

**GENOTYPE x LOCATION x MANAGEMENT AND GENETIC  
VARIABILITY OF FABA BEAN (*Vicia faba* L.) GENOTYPES BASED  
ON AGRO-MORPHOLOGY TRAITS**

**MSc THESIS**

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**Genotype x Location x Management and Genetic Variability of Faba  
Bean (*Vicia faba* L.) Genotypes Based on Agro-Morphology Traits**

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**Mesfin Tadele Deyasso**

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Final approval and acceptance of the thesis is contingent upon the submission of the final copy to the Council of Graduate Studies through the Graduate Council of the Department of Plant Sciences.

## **DEDICATION**

I dedicate this thesis to my lovely wife Ayinalem Dadi and my beloved family Beshade Wolde, Molash Hirpo and Tadele Deyasso who have sown the interest of learning in my mind and wishing me a great career throughout my life.

## **STATEMENT OF THE AUTHOR**

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

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## **ACRONYMS AND ABBREVIATIONS**

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	AMMI Stability Value
CS	Chocloate Spot Disease
CSA	Central Statistical Agency
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistics
GAM	Genetic Gain as Percent of the Mean
GCV	Genotypic Coefficient of Variation
GEI	Genotype by Environment Interaction
GLM	General Linear Model
GY	Grain Yield
HARC	Holetta Agricultural Research Center
HSW	Hundred Seed Weight
ICARDA	International Center for Agricultural Research in the Dry Areas
KARC	Kulumsa Agricultural Research Center
LR	Lime Rate
MoALR	Ministry of Agriculture and Livestock Resource
PCV	Phenotypic Coefficient of Variation
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
SNNPR	Southern Nation Nationalities and Peoples Region
UPGMA	Unweighted Pair group Method with Arithmetic Means



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# **Genotype x Location x Management and Genetic Variability of Faba Bean (*Vicia faba* L.) Genotypes Based on Agro-Morphology Traits**

## **ABSTRACT**

*Faba bean is an important source of protein for human and plays an important role in improving soil fertility. However, the productivity of the crop is low due to soil acidity in the highlands of Ethiopia. This research was conducted to estimate genetic variability, trait association and genotype x environment x management interaction on yield of faba bean genotypes at soil of pH 4.66, 4.96 and 4.49 at Holetta, Watebecha Minjaro and Jeldu respectively with and without lime application in 2017. The experiment comprised 50 faba bean genotypes arranged in randomized complete block design with three replications. The analysis of variance (ANOVA) for each management at each location and combined ANOVA over locations showed the presence of significant differences among genotypes for agronomic traits except number of seeds per pod. The ANOVA from AMMI model showed that environment, genotype and genotype x environment interaction contributed 58.05, 16.08 and 14.28%, to total sum square, respectively. The highest mean grain yield of 115.1 and 113.24 g/5plants obtained from Moti and CS20DK with lime over locations, respectively. Eighteen genotypes had mean yield advantage of 0.16 to 17.49% over the recently released variety Numan. However, soil acidity caused an overall mean yield reduction of 32.34% though varied number of genotypes produced higher mean grain yield under lime and without lime application over locations. Considering all stress indices, Wolki, Dosha, Obse, Hachalu and Numan were identified as relatively tolerant genotypes to soil acidity. Computed genotypic coefficient of variations ranged from 1.08-23.05 and 0.94-23.88% and penotypic from 1.20-23.26% and 1.11-24.07%, while heritability and genetic advance as percent of the mean ranged from 24.63 -98.22% and 35.06 - 98.45% and 2.0 - 47.13% and 1.64 - 48.89% without and with lime application, respectively. The highest values for all components computed recorded for hundred seeds weight (HSW) while all lowest values except for  $H^2$  computed for days to maturity. Plant height and HSW had positive and highly significant correlations with grain yield, besides HSW exerted positive direct effect on grain yield at genotypic level suggesting that HSW could be used for indirect selection of genotypes for high grain yield. The genetic distances estimated by Euclidean distances (ED) ranged from 1.23-11.52 and 1.04-11.06 with and without lime. The 50 genotypes were grouped into 10 distinct clusters by Unweighted Pair group Method with Arithmetic Means clustering method based on ED estimated from mean of genotypes for 12 traits over locations for both lime levels. The first three principal components (PC) accounted 77.35 and 77.57% of the total variations observed among genotypes without and with lime, respectively, though single or few traits were not identified as having much contribution than others traits to each PC. Genotypes Tumsa, Cool-0034, EKLS/CSR02019-2-4 and EH07015-7 were identified as relatively stable for yield from stability parameters of AMMI and GGE biplot models. It is therefore, concluded that soil acidity affected the production of faba bean and the presence of genetic variability among faba bean genotypes for yield, yield related traits and soil acidity stress tolerance indices suggested the higher chance of developing varieties for acid soils of central highlands of Ethiopia.*

**Keywords:** Grain yield, Soil acidity, Stability, Stress indices, Limed, Unlimed.

## 1. INTRODUCTION

Faba bean (*Vicia faba* L.,  $2n=2x=12$ ) is among the oldest crops in the world (Singh *et al.*, 2013). It is one of the earliest domesticated food legumes in the world, probably in the late Neolithic period (Torres *et al.*, 2006). The crop is known by many common names such as Faba bean, Fava bean, Broad bean, Horse bean, Windsor bean, Tick beans (small types), most of which refer to a particular subgroup rather than the whole species. It is known with common name of Bakela (Ethiopia), Fulmasri (Sudan), Fève (French) and Yeshil Bakla (Turkey) (Singh *et al.*, 2010).

Faba bean is produced through out the world in different agro-ecological regions in which China followed by Ethiopia, Australia, United Kingdom, France and Egypt are the leading producers (FAOSTAT, 2018). Ethiopia is the leading producer of faba bean in Africa (Akibode and Maredia, 2011) and the crop is the leading pulse crops in the country (Temesgen and Aemiro, 2012). It accounted for about 0.44 million ha (27.34%) and about 0.92 million tons (30.95%) of the total pulse crops production. Oromia followed by Amhara Regional States are the largest producers together accounting for about 83.20% of the country's faba bean production (CSA, 2017/18).

Faba bean is an important source of protein (Zhao *et al.*, 2017). It is a major source of protein rich foods in the developing countries for subsistence farmers (Asnakech *et al.*, 2016). It has a potential to a good meat substitute in many parts of the world where there is demand for non-animal protein sources (Crépona *et al.*, 2010). It is also used as animal feed in industrialized countries (Duc *et al.*, 2010; Tewodros *et al.*, 2015). The crop is also a source of cash to the farmers and foreign currency to Ethiopia (Tewodros *et al.*, 2015; Asnakech *et al.*, 2016; Gemechu *et al.*, 2016). The crop is widely used in rotation with cereals because it fix atmospheric nitrogen (Mulissa and Fassil, 2012; Tewodros *et al.*, 2015; Gemechu *et al.*, 2016). The yield of cereal crops following faba bean is improved and it reduce the amount of artificial nitrogen fertilizer applications for subsistence farmers (IFPRI, 2010). Realizing the potential importance of the crop, the national faba bean project has been made efforts and released 34 varieties for production (MoALR, 2017).



