GE as follows;

Population effects $\boldsymbol{\omega}=\sum g^{2}_{ij}$ and a sample estimated as;

$W_i = \sum_{j=1}^{q}(Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.J}} + \overline{Y_{..}})$ Where, Y_{ij} is the response of genotypes in the j^{th} location, $\overline{Y_{i.}}$ is the mean of the genotypes Y across locations, $\overline{Y_{.J}}$ the mean of the genotypes in j location and $\overline{Y_{..}}$ the grand mean. This equation implies the amount of sum of square represent by the i^{th} genotype to the sum of squares of the GE interaction effects. If $\boldsymbol{\omega_i}= 0$, the genotype is considered stable and if it is greater than 0 the genotype is considered unstable. This parameter also called ecovalency, and referred to it as genotype ability to answer to environmental changes.

2.9.3. Shukla's Stability Variance

Shukla (1972) proposed the variance component of each genotype throughout the environments is another related measure of phenotypic stability. Shukla defined the concept of stability variance as an unbiased estimate of the variance of genotype **i** across environments after the removal of environmental main effects. Since the genotype main effect is constant, the stability variance is thus based on the residual (GEij+ eij) matrix in a two way classification.

A genotype is stable if its stability variance (δ_i^2) is equal to environmental variance (δ_0^2) which means that δ_i^2=0. Relatively large value of (δ_i^2) will thus indicate greater genotype (i) instability. As the stability variance is the difference between the two sums of square; it can be negative but negative estimate of variance are not uncommon in variance component problems. Negative estimate of (δ_i^2) may be taken as equal to zero **(** Purchase, 1997).

2.9.4. Stability Parameters based on regression approach

The genotype-environment interaction is partitioned into a component due to linear regression coefficient (b_i) of the i^{th} genotype on environmental mean and a deviation (d_{ij}) (Crossa, 1990). When analyzing variety trials it is more usual to regresses the response of

a variety on to the mean response of all varieties in each environment rather than use an independent environmental score (Finlay and Wilkinson 1963, Kempton 1984).

Various attempts were made to characterize the behavior of genotypes in response to varying environments and the detailed discussion on G X E interaction and stability analysis are given by (Becker and Leon, 1988; Castelo *et al.,* 2016; Crossa, 1990 and Zobel *et al.,* 1988). There are direct relationships among many of the analytical methods used to analize genetic varation and genotype by environment interction in plant breeding.

According to Finlay and Wilkinson 1963, linear regression models used to compare the performance of a set of varieties evaluated in multiple sites and years in which, for each variety, a regression of their mean was obtained regarding the overall mean of all varieties in each site per year. The yield of each genotype is plotted against the mean yield of each environment and in which each genotype is represented using a fitted straight line.

In addition, each environment was classified as favorable or unfavorable according to the mean of all varieties in that environment. These authors have modeled environmental factors, simply in terms of the productivity response of genotypes. Thus, the varieties that have regression coefficients equal or close to one are considered varieties of mean stability. Among these, those that are associated with a high productivity have broad adaptation, and those associated with low productivity are weakly adapted to all environments. Varieties with coefficient significantly greater than 1.0 are considered especially adapted to favorable environments, but have low stability, and those which have coefficient lesser than 1, or tending to 0, are considered more stable and with adaptability to unfavorable environments.

Eberhart and Russell (1966) were improved the previous gap and proposed the use of the regression coefficient and the deviations from the straight line as parameters of stability aimed at helping to solve this problem. Introducing one more parameter, which accounts for unpredictable irregularities in response of genotypes to varying environments measured as the deviation from the regression (S^2di) lines, to characterize stable genotypes. According to Eberhart and Russell, sum of the mean square attributable to environments and G x E interaction is partitioned in to three components Environments (Linear), G x E (Linear) and (S^2di) (pooled deviation all over the genotypes). Values of bi close to 1 indicate a relatively stable genotype this definition is in accordance with the

dynamic concept, but, which tends to vary less with environmental change. A stable genotype is, thus, characterized by regression coefficient bi close to 1, and deviation from regression close to zero and those significantly deviating from unity (Eberhart and Russell 1966).

2.9.5. Additive Main effects and Multiplicative Interaction (AMMI) model

The Additive Main effects and Multiplicative Interaction (AMMI) model combines analysis of variance for the genotype and environment main effects with principal component analysis of the genotype-environment interaction which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model (Zobel *et al.*, 1988 and Kaya *et al.*, 2002).

The AMMI model first applies the additive analysis of variance (ANOVA) model to two-way data, and then applies the multiplicative principal components analysis (PCA) model to the residual from the additive model, that is, to the interaction (Gauch, 2013). It has proven useful for understanding complex genotype-environment interactions. The results can be graphed in a very informative biplot that shows both main and interaction effects for both genotypes and environments. Also, AMMI can partition the data into a pattern-rich model and discard noise-rich residual to gain accuracy (Hühn, 1996).

The AMMI methodology uses singular value decomposition (SVD) multivariate technique to reduce the information contained in a data array n x m (genotypes and environments, respectively) in vectors that accumulate, in a systematic manner (in order of importance), the greater part of variation contained in the data and, consequently, in G x E interaction. Since its disclosure, this methodology has been widely used for studies on adaptability in several important cultivated species such as wheat (Kempton, 1984; Gauch, 1988; Lule, *et al.*, 2014; Horn *et al.*, 2017; .Zobel *et al.*, 1988). The AMMI model is;

2.9.6. AMMI Stability Value

Another approach called the AMMI stability value (ASV), which is based on the first and second interaction principal component axis (IPCA) scores of the AMMI model for each genotype, has also been developed more recently and used by Tamene Temesgen *et al.*, (2015) to study the stability of faba bean genotypes in Ethiopia. ASV measures the distance from the genotype coordinate point to the origin in a two-dimensional scatter diagram of IPCA2 against IPCA1 scores. Genotypes with the lowest ASV values are

identified by their shortest projection from the biplot origin and considered the most stable.

2.9.7. Genotype plus Genotype by Environment Interaction (GGE) biplot

A biplot is a scatter plot that graphically displays a two-way data set by both factors in such a way that relationships between these factors can mask the real performance of the individual genotypes. GGE biplot analysis considers both genotype (G) and GE interaction effects and graphically displays GE interaction in a two-way table (Yan *et al*., 2000). Recently, the extensive usefulness of the GGE (genotype main effect (G) plus G x E interaction) biplot model provides breeders a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments.

The GGE biplot can be useful to display the which-won-where pattern of the data that may lead to identify high-yielding and stable cultivars and discriminating and representative test environments (Yan *et al.,* 2001). GGE biplot is an effective method based on principal component analysis (PCA) to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions. According to Yan and Hunt (2002) the polygon view of the GGE biplot indicates the best genotype(s) in each environment and group of environments. The polygon is formed by connecting the markers of the genotypes away from the biplot origin where all other genotypes contained within the polygon. The rays are lines that are perpendicular to the sides of the polygon or their extension (Yan and Kang, 2003).

2.10. G x E Interaction in Faba bean and other Legumes

Under Ethiopian condition, information regarding to G x E interaction in faba bean is lacking. Hence, information related to this work has been gathered in other Ethiopian pulse crops (Tamene Temesgen *et al.,* 2015; Abdalla *et al.*, 2015; Tezera Wallabo, 2000; Nleya *et al.,* 2000). Genotype × environment (G × E) interaction is of major importance for faba bean breeders, given that phenotypic response to change in environment is different among genotypes (TameneTemesgen *et al.,* 2015). They also have reported high G × E interaction effects in faba bean genotypes grown in Ethiopia particularly on quantitative traits such as seed yield that severely limit gain in selecting superior genotypes to speedup improved cultivar development process. For cultivars being selected

for a large group of environments, evaluating stability of performance and range of adaptation has become increasingly important.

According to Abadala (2016) yield instability is more common in faba bean than in most other crops. This may be due to its sensitivity to the environment in addition to the effects of various biotic limitations. Therefore, the author suggested tests of stability require trials over a number of seasons and/or locations (environments within the seasons). Similarly Temesgen Alene (2015) studied the genotype × environment interaction and stability of eight released varieties with local check across variable environments. All results proved that genotype × environment interaction play an important role in the productivity of faba bean genotypes. Hence, this test should be involved before recommending the genotype for particular environment(s).

Mussa and Yohanse (1997) reported significant differences among faba bean genotypes along with G X E interaction at three locations for three consecutive years. Stability analysis further showed that, non-significant differences among regression coefficients (bi) of various varieties studied for grain yield but deviation from regression (S^2di) was significant for eight of the genotypes showing their instability over environmental changes.

Abdalla *et al.,* (2015) revealed that environment, line or genotype and their interaction had a highly significant effect on mean number of pods per plant, number of seed per pod and 100 seed weight over the three consecutive seasons. In the meantime they also identified number of pod per plant and 100-seed weights were the most important contributors for seed yield.

Zhe *et al.,* (2010) also studied the effects of Genotype × Environment interaction on agronomic traits in Soybean and the significant influence of Genotype × environment interaction some agronomic traits. Furthermore, they also found the stable and suitable genotype for respective environment using "Which-won-where" analysis of the biplots for yield, protein, oil, and fatty acid. Similarly Nleya *et al.,* (2000) reported the protein concentration in faba bean seeds is influenced by Genotype (G), year (Y) and location (L) the grate part of the variation in protein concentration among faba bean genotype is due to heritable factors (Nleya *et al.,* 2000) Significant G x E interaction effects for protein of faba bean seed may occur (Picard, 1977) however, both reports conclude that the variation

due to G x E interaction was far smaller than variation due to genotype hence no important change in ranking of genotypes occurred in different environments.

Fekadu Gurmu *et al.,* (2012), explained that, GGE-biplot is among the best statistical methodologies that are used to analyze G x E interaction and graphically present the nature of G x E and stability of cultivars evaluated in a multi-environment trial. They found highly significant interaction effects, for G x L and L x Y. From the total variation the location contributed a much larger variation (80.5%) followed by genotype (11.1%) and GL interaction (5.0%).

Genotype x Environment interactions (GEI) has a major importance, because it provide information about the effects of different environments on cultivar performance and play a key role for assessment of performance stability of the breeding materials (Karadavut and Çetin Palta, 2010). GEI is the differential response of genotypes evaluated under different environmental conditions. It is a complex phenomenon as it involves environmental (agro-ecological, climate and agronomic) conditions and all physiological and genetic factors that determine the plant growth and development.

CHAPTER 3. MATERIALS AND METHODS

3.1. Descriptions of Experimental Area

The experiment was conducted at seven different locations from June to December, 2018 in the main cropping season under rain fed condition. These locations represent the varying agro ecologies of the major central faba bean growing areas of Ethiopia. The description of the test locations in terms of geographical position, altitude and climatic conditions and soil properties is given in Table 3.1

Table 3. 1. Summary of Experimental Locations

	Geographical position		Altitude	average	Temperature		agro-	Soil
Locations	Latitude	Longitude	m.a.s.l	rainfall	Min.	Max.	ecology	type
Asassa	07°06′12″N	39°11′32E	2300	620	5.8	23.6	THMH	Clay
Kulumsa	08°01′00″N	39°09′32E	2200	820	10.5	22.8	TSMMH	Clay
Bekoji	07°31′22″N	39°14′46E	2780	1010	7.9	16.6	CHMH	Clay
Holeta	09°04′12″N	38°29′45E	2400	1044	6.05	22.4	TMMH	Nitosol
Kofele	07°04′27″N	38°46′45E	2660	1211	7.1	18.0	CHMH	Nitosol
Debark	130 7’ N	37053’E	2900	1044	8.6	19.8	CHMH	Nitosol
Adet	110 16’ N	372 29’E	2240	1119.1	11.8	25.8	THMH	Nitosol

THMH: Tepid Humid Mid-Highland; TSMMH: Tepid Sub Moist Mid-Highland; CHMH: Cool Humid Mid-Highland; TMMH: Tepid Moist Mid-Highland.

3.2. Description of Experimental Materials

A total of twelve faba bean genotypes that comprise ten advanced breeding lines and two recently released varieties (standard checks) were used for field experiment. The list of genotypes, pedigree information and their code were described in Table 3.2

Table 3.2. Descriptions of Experimental Materials

Codes	Genotype	Pedigree
G1	Gora (standard check)	EH91020-8-2 X BPL44-1
G2	EH 010002-1-1	EH00126-1 X ILB938
G3	EH 010008-5	EKLS/CSR02017-1-4 X ILB938
G4	EH 010051-1	EKLS/CSR02018-1-1 X ATOM
G5	EH 010058-1	EKCSR/01004-2-1 X ATOM
G6	EH 010058-2	EKCSR/01004-2-1 X ATOM
G7	EH 09012-1	EH95132-1 X ILB938
G8	EH 09017-5	EH00014-1 X ILB4726
G9	EH 09021-1	EH01012-1 X ILB4726
G10	EH 09028-3	Wolki X ILB4726
G11	EH 09046-3	Wolki X ILB1563
G12	Tumsa (standard check)	Tesfa X ILB4726

3.3. Experimental Design and Procedure

The experiment was laid using a randomized complete block design (RCBD) with four replications. For each experimental unit a plot size of 4m by 1.6m (6.4m^2) was used with inter row spacing of 40cm and between plant spacing of 10cm.The spacing of 0.6m and 1.5 m was used between each experimental units and replications, respectively. All the agronomic practices were applied uniformly to the experimental units according to the recommendation. Fertilizer was applied to each plot at the rate of 121 kg NPS ha^{-1} at planting.

3.4. Data Collected

The data were recorded in plot and single plant basis according to descriptors of IBPGR and ICARDA 1985 developed for faba bean. All yield and yield related traits data were recorded on the two middle rows of each experimental unit (net plot size 3.2m^2). The plot-based data was collected from the entire rows. For individual plant based data was recorded from a total of five randomly taken plants from each plot and averaged for data analysis. The quality parameters Protein were measured in the food and nutrition laboratory of Kulumsa Agricultural Research Center.

3.4.1. Phenological and growth data

Days to Flowering: the number of days from planting to 50% plants of the plot starts to flower and recorded on plot base for each experimental unit.

Days to Maturity: The number of days starting from emergence to the date when 90%

of the pods became yellow or physiological maturity.

Plant Height: The average height of five randomly selected and pre-tagged plants in each plot, measured in centimeter from the ground surface to the top of the main stem at maturity.

3.4.2 Yield and yield related traits

Grain Yield (g): yield were measured from the harvestable plot area (two central rows) and adjusted to 10% moisture level using the following formula;

$$\text{Adjusted grain yield } (\frac{g}{plot}) = \frac{(100 - MC) \text{ x unadjusted grain yield}}{100 - standard\ mositure} \quad (10)$$

Number of pods per plant (NP/PL): The average number of pods counted on the five randomly selected and tagged plants in each plot.

Numbers of seeds per pod (NS/P): The number of seed per pod were recorded from three pods of five tagged plants in each plot and averaged before analysis.

Foliar Diseases (Chocolate spot and Rust): were recorded using (1-9) rating scale where 1 = immune (No visible disease symptom), 3= Slight, Some small discrete and a few large lesions (resistant), 5 = Medium, Some coalesced lesions, many spotting and some defoliation (moderately tolerance), 7 = Severe, Large coalesced lesions with about 50% defoliation, few dead stems/plants (susceptible) and 9 =Very severe, extensive lesion, severe defoliation stem girdling, many dead plants (highly susceptible). The disease was scored at weekly intervals starting from the first disease spot symptom appearance and continued until the final poding stage when the disease attained maximum (Villegas *et al*., 2012).

3.4.3. Protein content: The sequential extraction of protein was carried out according to the method described by (Gasim *et al.,* 2015). 50g sample of faba bean seed was taken for each plot and grinded with grinding machine. Then 0.25g flour from each independent sample (flour/solvent ratio 1:10 w/v) was sequentially extracted with each of distilled water (albumin), 1.0 mol/Litter Sodium chloride (NaCl) (globulin), 70% (v/v) aqueous ethanol (prolamin), and 0.1 mol/L and Sodium-hydroxide (NaOH) (glutelin) for 2 hour each at 25°C under continuous stirring. To extract most of the protein each extraction step was performed twice. The supernatants containing desired protein fractions were frozen,

concentrated, and the nitrogen content of each of these fractions was determined by the micro- Kjeldahl method (AOAC, 2003) which is %N multiplied by conversion factor 6.25.