Despite its diverse benefits and the availability of high yielding varieties ( $>3 \text{ t ha}^{-1}$ ) (MoALR, 2017), in Ethiopia the national average yield of faba bean  $2.11 \text{ t ha}^{-1}$  (CSA, 2017/18) has remained low compared to Egypt and United Kingdom  $3.47$  and  $3.83 \text{ t ha}^{-1}$ , respectively (FAOSTAT, 2018). The low average yield of the crop is attributed to susceptibility to biotic and abiotic stresses such as waterlogging, low moisture stress, poor cultural practices and soil acidity (Gemechu *et al.*, 2016) and coupled with poor crop management (Mussa *et al.*, 2008). Soil acidity is one of the major production limiting factors of faba bean in Ethiopia (Mulissa and Fasil, 2014; Endalkachew *et al.*, 2018). Soil acidity is a serious threat to crop production in Ethiopia that strong soil acidity affects 28.1% of the entire country and 43% of the agricultural land mostly in the highlands of the three potential regions (Oromiya, Amhara and Southern Nation Nationalities and Peoples region) (Tegbaru, 2015). Soil acidity is associated with low nutrient availability and it is a major yield-limiting factor for bean production (Fageria *et al.*, 2012). Soil acidity is a significant problem that agricultural producers in tropical and subtropical regions are facing and limit legume productivity (Bordeleau and Prevost, 1994).

Acid soils occur widely in the highlands of Ethiopia where the rainfall intensity is high that leaches substantial amounts of exchangeable bases as a result most of the soils have a pH range of 4.5 to 5.5 with low organic matter and nutrient availability (Temesgen *et al.*, 2011). Soils with  $\text{pH} < 5.5$  resulted retardation of plant growth and low yields of faba bean because acid soils associated with low P availability and deficiency of Ca and Mg or toxicity of Al, Fe and Mn (Dodd and Mallarino, 2005). Furthermore, Getachew *et al.* (2005) reported that acid soils could expose faba bean to greater chocolate spot infection thereby reducing yield. Faba bean is generally acknowledged as being sensitive to soil acidity; and it successfully grows on slightly acidic soils (Chris and Stephen, 2009; Burns *et al.*, 2017).

The pH of soils varies in different parts of Ethiopia. Soils of western highlands of Ethiopia are categorized as moderate to strongly acidic and reduces yield of faba bean (Abebe and Tolera, 2014). A pH of 4.49 to 4.94 are measured from soil samples from three locations (Holetta, Watebecha Minjaro and Jeldu) of central Ethiopia which is considered as strongly acid ( $\text{pH} < 5.5$ ) (Alemu *et al.*, 2016). Improving the productivity of acid soil is major priority as a demand of food and raw materials are increasing rapidly. This can be achieved

by adding limestone to the soil (Maheshwari, 2006). The use of lime is a potential option for soils sustainable management among the other options for restoring soil health and fertility. It is an effective and widespread practice to improve crop yields on acid soils and it make the soil environment better for leguminous plants and associated microorganisms as well as increase concentration of essential nutrients by raising its pH and precipitating exchangeable aluminum (Kisinyo *et al.*, 2012). Different methods can be employed to overcome low production of faba bean on acidic soils ranging from liming of soils (Achalu *et al.*, 2013) to that of selecting host to effective rhizobia species to achieve effective symbiosis (Mulissa and Fassil, 2011). The effect of  $Al^{3+}$  toxicity is ameliorated by the application of P-containing fertilizers (Atemkeng *et al.*, 2011). However, some of these options are less effective if cultivars are sensitive to acid soil and either not available to farmers or farmers are poor to purchase the materials (Sun *et al.*, 2008).

The utilization of soil acidity tolerant genotypes is an important strategy in improving bean yields and reducing cost of production (Fageria *et al.*, 2012). Acid tolerant crop varieties reduce the amounts of lime required (Adane, 2014). The use of acid tolerant varieties remains the first option and low cost if the use of lime is beyond the reach of smallholder farmers. However, faba bean varieties released so far in Ethiopia were not tested and recommended for areas with soil acidity stress. Abebe and Tolera (2014) reported significant effect of lime application on grain yield of faba bean on acid soils of western highlands of Ethiopia. Some other workers reported the significant effects of genotype x environment interaction on grain yield of faba bean in different sets of environments in Ethiopia (Gemechu and Mussa, 2009; Million and Habtamu, 2012; Tamene *et al.*, 2015).

The national and regional variety trials have been part of the faba bean breeding program in national research system for many years in Ethiopia. However, the genotype by environment interaction and stability of faba bean genotypes for yield under different levels of acid soils has not been much studied and documented in central Ethiopia. Similarly, study on soil acidity problems and response to lime application have been done in some part of the country, however, information on the stability of genotypes and heritability of traits under soil management across locations is scanty. Therefore, identifying stable genotypes under acid soil stresses and non-stress environments, traits correlated with yield, genetic variability and estimating broad sense heritability of traits is

of a paramount importance for breeding faba bean genotypes adaptable to acidic soils. Hence, this study was initiated with the following objectives.

### **Objectives**

- To estimate genetic variability in faba bean genotypes under soil acidity stress and non-stress conditions;
- To determine association among characters and the direct and indirect effects of characters on yield of faba bean genotypes; and
- To assess effect of genotype x environment x management interaction on grain yield of faba bean and determine stability of genotypes for yield.

## 2. LITERATURE REVIEW

### 2.1. Origin and Botany of Faba Bean

Faba bean is one of the earliest domesticated cool season food legumes originated in the Middle-East in the prehistoric period (McVicar *et al.*, 2013). It is now widespread and cultivated in Europe, Africa, Central Asia, China, South America, USA, Canada and Australia. It is believed that the crop was introduced to Ethiopia from the Middle East *via* Egypt around 5000 B.C. immediately after domestication (Torres *et al.*, 2006) and now Ethiopia is considered as one of the centers of secondary diversity for faba bean (Yohannes, 2000; Torres *et al.*, 2006).

Faba bean is an annual herb with stiff and upright stems, unbranched 0.3-2 m tall, with one or more hollowed stems from the base (Bond *et al.*, 1985). The leaves are alternate consisting of 2-6 leaflets each up to 8 cm long. Flowers are large, white with dark purple markings, borne on short pedicels in clusters of 1-5 on each auxiliary raceme usually between the 5<sup>th</sup> and 10<sup>th</sup> node; one to four pods develop from each flower cluster, and growth is indeterminate. It has a robust tap root with profusely branched secondary roots. About 30% of the plants in a population are cross-fertilized and the main insect pollinators are honey bees (Bond *et al.*, 1985).

Faba bean is mainly cultivated in the mid and high altitude areas of Ethiopia. It grows at elevations from 1800 to 3000 meters above sea level, with evenly distributed annual rainfall of 700mm - 1000mm during the growth season (Mussa and Gemechu, 2006; Mussa *et al.*, 2008). Faba bean grow on nitosols and cambisol type of soils (Gemechu and Mussa, 2002). It can also grow on vertisol and tolerate water logging than lentil, field pea and common bean (McVicar *et al.*, 2013).

### 2.2. Genetic Resources of Faba Bean

Knowledge of genetic diversity is valuable for germplasms conservation, individual, population, variety or breed identification. Since International Center for Agricultural Research in the Dry Areas (ICARDA) has global mandate on faba bean, it houses 9320 germplasm accessions of faba bean in its Gene Bank (Maalouf, 2011), China Institute of

Crop Science 5229 and Ethiopia Biodiversity Conservation and Research Institute (EBCRI) has 1208 germplasm accessions (Anonymous, 2009).

The agro-biodiversity is the most important component of plant genetic resources, which exists in the primitive forms of cultivated plant species and landraces, obsolete and modern cultivars, weedy types, wild species, genetic stocks, and breeding lines (Kumar *et al.*, 2011). Selection and improvement of crops through breeding to ensure the food security needs the genetic resource as a basic material. The genetic variation among genotypes of various legume crops is being vastly eroded as the modern cultivars are replacing the traditional cultivars over large areas across the world (Duc *et al.*, 2010). On the other hand, the genetic diversity is threatened for breeding the crops for future generations due to the destruction of wild relatives of the cultivated crop species (Wang *et al.*, 2012).

The existence of genetic diversity of faba bean is reported from morphological characterization of faba bean accessions collected from different regions of Ethiopia (Gemechu *et al.*, 2005). Likewise, molecular study using SSR markers of Ethiopian faba bean germplasms collections showed the presence of high genetic diversity (Asnakech, 2014). This information implies the existence of genetic diversity in Ethiopian faba bean genotypes.

### **2.3. Importance and Production Potential of Faba Bean**

Faba bean is used as a source of protein in human diets, as fodder and a forage crop for animals (Maalouf, 2011). It plays a significant role in soil fertility restoration as suitable rotation crop by fixing atmospheric nitrogen; thereby result in savings for smallholder farmers from less fertilizer use (IFPRI, 2010). Therefore, it is a very valuable legume crop that contributes to the sustainability and diversification of cropping systems through improving soil health, decreasing disease, pest and weed buildup (Jensen *et al.*, 2010). It is also grown for green manure production or as a rotation crop with cereals (McVicar *et al.*, 2013). Legumes have the ability to improving soil fertility (Tewodros *et al.*, 2015). Ethiopian farmers are also aware of the role of the crop and widely use in rotation with cereals (Mulissa and Fassil, 2012; Gemechu *et al.*, 2016). From the economic perspective, the crop is a source of cash to the farmers and foreign currency to the country (Tewodros *et al.*, 2015; Asnakech *et al.*, 2016; Gemechu *et al.*, 2016).

Faba bean seed, generally recognized to having good nutritional value, has long history of uses in human foods or animal feeds (Duc *et al.*, 2010; Jensen *et al.*, 2010). This is the result of its valuable and digestible major seed components, starch and proteins. Faba bean genotypes display a large genetic variability for starch, protein and fiber contents (Duc *et al.*, 2011). It is confirmed that faba bean is rich in protein and other nutritional contents (Crépona *et al.*, 2010; Fekadu *et al.*, 2012). In Ethiopia, faba bean is a cheap source of protein for the poor high land inhabitants whose diet is mainly dominated by cereal foods and who cannot afford to purchase animal products.

Ethiopia is the second largest faba bean producer next to China and followed by Australia, France and United Kingdom. These countries accounted more than 75% of world production. China alone produced 34% of all faba beans production (FAO, 2014). Faba bean is leading the country's pulse category in area and production and grown on about 437,106.04 ha of land (27.34%) of the total area covered by pulse and about 0.92 million ton (30.95%) of the total pulse production. Faba bean is produced in different regions of the country, Oromia, Amahara, Tigray, Southern Nation Nationalities and Peoples Region (SNNPR), and Benishangul-Gumuz regional states. Oromia region is the largest (0.48 million ton) faba bean producer in the country followed by Amhara region (0.28 million ton). The two regions together share about 83.20% of the country's faba bean production (CSA, 2017/18). In 2016/2017 cropping season the total area under faba bean cultivation is estimated to be 0.43 million ha of land from which 8.8 million tons are produced (MoALR, 2017). Faba bean is produced in different regions with the required minimal rainfall pattern (Gemechu *et al.*, 2016).

#### **2.4. Production Constraints of Faba Bean**

In spite of its diverse benefits and high production, the productivity of faba bean has remained very low in Ethiopia 2.11 t ha<sup>-1</sup> (CSA, 2017/18) compared to Egypt and United Kingdom 3.47 and 3.83 t ha<sup>-1</sup>, respectively (FAOSTAT, 2018). Lower yield as a result of acid soil were reported compared to the national average yield of faba bean in Ethiopia at pH 5.1 (Degife and Kiya, 2016). The major production constraints of faba bean that attributed to lower productivity and product quality in Ethiopia are associated with stresses from the adverse conditions for crop growth and production imposed by biological (biotic

stresses) and environmental (abiotic stresses) factors, coupled with poor crop management (Gemechu *et al.*, 2016) and the inherent biological limitations (Mussa and Gemechu, 2006).

The biotic factors include diseases, chocolate spot (*Botrytis fabae*), rust (*Uromyces Vicia fabae*), black root rot (*Fusarium solani*), foot rot (*Fusarium avenaceum*), “faba bean gall” (*Olpidium viciae*), insects, African bollworm (*Helicoverpa armigera*), bean bruchids (*Callosobruchus chinensis*) and broad-leaved weed, grass weeds, and parasitic weed (*Orobancha crenata*). Abiotic factors include waterlogging, moisture stress, soil acidity and poor cultural practices (Gemechu *et al.*, 2016). Among abiotic stresses soil acidity associated with low nutrient availability is one of the major production limiting factors of faba bean in the highlands of Ethiopia (Endalkachew *et al.*, 2018) and related stresses (Mulissa and Fasil, 2014). Soil acidity has a dramatic impact on most chemical and biological processes of a crop (Jensen *et al.*, 2010).

## **2.5. Soil Acidity as Production Constraint of Faba Bean**

Soil acidity is a worldwide problem, and sensitivity to acid soils limits the usage of faba bean in some cropping systems. Besides the simple matter of low pH, soil acidity is associated with high availability of  $Al^{3+}$  (Atemkeng *et al.*, 2011). It is one of the major soil chemical constraints which limit agricultural productivity in the mid and highlands of Ethiopia (Workneh, 2013). Soil acidity has become a serious threat to crop production in most highlands of Ethiopia in general and in the western part of the country in particular (Hirpa *et al.*, 2013). Currently, it is estimated that 28.1% of the entire country and 43% of the agricultural land mostly in the highlands of the three high potential regions (Oromia, Amhara and SNNPR) are affected by soil acidity (Tegbaru, 2015). Thus soil acidity is one of the environmental factors that limit plant production because it is often associated with increased Aluminium (Al) and Manganese (Mn) toxicity and limit calcium and Phosphorus (P) up take by plants (Hungria and Vargas, 2000). Soil acidity hinders legume production more than any other crops as it affects the complex symbiotic association of the legume host and the symbiotic bacteria (Graham, 1992).

Soil acidity is a natural process with major difficulties on plant growth. As soils become more acid, particularly when the pH drops below 4.5, it becomes increasingly difficult to produce food crops. As soil pH declines, the supply of most plant nutrients decreases while aluminum and a few micronutrients become more soluble and toxic to plants (Harter, 2007). In practical terms, soils pH between 6.6 and 7.3 are considered as neutral. Soils in the range 5.6 to 6.5 are moderately acid and below 5.5 strongly acid (Alemu *et al.*, 2016).

### **2.5.1. Causes of Soil Acidity**

Soil acidity is caused by various mechanisms that make imbalance of the carbon and nitrogen cycles such as, composition of soil parent materials, excretion of H<sup>+</sup> from plant roots to balance excess uptake of cations over anions, continuous use of acid forming nitrogen fertilizers (Urea, DAP etc) and accumulation of organic matter that contains different acid functional groups from which these ions can dissociate. The cause of soil acidity in the highlands of Ethiopia is mainly high amount of rainfall that exceeds evapotranspiration that leaches substantial amounts of exchangeable bases from the soil surface. As a result, most of the soils have a pH range of 4.5 to 5.5 and low nutrient availability (Temesgen *et al.*, 2011). Agricultural practices like leaching of nitrate nitrogen and erosion of topsoil organic matter aggravate soil acidity.

### **2.5.2. Impacts of Soil Acidity on Faba Bean Production**

Soil acidity is a significant problem that agricultural producers in tropical and subtropical regions are facing and limit legume productivity (Bordeleau and Prevost, 1994). Acid soil infertility is a result of severe chemical imbalance caused by toxic levels of exchangeable aluminum, manganese and hydrogen ions. This resulted in parallel critical deficiency of available nitrogen, phosphorus, potassium, calcium, magnesium, zinc and molybdenum which limits the growth and production of legumes (Fageria, 2002). Phosphorus nutrition plays important role in legumes and symbiotic N<sub>2</sub> fixation. The formation of seeds and fruits is especially depressed in plants suffering from P deficiency. Thus, not only yields but also poor quality seeds and fruits are obtained from P deficient soils (Fageria, 2009). It has been reported that faba bean requires high P for energy expenditure for nodule formation (Kopke and Nemecek, 2010). In acid soils P fixation takes place thereby availability of P is too low.