Thousand seed weight (TSW (g)): random sample of 1000 seeds were counted from the harvested plot yields immediately after grain moisture determination and was weighed in grams. The weights then adjusted to 10% seed moisture level.

3.5. Data Analysis

Different statistical software packages were employed to analyze the data. The analysis of variance for each location and combined analysis of variance over locations, Shukula stability variance, Eberhart and Russel's (1966) stability and Wricke's ecovalence were computed using the SAS software. AMMI and GGE biplots were analyzed using GEA-R version 2.0 (CIMMYT, 2015) and GenStat 18th edition (2012).

3.5.1. Analysis of variance

All collected data were subjected to analysis of variance (ANOVA) for individual location and combined over all locations according to Gomez and Gomez (1984). Bartlett's tests of homogeneity of variances were made to see the homogeneity of error variances of the individual location experiments and after proving the homogeneity of variances the combined analysis of variance across locations were performed. In the combined analysis the locations and location x genotype interaction were treated as random factors while genotypes were fixed (Dia *et al.,* 2016). The mean comparison was done using Duncan Multiple Range Test (DMRT) at the 5% probability level. The standard ANOVA table and its associated expected mean square according to the RCBD design for the individual location and combined analysis was presented in Table 3.3 and Table 3.4 respectively.

Table 3. 3. Outline of Analysis of Variance for Individual Location

Sources	DF	SS	MS	Expected MS
Replication (R)	(r - 1)	SS_r	MS_R	$\sigma^2e + g\sigma^2r$
Genotypes (G)	(g - 1)	SS_g	MS_G	$\sigma^2e + r\sigma^2g$
Error (e)	(r - 1) (g - 1)	SS_e	MS_e	σ^2e

SS_r =sum square of replication, SS_g = sum square of genotypes, SS_e= sum square of error, MS_e = mean squares due to error, MS_G = mean squares due to genotypes, MS_R = mean squares due to replications.

The genotype by location interaction was tested against the pooled error and it was used as an error term to test the genotype by location interactions. The genotypes (fixed factors) were tested against either the genotype by location interaction if either of these two were

found to be significant using the genotype by location interaction as an error term. F-test was used to detect significant effects of the source of variation from the ANOVA table.

Individual location ANOVA model; $Y_{ij} = \mu + G_i + B_j + \epsilon_{ij}$ Where, Y_{ij} = observed value of genotype i in block j, μ = grand mean of the experiment, G_i = effect of genotype i, B_j = the effect of block j, ϵ_{ij}= random error effect of genotype i in block j.

Table 3.4. Skeleton of Combined Analysis of Variance Over location

Sources	DF	MS	Expected MS	F- ratio
Total	ERG- 1			
Environment (E)	E - 1	MS_E	$\sigma^2e + g\sigma^2R(E) + RG\,\sigma^2E$	MSE/MSGE
Rep/ Env't (R)	E(R -1)	MSR	$\sigma^2e + g\sigma^2R(E)$	
Genotype (G)	(G - 1)	MSG	$\sigma^2e + g\sigma^2GE + ER\,\sigma^2G$	MSG/MSGE
G x E Interaction	(E- 1) (G - 1)	MSGE	$\sigma^2e + g\sigma^2GE$	MSGE/MSe
Pooled Error (e)	E (G - 1) (R-1)	MSe	σ^2e	

G = number of genotypes, E = number of environments, MSE = mean squares due to environments, MSR = mean squares due to block (locations), MSG = mean squares due to genotypes, MSGE = mean squares due to G x E and MSe = mean squares due to residual and R = number of replications.

The combined ANOVA model $Yijk = \mu + Gi + Ej + GEij + Bk(j) + \epsilon ijk$ Where, Yijk, is the total variation of the response variable, μ the grand mean, Gi the treatment effect, Ej the location effect, Bk(j) the effect of the replication within location, GEij the interaction effect between genotype vs. location and ϵijk the residual.

3.5.2. Eberhart and Russell (1966) Regression based Stability Analysis

The stability model proposed by Eberhart and Russell (1966) was employed to analyze the data over seven environments. According to this model, environment and GEI component were further partitioned into environment (linear), G x E (linear) and pooled deviations from regression. Mean performance of genotype, regression coefficient (bi) and deviation from regression ($S^2_{di)}$) were employed based on the following equation;

$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ Where; Y_{ij} = Mean of i^{th} genotype in j^{th} environment. μi = the grand mean βi = the regression coefficient of the i^{th} genotype on environmental index and I_j = the environmental index obtained by the difference between the mean of each environment and the grand mean, $I_j = X_j - \mu_i$

δ_{ij} = the regression deviation of the i[th] cultivar in the j[th] environment. The two stability parameters, regression coefficient (bi) and variance of the regression deviations (S^2di) were estimated as:

$$\text{bi} = \frac{(\sum y_{ij} l_j)}{\sum \text{I}^2\text{j}}$$

Where, $\sum y_{ij} l_j$ = the sum of products of the i[th] observation in the j[th] environment and the environmental index, and $\Sigma\ I^2_j$ = the sum of squares of environmental index. Therefore, the performance of each variety could be predicted by using the estimates of the parameters, $\hat{Y}_{ij} = x_i + b_i I_i$ where x_i is the estimate of μ. The second stability parameter is the mean square deviation from linear regression and could be estimated first by squaring the deviation $\delta_{ij} = (Y_{ij} - \acute{y}_{ij})$ to provide an estimate of another stability parameter (S^2di) that could be calculated as:

$$S^2{}_{di} = \frac{1}{E-2}[\sum_{j=1}^{e}(\bar{y}_{ij} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...})^2 - (b_i - 1)^2 \sum_{j=1}^{e}(y_{.j.} - y_{...})^2]$$

Where b_i is the linear regression coefficient, $\bar{y}_{ij}$is the mean performance of genotype *i* in the j^{th} environment $\bar{y}_{i..}$ and $\bar{y}_{.j.}$ are the genotype and environment means, respectively, $\bar{y}_{...}$ is the overall mean. The deviation sums of squares are the sums of variance due to deviation from regression divided by (E -2), and subtracting pooled error mean square, where *E* stands for the number of environment at which each variety was tested (Eberhart and Russell, 1966).

The regression coefficients (bi) = tested for the significance of difference from unity using t-test whereas, the significance of the S^2di from zero was tested using the F-test by comparing the deviation from regression with pooled error estimate.

Table 3.5. ANOVA table for stability based on Eberhart and Russell Model

Source	DF	M.S.S.	F test
Genotype (V)	(v-1)	MS_1	MS_1/MS_3
Environment (E)	v (n-1)		
Environment (E) (linear)	1		
Genotype × Environment (GXE) (linear)	(v-1)	MS_2	MS_2/MS_3
Pooled deviations	v (n-2)	MS_3	MS3/MS4
Pooled error	n (r-1) (v-1)	Me	
Total	(nv-1)		

DF degree of freedom n= Number of environments**,** v= Number of genotypes r = Number of replications

3.5.3. Shukla Stability Variances (Sh-σ^2i)

Shukla (1972) defined the stability variance of genotype i as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual ($GE_{ij}+e_{ij}$) matrix in a two-way classification. The stability statistics is termed "stability variance" (σ^2i) and is estimated as follows:

$$\delta^2{}_i = \frac{1}{(G-1)(G-2)(E-1)}[G(G-1)\sum_j(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2 - \sum_i\sum_j(Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2]$$

Where Y_{ij} is the mean yield of the ith genotype in the jth environments,$\overline{Y}_{.j}$ is the mean of all genotypes in jth environment, $\overline{Y}_{i.}$ is the mean of all environments in ith genotype and $\overline{Y}_{..}$is the mean of all genotypes in all environments.

3.5.4. Wricke's Ecovalence

Based on the Ecovalence term the relative contribution of genotype 'i' to the overall genotype-environment interaction and the GEI mean square as the criteria for stability was estimated to understand the stability of each genotype with respect to the measured traits. The ecovalence (Wi) or stability of the ith genotype is its interaction with the environments, squared and summed across environments, and expressed as;

$$\omega\text{i} = \sum_{j=1}^{q}(Y_{ij} - \overline{Y_{i.}} - \overline{Y_{.J}} + \overline{Y_{..}})$$

Where, (Y_{ij} is the mean performance of genotype i in the jth environment. $\overline{Y_{i.}}$ is the marginal mean of the ith genotype. $\overline{Y_{.J}}$ is the marginal mean of the jth environment. $\overline{Y_{..}}$ is the overall mean.

3.5.5. Additive Main effect and Multiplicative Interaction (AMMI) model

AMMI analysis first fits the additive main effects of genotypes and environments by the usual analysis of variance and then describes the non-additive part, genotype-environment interaction, by principal component analysis. The AMMI analysis was performed using the following model suggested by Crossa *et al*., (1990).

: $$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{n} \lambda_n \alpha_{in}\, y_{jn} + e_{ijk}$$

Where, Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment, μ is the grand mean, G_i is the mean of the i^{th} genotype minus the grand mean, E_j is the mean of the j^{th}

environment minus the grand mean, λ_n is the square root of the Eigen value of the principal component analysis (PCA) axis α_{in} and y_{jn} are the principal component scores for PCA axis n of the i^{th} genotype and j^{th} environment and e_{ijk} is the error term.

To estimate the unknown model parameters usually first uses row/column means for the main effects and then performs a singular value decomposition of the residual matrix for the interaction parameters. This classical approach corresponds essentially to a least square fit of the full model. That is, estimates of the overall mean (μ) and the main effects (G_i and E_j) are obtained in the context of a simple two-way ANOVA of the array of means $Y_{(gxe)}$. The residuals from this array then constitute the array of interactions $Z_{gxe} = z_{ij}$, Where, $z_{ij} = y_{ij} - y_{i.} - y_{.j} + y..$ and the multiplicative interaction terms are estimated from the singular value decomposition (SVD) of this array. Thus, λk is estimated by the k^{th} singular value of Z, αik is estimated by i^{th} element of the left singular vector αk (g x1) and γ jk is estimated by j^{th} element of the right singular vector γ k' (1x k) associated with λk (Zelalem Tazu, 2011).

Table 3.6. AMMI analysis of variance for "n" number of PCA

Sources of variation	DF	Sum of square
Environment (E)	e-1	SSE
Rep within environment (R/E)	e(r-1)	SSR/E
Genotype (G)	g-1	SSG
Genotype x Environment interaction (G x E)	(g-1)(e-1)	SSGxE
PCA-1	v1=g+e-1-(2x1)	$r\lambda^2_1$
PCA-2	v2=g+e-1-(2x2)	$r\lambda^2_2$
.	.	.
.	.	.
.	.	.
PCA-n	vn=g+e-1-(2xn)	$r\lambda^2_n$
Experimental error (e)	e(g-1)(r-1)	SSe

Computations of the SS and DF for genotype, environment and genotype x environment follow the standard procedure but the SS and DF for interaction components are described using Gollob's (1968) approach (Table 3.7)

3.5.6. Estimation of AMMI Stability Value

The AMMI model does not make provision for a quantitative stability measure, such measure is essential in order to quantify and rank genotypes according to their stability. This stability value was calculated in the excel spread sheet using the formula developed by (Purchase *et al.*, 1997).

$$\text{ASV} = \sqrt{\left[\left(\frac{\text{SSIPCA1}}{\text{SSIPCA2}}\ \text{IPCA1 score}\right)^2 + (\text{IPCA2 score})^2\right]}$$

Where, ASV = AMMI's stability value, SSIPCA1 = sum square of interaction principal component axis one, SSIPCA2 = sum square of interaction principal component axis two.

3.5.7. Stability Analysis using GGE biplot

Genotype plus genotype by environment interaction (GGE) analysis partition the G + GE effects into principal components through singular value decomposition of environmentally centered yield data. The GGE biplot model of *t* principal components is given as follows:

$$\overline{Y_{ij}} - \mu i - \beta j = \sum_{k=1}^{t} \lambda\kappa\ \sigma i\kappa\ \gamma j\kappa + \varepsilon ij$$

Where, $\overline{Y_{ij}}$= the performance of genotype i in environment j, μi= the grand mean, β*j* = the main effect of environment j, k = the number of principal components (PC); λ*k* = singular value of the kth PC; and α*ik* and γ*jk* = the scores of ith genotype and jth environment, respectively for PC k; ε*ij* = the residual associated with genotype i in the environment j. Usually only the first two PCs are used especially if they account for the major portion of the G x E interaction. Therefore, the basic model for GGE biplot is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

Where, Y_{ij} is the mean for the i^{th} genotype in the j^{th} environment, μ is the grand mean β_j is the main effect of environment j, λ_1 and λ_2 are the singular values of the 1st and 2nd principal components (PC1 and PC2), ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, respectively, for genotypei^{th}, η_{j1} and η_{j2} are the eigenvectors for the j^{th} environment for PC1 and PC2 and ϵ_{ij} is the residual error term. To statistically compare the stability analysis procedures, Spearman's rank correlation coefficients were computed (Steel and Torrie, 1980) using SAS, 2000 software to compare all possible pairs of stability measure

which were used for this experiment. Spearman's rank correlation coefficient (r_s) was computed as follow: $$rs = \frac{6\sum d^2 i}{n(n^2-1)}$$

Where, $\sum d^2_i = \sum (x_i - Y_i)^2$ x_i, indicates the ranking order or number of the i^{th} genotype for the first parameter, Y_i indicates the ranking order of the i^{th} genotype of the second parameter, then $d^2 = x_i - Y_i$ (i=1, 2, 3…n), n is number of genotypes or samples used for the experiments. The significance of rank correlations on any of two stability measures was tested by means of student's t-test as described by Steel and Torrie (1980) using the following formula with n-2 degree of freedom;

$$t = \frac{rs\sqrt{n-2}}{\sqrt{1-r^2 s}}$$

CHAPTER 4. RESULTS AND DISCUSSION

Major findings of this multi-location testing experiment were summarized and presented in such a way that results from the study on agronomic traits (phenology traits, growth character, yield and yield components), Major disease (chocolate-spot and rust) and quality studies were separated. The study on phenology traits comprises days to flowering (FLD), days to maturity (DTM), growth character comprises plant height (PH), yield and yield components comprise yield, number of pod per plant (NP/PL), number of seed per pod (NS/P). While the quality study encompasses thousand seed weight (TSW) and protein content were separately discussed.

4.1. Analysis of Variance at Individual Location

4.1.1. Grain yield

The analysis of variance at individual locations indicated that grain yield was significant ($P \leq 0.01$) among tested genotypes over five testing environments except Holetta and Kofele (Appendix Table 1). This showed the tested genotypes have high genetic variability for this trait and the two locations (Holetta and Kofele) showed low discriminating power than the other locations. Similar findings in grain yield performance of faba bean genotypes were reported by (Tekalgn Afeta, 2018, Tamene Temesgen *et al.*,, (2015) and Temesgen Alene, 2015).

Since yield is the final result from the interaction of various plant characters and the environmental factors during the life span of the plant development, the ranking of genotypes based on grain yield can be considered as a reliable measure for genotypic performance. Thus, the three highest genotypes were G11 (4242 kg/ha), G4 (4065 kg/ha) and G8 (4056 kg/ha) at Assasa whereas; the three lowest yielder genotypes were G2 (680. kg/ha), G9 (743.1 kg/ha) and G8 (778.7 kg/ha) at Adet (Table 4.1). This is because of hail damage at the time of flowering and seed setting causes yield reduction at Adet and Debark besides to variation on soil fertility and uneven rainfall distribution.