Soil acidity is the major constraints of faba bean production in the highlands of Ethiopia (Endalkachew *et al.*, 2018). Most legumes prefer pH > 5.0 to a depth of at least 20cm. Acidic layers below 5 cm adversely affect root growth, nodulation, plant vigour and the nitrogen fixation potential of acid-sensitive pulses (Burns *et al.*, 2017). Faba bean grows best in soils with pH ranging from 6.5 to 9.0 (Jensen *et al.*, 2010) and poorly perform at a pH values of 5 or less (French & White, 2005). However, some accessions remain productive in soil with pH as low as 4.5 (Singh *et al.*, 2012). In acid soil Aluminum and Manganese toxicities provide a hostile environment to root growth (Ouertatani *et al.*, 2011). Poor soil fertility associated with low soil pH adversely affect the growth and yield of faba bean (Endalkachew *et al.*, 2018). It was reported that faba bean varieties gave lower yield compared to the national average yield (1.52 t ha<sup>-1</sup>) in Ethiopia due to strong acidic status of the soil (pH 5.1) and the highest seed yield was harvested from variety Moti followed by Gora, Walki and Geblecho 1.03, 1.01, 0.99 and 0.95 t ha<sup>-1</sup> and the lowest from Hachalu and CS20DK 0.68 and 0.69 t ha<sup>-1</sup>, respectively (Degife and Kiya, 2016).

Acid soils might expose faba bean to greater chocolate spot infection thereby reduce yield and it was also suggested that acid soil reduce plant vigour and increase disease susceptibility (Getachew *et al.*, 2005; Elliot and Whittington, 2009). Response of faba bean genotypes to soil acidity at early stage was diverse. Some genotypes showed less than 3% reduction in root length in acid condition, whereas other genotypes showed significant reductions 30-40% hindrance in root growth. Specifically, Dosha, NC 58 and Kassa were tolerant to acidity showing less than 3% reduction in taproot length (Kiflemariam *et al.*, 2017). Similar results were reported in soybean that acid soil affects root growth, agronomic and yield traits and also increase in soil acidity have a deleterious effect on the overall growth of the crop (Michael *et al.*, 2011).

## **2.6. Management Strategies of Soil Acidity**

In order to feed the increasing population from existing natural resources, significant advances are required in the field of agricultural production. Increasing agricultural productivity from the existing arable land in an environmentally friendly manner; however, is a big challenge for the global agricultural system (Robertson and Swinton, 2005). More

specifically, increased efforts are needed to raise crop productivity from acid affected soils by combining crop production and management practices and genetic improvement of crops that are environmentally sustainable and socially acceptable.

To improve production and productivity of faba bean in soil acidity problem areas, different strategies need to be implemented: use of soil acidity tolerant genotypes or fitting the genotype to the environment for sustainable production or using soil management practices to fit the environment to genotypes, use of integrated biological (tolerant genotype) and appropriate soil management practices such as liming. Therefore, soil acidity problems for faba bean production can be overcome by growing genotypes which are adapted to acid soil condition in circumstances where other soil amendment strategies are not readily practical. However, this is not possible until these tolerant genotypes are developed.

#### **2.6.1. Soil Amendment (Liming)**

Liming acid soil makes the soil environment better for leguminous plants and associated microorganisms as well as increase concentration of essential nutrients by raising its pH and precipitating exchangeable aluminum (Kisinyo *et al.*, 2012). The amount of lime needed to achieve a certain pH depends on the pH and the buffering capacity of the soil. The buffering capacity is related to the cation exchange capacity. Soils with a high buffering capacity require larger amounts of lime to increase the pH than soils with a lower buffering capacity (Derib, 2014).

Lime requirement refers to the amount of lime required to neutralize all or part of the acidity in soil (both solution and reserve) from an initial level to a desired or target less acid condition. The target level of soil acidity depends both on the soil and crop type. The lime rate depends on the tolerance level of crops and reserve acidity of soil which maintains a given concentration of toxic  $H^+$  and  $Al^{3+}$  in soil solution. Neutralization of soil acidity involves not only neutralization of  $H^+$  in soil solution but also all or part of the soil's reserve acidity (Eshetu, 2011). A lime requirement test is necessary for determining the correct amount of lime to apply because over-applications may decrease soil productivity. Consequently, for soils having less than pH 5.5 performing a lime requirement test where legumes are grown is vital necessary (Mahler, 2000).

A previous report on faba bean evaluated with and without lime application on acid soil showed that liming significantly influenced all the growth parameters; particularly pronounced for plant height and pod number. Applied lime enhanced nutrient use efficiency of both P and K and this is reflected by increased pod number per plant. Thus, application of lime and mineral fertilizers together further increased grain yield (Ouertatani *et al.*, 2011). Similarly, studies indicated that significant grain yield increment resulted from neutralization of excess acidity over time with lime (Fuentes *et al.*, 2006). However, lime is slow acting of long duration (Follet *et al.*, 1981). As a result, a significant increase in yield is expected in the next planting season (Adane, 2014). Amelioration of acid soils by surface application of lime and other materials is the main commercially available option. However, lime application on surface soil generally does not have a rapid effect in reducing the subsoil acidity and mixing lime with the subsoil is generally not economically feasible. Therefore, selecting and growing acid-tolerant cultivars may be a sustainable approach for the better growth and productivity of pulse crops on acid soils (Hynes and Mokolobate, 2001).

### **2.6.2. Use of Soil Acidity Tolerant Crops**

The use of acid tolerant crops and pasture is a low cost input that is easily adopted and can often change the cost portion to value more favorable for initiating lime use. The choice of crops with better yield potential is obviously important for economic reasons. However, the choice of variety is also an important management strategy to offset acidification and plants that tolerate soil acidity use water through a better root growth (Coventry *et al.*, 1997). In Ethiopian Triticale, Oat and Potato grow on acid problematic areas and considered as acid tolerant crops.

Cultivated crops vary in their tolerance to soil acidity. Therefore, selecting and growing species and variety adaptable to acidic soils is one solution (Scott *et al.*, 1997). Study on soil acidity stress tolerance of faba bean is scanty. Nevertheless, wide diversity exists among faba bean landraces for agro-ecological adaptation (French & White, 2005) and biotic and abiotic stress resistance (Khazaei *et al.*, 2013). So far in Ethiopia lime based managements of acid soil were conducted in different location with different crops soybean (Workneh, 2013), haricot bean (Adane, 2014), faba bean (Endalkachew *et al.*,

2018). These authors reported that, the limitation of lime application with its wider utility is that the amount of lime needed per hectare is in tons and the cost also is not affordable by small scale farmers (Workneh, 2013; Adane, 2014; Endalkachew *et al.*, 2018). Therefore, use of soil acidity tolerant crops in acid prone areas is eco-friendly and economically feasible alternative when considered as a management option.

## **2.7. Breeding Faba Bean Tolerance to Soil Acidity**

Faba bean breeding strategy in Ethiopia targets specific adaptation for exploiting genetic potential of cultivars that are responsive to optimum environments and for widely adapting (stable) varieties that consistently perform better under various environments. In addition, breeding for specific adaptation of crop cultivars that can adapt under resource poor environments like soil acidity prone areas is very important. Under stressed condition the ultimate goal is to fit the cultivars to the environment by developing varieties with modest demand for resources and having resistance and better performance under stressed conditions (Gemechu *et al.*, 2016).