Table 4.1. Mean value of grain yield (kg ha^{-1}) for individual location

	Testing Locations							
Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holetta	GM
G1	3359^{bc}	3037^{cde}	4043^{a}	3358^{ab}	985.6^{abc}	1466^{ab}	4656^{ab}	2986^{abc}
G2	3948^{abc}	3070^{cde}	3881^{ab}	3211^{ab}	680.6^{c}	1486^{ab}	4445^{ab}	2960^{abc}
G3	3970^{abc}	3695^{ab}	3935^{a}	2950^{ab}	949.8^{abc}	1358^{bc}	4710^{ab}	3081^{abc}
G4	4065^{ab}	2981^{cde}	3604^{ab}	3396^{ab}	902.6^{abc}	1560^{ab}	4861^{a}	3053^{abc}
G5	3446^{bc}	3190^{bcde}	3810^{ab}	2990^{ab}	1249.2^{ab}	1912^{a}	4616^{ab}	3030^{abc}
G6	3972^{abc}	3440^{abc}	3900^{ab}	3242^{ab}	1050.1^{abc}	1571^{ab}	4395^{ab}	3081^{abc}
G7	3313^{c}	2780^{e}	3480^{ab}	2738^{b}	778.1^{bc}	918^{c}	4500^{ab}	2644^{d}
G8	4056^{ab}	3520^{abc}	4032^{a}	3172^{ab}	773.7^{c}	1684^{ab}	4638^{ab}	3125^{ab}
G9	3869^{abc}	2826^{de}	3266^{b}	3236^{ab}	743.1^{c}	1645^{ab}	4479^{ab}	2866^{c}
G10	3656^{abc}	3357^{abcd}	3453^{ab}	3610^{a}	816.1^{bc}	1279^{bc}	4097^{b}	2895^{bc}
G11	4242^{a}	3748^{a}	3268^{b}	3011^{ab}	1155.9^{abc}	1362^{bc}	4761^{ab}	3078^{abc}
G12	3948^{abc}	3297^{a-e}	4086^{a}	3207^{ab}	1317.5^{a}	1674^{ab}	4672^{ab}	3172^{a}
EM	3820.5	3245.1	3729.8	3176.7	950.2	1492.9	4569.2	2997.8
CV%	13.2	14.6	12.8	15.1	20.2	18.6	9.1	

CV= Coefficient Variability, EM= Environment Mean and GM=Genotype Mean

At Bekoji, the highest and lowest yielder genotypes were G12 (4086 kg/ha), G1 (4043 kg/ha) and G9 (3266 kg/ha), G11 (3268 kg/ha) respectively. Among the total genotypes tested in this experiment, the seven genotypes (G3, G4, G5, G6, G8, G11 and G12) had higher grain yield than the grand mean (2997.8 kg/ha). Generally among the tested environments Adet (950.2 kg/ha) and Debark (1492.9 kg/ha) showed poor yield (Table 4.1). The yield reductions were occurred due to the very low rainfall distribution during flowering period and flower abortion due to hail damage. Sonia *et al.*, (2013) also reported the significant negative effect of stresses i.e. drought on grain yield potential if it happens at any stage of crop growth.

At Assasa, G4, G8 and G11were high yielding genotype with mean grain yield value of 4065.4, 4056 and 4242 kg/ha respectively with relative to standard check Gora (G1) and Tumsa (G12). With regard to yielding performance, G2 ranked last at Adet with mean yield of 680.6 kg/ha, and 5^{th} at Assasa with mean grain yield of 3948.4 kg/ha. This indicated the genotype responded differently to the different environmental conditions. Tamene Temesgen *et al.,* (2015) also reported that yield of faba bean genotypes was highly influenced by environment and can cause differential response of the genotypes.

4.1.2. Phenological, disease and yield component traits

The analysis of variance at individual environments showed significant differences ($P \leq 0.01$ and $P \leq 0.05$) among genotypes in days to flowering at all testing environments except at Debark, days to maturity at five locations except Assasa and Holetta, and plant height at four environments but it was non-significant at Assasa, Kofele and Adet. Pod per plant was significant at Kulumsa, Kofele and Debark but number of seeds per pod was not significantly different among locations and genotypes except at Holetta. Chocolate spot were significant at Holetta. However, 1000seed weight was showed highly significant difference at six environments except Assasa. Similarly leaf rust was significant at Kulumsa and Adet (Appendix Table 1). This kind of variation indicated that phenological and yield component traits are significantly affected by environment in addition to variation of their genetic compositions and incidences of disease were dependent on environmental condition

4.2 Combined Analysis of Variance over location

4.2.1. Analysis of variance for grain yield

The combined ANOVA revealed highly significant differences among genotypes, environments at ($p<0.01$) and the interactions was significant at $p<0.05$) for grain yield (Table 4.2). These results depicted the presence of genetic variability among genotypes and the location was diverse. Moreover, the significant G x E interaction indicated the differential response of genotypes grown across environments (Zelalem Tazu, 2011 and Iyad *et al.*, 2004). From the total variation, the highest proportion accounted for the environment (88.4%) whereas the G x E contribution is very low (2.7%). The large percentage of the total variation accounted by environment is an indication that the major factor that influence yield performance of the tested genotypes is the environment. Relatively large proportion of Genotype x Environment interaction when compared to that of genotypes main effect indicated that the variable phenotypic expression of genotype across the environments (Falconer and Mackay, 1996).

Table 4.2. Combined ANOVA for grain yield tested across seven environments

Source of variation	DF	SS	MS	% Explained
Environment	6	491153461.8	81858910.3**	88.4
Rep/Environment	21	8672058.8	412955.2	1.6
Genotype	11	6319688.2	574517.1**	1.1
Genotype X Environment	66	15007947.1	227393.1*	2.7
Error	231	34655688.1	150024.6	
Total	335	555808844		

DF= degree of freedom, SS = sum of squares, MS = mean squares, *, ** = significance difference ($p \leq 0.05$) and ($p \leq 0.01$), respectively

The significant G x E interaction is showed, the effects of genotypes and environments are statistically non-additive or the performance between genotypes depends on the environment). Despite, in this study the G x E interaction is not serious, it is difficult to interpret the results and identify superior genotypes across diverse environments in the presence of high significant G x E interactions. This finding is in agreement with those reported by Annathurai *et al.,* (2012) who found that faba bean varieties and breeding lines express a significant level of genotype x environment interaction for yield.

The mean yield of the genotypes evaluated in this experiment ranges from 2643.9 kg/ha (G7) to 3171.8 kg/ha (genotype 12) while the mean yield of the environment range from 950.1 (Adet) to 4569.1 (Holetta) (Table 4.1). The relative means of genotypes across environments are adequate indicators of genotypic performance only in the absence of genotype by environment interaction. However, in the presence of G x E interaction, genotype means across environments cannot explain how genotypes differ in relative performance over the environments.

The ranking of genotypes based on yield showed G12, G8, and G6 were the three highest performing genotypes across the tested environment. When the ranking of genotypes remains constant in diverse environments and the interaction is significant, due to change in magnitude of response of genotypes; this interaction is a non-cross-over type (Kang, 2017). If the interaction is significantly different from one environment to another or significant change in rank occurs, the interaction is crossover type. In the present study, the interaction was crossover type since ranking of genotypes changed at each location. This showed the existence of cross over type of interaction in the current study.

4.2.2. Growth, phenological and yield related traits

The combined analysis of variance showed highly significance difference among genotypes, environments and genotype by environment interaction effects for all studied traits except for number of seed per pod and chocolate spot which showed non-significant GEI (Table4.3). This result is in line with Abdalla *et al., (*2015) who found none significant result on Chocolate spot and number of seed per pod.

Table 4.3. Mean squares of growth, phenological, disease and yield component traits

	Mean Square due to			
Traits	Environment df (6)	Genotype df (11)	G X E df (66)	Pooled error df (231)
Days to Flowering	1578.4**	134.4**	9.8**	2.8
Days to Mature	11556.5**	66.8**	10.3**	4.5
Plant Height	20210.8**	284.7**	34.3*	35.8
Pod per plant	770.5**	12.0**	6.7**	3.6
Seed per pod	2.7**	0.3**	0.1^{ns}	0.1
1000 seed weight	1225150.4**	79502.9**	7019.5**	3359.9
Chocolate spot	55.7**	0.9*	0.4^{ns}	0.4
Rust	93.8**	0.9**	0.5**	0.2
Protein content	1909.5**	29.5**	74.3**	2.1

**,*, ns= highly significance (P≤0.01) and significant (P≤0.05) non-significant difference respectively

Days to Flowering and Maturity

The overall mean comparison showed genotype G8 (EH 09017-5) was early flowering and early maturing genotype (53.1 and 141.8 days) and at the same time G9 (EH 09021-1) was characterized as late flowering and late mature genotype across locations (Table 4.4). On the other hand late flowering and late mature genotypes were found at Bekoji for example G9 (Appendix Table 1 and 2). The major causes of these variations may be due to differences in altitudes and temperatures across environments. Similar results were reported by Asfaw Tilaye *et al.,* (1994) altitudinal difference has negative impact on crop phenology; the lower the temperature the longer is the period of days to flower and maturity and vice versa.

Table 4.4. Mean performance for phenological, disease score, quality and yield related traits

Genotypes	FLD	MTD	PLH	PPL	SPP	CHS	Rust	TSW	Protein
G1 (S.C.)	55.5^{c}	146.0^{ab}	127.5^{a}	11.8^{a}	2.6^{b}	2.9^{b-e}	2.9^{bcde}	797.2^{f}	25.3^{cd}
G2	53.0^{e}	142.9^{gh}	121.1^{cd}	10.8^{b}	2.7^{b}	3.3^{a}	3.3^{a}	814.7^{ef}	26.1^{ab}
G3	54.1^{d}	144.4^{def}	125.8^{ab}	10.6^{bc}	2.7^{b}	2.8^{cde}	2.8^{bde}	903.5^{c}	25.3^{bcd}
G4	56.0^{c}	144.4^{def}	125.0^{ab}	10.9^{b}	2.9^{a}	3.2^{a}	3.3^{a}	896.2^{c}	25.8^{abc}
G5	54.3^{d}	145.5^{bcd}	122.9^{bc}	9.2^{d}	2.7^{b}	3.0^{a-d}	3.0^{abcde}	941.3^{ab}	23.8^{ef}
G6	53.4^{de}	142.8^{gh}	119.2^{de}	9.2^{d}	2.6^{b}	3.1^{abc}	3.1^{abcd}	814.8^{ef}	25.2^{cd}
G7	56.9 ^{b}	144.1^{ef}	120.7^{cd}	10.4^{bc}	2.6^{b}	2.9^{b-e}	2.9^{bcde}	840.8^{e}	25.2^{cd}
G8	53.1^{e}	141.8^{h}	122.5^{bcd}	10.5^{bc}	2.6^{b}	3.0^{a-e}	3.1^{ab}	855.6^{d}	26.5^{a}
G9	59.5^{a}	147.0^{a}	122.8^{bc}	10.3^{bc}	2.6^{b}	2.7^{e}	2.8^{e}	924.7^{bc}	23.6^{f}
G10	59.0^{a}	145.9^{abc}	117.0^{e}	10.4^{bc}	2.7^{b}	2.8^{cde}	2.9^{bcde}	960.3^{a}	26.6^{a}
G11	54.2^{d}	143.2^{fg}	120.2^{cde}	9.6^{cd}	2.6^{b}	3.1^{ab}	3.1^{abc}	901.2^{c}	24.6^{de}
G12 (S.C.)	54.1^{d}	144.8^{cde}	126.7^{a}	10.7^{bc}	2.7^{b}	2.8^{de}	2.8^{de}	896.3^{c}	23.9^{ef}
Mean	55.3	144.4	122.6	10.5	2.7	3.4	3	878.9	25.2
CV (%)	3	1.5	4.9	18.1	12.6	18.3	17.3	6.6	5.8

FLD = Days to flower, DTM = days to mature, PPL = pod per plant, SPP = seed per pod, PLH = plant height, CHS = chocolate- spot, TSW= thousand seed weight and S.C = standard check

A Significant interaction for time to flowering and maturity between genotype and environment suggesting that, genotypes differed in their sensitive to environmental conditions. However, the results for days to maturity found from this study is not similar with Iyad *et al.*, (2012) who found that non-significant differences among genotypes and environments under irrigated and rain fed conditions.

Table 4.5. Mean values of phenological, yield related traits and disease score of faba bean genotypes of each environment

Environment	FLD	MTD	PLH	PPL	SPP	CHS	Rust	TSW	Protein
Assasa	51.5	126	135.9	6.8	2.9	3.4	4.5	1198.2	19.4
Kulumsa	52.6	124.7	126.1	14.1	2.8	3	3.6	803.1	21.6
Bekoji	64.1	154.1	103.9	13.9	2.9	3.8	2.5	822.4	31.6
Kofele	59	158.9	127.4	15.5	2.9	5.7	5	809.1	33.8
Adet	50.3	136.3	125	7.6	2.4	2.9	1.9	701.7	19.9
Debark	60.2	148.2	88.7	5.7	2.5	2.7	1.9	954.9	29.9
Holetta	49.3	162.7	151.1	9.7	2.4	2.5	1.3	862.8	20
Mean	55.3	144.4	122.6	10.5	2.7	3.4	3	878.9	25.2
CV	3	1.5	4.9	18.1	12.6	18.3	17.3	6.6	5.8

FLD = Days to flower, DTM = days to mature, PPL = pod per plant, SPP = seed per pod, PLH = plant height, CHS = chocolate- spot, TSW= thousand seed weight

Generally, the mean ranges of genotypes were 53.0-59.5 days for flowering and 141.8-147 days for maturity (Table 4.4). Whereas, the mean range of environments 49.3-64.1 days for flowering and 126-162.7 days for maturity (Table 4.5).

Pod per plant and number of seeds per pod

The mean value for number of pods per plant recorded ranged from lowest, 4.5 pods for G3 (EH 010008-5) at Debark to highest, 18.8 pods for G2 (EH 010002-1-1) at Kofele (Appendix Table 5). This kind of variation might be happened due to more favorable soil moisture at Kofele during flower formation and pod setting as compared with Debark because these two stages are sensitive to shortage in soil moisture content. Number of seed per pod was highly significant due to environment and genotype but the interaction is non-significant this indicates that the trait is relatively stable across different environments.

Number of pods per plant is an important selection criterion for the development of high yielding genotypes and is strongly influenced by environment in faba bean (Abdalla *et al.*, 2015). Number of pods per plant was highest at Kofele and least at Debark (Appendix Table 5). The highest mean number of pods per plant were recorded for genotypes EH 010002-1-1 (18.8) and Gora (17.8) at Kofele followed by EH 010051-1 (17.5) and 17.0 at Kulumsa and Bekoji respectively, (appendix Table 6). These results are consistent with the findings of Abdalla *et al.,* (2015). These results indicate variability for number of pods per plant and its sensitiveness to environmental fluctuations.

Plant Height

The tested genotypes showed different response for plant height across the tested environments. Based on the mean value result presented in (appendix Table 4), the tallest plant height was recorded at Holetta (151.1 cm) while the shortest plant height was recorded at Debark (88.7 cm). The variation was happened due to differences in soil moisture and soil nutrient content. Similarly the genotypes mean value across seven locations was varied from tallest Gora (127.5 cm) to shortest genotype (EH 09028-3) 117.0 cm (appendix Table 4).

4.2.3. Disease reactions

In addition to grain yield and other yield related components, G X E interaction and stability analysis were also performed with respect to major disease such as Chocolate-spot and rust. These two major fungal diseases were recorded across tested locations using

1-9 scoring scale 1 as immune or resistance and 9 as highly susceptible (Villegas *et al*., 2012).

The Mean square of combined analysis of chocolate-spot and rust were showed highly significant differences due to environment and genotypes. This was clearly demonstrated the influence of environmental variation on disease pressure and different genotypes reacted differently for chocolate-spot and rust disease severity. However, non-significance differences were observed for chocolate-spot among genotypes in contrast to rust G X E interaction. This indicates the genotypes exhibits a similar disease reaction for chocolate-spot and differential disease reaction response for rust at all tested environments.

The highest chocolate spot incidence was recorded at Kofele followed by Bekoji and Assasa with 5.7, 3.8 and 3.4 score of mean infection, respectively (Appendix Table 7). Despite genotypes were not highly infected by rust across the tested locations, the disease was more recorded at Kofele followed by Kulumsa with mean infection of 5 and 3.6 score respectively and the lowest chocolate spot and rust score was recorded at Holetta, Debark and Adet (Appendix Table 7 and 8). Therefore, evaluation of faba bean materials for their resistance against major diseases at the above hot spot area would be desirable in crop breeding program.

4.2.4. Protein content and thousand seed weight

The high genotype x environment interaction effect indicated the differential performance of genotypes for protein content and thousand seed weight across tested environments. High significant effect among the environment showed the importance of environments for the differential expression of the genotypes for seed weight and protein content. Similar reports were presented by Nleya *et al.,* (2000) they stated that, nutritional quality and culinary quality of food legumes are subjected to variation caused by environmental factors particularly significant G x E interaction exist for most quality traits.

The highest thousand seed weight (960.3g) and protein content (26.6%) were recorded from G10 and the lowest 1000 seed weight and lowest protein content were obtained from G1 (Gora) standard check (797.2g) and G9 (23.6%) respectively (Table 4.5). Similarly G8 and G5 were best genotypes in protein content (26.5%) and (25.8%) respectively with relative to grand mean (25.2%).

In terms of individual environment the highest seed protein content were recorded at Kofele (33.8%), Bekoji (31.6%) and Debark (29.9%), respectively. The lowest protein content was recorded at Assasa (19.4%), Adet (19.9%) and Holetta (20%). The highest thousand seed weight were recorded at Assasa (1198.2g), Debark (954.9g) and Holetta (862.8g) whereas the lowest 1000 seed weight were recorded at Adet (701.7g) followed by Kulumsa (803.1g) (Table 4.6). This kind of variation occurred because of variation in soil type, amount of rainfall distribution or terminal moisture stress at the time of seed development

4.3. Stability Analysis

It is widely understood that the yield stability has particular important in developing countries where control over disease and insects is limited. In general knowing about environment through G x E study is the most important in breeding program. Because it is helpful to decide the number of appropriate testing sites for effective and efficient output to estimate the genetic variability and environmental variance devoid by G x E interaction. The selection efficiency can be increased with a careful estimation of G x E interaction (Tezera wallabo, 2000) and this information is in adequate in faba bean breeding program in Ethiopia.

Genotypes did not respond similarly for the recorded traits across the changing environments because of genotype by environment interactions. That showed the analysis of variance and estimation of variance components alone do not provide genuine explanation of genotype by environment interaction (Abel Moges, 2017). Hence, several authors developed various stability models as selection and evaluation criteria. Therefore, different stability models were used in this study to measure grain yield stability of faba bean genotypes.

4.3.1. Eberhart and Russell stability analysis

This model is important for analyzing and interpreting the non-additive structure (interaction) of two-way classification data is the joint linear regression method. This approach has been extensively used in genetics, plant breeding, and agronomy for determining yield stability of different genotypes or agronomic treatments (Crossa, 1990).

The regression coefficient (*bi*) revealed the linear response of genotypes across diverse environments or goodness of the environmental conditions whereas; the deviations from regression actually measure the genotype performance or consistency (Eberhart and Russell, 1966). Larger regression values (bi > 1) describe higher sensitivity to environmental change i.e. below the average stability value and have better performance at favorable environments. Lower regression coefficients (bi < 1) describe lower sensitivity to environmental change and better performance in poor environments, but above average stability value in good-performing environments.

Table 4.6. Analysis of Variance of faba bean mean grain yield by Eberhart and Russel's Model

Source of Variations	DF	SS	MS
Total	83	128120274.3	1543617.8
Genotype (G)	11	1579922.0	143629.3**
Environment (E) + (G x E)	72	126540352.2	1757504.9**
E (Linear)	1	122788365.5	122788365.5**
G x E (Linear)	11	437113.8	39737.6*
Pooled Deviation	60	3314873.0	55247.9
G1	5	394547.8	78909.6
G2	5	120086.7	24017.3
G3	5	249189.2	49837.8
G4	5	235987.2	47197.4
G5	5	234080.0	46816.0
G6	5	83593.3	16718.7
G7	5	207413.3	41482.7
G8	5	138414.0	27682.8
G9	5	338440.3	67688.1
G10	5	503191.6	100638.3
G11	5	718902.3	143780.5
G12	5	91027.2	18205.4
Pooled Error	252	10831936.7	42983.9

In the present study the regression coefficient (bi) values ranged from 0.85 (G5) to 1.075 (G3). The genotypes (G1, G5, G6, G9, G10 and G12) were found significant when tested for bi=0. In contrast, genotypes such as G2, G3, G4 and G8 were found significant for bi=1. G11 and G6 showed bi value is equal to 1 or close to one. In general, stable genotype was defined as one, which showed high mean yield, regression coefficient bi is around unity and deviation from regression S^2di components close to zero. According to this stability model, genotypes which had the smallest S^2di values were G7, G8, and G5 can be regarded as more stable genotypes. Among these, genotype G8 can be considered as best genotypes, judging from its mean yield (3125.3kg/ha) and deviations from regression (-15301.1). In contrast, G11, G10 and G1 can be grouped as unstable genotypes (Table 4.7). The significant S^2di component indicates that the behavior of genotypes is highly unpredictable and they are not suitable where the environment is changing (Table 4.7).

This study is in agreement with Mussa and Yohanse (1997) reported significant differences among faba bean genotypes along with G X E interaction at three locations for

three consecutive years. Stability analysis further showed that, non-significant differences among regression coefficients (bi) of various varieties studied for grain yield. In contrast the deviation from regression (S^2di) was significant for eight of the genotypes showing their instability over environmental changes.

When bi value is close to 1, it indicates that the genotype is stable and behaves similar to the average across all environments. A genotype with bi value is equal to one and S^2di = 0 interpreted as stable with desirable mean yield. However, usually, S^2di is considered as stability parameter rather than bi, which are more about responsiveness of genotypes (Eberhart and Russel, 1966; Becker and Leon, 1988).

Table 4.7. Mean grain yield, various stability analysis and the ranks of 12 faba bean genotypes across seven environments.

GEN.	YLD	R	Wi	R	σ^2	R	bi	R	S^2di	R	Pi	R
G1	2986.4	8	394966.3	9	60584.1	9	0.99	1	35925.7	10	125827	5
G2	2960.2	9	149304.9	3	11451.8	3	1.05	8	-18966.5	6	109536	4
G3	3081.3	4	306957.3	7	42982.3	7	1.08	10	6854	5	171680	9
G4	3052.7	6	264156.1	6	34422	6	1.05	8	4213.6	4	157074	8
G5	3030.3	7	443873.1	10	70365.5	10	0.86	11	3832.1	3	151769	6
G6	3081.4	3	91660.5	1	-77.1	1	0.97	4	-26265.2	9	155563	7
G7	2643.8	12	217111.4	5	25013.1	5	1.03	3	-1501.2	1	15553	1
G8	3125.3	2	181604.3	4	17911.7	4	1.07	9	-15301.1	2	197532	11
G9	2866.3	11	349635	8	51517.8	8	0.97	5	24704.2	7	88481	2
G10	2895.4	10	517233.1	11	85037.5	11	0.96	6	57654.4	11	99607	3
G11	3078.2	5	722113.6	12	126013.6	12	1.02	2	100796.6	12	195584	10
G12	3171.8	1	113371.1	2	4265	2	0.95	7	-24778.4	8	205220	12

Where R= rank, bi = regression coefficient, $S^2{}_{di}$ = deviation from regression, W_i = Wricke's Ecovalence Analysis, δ^2 = Shukla's Stability Variance, Pi = Cultivar performance superiority measure, GEN = genotypes YLD = grain yield

Genotypes characterized by regression coefficient (bi) close to one have average stability over all environments accordingly, G1 (bi = 0.99) and G11 (bi= 1.02) respectively and indicated as wide adaptable genotypes. Similarly G2, G3, G4, and G8 have a regression coefficient bi value significantly greater than 1 (1.05, 1.06, 1.05 and 1.07), respectively. This showed that genotypes are very sensitive when the environment is changed (small changes in environment large variation in yield). These genotypes produced below average stability over location that means specifically adapted to high-yielding environments but poorly adapted in low-yielding environments.

On the other hand genotypes with low value of regression coefficient (bi <1) for instance G5 (bi= 0.857) exhibited opposite type of adaptation very little change despite large change in environments (above average stability). This genotype produced above average yield in low-yielding environments but being insensitive to environmental change it yields relatively small grain yield in high-yielding environments.

4.3.2. Wrickes stability variance

The contribution of each genotype to the sum of square of the G X E interaction is considered as a stability measures (Wricke, 1962). This stability measure is considered as a dynamic concept and popularly known as "Eco-valence" (Wi). This parameter is estimated by the decomposition of the sum of squares of the G x E interaction in to its components. According to the eco-valence (Wi) the stability of the i^{th} genotype is its interaction with environments squared and summed across environments. Genotypes with low ecovalence have smaller interaction or fluctuation across environments and therefore, are stable. Accordingly, G6 and G12 are the stable genotypes according to the Wricke's ecovalence measures of stability (Table 4.7). Moreover, G12 is the one with high yield and more stable genotype across the tested environments. The most interactive and unstable genotypes were G11 followed by genotypes G10 and G5 with mean grain yield ranked 5^{th} 10^{th} and 7^{th} respectively. In contrast, the most stable or low interactive genotypes were G6, G12, G2 and G8 with yield response ranked 3^{rd}, 1^{st}, 9^{th} and 2^{nd} respectively (Table 4.7).

4.3.3. Shukla's Stability Variance

Shukla (1972) proposed that, the variance component of each genotype throughout environments is another related measure of phenotypic stability. Shukla defined the concept of stability variance by modifying ecovalence's stability to provide an unbiased estimate of the variance of genotype i across environments after the removal of environmental main effects. Since the genotype main effect is constant, the stability variance is thus based on the residual (GE_{ij}+ e_{ij}) matrix in a two-way classification.

This stability statistics is termed as stability variance (δ_i^2). A genotype is stable if its stability variance (δ^2_i) is equal to environmental variance (δ^2_0) which means that $\delta^2 i=0$. Thus, relatively large value of (δ^2_i) will indicate greater genotypic instability. According to Shukula stability parameter the most stable genotypes were G6, G12 and G2; this observation means that genotypes showed lower differential responses to the changes in

the growing environment and contributed minimally to the sum of squares of the interaction effect regarding of their high yielding ability. Similarly the most unstable genotypes were G11, G10 and G5 (Table 4.7). The result obtained based on Shkula and Wrick's stability measure were identical and identify similar stable genotypes across the environment. Similar findings also reported by (Mulusew Fikere *et al.*, 2008).

4.3.4. Cultivar superiority measure (Pi)

The smaller the values of Pi the smaller the distance of the genotype from the maximum yield; that indicate the better the genotype. Pi values were measured on overall location mean; it represents superiority in the sense of general adaptability or wide adaptation (Crossa, 1990). Therefore, ideal genotype is the one, which have lowest Pi value and the small contribution for genotype by environment interactions. According to this stability model G7, G9 and G10 were considered as stable despite lower in terms of mean grain yield. However, G12, G8 and G11 were considered unstable though highest in grain yield (Table 4.7). The application of this stability parameter was reported in various researchers (Purchase, 1977 and Lin and Binns 1988) as cultivar superiority measure to select the stable faba bean genotypes.

4.3.5. Additive Main effects and Multiplicative Interaction (AMMI) model

The grain yield data were subjected to AMMI analysis of variance by combining ANOVA with additive main effects and multiplicative effects into single model for 12 faba bean genotypes over seven locations (Table 4.8). The results showed that highly significant difference ($p<0.01$) for genotypes, environments and genotype and environment interactions.

According to the AMMI ANOVA result the treatments accounted 92.2% from the total variation; environment, genotype and interaction contributed 88.4 %, 1.1 % and 2.7% from the total treatment variations, respectively. From the treatment component environment contributed the largest source of variation this finding is similar with Agegnehu Mekonen (2017) report on bread wheat, who found large portion of variations was accounted by environment followed by interaction.

Table 4.8. AMMI analysis of Variance for mean grain yield across seven environments

Source	DF	SS	MS	Explained (%)
Total	335	555808844	1659131	
Treatments	83	512481097	6174471**	92.2
Genotypes	11	6319688	574517**	1.1
Env.t	6	491153462	81858910**	88.4
Rep/Env.t	21	8672059	412955	1.6
Interactions	66	15007947	227393*	2.7
IPCA 1	16	5100778	318799**	34
IPCA 2	14	3568960	254926*	23.8
IPCA 3	12	2644506	220375^{ns}	17.6
Residuals	36	6338210	176061	1.14
Error	231	34655688	150025	6.2

DF = degree of freedom, SS = sum square, MS = mean square, ** and * significant difference at 1% and 5%

The magnitude of the environment was 8.0 times greater than the genotype by environment interaction (Table 4.8). The significance of MS of environment indicated the test environments are very diverse and causing most of the variations in seed yield. The genotype by environment interactions was decomposed into IPCA. The first and the second interaction principal component axis explained 34.0% ($p< 0.01$) and 23.8% of the total G x E interaction (Table 4.8). The two IPCAs explained about the 57.8 % of the total genotype x environment interaction sum of square.

AMMI Stability Value (ASV), IPCA1 and IPCA2 scores for each genotype were also computed and presented in Table 4.9. ASV is the distance from the coordinate point to the origin in a two-dimensional scatter diagram of IPCA1 scores against IPCA2 scores. The larger the IPCA scores, either positive or negative the more specifically adapted genotype to a certain environments, whereas, the smaller the IPCA scores, the more stable the genotype in all environments.

Table 4.9. Mean grain yield (GY) (kg ha^{-1}), AMMI stability value (ASV) and genotypic IPCA1 and IPCA 2 score for tested genotypes

Genotypes	GY	Rank	IPCAg[1]	IPCAg[2]	ASV	Rank
G1	2986	7	17.0	1.5	24.3	11
G2	2960	8	1.9	-4.8	5.5	3
G3	3081	3	-8.3	14.1	18.4	9
G4	3053	5	-0.4	-11.3	11.3	6
G5	3030	6	12.2	7.2	18.8	10
G6	3081	3	-2.0	1.2	3.1	1
G7	2644	12	4.8	7.4	10.1	5
G8	3125	2	-2.6	3.3	4.5	2
G9	2866	10	-0.9	-16.0	16.1	8
G10	2895	9	-4.0	-12.8	14	7
G11	3078	4	-23.2	4.8	33.5	12
G12	3172	1	5.5	5.4	9.6	4

Where, IPCAg1 and IPCAg2 = interaction principal component axis one and two for each genotype

Therefore, based on ASV the genotype G6, G2, G12 (Tumsa) and G8 had the lowest AVS score thus, which were widely adapted across environments. However, the genotypes such as the standard check G1 (Gora), G3, G5 and G11, which had the highest ASVs, were unstable genotypes over the testing environments (Table 4.9).

According to AMMI analysis the genotype and environmental scores of AMMI-2 (interaction IPCA one and IPCA two) are presented in (Table 4.9 and 4.10), respectively. The IPCA score indicated the stability or general adaptability of genotype/s across environments. The larger the IPCA score, either positive or negative, as its order of importance, the more specifically adapted a genotype to certain environments.

The closer the IPCA scores near zero, the more stable or adapted genotype in overall test environments. Similarly environment scores from AMMI analysis regarding to interaction also interpreted as environments with large IPCA scores are more discriminating of genotypes, while environments with low IPCA scores or near to zero revealed small interaction across genotypes and low discrimination power among genotypes (Gauch and Zoble, 1996).

The combination of environment and genotype IPCA scores of the same signs indicated positive specific interaction effect, whereas, combination of opposite signs have negative specific interactions. Accordingly, G1, G2, G5, G7 and G8 with E3 (Bekoji), E5 (Adet) has positive specific interaction effect with E7 (Holetta) whereas, genotypes G1, G2, G5,

G7 and G8 have negative specific interaction effect with E1 (Assasa). Environment/s which has same signs of interaction IPCA scores discriminate genotypes similarly and environments having opposite sign of interaction discriminating genotypes differently for example Assasa and Bekoji or Kulumsa and Kofele these are main contributors for rank change of genotypes performance Table 4.10.