Selection of parents having genes for efficient use under low soil fertility and tolerance to soil acidity stress needs to be identified for use in hybridization, as genetic manipulation is preferred to the continual manipulation of the growing environment. As stated by Mussa *et al.* (2008) due to production cost and environmental concerns particularly to the resource-poor farmers do not justify the economics to apply external inputs in faba bean production. Therefore, the identification of acid soil tolerant genotypes as a source of parental materials for hybridization to develop tolerant genotypes becomes the best option for sustainable production in soil acidity prone areas.

Sources of tolerance to abiotic production constraints of faba bean in Ethiopia such as soil acidity or low soil pH, poor soil fertility and frost have not yet been identified although genetic variability for most of the stresses is expected to exist (Mussa *et al.*, 2008). Breeding success for different biotic and abiotic stresses have been reported in faba bean for chocolate spot disease (Tamene *et al.*, 2015; Asnakech *et al.*, 2016) and for high moisture stress (water logging) (Mussa *et al.*, 2008) by identifying different materials for sources of tolerance introduced from ICARDA and collected from areas with water logging problem as source of resistance for hybridization. As a strategy of last alternative,

where soil pH has fallen to values less than 6.0, plant breeding or biotechnology to improve resistance of plants to acidity is necessary (Conyers *et al.*, 2005). Genetic improvement of crops to improve productivity is preferred to the continual manipulation of the growing environment because of unaffordable production costs by resource-poor farmers to purchase inputs. Varietal selection on target production environment is very important to maximizing gains from breeding efforts (Gemechu, 2007a). Thus, breeding acid soil tolerant genotypes has to be done in acid prone environments.

The previous effort to identify soil acidity tolerant faba bean genotypes showed that, there were great variation among genotypes with acidity tolerance level ranging from 3% to 40% hindrance in taproot growth at pH 4.5 (Kiflemariam *et al.*, 2017). The information indicates the need to evaluate faba bean genotypes for acid tolerance and the chance of getting soil acidity stress tolerant faba bean genotypes from the existing genetic resource.

## **2.8. Genetic Variability in Faba Bean**

### **2.8.1. Phenotypic and Genotypic Coefficients of Variation**

The knowledge of phenotypic (PCV) and genotypic (GCV) coefficients of variation helps to determine the type of breeding strategy to be followed. The close correspondence between the GCV and PCV variation in faba bean has been reported that variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors (Solieman and Ragheb, 2014; Hamza *et al.*, 2017; Mostafa *et al.*, 2017). The high phenotypic and genotypic coefficients of variation is an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding (Ejigu *et al.*, 2016).

The high PCV values than GCV implies greater influence of environmental factors for the phenotypic expression of these traits that make difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the traits. Haridy and El-Said (2016) and Sekhon *et al.* (2017) reported high environmental variance than genotypic variance for days to 90% maturity and plant height and days to 50% flowering, days to 90% maturity and plant height, respectively. Likewise, Hamza *et al.* (2017) reported high phenotypic variance for days to 50% flowering and plant height.

### 2.8.2. Heritability and Expected Genetic Advance

The magnitude of heritability also helps in predicting the behavior of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement (Allard, 1960). The traits with high to moderate heritability, indicates that it may respond moderate to high for phenotypic selection (Singh and Ceccarelli, 1996). Many authors (Gemechu and Mussa, 2009; Million and Habtamu, 2012; Tafere *et al.*, 2013; Bakhiet *et al.*, 2015; Sharifi, 2015; Hamza *et al.*, 2017) also reported high estimates of broad sense heritability for hundred seed weight and grain yield in faba bean genotypes at varied environments and number of genotypes. El-Badawy *et al.* (2012) and Asnakeh (2014) reported high heritability for chocolate spot disease.

The genetic gain expected from selection of the top 5% of the genotypes, as a percent of the mean indicates the genetic progress that can be made in the breeding program (Allard, 1960). High genetic advance as percent of the mean (GAM) were reported for number of pod per plant (Million and Habtamu, 2012; Bakhiet *et al.*, 2015). Low GAM was reported for hundred seed weight and grain yield (Hamza *et al.*, 2017). Million and Habtamu (2012) reported GAM values of 12.32% for number of seeds per plant and 35.46% for seed yield. It was suggested by Johnson *et al.* (1955) the importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much progress can be made through selection and selection based on phenotypic performance of genotypes would be effective to improve traits that have high genetic advance as percent of mean coupled with high heritability estimates because high heritability will not always be associated with high genetic advance.

It was reported that heritability and genetic advance values did not show similar trend under favorable and unfavorable environments (Singh, 2002; Gemechu *et al.*, 2015). Favorable environment show higher estimates of heritability and genetic advance values than unfavorable environment (Singh, 2002). Likewise, Gemechu *et al.* (2015) reported that heritability values 60-93% and 59-93% and genetic advance 4-62% and 4-79% in the absence and presence of phosphorus, respectively in chick pea. Under unfavorable conditions the values of heritability and genetic advance may be masked due to a greater genotype by environment interaction (Rosielle and Hambin, 1981).

## 2.9. Genotype by Environment Interaction

The differential response of genotypes to changing environmental conditions is known as genotype x environment interaction (GEI). GEI is important for breeding program because it brings about differences in the performance of a test material in several locations. The GEI determines whether a genotype is widely adapted or has specific adaptation. Differential responses of crop varieties to variable environmental conditions limit accurate yield estimates and identification of high yielding stable ones. In order to identify stable genotypes, the GEI can be evaluated using stability statistics that are assignable to each genotype evaluated across a range of environments (Fernandez, 1991). Environment is the sum total of physical, chemical and biological factors that influence the development of an organism (Dabholkar, 1992).

Baker (1988) defined GEI as the difference between the phenotypic value and the value expected from the corresponding genotypic and environmental values. Conducting multi-environment trial enables to identify adaptability of a crop variety and this helps to understand the nature and magnitude of GEI. The GEI is an important feature of crop improvement that should be considered in a breeding program aimed at developing crop varieties for multi-environments (Fekadu *et al.*, 2012). The presence of a significant GEI for quantitative traits, such as grain yield, can seriously limit genetic gains in selecting superior genotypes for the development of improved varieties because environmental variation causes differential genotypic responses that result in rank changes of genotypes (Kang, 1990). The presence of significant GEI reduces the association between genotype and phenotype and thereby reduces the genetic advance; the best option is either to exploit it by selecting superior genotypes for specific environments or to avoid it by selecting widely adapted and stable genotypes across a wide range of environments (Ceccarelli, 1989). The determination of grain yield stability of genotypes enables breeders for cultivar recommendations despite the variable environmental conditions (Yan *et al.*, 2007). Therefore, information on GEI is important to plant breeders for the development, selection and recommendation of cultivars that are suitable for growth in different environments.

Various analysis methods have been used to explore GEI and to identify superior genotypes with wide or specific adaptation to different environments. The additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype x environment interaction effects (GGE-biplot) model are the two frequently used models for statistical analyses of multi-environment trials (Gauch *et al.*, 2008). It is better to use more than one stability statistics model to provide an accurate picture because of the genotype's multivariate response to varying environments (Lin *et al.*, 1986).

### **2.9.1. AMMI Stability Model**

The additive main effects and multiplicative interaction (AMMI) model is one of the multivariate analysis techniques. It combines the analysis of variance of genotypes and the environment main effects with principal component analysis of the GEI into a unified approach (Gauch and Zobel, 1996). The results can be graphically represented in an easily interpretable and informative biplot that shows both main effects and GEI. The AMMI model has been used extensively with great success over the past years to analyze and understand various crops GEI (Yau, 1995).

The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach to understand GEI and obtain better yield estimates. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance over diverse environments. Genotypes represented by points near the origin of axes reveal limited GEI. On the contrary, genotype that is far from the origin has a much better response to environments and for which the angle formed between the genotype points, the origin and the environment point is small (Mulusew *et al.*, 2008). The results of AMMI can be graphically represented in an easily interpretable and informative biplot, which shows both main effects and GEI (Gauch and Zobel, 1996). The importance of AMMI to identify superior genotypes for specific or wide adaptation has been proved and applied for faba bean (Mulusew *et al.*, 2008; Teklay *et al.*, 2015; Asnakech *et al.*, 2017). The AMMI model gives information on main and interaction effects (Fasahat *et al.*, 2014). However, AMMI is incapable to found close relationship between high performance and stability (Carbonell *et al.*, 2004).



### 2.9.2. GGE-Biplot

The GGE-biplot approach is preferred to AMMI since only G and GEI are important and E is not important, and therefore only these components must be simultaneously considered (Yan *et al.*, 2007). The GGE biplot analysis best identifies GEI pattern of data and clearly shows which variety performs best in which environments, and thus facilitates mega-environment identification than AMMI. Otherwise, both GGE and AMMI models are equivalent as far as their accuracy is concerned. It is one of the most frequently used analysis methods to investigate the stability of genotypes over environments. The GGE biplot is a visual statistical tool for examining the performance of genotypes tested in different environments (Yan, 2001). The GGE biplot model has been utilized to identify breeding lines and cultivars of faba bean that are resistant to chocolate spot diseases (Asnakech *et al.*, 2017) and for parasitic weed broomrape resistance (Teklay *et al.*, 2015). In most cases environment main effect is the major source of genotypic variation (Yan, 2001). This large yield variation due to environments is not relevant to cultivar evaluation and mega-environment investigation (Gauch and Zobel, 1996). Therefore, G and GE interaction are the only important components for yield variation. Similarly, most of the previous GEI studies on faba bean revealed that environment accounts for the major portion of the yield variation (Mulusew *et al.*, 2008; Fekadu *et al.*, 2012; Teklay *et al.*, 2015; Asnakech *et al.*, 2017).

Where environmental differences are great, as in drained and un-drained waterlogged Vertisols, it may be expected that genotype by environment interaction effect is also high. In such cases, care must be taken not to use statistical models that omit inclusion of the GEI effects unless otherwise proven that the performance of the given crop or the given trait is not considerably influenced by environmental fluctuations (Gemechu and Mussa, 2009). Since faba bean is grown across a wide range of environments in the highlands of Ethiopia, it is exposed to the effect of GEI. It is very essential to study the nature and magnitude of GEI and stability of faba bean genotypes in Ethiopia. There is little information concerning the GEI and cultivar stability on faba bean in Ethiopia (Fekadu *et al.*, 2012). The investigation of GEI in multi-environment trials is thus important in the development of soil acidity tolerant, high yielding and stable faba bean genotypes.

### 3. MATERIALS AND METHODS

The experiment was conducted at three locations of two districts at Welmera (Holetta and Watebecha Minjaro) and Jeldu district. The experimental materials and site descriptions are presented hereunder.

#### 3.1. Description of the Study Sites

The experiment was conducted during 2017 main cropping season under rain fed condition at three locations Holetta, Watabecha Minjaro and Jeldu. Holetta agricultural research center is located at 09<sup>0</sup> 00'N, 38<sup>0</sup> 30'E at an altitude of 2400m above sea level. It is 29 km away from Addis Ababa on the road to Ambo and characterized with annual rainfall of 1072 mm, mean relative humidity of 58.8%, and mean maximum and minimum temperature of 24.1<sup>0</sup>C and 6.6<sup>0</sup>C, respectively. The soil of the center is Nitosol (Gemechu, 2007b) which is characterized with pH 4.66.

Watabecha Minjaro is located at 09<sup>0</sup> 05' 55" N, 38<sup>0</sup> 36' 21" E, and altitude 2565 meter above sea level in the central highlands of Ethiopia. The site is typically characterized by flat plains with cool subtropical climate. Annually receives about 1100 mm rainfall. The mean maximum and mean minimum temperatures are 23.3<sup>0</sup>C and 8.7<sup>0</sup>C, respectively. The soils is categorized as Nitisols with deep red and well-drained tropical soil having a pH range of 4.5 to 5.5, contain low organic matter (<20 g kg<sup>-1</sup>) and low nutrient availability (Temesgen *et al.*, 2017).

Jeldu sub- station is one of the cool season crops trial sites which is located at an altitude of 2800m above sea level at 09<sup>0</sup> 16'N and 38<sup>0</sup> 05'E. It receives average annual rain fall of 1200 mm with an average annual maximum and minimum temperature of 16.9<sup>0</sup>C and 2.06<sup>0</sup>C respectively (Wondimu *et al.*, 2011). The area has a soil pH of 4.49.

#### 3.2. Experimental Materials and Design

A total of 50 faba bean genotypes were used in the study: 22 released varieties and 28 pipe line materials that were collected from Holetta Agricultural Research Center (HARC) and Kulumsa Agricultural Research Center (KARC) (Table 1). Additionally, a product of Derba Cement Factory limestone (CaO) collected from HARC was used.

The experiment was arranged in Randomized Complete Block Design (RCBD) with three replications using adjacent block technique (growing the two sets adjacent to each other). Each block was divided into two adjacent sub-blocks to accommodate both with and without lime plots. The spacing between adjacent and within blocks were 1.5 and 2m respectively. The experimental plots consisted of one row of 4m length and 40cm row spacing continuously and 10cm between plants (1.6m<sup>2</sup>). Undamaged clean seeds of each genotype were selected to a reasonably uniform size by hand sorting and whole set of genotypes were planted separately in alternating adjacent sub-blocks with and without lime in side-by-side pairs.

One sub-block in each block was limed and not to the other sub-block. Blended Fertilizer was applied at the rate of 19 kg N, 38 kg P<sub>2</sub>O<sub>5</sub> and 7 SO<sub>4</sub> in the form of NPS (121kg/ha) that can substitute DAP in each area during planting. One faba bean variety (Dosha) was planted as a border row in each block to avoid border effect. The other agronomic practices were carried out uniformly to all genotypes as per the recommendations made by the national research system for faba bean. Five random faba bean plants in each row were used for data collection to determine yield and yield components.

Table 1. Description of 50 faba bean genotypes used in the study

No.	Genotypes	Code	Year of release	Origin	Seed source
1	Cool-0030	G1	---	Collection	HARC
2	Wolki <sup>¥</sup>	G2	2008	Hybridization	HARC
3	EKLS/CSR02012-2-3	G3	---	Hybridization	KARC
4	Obse	G4	2007	Hybridization	HARC
5	NC58	G5	1978	Collection	HARC
6	Ashebeka <sup>¥</sup>	G6	2015	Hybridization	KARC
7	Hachalu <sup>¥</sup>	G7	2010	Hybridization	HARC
8	Degaga	G8	2002	Introduction	HARC
9	EH09031-4	G9	---	Hybridization	HARC
10	Holetta-2	G10	2001	Introduction	HARC
11	EH09007-4	G11	---	Hybridization	HARC
12	EH07023-3	G12	---	Hybridization	HARC
13	EK05006-3	G13	---	Hybridization	KARC
14	EKLS/CSR02014-2-4	G14	---	Hybridization	KARC
15	Numan	G15	2016	Hybridization	KARC

“---” = pipeline genotypes, ¥ = Varieties released for areas with waterlogging problems, HARC and KARC= Holeta and Kulumsa Agricultural Research Center, respectively.

Table 1. Continued.