Table 4.10. Environment mean grain yield, IPCAe1 and IPCAe2 score

Environments	Environment mean	IPCAe[1]	IPCAe[2]
Assasa	3820	-19.6	-7.4
Kulumsa	3245	-17.5	12.2
Bekoji	3730	17.7	11.7
Kofele	3177	5.2	-22.0
Adet	950	3.8	7.1
Debark	1493	9.0	-6.5
Holetta	4569	1.4	4.9

Where, IPCAe1 and IPCAe2 = interaction principal component axis one and two for each environment

As shown in Table 4.10) environments were variable for both interaction and main effects. Among the testing environments, Assasa (E1) recorded the largest negative IPCA-1 scores and ranked second in environmental average mean grain yield (3820 kg/ha) relative to the rest of the environments. Following Assasa; Bekoji (E3) had largest positive IPCA-1 scores with above average mean grain yield. These two environments were highly interactive environments, which contributed the largest interaction effects.

On the other hand Holetta (E7), Kofele (E4) and Adet (E5) scored the least positive IPCA-1 score associated with highest average mean grain yield except Adet indicating their minimal contribution to the GEI and less discriminating power of the genotypes. The other environments were found in between of the highest and the lowest interactive environments. The tested genotypes relatively explained their genetic potential at five environments namely; Kofele (E4), Bekoji (E3), Assasa (E1), Kulumsa (E2) and Holetta (E7), providing above average grain yield. These environments are classified as high yielding (high potential) environments, whereas, Adet (E5) and Debark (E6) recorded below average grain yield, and hence clustered under low yielding (poor) environments (Table 4.10). According to AMMI-2 biplot graph the first two axis accounted 57.78% of the interaction SS (fig. 4.1). Since the interaction component of the AMMI model is based on the product of interaction PCA scores, the genotypes or environments has small interactions appears close to the center of the axes. Therefore, from the present study

genotypes G6, G8, and G2, revealed small interaction and they were considered as relatively stable genotypes. Conversely, genotypes such as G11, G3, G9 and G1 are relatively far apart from the origin and thus showed strong interaction effects (Figure 4.1).

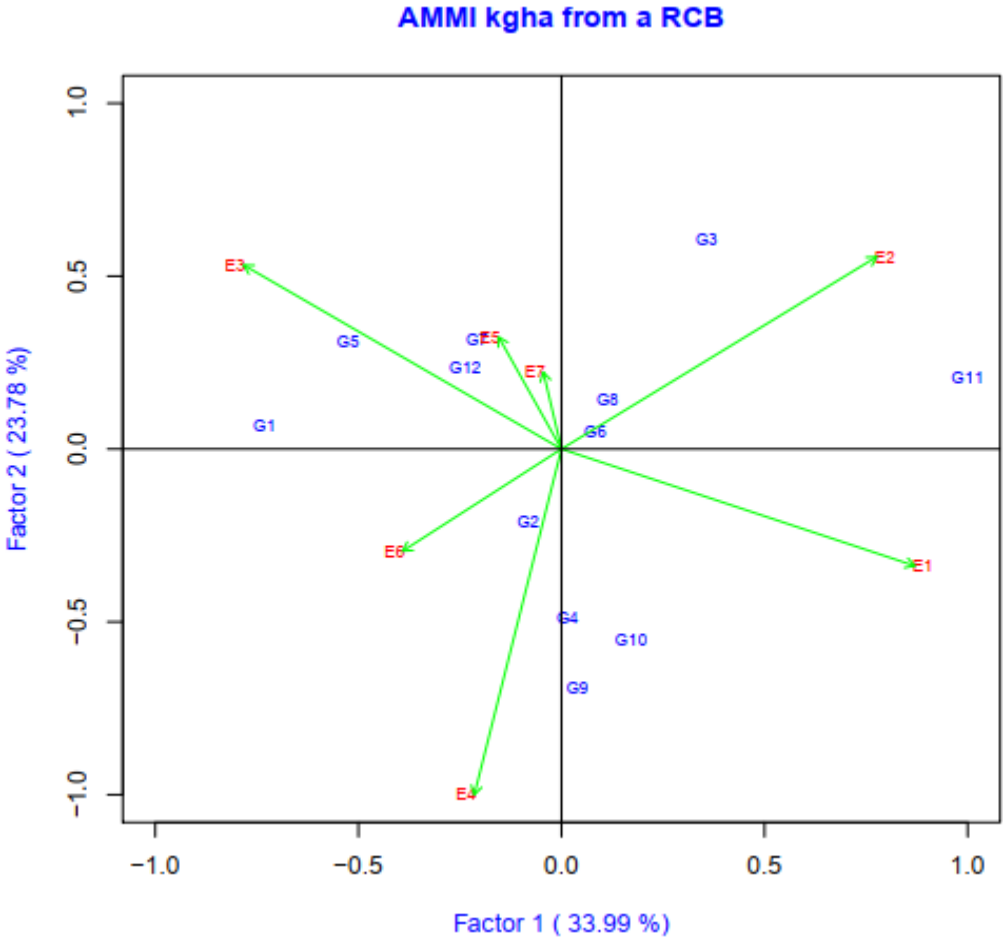

Figure 4.1 AMMI-2 biplot for grain yield (kg/ha) showing the interaction of IPCA2 against IPCA1 score of 12 faba bean genotypes (G) grown at seven environments (E)

A high absolute IPCA1 score of the genotype far from the origin shows variable performance of the genotype across the environment and reflects instability across environments. In this study the genotype G11 and G3 specifically adapted to E2 and E1 Genotypes G11, G3, G8, and G12 and environments E1, E2 and E7 on Fig. 4.1 have large magnitude of IPCA1 score that showed high interaction. There are no genotypes suitable or adaptable for E5 and E6 Fig.4.1 among the tested genotypes this indicates the environments were not favorable for the evaluated genotypes.

The AMMI-1 biplot Fig. 4.2 is the most known and important component of AMMI analysis. The ordinate (y- axis) represent PCA1and abscissa (x-axis) represent the main effect (genotype and environment) scores. Therefore, it provides opportunity to visualize

the mean performance of genotype and environment as well as stability using IPCA1 simultaneously. The IPCA1 score for 12 genotypes and seven environments were plotted against the mean yield of genotypes and environments Figure .4.2

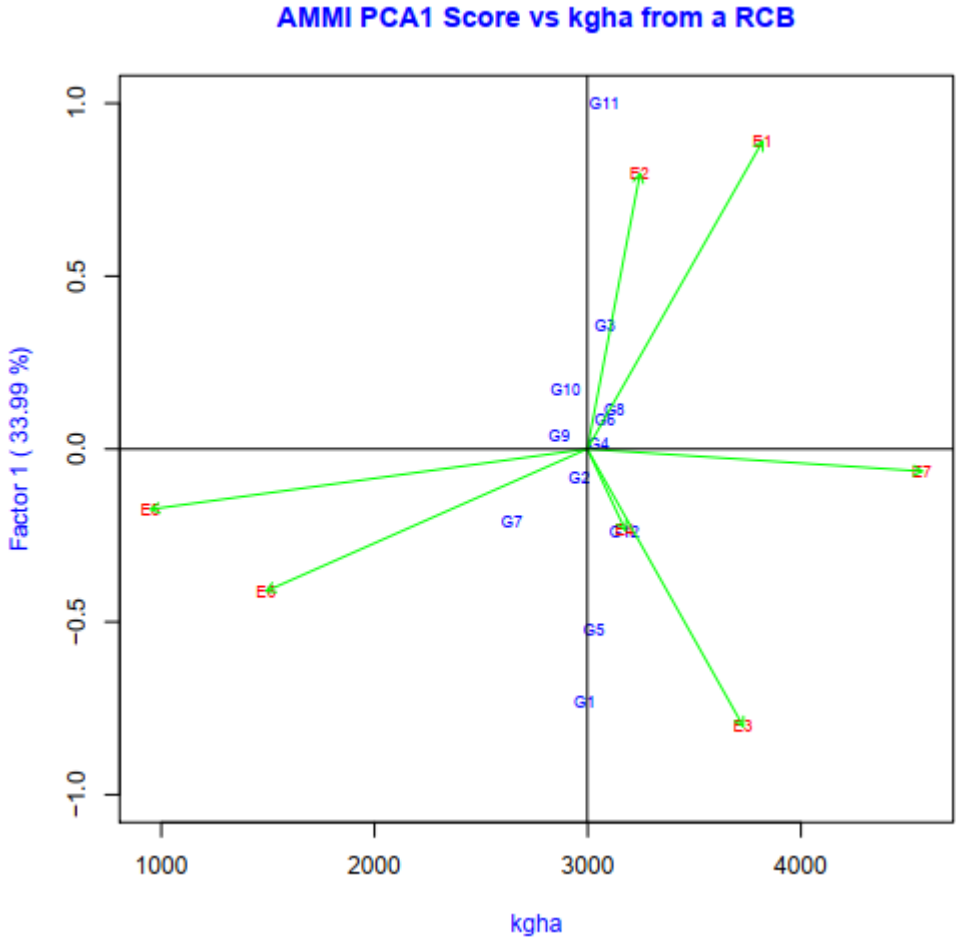

Figure 4.2 Mean grain yield of faba bean genotypes plotted against with IPCA1score across seven environments.

Genotypes or environments on the right side of the midpoint of the axis have higher yields than those on the left hand side. Therefore, all genotypes found on the right side of the midpoint of the x-axis except G7, G9 and G10 are relatively better yielding genotypes (Fig. 4.2). According to AMMI-1 biplot genotype G12 generally exhibited highest mean grain yield with highest additive main effect and plotted with E4 (Kofele), E3 (Bekoji) and E7 (Holetta). But G12 is specifically adapted to E4 and E3. Genotypes (G7) categorized under low yielding genotypes, which is shown at the lower left quadrant of the biplot. Generally G11 was the most unstable genotype identified by the AMMI model (Fig. 4.2).

Genotypes and environments close to each other or the same parallel line indicated having similar performance for given trait relative to coordinate. Hence, genotypes G1 and G5 were relatively adapted to environments E3; G12 best at E4. G2, G6, G8 and G10 more

adapted to E4 and E7. Genotype G11 was more adapted to at environments E1 and E2 (Fig. 4.2).

4.3.6. Best Genotype Selection using AMMI model

In the variety development processes, Multi-environment yield trial is crucial to select the best genotypes either for specific environment or general adaptable before recommending varieties for future production. In the present study the AMMI model selected four best adaptable genotypes for each testing environment. Accordingly, the standard check G12 (Tumsa) was best at E3, E6, E5 and E7 whereas, G11 was best at E1 and E2; G4 was best at E4. The next adaptable genotype at E5, E7 and E2 was G3 followed by G8 (Table 4.11).

On the other hand, the mean grain yield at individual location ranged from 950 kg/ha to 4569 kg/ha at Adet and Holetta, respectively. This indicated the existence of high variation among environments that can be due to difference in temperature, soil variation pest and disease and amount of precipitation. Consequently the performance of genotypes varies from location to location.

Table 4.11. Selection of best faba bean genotypes per environment by AMMI model

			The first four AMMI genotype recommendation			
Environment	Mean Yield	Score	1st	2nd	3rd	4th
E1	3820	-19.6	G11	G8	G4	G3
E2	3245	-17.5	G11	G3	G8	G12
E3	3730	17.7	G12	G5	G1	G8
E4	3177	5.2	G4	G9	G10	G12
E5	950	3.8	G12	G3	G8	G5
E6	1493	9.1	G12	G1	G4	G5
E7	4569	1.4	G12	G3	G8	G6

Where, E1= Assasa, E2= Kulumsa, E3= Bekoji, E4= Kofele, E5=Adet, E6= Debark and E7=Holeta , number in the bracket is mean grain yield in kg ha^{-1}

4.3.7. Stability Analysis using GGE biplot

GGE biplot is a data visualization tool, which graphically displays G x E interaction in a two-way table (Yan *et al.,* 2000). Moreover, GGE biplot is an effective tool for mega-environment analysis "which-won-where" pattern, where by particular genotypes can be recommended to specific mega-environments, genotype evaluation the mean performance and stability and environmental evaluation; the power to discriminate among genotypes in target environments (Yan *et al.,* 2000).

Evaluations of genotype mean yield performance in the given environment

The ranking of 12 faba bean genotypes based on their mean yield and stability is described in (Fig. 4.3). The PC1 and PC2 together explained 58.14% of the total G X E interaction. As Yan *et al.* (2000) pointed out PC1 approximated the genotype main effect or mean performance and PC2 approximate the GGE interaction effect, which is used to measure genotypes instability.

The line passing through biplot origin and the environment E1 axis is indicated by arrow head solid striate line called E1 axis. The projection of genotype markers onto this axis approximates the mean yield of the genotypes. Accordingly, the biplot organized the orders of genotypes based on mean yield performance relative to environment E1 hence, G11>G3>G8>G6>G4>G12>G2>G10>G9>G5, > G1>G7.

The line passing through the biplot origin and perpendicular to the E1 axis separates genotypes that yielded below the mean or in the left hand side (G7, G9, G10, G2, and G1) and genotypes that yielded above the mean were all other genotypes found in the right hand side. Despite inconsistencies in yield rank, the agreement was found between GGEbiplot (Fig. 4.3) and simple arithmetic mean method, which took into accounts both genotype effect and G x E interaction effect (Zhang *et al.*, 2016).

The AEC vertical axis indicated yield stability measure of genotypes. The smaller the length of the line perpendicular to the horizontal AEC axis indicated the more stable the genotype and vice versa. Accordingly, G2 and G4 were the best stable genotypes, whereas G12 and G7 were the most unstable genotypes relative to other genotypes. In general, G11 and G3 were not only showed higher yield but also the best stable genotypes. Conversely, genotype G7 was low yielding and less stable (Figure 4.3).

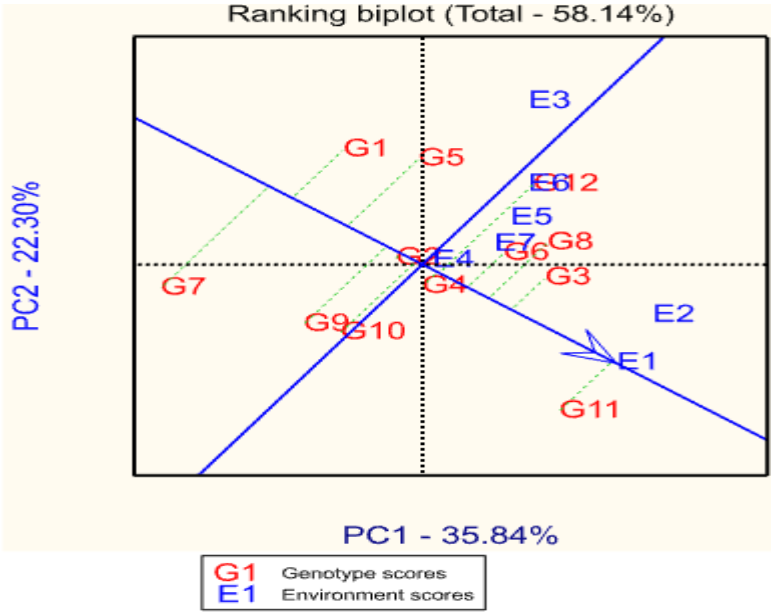

Figure 4.3 Ranking of the genotypes based on performance in E1 (Assasa) environment.

Relationship among environments and discriminating versus representativeness

The other application of GGE biplot is measuring representativeness to define an average environment and use it as a reference or benchmark. Therefore, the GGE graphical display result shows us an average environment is indicated by solid red line with arrow headed (Fig. 4.4). The discriminating power vs. representative view of GGE biplot identifies test environments that effectively identify superior genotypes for mega-environments. An ideal test environment is a virtual environment that has ability to discriminate the genotype and represent the mega-environment. Test environment with longest vectors from biplot origin are more discriminating of the genotypes hence, E3, E1 and E2 considered more discriminating environments for the testing genotypes and least representative due to large deviation from AEC. However, these environments are important for selecting specifically adapted genotypes.