No.	Genotypes	Code	Year of release	Origin	Seed source
16	Bulga 70	G16	1994	Collection	HARC
17	EK05001-1	G17	---	Hybridization	KARC
18	Dosha	G18	2008	Collection	HARC
19	Gora	G19	2012	Hybridization	KARC
20	EH08035-1	G20	---	Hybridization	HARC
21	Wayu	G21	2002	Collection	HARC
22	EKLS/CSR02023-2-1	G22	---	Hybridization	KARC
23	Mesay	G23	1995	Hybridization	HARC
24	EH09004-2	G24	---	Hybridization	HARC
25	EH06088-6	G25	---	Hybridization	HARC
26	EKLS/CSR02017-3-4	G26	---	Hybridization	KARC
27	Kasa	G27	1980	Collection	HARC
28	Cool-0025	G28	---	Collection	HARC
29	EH06070-3	G29	---	Hybridization	HARC
30	EKLS/CSR02010-4-3	G30	---	Hybridization	KARC
31	Cool-0031	G31	---	Collection	HARC
32	Cool-0018	G32	---	Collection	HARC
33	EKLS/CSR02028-1-1	G33	---	Hybridization	KARC
34	EK 05037-4	G34	---	Hybridization	KARC
35	Cool-0035	G35	---	Collection	HARC
36	KUSE2-27-33	G36	1979	Introduction	HARC
37	EH07015-7	G37	---	Hybridization	HARC
38	Cool-0024	G38	---	Collection	HARC
39	Selale <sup>¥</sup>	G39	2002	Collection	HARC
40	Moti	G40	2006	Hybridization	HARC
41	EH06027-2	G41	---	Hybridization	HARC
42	EKLS/CSR02019-2-4	G42	---	Hybridization	KARC
43	EH09002-1	G43	---	Hybridization	HARC
44	Tumsa	G44	2010	Hybridization	HARC
45	Gebelcho	G45	2006	Hybridization	HARC
46	EK05037-5	G46	---	Hybridization	HARC
47	Didi'a <sup>¥</sup>	G47	2014	Hybridization	KARC
48	Cool-0034	G48	---	Collection	HARC
49	CS20DK	G49	1977	Collection	HARC
50	Tesfa	G50	1995	Introduction	HARC

“---” = pipeline genotypes, ¥ = Varieties released for areas with waterlogging problems, HARC and KARC= Holeta and Kulumsa Agricultural Research Center, respectively.

### **3.3. Experimental Procedure**

#### **3.3.1. Treatment Application and Field Activities**

All field activities were done with standard production practices developed for faba bean. The land was cultivated by tractor at Holetta and Jeldu and by oxen plough at Watebecha Minjaro and pulverized by hand and rows were made to plant the seeds. As suggested by Temesgen *et al.* (2017) lime was applied one month ahead of planting to give time for incorporation on block bases at each location based on the lime requirement of the locations as a result of soil test. Planting of the experiment was done in July 2017 at all locations. Fertilizer was applied during planting in the form of NPS (19 kg N, 38 kg P<sub>2</sub>O<sub>5</sub> and 7 SO<sub>4</sub> using a rate of 121 kg ha<sup>-1</sup>. Weeding was carried out timely to eliminate any external competition by weeds. Harvesting was done in November 2017 at Holetta and Watebecha Minjaro and in December 2017 at Jeldu. `

#### **3.3.2. Soil Sampling, Preparation and Analysis**

Prior to planting, ten surface soil samples (20 cm depth) were taken randomly from representative spots of the entire experimental field using an auger and composited to one representative sample. The composite sample was air-dried at room temperature, thoroughly mixed and ground to pass through a 2mm sieve and then analyzed for: particle size distribution (soil texture), pH, organic carbon, cation exchange capacity, exchangeable bases (Na, K, Ca and Mg), total nitrogen, available Phosphorus, exchangeable acidity, extractable aluminium and micro nutrients (Zn, Fe, Mn and Cu). One soil sample for bulk density analysis at each location was taken by core sampler. Moreover, after harvesting, surface soil samples 0-20 cm were collected randomly from five spots in each lime treated blocks and analyzed to know the level of increment in parameters analyzed before planting with the exception of soil texture and bulk density.

Soil bulk density was determined using a core sampler and soil pH was determined by potentiometric method at 1:2.5 soils: water ratio (Van Reeuwijk, 1992). Cation exchange capacity was determined by 1M ammonium acetate method at pH 7 (Chapman, 1965) whereas organic carbon was determined by the Walkley and Black method (Walkley and Black, 1934) and total nitrogen by the micro-Kjeldhal method (Jacson, 1958), available P was determined by the Olsen method (Olsen *et al.*, 1954). Soil particle size distribution

was determined by the hydrometer method (Bouyoucus, 1962). Exchangeable Na, K, Mg and Ca were determined by Ammonium acetate- AAS method and extractable Al, Fe, Zn, Mn and Cu by DTPA-AAS method. Analysis of all the soil parameters was done at Holetta agricultural research center soil and plant analysis laboratory.

### 3.3.3. Lime Rate Determination and Application

Lime rate (LR) was determined based on the soil laboratory analysis results and applied uniformly on the lime treated blocks one month ahead of planting. The amount of lime applied was determined using the exchangeable acidity, bulk density of the soil as well soil depth (Plough depth) and area of the experimental plot based on the equation presented below (Hellmuth, 2016).

$$LR \left( \text{CaO} \left( \frac{\text{kg}}{\text{ha}} \right) \right) = \frac{EA \left( \frac{\text{cmol}}{\text{kgsoil}} \right) * DS(\text{m}) * A(\text{m}^2) * \rho b \left( \frac{\text{g}}{\text{cm}^3} \right)}{2} * LF$$

Where: LR= Lime rate; EA= Exchangeable acidity; DS= Depth of soil; A= Area of land;  $\rho b$  = Bulk density; LF= Liming factor/adjustment factor (LF= 2) is determined based on crop response.

The lime requirement for each site varies depending on the soil test results. Therefore, the total area lime applied were 240m<sup>2</sup> at each site of three blocks with 80m<sup>2</sup> each. The lime rate applied at each location presented as follows:

$$LR (\text{Holetta}) = 1.01 \text{ cm/kg} \times 0.15 \text{ m} \times 80 \text{ m}^2 \times 1.26 \text{ g/cm}^3 = 15.2 \text{ kg/block}$$

$$LR (\text{Watebecha Minjaro}) = 0.98 \text{ cm/kg} \times 0.15 \text{ m} \times 80 \text{ m}^2 \times 1.12 \text{ g/cm}^3 = 13.2 \text{ kg/block}$$

$$LR (\text{Jeldu}) = 3.36 \text{ cm/kg} \times 0.15 \text{ m} \times 80 \text{ m}^2 \times 1.05 \text{ g/cm}^3 = 42.3 \text{ kg/block}$$

The lime rate applied were 1.91, 1.65 and 5.29 t/ha at Holetta, Watebecha Minjaro and Jeldu respectively.

### 3.4. Data Collection

#### 3.4.1. Data Recorded on Plot Basis

**Days to 50% flowering:** Number of days from planting to the date on which 50% of plants in the plot produce at least their first flower.

**Days to 90% physiological maturity:** Number of days from the date of planting to the date on which 95% of the pods reach physiological maturity.

**Grain filling period:** The number of days between days to 50% flowering and days to 90% physiological maturity.

**Hundred Seed Weight (g):** The weight in gram of one hundred randomly taken seeds from each experimental plot adjusted to standard moisture content for pluses (10%).

**Chocolate spot disease:** The severity of chocolate spot disease was recorded using the scale of Bernier *et al.* (1993), as follows: 1 = no disease symptoms or very small spots (highly resistant), 3 = few small disease lesions (resistance), 5 = some coalesced lesions, with some defoliation (moderately resistant), 7 = large coalesced sporulating lesions, 50% defoliation some dead plants (susceptible), 9 = extensive, heavy sporulation, stem gridling, blackening and death of more than 80% of plants (heavily susceptible).

#### 3.4.2. Data Recorded on Plant Basis

Data for the following traits were recorded on five randomly pre-tagged plants from each experimental plot. The average of the five plants in each experimental plot was used for statistical analysis.

**Plant Height (cm):** The average height of five plants in each plot measured in centimeter from the ground surface to the top of the main stem at maturity.