If the test environment has a very short vector or is close to biplot origin, these environments are non-discriminating hence, less useful therefore, E4 and E7 were exhibited these characters this may be due to unfavorable rainfall conditions. Similarly, the test environment that has small angle with AEC (the average coordinates of all test environments) is more representative of the mega-environment than those that have larger angles with it for instance the angle between E3 and E1 revealed almost right angle hence,

these environments were not good representative of an ideal environment as supported by Dia *et al.*,(2016).

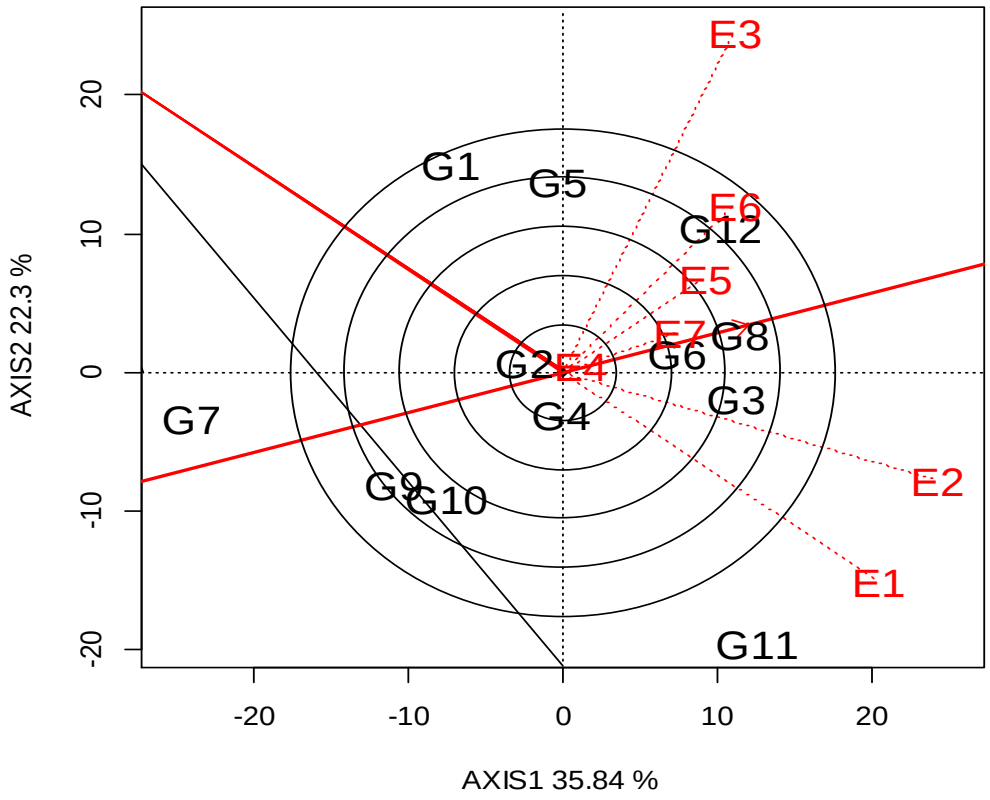

Figure 4.4 Discrimitiveness Vs. representativeness view of GGE biplot.

Although MET are conducted primarily for genotype evaluation, they can also be used in evaluating environments. An ideal environment should be highly differentiating of the genotypes and at the same time representative of the target environment. Assuming that the test environments used in the MET are representative samples of the target environment, the ideal environment should be located on or close to the mean environment axis. Despite environments found on to the center of the concentric circles represents the ideal environment, E4 and E7 were not represent ideal rather representative because of non-discriminating of genotypes very well (Fig. 4.4). Therefore, E2 found to be ideal environment since it is close to the mean environment axis i.e. representative and has ability to discriminating of genotypes. An environment is more desirable if it is closer to the 'ideal' environment. Therefore, E5, and E7 were relatively highly desirable or representative test environments, whereas E1, E2 and E3 were relatively more discriminate environments but not representative test environments for mean environment.

Visual identification of the best genotype(s) in each environment

The 'which-won-where' or polygon view of the GGE biplot is an effective visual tool in mega-environment analysis. The perpendicular lines to the polygon sides divide the biplot into sectors. If environments fall into different sectors, this suggests that different genotype won in different sector and thus genotype x environment interaction or crossover pattern exist. The winning genotype for a sector is the vertex genotype. Conversely, if all environments fall into a single sector, this indicates that a single genotype had the highest yield in all environments G12 was best yielding in E5 (Adet), E7 (Holetta), E3 (Bekoji), E6 (Debark) and E4 (Kofele) (fig. 4.5).

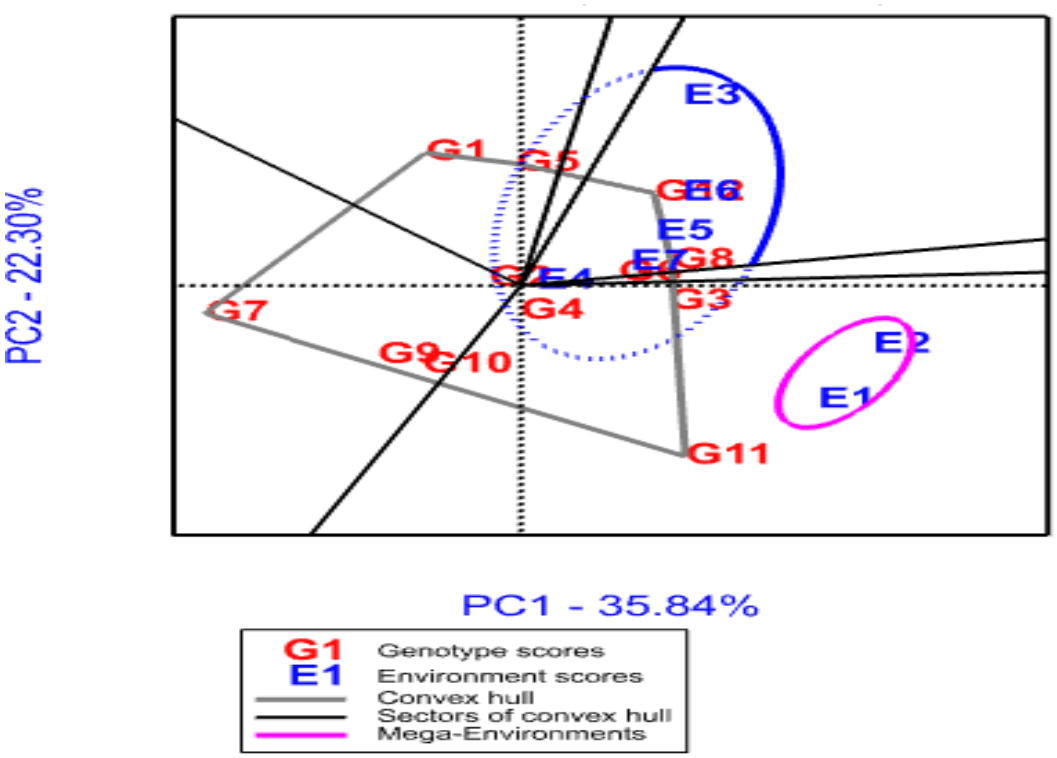

Figure 4.5 Polygon view of the GGE biplot show the "which-won-where" pattern.

According to Dia *et al.*, (2016) dividing target environment or location into mega-environment is recommended if crossover patterns are repeatable across year. Thus, similar results found from this study where the locations fall within one sector considered as one mega-environment such as E1 and E2 fall in one mega-environment (Fig.4.5). A further extended application of the biplot geometry is to visually identify the highest yielding genotypes for each of the environments in a single step. For this purpose, the genotypes that were located far away from the biplot origin were connected with straight

lines so that a polygon or vertex hull were formed with all other genotypes contained within the vertex hull (Fig. 4.5).

Therefore, the vertex genotypes (G1, G11, G12 and G7) were the most responsive genotypes to the environments; they were either the best or the poorest genotypes in some or all of the environments. Perpendicular lines to the sides of the vertex hull were drawn, starting from the biplot origin, to divide the biplot into different sectors or quadrants, each having a vertex genotype (Figure 4.5). The vertex genotype for each quadrant was the one that gave the highest yield for the environments that fall within that quadrant. Thus, genotype G11was gave the highest yield in environments E1 and E2; similarly G12 was gave the highest yield in environments E4, E7, E5, E3 and E6.

The other vertex genotypes found in the lower left quadrant and far from the origin was G7 and not gave the highest yield in any of the tested environments. Hence, this genotype is the poorest genotypes in some or all of the test environments. According to the polygon section, visual comparison of two genotypes in different environments, the line perpendicular to the polygon side that connects genotypes G12 and G11 facilitates the comparison between them. Genotype G12 yielded higher than G11 in all environments except E4 since all environments were on the side of G12.

The longer the projection of a genotype, regardless of direction, the greater the GE associated with the genotype, which is a measure of variability or instability of the genotype across environments. Thus, the performance of genotypes G11, G7, G1, G9 and G10 were highly variable (less stable), whereas genotypes G2, G6 and G4 were highly stable (Fig.4.6) however stability per se is not necessarily a positive factor.

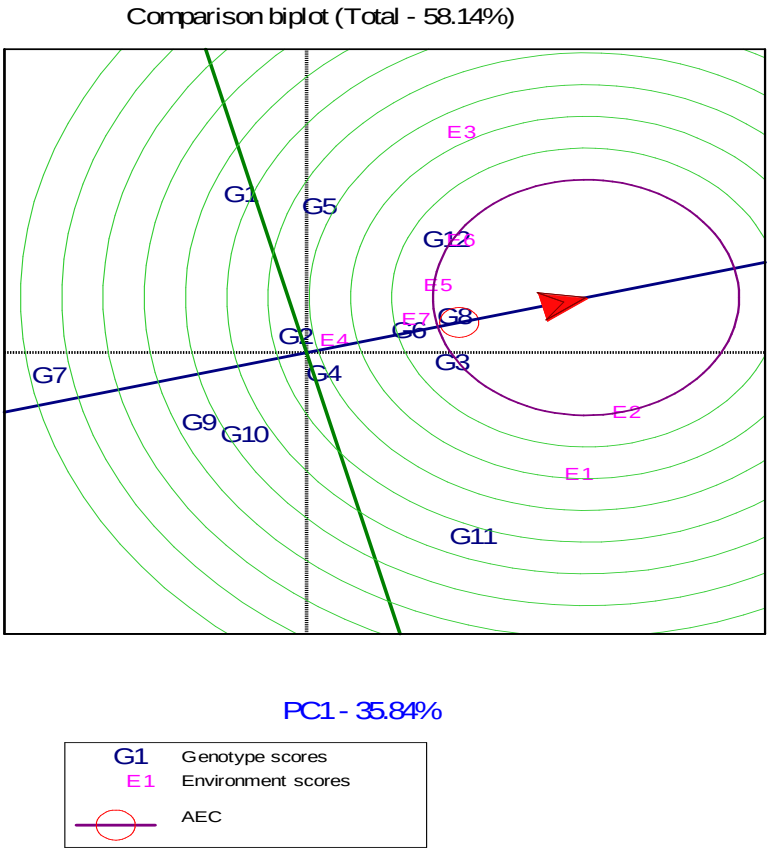

Figure 4.6 Ranking of genotypes with respect to ideal genotype.

The center of the concentric circles in Figure 4.6 represents the position of an 'ideal' genotype according to this G8 was considered as an ideal genotype which is defined by a projection on to the mean-environment axis that equals the longest vector of the genotypes that had above average mean yield and by a zero projection on to the perpendicular line (zero variability across environments). A genotype is more desirable if it is closer to the 'ideal' genotype. Thus, genotypes G6, G12 and G3 were more desirable than genotypes that were far from the concentric circle or ideal genotype. The low-yielding genotypes G7, G9, G1 and G10, were of course, undesirable because they were far away from the 'ideal' genotype (Fig.4.6).

Ranking test environments with relative to ideal environment

Average environmental axis (AEA) is a line passing through the origin and pointing to the positive direction with its distance equal to the longest vector. Besides, an ideal environment is a point on the AEA in the positive direction of the biplot origin and is equal to the longest vector of all environments (Yan and Tinker, 2006). According to this E7 is identified as ideal environment despite far from the concentric circle, it is close to

the mean environment axis. However, E5, E6, were identified as desirable representative environments. Though there was no ideal environment, E2 was better environment relative to other environments; E1 and E3 had longest projection form biplot origin and had better performance (Fig.4.7)

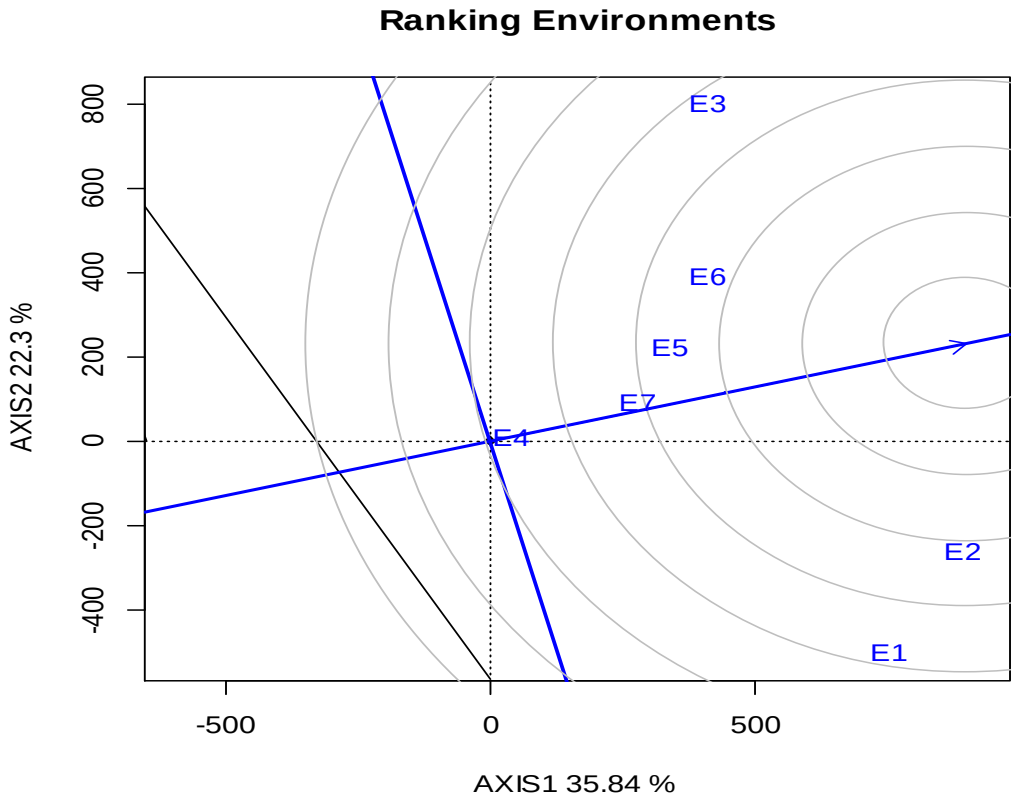

Figure 4.7. Ranking environments relative to ideal environment

4.4. Comparison of Stability parameters and Spearman's Rank Correlation

Spearman's rank correlation was performed between seven stability parameters and the overall mean grain yield (Table 4.12). The results described that some stability parameters were significant ($P \leq 0.01$) and positively correlated with the mean grain yield and other stability parameters.

Table 4.12.The Spearman's rank correlation coefficients for all stability measures

	Yield	Wi	σ^2	Bi	S^2di	Pi	ASV
Yield	1						
Wi	-0.077^{ns}	1					
σ^2	-0.077^{ns}	1**	1				
bi	-0.010^{ns}	-0.222^{ns}	-0.222^{ns}	1			
S^2di	-0.131^{ns}	0.953**	0.953**	-0.05^{ns}	1		
Pi	0.978**	0.043^{ns}	0.043^{ns}	0.017^{ns}	-0.010^{ns}	1	
ASV	0.026^{ns}	0.885**	0.885**	0.158^{ns}	0.854**	0.135^{ns}	1

Where, σ^2 Shukula stability variance, Pi = Lin and Binn's cultivar performance measure, Wi = Wricke's ecovalence, bi = regression coefficient and S^2di = deviation from regression, ASV = AMMI stability value, S^2i= environmental variance and CVi = coefficients of variability *, ** significant at P≤0.05 and P≤0.01 respectively ns = non-significant

Lin and Binn's procedure shows highly positive rank correlation Pi (r = 0.978**) with mean grain yield. This indicates that selection for yield would change yield stability leading to the development of genotypes that are specially adapted to environments with optimal growing conditions. This finding is similar with earlier reports which indicated the presence of strong positive correlation between grain yield and Pi (Tamene Temesgen *et al.,* 2015). Similarly, Pi is non-significant and positively rank correlated with other stability statistics except S^2di.

ASV shows positive and highly significant rank correlations with Wricke (r =0.885**), Shukula (r = 0.885**) and deviation from regression (r = 0.854**). In contrast the non-significant positive rank correlations was observed between mean yield, regression coefficient and cultivar performance (r = 0.026^{ns}, 0.158^{ns} and 0.135^{ns} respectively) and ASV. Positive and highly significant rank correlations were also observed between Shukula, Wrickes, and deviation from regression. All stability statistics were showed non-significant and negative rank correlation with mean yield except ASV and Pi.

The Wrickes procedure of stability parameter shows the highest significant positive correlation with Shukula (r = 1**) indicated that the two procedures are similar for ranking purposes. Purchase, (1997) and Tamene Temesgen *et al.* (2015) suggested significant positive correlation between different stability parameters revealed that these parameters would provide similar result in stability ranking of genotypes. The non-significant and negative significant correlation among yield and stability parameters described that stability parameters provide information that cannot be collected based on the average yield only (Eyeberu Abere, 2017).

5. CONCLUSIONS AND RECOMMENDATIONS

Combined analysis of variance indicated that, the effect of environment, genotype and genotype by environment interaction were highly significant for grain yield, yield related components and quality traits. The result also indicated the large percentages of the variation caused due to the environment that caused the occurrence of G x E interaction. This observed pattern of interaction revealed that genotypes respond differently from one environment to another that causes variation in relative ranking of genotypes from location to location. Therefore, requires the detail analysis to make recommendation for specific or wide adapted genotypes.

From combined analysis of variance the highest thousand seed weight and protein content were recorded from G10. The result also showed genotypes G8 and G5 recorded high protein content and grain yield. This revealed the potential of the new candidate genotypes to increase faba bean production and productivity with desirable quality in Ethiopia.

Different stability statistics such as Wi, AMMI, ASV, S^2di, bi, σ^2, GGE and Pi were found to be useful in detecting the phenotypic stability of the genotypes studied and exploited the effects of G x E interaction and to make recommendation of a genotypes based on the mean performance and stability simultaneously. Based on these G6, G12, and G8 were the most stable and high yielder genotypes by most stability parameters with relative to the grand mean and standard checks G1 (Gora) and G12 (Tumsa).

The result of this study showed that most of the tested genotypes were moderately susceptible for chocolate spot and rust infestation except G9. This showed the importance of urgent action to develop resistant genotypes for chocolate spot and rust disease to stabilize the faba bean production in the country.

In this study, the GGE biplot was able to identify environments (E3, Bekoji; E1 Assasa and E2, Kulumsa) as better environment with discriminating ability and the other environments such as E2, E5, E6, and E7 were found to be more representative and geographically close to each other and may generate similar information. Hence, to conduct the MET effectively with limited resources, discriminative locations encompassing representative locations may be included, rather than extending the trials extensively over related locations. Moreover the which-won-where view of the GGE biplot analysis has demonstrated existence of two mega-environments that include E1 and

E2 in one group the winning genotype for this mega-environment is G11 and the other environments grouped the second mega-environment and G12 is adaptable for the respective environments. The breeding program should look in detail to understand the effect of G x E interaction on the performance of the genotypes and understand the stability of the genotypes to classify them as specific and widely adapted genotypes before any recommendation to the users.

Generally the information generated from this research has important implications in GEI studies. However, the findings of this study are based on only seven environments, one cropping season and limited number of quality parameters. Thus further studies using more diverse locations and seasons in more number of quality traits attributes is required to generate more reliable information on the effect of genotype, environment and their interaction that allows us to make recommendations and select the best genotypes for future commercial production and parental selection for the breeding program.

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7. APPENDIX

Appendix Table 1 Mean square values of replication, genotypes and error for individual location

		locations						
Traits	SV	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta
YLD	Rep	566078.3	773896.7	554098.6	41033	430100.5	128250.8	397228.3
	GEN	566078.3*	408244.4**	363457.2*	212539.2^{ns}	172534.7*	251292.1*	163110.4^{ns}
	Error	186212.1	113520	152401.2	252101.7	80941.2	107755.2	157241.1
DTF	Rep	2.33	3.13	2.17	10.36	2.03	3.52	1.14
	GEN	3.64*	34.61**	37.65**	34.86**	54.63**	5.32 ns	22.63**
	Error	1.73	1.37	1.42	2.83	4.15	4.13	3.68
DTM	Rep	1.25	6.02	6.24	1.19	18.91	27.89	13.85
	GEN	6.86ns	7.57*	23.14**	30.11**	23.10*	35.65**	2.23 ns
	Error	3.6	2.7	1.5	5.14	9.86	6.15	2.37
PLH	Rep	107.4	1.2	53.5	20.7	74.5	88.7	334.3
	GEN	48.23ns	5.16**	140.37**	50.1^{ns}	49.9 ^{ns}	98.2*	98.7*
	Error	31.82	1.33	25.65	38.58	68.85	35.24	49.01
PPL	Rep	0.5	1.91	16.91	18.78	0.16	3.26	2.85
	GEN	2.88^{ns}	18.43**	6.29^{ns}	14.86*	1.39 ^{ns}	2.72*	5.37 ^{ns}
	Error	2.09	6.41	4.44	5.94	1.6	1.09	3.41
SPP	Rep	0.3	0.08	0.35	0.06	0.43	0.11	0.22
	GEN	0.08^{ns}	0.14^{ns}	0.07^{ns}	0.11^{ns}	0.17^{ns}	0.08^{ns}	0.42*
	Error	0.08	0.17	0.13	0.07	0.1	0.06	0.19
TSW	Rep	17121.4	40.4	2384.2	991.7	12666.2	1530.3	3830.3
	GEN	10057.6ns	18140.6**	17324.8**	28185.9**	17921.5**	16807.8**	13181.6**
	Error	8806	2575.1	1200.4	2334.8	3467.7	3569.3	1565.8
CHS	Rep	0.14	0.31	1.14	2.06	4.83	0.06	0.24
	GEN	0.11^{ns}	0.17^{ns}	0.45^{ns}	0.42^{ns}	1.33 ^{ns}	0.38 ^{ns}	0.48*
	Error	0.29	0.09	0.23	1.09	0.68	0.19	0.18
Rust	Rep	0.59	0.13	7.36	0.13	0.13	0.19	1.22
	GEN	0.50^{ns}	0.82**	0.67^{ns}	0.84^{ns}	0.61**	0.05^{ns}	0.24^{ns}
	Error	0.33	0.19	0.44	0.47	0.1	0.05	0.13
PC.	Rep	2.9	0.01	0.95	1.3	0.45	2.8	0.06
	GEN	65.3**	61.2**	51.0281**	17.5**	20.6**	43.89**	103.3**
	Error	2.3	0.02	0.83	1.1	0.41	3.3	0.011

Where, SV = source of variation, YLD=grain yield, DTF = days to flowering, DTM = Day s to mature, PLH = plant height (cm), PPL = pod per plant, SPP= seed per pod, TSW = tho usand seed weight (gm), CHS = chocolate spot (1-9) scale, PC = Protein content

Appendix Table 2 Means value for days to flowering of 12 faba bean genotypes tested across seven environments

Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holetta	GM
Gora (S.C.)	52.3ab	52.1cd	65.0bc	59.8bc	51.0c-e	58.8a	50.0a	55.5^{c}
EH 010002-1-1	51.0abc	49.3e	62.3de	55.0e	47.3fg	59.0a	47.0a	53.0^{e}
EH 010008-5	52.0abc	51.0de	62.3de	56.3e	48.0efg	60.5ab	48.3a	54.1^{d}
EH 010051-1	51.5abc	53.3c	64.5c	59.8bcd	52.5cd	61.3ab	49.0a	56.0^{c}
EH 010058-1	50.5bc	50.8 de	62.5de	56.5e	50.3c-f	61.0ab	49.0a	54.3^{d}
EH 010058-2	51.3abc	50.3de	60.8e	57.3ce	45.8g	60.5ab	48.0a	53.4^{de}
EH 09012-1	52.0ac	56.0b	66.5b	62.0ab	53.3ac	60.8ab	47.5a	56.9 ^{b}
EH 09017-5	51.5abc	50.5de	61.3de	57.0e	45.8g	58.8a	47.3a	53.1^{e}
EH 09021-1	52.8a	57.0ab	70.3a	63.8a	56.3a	62.5b	54.3b	59.5^{a}
EH 09028-3	53.0a	58.5a	69.0a	63.5a	56.3ab	59.0a	53.8b	59.0^{a}
EH 09046-3	50.0c	50.7de	62.0de	60.0b	47.3fg	60.0ab	49.5a	54.2^{d}
Tumsa (S.C.)	50.3bc	51.5ce	62.8d	56.3e	50.0d-f	60.3ab	48.0a	54.1^{d}
EM	51.5	52.6	64.1	59	50.3	60.2	49.3	55.3
CV%	2.6	2.2	1.9	2.9	4.3	3.4	3.9	

Means within each column followed by the same letter(s) are not significantly different at P ≤ 0.05 according to DMRT. CV = coefficient of variation, EM =Environment mean GM= genotype mean

Appendix Table 3 Overall means value for days to maturity of 12 faba bean genotypes tested across seven environments.

Genotypes	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	GM
Gora (S.C.)	126.8^{ab}	125.2^{bcd}	156.2^{e}	160.5^{bd}	138.2^{bcd}	153.0^{f}	162.2^{a}	146.0^{ab}
EH 010002-1-1	124.5^{a}	123.2^{ab}	151.8^{a}	156.8^{b}	134.3^{abc}	148.2^{b-e}	161.5^{a}	142.9^{gh}
EH 010008-5	125.5^{a}	124.5^{a-d}	152.5^{abc}	159.0^{b}	137.0^{a-d}	149.2^{c-f}	163.0^{a}	144.4^{def}
EH 010051-1	124.8^{a}	124.8^{bcd}	156.5^{e}	159.5 ^{b}	134.5^{abc}	146.8^{abc}	163.8^{a}	144.4^{def}
EH 010058-1	124.8^{a}	125.8^{bcd}	154.2^{cd}	159.8^{bc}	140.2^{d}	150.2^{c-f}	163.2^{a}	145.5^{bcd}
EH 010058-2	125.2^{a}	123.8^{ab}	152.2^{ab}	157.5^{b}	134.2^{abc}	144.0^{a}	162.5^{a}	142.8^{gh}
EH 09012-1	126.5^{ab}	125.8^{bcd}	156.0^{de}	157.8^{b}	132.8^{a}	147.8^{a-e}	162.2^{a}	144.1^{ef}
EH 09017-5	126.5^{ab}	122.0^{a}	151.5^{a}	153.2^{a}	133.8^{ab}	144.0^{a}	161.5^{a}	141.8^{h}
EH 09021-1	129.0^{b}	126.8^{d}	158.8^{f}	163.2^{d}	136.8^{a-d}	151.8^{ef}	163.0^{a}	147.0^{a}
EH 09028-3	127.2^{ab}	126.5^{cd}	154.2^{cd}	163.2^{cd}	139.2^{cd}	147.0^{a-d}	163.8^{a}	145.9^{abc}
EH 09046-3	125.8^{a}	124.5^{a-d}	151.0^{a}	157.8^{b}	136.0^{a-d}	145.0^{ab}	162.5^{a}	143.2^{fg}
Tumsa (S.C.)	125.0^{a}	124.0^{abc}	153.8^{bc}	158.5^{b}	138.5^{bcd}	151.0^{def}	163.0^{a}	144.8^{cde}
EM	126	124.7	154.1	158.9	136.3	148.2	162.7	144.4
Cv	1.6	1.6	1.7	2.1	2.7	2.6	1.1	

Means within each column followed by the same letter(s) are not significantly different at P ≤ 0.05 according to DMRT.

Appendix Table 4 Mean value for plant height (cm) of 12 faba bean genotypes tested across seven environments

Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holetta	G/mean
Gora (S.C.)	137.5^{ab}	126.2^{bc}	114.8^{e}	131.5^{a}	126.8^{a}	95.8^{d}	160.0^{c}	127.5^{a}
EH 010002-1-1	131.5^{a}	124.5^{ab}	101.5^{bc}	125.5^{a}	123.5^{a}	92.7^{bcd}	148.2^{ab}	121.1^{cd}
EH 010008-5	136.8^{ab}	125.5^{bc}	110.0^{de}	129.5^{a}	131.0^{a}	91.8^{a-d}	155.8^{bc}	125.8^{ab}
EH 010051-1	140.2^{ab}	127.0^{c}	101.8^{bc}	133.0^{a}	125.8^{a}	93.9^{cd}	153.2^{abc}	125.0^{ab}
EH 010058-1	132.0^{a}	127.0^{c}	106.2^{bcd}	127.5^{a}	125.8^{a}	91.3^{a-d}	150.2^{abc}	122.9^{bc}
EH 010058-2	134.0^{ab}	126.0^{bc}	99.0^{ab}	123.0^{a}	120.5^{a}	85.8^{abc}	145.8^{ab}	119.2^{de}
EH 09012-1	133.5^{ab}	126.5^{c}	101.2^{bc}	124.0^{a}	126.5^{a}	83.2^{ab}	149.8^{abc}	120.7^{cd}
EH 09017-5	139.8^{ab}	123.5^{a}	107.8^{cde}	125.0^{a}	122.8^{a}	85.4^{abc}	153.8^{bc}	122.5^{bcd}
EH 09021-1	136.2^{ab}	127.2^{c}	103.0^{bcd}	126.5^{a}	127.8^{a}	85.6^{abc}	153.5^{abc}	122.8^{bc}
EH 09028-3	131.8^{a}	127.2^{c}	92.0^{a}	124.8^{a}	119.0^{a}	82.2^{a}	142.0^{a}	117.0^{e}
EH 09046-3	136.2^{ab}	126.2^{bc}	101.5^{bc}	125.8^{a}	122.2^{a}	83.3^{ab}	146.5^{ab}	120.2^{cde}
Tumsa (S.C.)	141.8^{b}	126.2^{bc}	108.5^{cde}	133.2^{a}	129.0^{a}	94.1^{cd}	154.2^{bc}	126.7^{a}
EM	135.9	126.1	103.9	127.4	125	88.7	151.1	122.6
Cv%	4.7	1.2	7.1	5	6.4	8.2	5.9	

Appendix Table 5 Means value for pod per plant of 12 faba bean genotypes tested across seven environments

Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	GM
Gora (S.C.)	8.4^{b}	16.75^{cd}	14.8^{ab}	17.8^{cd}	8.6^{b}	6.5^{cd}	10.3^{ab}	11.8^{a}
EH 010002-1-1	7.5^{b}	10.50^{a}	13.8^{ab}	18.8^{d}	7.5^{ab}	7.1^{d}	10.3^{ab}	10.8^{b}
EH 010008-5	7.1^{ab}	15.00^{bcd}	14.8^{ab}	15.0^{a-d}	8.0^{ab}	4.5^{a}	9.8^{ab}	10.6^{bc}
EH 010051-1	6.9^{ab}	17.50^{d}	17.0^{b}	13.0^{ab}	7.5^{ab}	5.2^{abc}	8.8^{ab}	10.9^{b}
EH 010058-1	4.9^{a}	13.50^{a-d}	14.0^{ab}	12.0^{a}	7.1^{ab}	5.2^{abc}	7.5^{a}	9.2^{d}
EH 010058-2	6.5^{ab}	14.50^{a-d}	13.3^{a}	14.3^{abc}	8.0^{ab}	6.0^{a-d}	10.0^{ab}	9.2^{d}
EH 09012-1	6.3^{ab}	15.00^{bcd}	13.0^{a}	16.3^{bcd}	7.1^{ab}	6.2^{bcd}	9.5^{ab}	10.4^{bc}
EH 09017-5	7.1^{ab}	12.00^{ab}	13.8^{ab}	14.8^{a-d}	7.9^{ab}	5.7^{a-d}	11.3^{b}	10.5^{bc}
EH 09021-1	6.3^{ab}	13.75^{a-d}	14.3^{ab}	15.0^{a-d}	7.3^{ab}	6.3^{bcd}	10.3^{ab}	10.3^{bc}
EH 09028-3	6.6^{ab}	11.75^{ab}	12.5^{a}	16.0^{bcd}	7.8^{ab}	4.6^{ab}	7.8^{a}	10.4^{bc}
EH 09046-3	6.5^{ab}	16.50^{cd}	13.5^{a}	16.0^{a-d}	6.3^{a}	4.8^{abc}	11.0^{b}	9.6^{cd}
Tumsa (S.C.)	7.3^{ab}	13.00^{abc}	12.3^{a}	17.3^{cd}	8.0^{ab}	6.3^{bcd}	10.0^{ab}	10.7^{bc}
EM	6.8	14.2	13.9	15.5	7.6	5.7	9.7	
CV	21.4	17.9	17.1	15.7	16.7	18.4	19.1	

Means within each column followed by the same letter(s) are not significantly different at $P \leq 0.05$ according to DMRT. EM = Environment mean and GM = genotype mean and CV Coefficient of variation

Appendix Table 6 Mean value for seeds per pod of 12 faba bean genotypes tested across seven environment

Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	GM
Gora (S.C.)	2.7^{a}	2.8^{a}	2.8^{a}	3.0^{b}	2.3^{ab}	2.6^{b}	2.3^{ab}	2.6^{b}
EH 010002-1-1	2.9^{ab}	2.8^{a}	3.0^{a}	2.8^{ab}	2.4^{ab}	2.6^{b}	2.3^{ab}	2.7^{b}
EH 010008-5	2.9^{ab}	2.8^{a}	2.8^{a}	3.0^{b}	2.3^{ab}	2.6^{ab}	3.0^{c}	2.7^{b}
EH 010051-1	3.2^{b}	3.0^{a}	3.0^{a}	3.0^{b}	2.6^{b}	2.8^{b}	3.0^{c}	2.9^{a}
EH 010058-1	2.9^{ab}	2.8^{a}	2.8 ^{a}	3.0^{b}	2.7^{b}	2.4^{ab}	2.8^{bc}	2.7^{b}
EH 010058-2	2.8^{ab}	3.0^{a}	2.8 ^{a}	2.5^{a}	2.2^{ab}	2.5^{ab}	2.3^{ab}	2.6^{b}
EH 09012-1	2.9^{ab}	2.8^{a}	3.0^{a}	3.0^{b}	2.3^{ab}	2.5^{ab}	2.0^{a}	2.6^{b}
EH 09017-5	2.9^{ab}	3.0^{a}	2.8 ^{a}	3.0^{b}	2.0^{a}	2.2^{a}	2.5^{abc}	2.6^{b}
EH 09021-1	2.9^{ab}	2.5^{a}	2.8^{a}	2.8^{ab}	2.3^{ab}	2.5^{ab}	2.3^{ab}	2.6^{b}
EH 09028-3	3.0^{ab}	3.0^{a}	3.0 ^{a}	3.0^{b}	2.5^{b}	2.4^{ab}	2.3^{ab}	2.7^{b}
EH 09046-3	2.7^{a}	2.5^{a}	3.0^{a}	3.0^{b}	2.4^{ab}	2.3^{ab}	2.3^{ab}	2.6^{b}
Tumsa (S.C.)	2.9^{ab}	3.0^{a}	2.8^{a}	3.0^{b}	2.5^{b}	2.6^{ab}	2.3^{ab}	2.7^{b}
EM	2.9	2.8	2.8	2.9	2.3	2.4	2.4	2.7
Cv	9.8	14.5	12.5	9.1	13.4	9.5	18.1	

Appendix Table 7 Mean value for Chocolate- spot disease severity (1-9) scale of 12 faba bean genotypes tested across seven environments in 2018/19

Genotypes	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	G/Mean
Gora (S.C.)	3.5^{a}	3.0^{b}	4.0^{ab}	5.5^{a}	2.8^{ab}	2.8^{ab}	2.5^{abc}	2.9^{b-e}
EH 010002-1-1	3.5^{a}	3.5^{a}	3.3^{ab}	6.3^{a}	3.5^{a}	2.8^{ab}	3.0^{a}	3.3^{a}
EH 010008-5	3.3^{a}	2.8^{b}	3.5^{ab}	5.8^{a}	2.5^{ab}	3.0^{a}	2.3^{bc}	2.8^{cde}
EH 010051-1	3.5^{a}	3.3^{ab}	3.3^{ab}	5.3^{a}	3.0^{a}	3.0^{a}	2.8^{ab}	3.2^{a}
EH 010058-1	3.5^{a}	2.3^{b}	3.3^{b}	6.0^{a}	3.0^{a}	2.8^{ab}	2.3^{bc}	3.0^{a-d}
EH 010058-2	3.3^{a}	3.0^{b}	4.0^{ab}	5.3^{a}	3.3^{a}	2.5^{abc}	3.0^{a}	3.1^{abc}
EH 09012-1	3.5^{a}	3.0^{b}	4.0^{ab}	5.8^{a}	3.3^{a}	2.8^{ab}	2.5^{abc}	2.9^{b-e}
EH 09017-5	3.3^{a}	3.0^{ab}	3.8^{ab}	5.8^{a}	3.8^{a}	2.3^{bc}	3.0^{a}	3.0^{a-e}
EH 09021-1	3.5^{a}	3.0^{b}	3.3^{b}	5.5^{a}	1.5^{b}	2.0^{c}	2.3^{bc}	2.7^{e}
EH 09028-3	3.0^{a}	3.0^{ab}	4.3^{a}	6.0^{a}	2.5^{ab}	3.0^{a}	2.0^{c}	2.8^{cde}
EH 09046-3	3.5^{a}	3.0^{ab}	4.3^{a}	5.8^{a}	3.0 ^{a}	2.5^{abc}	2.5^{abc}	3.1^{ab}
Tumsa (S.C.)	3.3^{a}	3.3^{ab}	3.8^{ab}	5.3^{a}	3.0^{a}	2.8^{ab}	2.3^{bc}	2.8^{de}
EM	3.4	3	3.8	5.7	2.9	2.7	2.5	2.7
CV%	14.5	11.7	15.3	17.6	20.5	17.9	20	16.8

Means within each column followed by the same letter(s) are not significantly different at P ≤ 0.05 according to DMRT. EM = Environment mean, GM = genotype mean, CV = Coefficient of variation

Appendix Table 8 Mean value for rust disease score (1-9) scale of 12 faba bean genotypes tested across seven environments in 2018/19

Genotypes	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	G/Mean
Gora (S.C.)	2.3^{ab}	3.5^{bc}	2.0^{ab}	4.8^{abc}	2.3^{a}	2.0^{a}	1.3^{ab}	2.9^{b-e}
EH 010002-1-1	2.5^{ab}	4.5^{a}	3.0^{a}	5.0^{abc}	2.0^{a}	2.0^{a}	1.8^{a}	3.3^{a}
EH 010008-5	2.3^{ab}	3.0^{c}	2.8^{ab}	4.8^{abc}	1.8^{a}	2.0^{a}	1.3^{ab}	2.8^{cde}
EH 010051-1	2.8^{ab}	3.8 ^{b}	3.0^{a}	5.8^{a}	2.0^{a}	2.0^{a}	1.3^{ab}	3.2^{a}
EH 010058-1	2.3^{ab}	3.5^{bc}	2.8^{ab}	5.3^{ab}	2.0^{a}	1.8^{a}	1.5^{ab}	3.0^{abcd}
EH 010058-2	2.8^{ab}	3.5^{bc}	2.5^{ab}	5.5^{ab}	2.0^{a}	2.0^{a}	1.5^{ab}	3.1^{abc}
EH 09012-1	2.3^{ab}	3.5^{bc}	1.8^{b}	5.0^{abc}	2.3^{a}	1.8^{a}	1.3^{ab}	2.9^{b-e}
EH 09017-5	2.8^{ab}	4.0^{ab}	2.8^{ab}	5.0^{abc}	2.0^{a}	1.8^{a}	1.3^{ab}	3.0^{a-e}
EH 09021-1	2.0 ^{b}	3.5^{bc}	2.3^{ab}	4.0^{c}	2.0^{a}	2.0^{a}	1.0^{b}	2.7^{e}
EH 09028-3	2.5^{ab}	3.0^{c}	3.0^{a}	5.0^{abc}	1.0^{b}	2.0^{a}	1.3^{ab}	2.8^{cde}
EH 09046-3	3.3^{a}	4.0^{ab}	2.5^{ab}	5.3^{ab}	1.3^{b}	2.0^{a}	1.8^{a}	3.1^{ab}
Tumsa (S.C.)	2.5^{ab}	3.0^{c}	2.3^{ab}	4.5^{bc}	2.3^{a}	2.0^{a}	1.0^{b}	2.8^{de}
EM	2.5	3.6	2.5	5	1.9	1.9	1.3	3
CV%	23.1	12.3	22.2	13.7	16.8	11.7	23.4	17.6

Appendix Table 9 Mean value for thousand seed weight in (g) of 12 faba bean genotypes tested across seven environments in 2018/19

	Locations							
Genotypes	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	G/Mean
Gora (S.C.)	1132^{b}	704.0^{e}	742.2^{fg}	719.2^{e}	604.5^{cd}	872.5^{cd}	806.0^{efg}	797.2^{f}
EH 010002-1-1	1208^{b}	732.0d^{e}	769.2^{ef}	732.5^{e}	577.0^{d}	895.0^{bcd}	788.5^{fg}	814.7^{ef}
EH 010008-5	1246^{b}	762.0c^{e}	821.^{cde}	860.5^{c}	731.5^{ab}	1001.0^{a}	902.2^{abc}	903.5^{c}
EH 010051-1	1220^{b}	845.0^{ab}	882.2^{ab}	806.0^{d}	656.0^{bcd}	979.0^{ab}	885.2^{bcd}	896.2^{c}
EH 010058-1	1134^{b}	895.2^{a}	924.8^{a}	887.2^{b}	742.5^{ab}	1054.0^{a}	951.8^{a}	941.3^{ab}
EH 010058-2	1244^{b}	723.2^{de}	713.8^{g}	735.5^{e}	663.8^{bcd}	860.5^{d}	763.2^{g}	814.8^{ef}
EH 09012-1	1114^{b}	762.0^{ce}	816.0^{ce}	753.2^{e}	707.2^{b}	905.8^{bd}	827.0^{def}	840.8^{e}
EH 09017-5	1205^{b}	787.0^{bd}	782.2^{df}	758.8^{e}	695.2^{bc}	902.5^{bd}	858.2^{ce}	855.6^{d}
EH 09021-1	1205^{b}	844.0^{ab}	831.0^{bd}	927.^{b}	745.8^{ab}	1022.8^{a}	897.0^{ac}	924.7^{bc}
EH 09028-3	1176^{b}	901.0^{a}	917.8^{a}	971.8^{a}	816.5^{a}	1005.5^{a}	933.8^{ab}	960.3^{a}
EH 09046-3	1277^{a}	858.8^{ab}	807.5^{ce}	751.5^{e}	744.2^{ab}	1000.2^{a}	869.0^{cd}	901.2^{c}
Tumsa (S.C.)	1216^{b}	823.0^{ac}	861.0^{bc}	806.^{d}	736.4^{ab}	959.8^{ac}	871.5^{bd}	896.3^{c}
EM	1198	803.1	822.4	809.1	862.8	954.9	862.6	901.8
CV%	7.8	6.3	4.2	6	4.6	6.3	4.8	5.7

Means within each column followed by the same letter(s) are not significantly different at P ≤ 0.05 according to DMRT. EM = Environment mean, GM = genotype mean, CV = Coefficient of variation

Appendix Table 10 Mean value for Crude protein content of 12 faba bean genotypes tested across seven environments in 2018/19

Genotype	Assasa	Kulumsa	Bekoji	Kofele	Adet	Debark	Holeta	G/mean
Gora (S.C.)	23.9^{a}	24.6^{c}	22.5^{a}	20.8^{de}	20.8^{b}	10.6^{f}	16.4^{i}	25.3^{cd}
EH 010002-1-1	24.9^{a}	24.5^{b}	23.0^{a}	19.0^{f}	20.4^{b}	16.5^{d}	10.2^{k}	26.1^{ab}
EH 010008-5	20.4^{bc}	23.9^{d}	20.3^{b}	21.4^{cde}	20.7^{b}	19.6^{bc}	16.9^{h}	25.3^{bcd}
EH 010051-1	19.9^{c}	22.4^{ef}	18.22^{c}	22.2^{bcd}	22.6^{a}	20.1^{ab}	18.2^{g}	25.8^{abc}
EH 010058-1	20.9^{bc}	17.9^{i}	11.95^{e}	20.4^{ef}	23.2^{a}	16.4^{d}	22.6^{e}	23.8^{ef}
EH 010058-2	12.2^{e}	22.2^{f}	20.2^{b}	20.4^{ef}	20.7^{b}	19.5^{abc}	23.5^{d}	25.2^{cd}
EH 09012-1	20.3^{bc}	26.7^{a}	22.4^{a}	16.4^{g}	19.8^{b}	13.5^{e}	22.2^{f}	25.2^{cd}
EH 09017-5	20.9^{bc}	21.5^{h}	22.7^{a}	20.4^{e}f	14.5^{d}	22.4^{a}	24.7^{a}	26.5^{a}
EH 09021-1	19.0^{c}	17.6^{j}	20.4^{b}	22.6^{abc}	19.7^{b}	19.3^{bc}	12.2^{j}	23.6^{f}
EH 09028-3	22.6^{ab}	21.9^{g}	19.5^{bc}	23.4^{ab}	17.7^{c}	21.1^{ab}	24.7^{a}	26.6^{a}
EH 09046-3	15.4^{d}	12.4^{k}	20.7^{b}	24.1^{a}	20.0^{b}	17.0^{cd}	24.4^{b}	24.6^{de}
Tumsa (S.C.)	12.8^{e}	22.5^{e}	13.3^{d}	21.7^{cde}	18.3^{c}	18.5^{bcd}	23.8^{c}	23.9^{ef}
EM	19.4	21.6	19.6	21.1	19.9	17.9	20.1	25.2
CV%	7.8	0.7	4.6	5	3.4	10.1	0.5	

Means within each column followed by the same letter(s) are not significantly different at $P \leq 0.05$ according to DMRT. EM = Environment mean, GM = genotype mean, CV = Coefficient of variation

8. BIOGRAPHICAL SKETCH

The author was born in 1989 at North Wollo Zone, Amhara National Regional State, Ethiopia. He attended his junior education in Weyniye Primary School from 1997 to 2005 and his Secondary education in Woldia Secondary and preparatory school from 2006 to 2010. The author was joined Wolaita Sodo University in October 2011 and graduated with BSc. degree in plant science on July 13, 2013. Then the author was employed by Gewane Agricultural TEVT College in Afar National regional state Ethiopia.

After six month teaching service, he was employed by Ethiopian Institute of Agricultural Research (EIAR) Addis Ababa based under Kulumsa agricultural research center on May 2014 as a junior plant breeder until he joined the School of Graduate Studies at Bahir Dar University in September 2017 to pursue his Master of Science degree (MSc.) in Agriculture (Plant Breeding).