**Number of podding nodes per plant:** The average number of podding nodes of five plants in each plot.

**Number of pods per podding node:** The average number of pods per podding nodes of five plants in each plot.

**Number of pods per plant:** The average number of pods of five plants in each plot.

**Number of seeds per pod:** Average number of seeds of five random sample pods in each plot.

**Grain yield (g/5 plants):** Grain yield in gram from five random plants at the middle of the row adjusted to standard moisture content for pluses (10%) as follows:

Adjusted yield = Correction factor (CF) x unadjusted yield. Where, CF = (100- Moisture content)/90

**Economic growth rate:** Grain yield (g/5 plant) divided by grain filling duration and then multiplied by 100.

**Grain production efficiency:** Grain filling duration divided by duration of vegetative period and then multiplied by grain yield (g/5 plant).

### 3.4.3. Stress Tolerance Indices of Soil Acidity

The yield variation due to soil acidity stress in lime untreated plots relative to the respective lime treated plots were calculated to evaluate the sensitivity of tested genotypes in the absence of lime treatment at all tested locations using soil acidity stress indices which is given in Table 2 as suggested by the respective authors.

Table 2. List of stress tolerance indices

Stress index	Formula	Reference
Relative yield reduction	$1-(YS/YP)$	Pimratch <i>et al.</i> , 2008
Stress tolerance index	$(YP \times YS) / \mu YS$	Fischer & Maurer, 1998; Fernandez, 1992
Stress susceptibility index	$\frac{YP-YS}{YP \times (1 - [\frac{\mu YS}{\mu YP}] )}$	Fischer & Maurer, 1998; Fernandez, 1992
Mean productivity	$(YP + YS) / 2$	Rosielle & Hamblin, 1981
Geometric mean productivity	$(YS \times YP)^{1/2}$	Fernandez, 1992
Harmonic mean	$2(YP \cdot YS) / (YP + YS)$	Fernandez, 1992
Yield index	$YS / \mu YS$	Gavuzzi <i>et al.</i> , 1997

Where, YP = seed yield from non-stressed plot of a given genotype, YS = seed yield from stressed plot of the same genotype,  $\mu YS$  = mean grain yield of all lime untreated plots,  $\mu YP$  = mean grain yield of all lime treated plots,  $\mu$  = mean.



### 3.5. Data Analysis

#### 3.5.1. Analysis of Variance

The SAS computer package version 9.3 statistical software (SAS Institute, 2010) was used to test for presence of outliers and normality of residuals. Data based on disease score (1-9 scale data) were converted in to percentage as 0, 4, 15, 30, 50, 70, 86, 96 and 100 respectively (Mussa *et al.*, 2008) and percentage values were ARCSINE transformed for statistical analysis (Gomez and Gomez, 1984) and untransformed means were presented otherwise. For multivariate analysis like cluster, distance and principal component analyses, records on all traits were pre- standardized to means of zero and variances of unity before clustering to avoid bias due to differences in measurement scales (Manly, 1986).

All data were subjected to analysis of variance (ANOVA) for RCBD as per the procedure indicated by Gomez and Gomez (1984) using SAS software version 9.3 statistical software package (SAS Institute, 2010). The SAS GLM (General Linear Model) procedure was employed for the analysis of variance. Analysis of variance was conducted for data collected from each location and management level (with and without lime application) separately and combined.

For combined analysis of variance, the homogeneity of error variance was tested using the F-max method of Hartley (1950), which is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller mean square of error. If the larger error mean square is less than three-fold than the smaller error mean square, the error variance was considered homogeneous (Gomez and Gomez, 1984).

$$F - \text{ratio} = \frac{\text{Larger MSE}}{\text{Smaller MSE}}$$

Accordingly, the error variances were homogenous for each with and without lime environments; therefore, combined ANOVA for data collected from with and without lime environments for each location were conducted. The error variances for separate management levels were homogeneous over locations and over locations and management levels, therefore, overall combined ANOVA for with and without lime environments over locations and management levels were made and mean comparison of genotypes were on

the basis of pooled means for the traits exhibited homogeneous error variances. For heterogeneous traits mean computed based on performance at each individual locations.

Existence of significant difference among the genotypes, locations, management level and their interaction were determined using the F-test in all the cases. Mean separation at 1% or 5% probability levels was done using Duncan's Multiple Range Test (DMRT) following Gomez and Gomez (1984), whenever genotype differences were significant.

According to Gomez and Gomez (1984), analysis of variance conducted to quantify the total variation among the genotypes under both lime levels at individual location (a) and combined at each location and over locations at each lime level and combined as six environments (b) and over locations and lime levels (c) used ANOVA models presented as follows:

$$P_{ij} = \mu + B_i + G_j + e_{ij} \dots\dots\dots (a)$$

$$P_{ijk} = \mu + B_i(m_k) + G_j + M_k + (GM)_{jk} + e_{ijk} \dots\dots\dots (b)$$

$$P_{ijkl} = \mu + B_i(L_k M_l) + G_j + L_k + M_l + (GL)_{jk} + (GM)_{jl} + (LM)_{kl} + (GLM)_{jkl} + e_{ijkl} \dots\dots\dots (c)$$

Where  $P_{ij}$  = phenotypic observations on genotypes in block i ( $i = 1 \dots B$  and  $j = 1 \dots G$ ),  $P_{ijk}$  = phenotypic observation on genotype j in block i (at management k)  $P_{ijkl}$  = phenotypic observation on genotypes j in block i (at location k and management l), G, B, M and L = number of genotypes, blocks, managements and locations respectively,  $\mu$  = grand mean,  $B_i$  = the effect of block I,  $B_i(M)_k$  = the effect of block i (within management k),  $B_i(L_k M_l)$  = the effect of block i (with location k at management l)  $G_j$  = the effect of genotype j,  $m_k$  and  $M_l$  = the effect of management k and l,  $L_k$  = the effect of location k,  $(GM)_{jk}$  &  $(GM)_{jl}$  = the interaction effect between genotype j and management k and l,  $(LM)_{kl}$  = the interaction effect between location k and management l,  $(GLM)_{jkl}$  = the interaction effect between genotype j, location k and management l,  $e_{ij}$ ,  $e_{ijk}$  and  $e_{ijkl}$  = the residual or effects of random error.

### 3.5.2. Genetic Variability Components

Heritability in broad sense, expected genetic advance as percent of the mean, phenotypic and genotypic variances and coefficient of variations and genetic diversity were computed considering only traits that mean squares for genotype exhibit significant differences.

#### 3.5.2.1. Phenotypic and genotypic variability

Phenotypic and genotypic variances at each location were estimated according to the methods suggested by Burton and De vane (1953) as follows:

$$\sigma^2g = \frac{MSg - MSe}{r}$$

$$\sigma^2p = \sigma^2g + \sigma^2e$$

Where,  $\sigma^2g$ = genetic variance,  $MSg$ = mean square due to genotypes,  $MSe$ = error mean square,  $\sigma^2p$ = phenotypic variance,  $\sigma^2e$ = environmental variance and  $r$ = number of replications.

For combined ANOVA genotypic and phenotypic variances were performed by partitioning the total variance into components due to genotype ( $g^2$ ), location ( $l^2$ ) and genotype by location interaction ( $gl^2$ ) effects and error variance ( $e^2$ ) from the analysis of variance by assuming various observed mean squares equal to their expected mean squares (Table 3) as suggested by Singh and Chaudhary (1985).

$$\sigma g^2 = [(\sigma e^2 + R\sigma gl^2 + RL\sigma g^2) - (\sigma e^2 + R\sigma gl^2)]/RL$$

$$\sigma gl^2 = [(\sigma e^2 + R\sigma gl^2) - (\sigma e^2)]/R$$

$$\sigma^2p = \sigma g^2 + \sigma gl^2/L + \sigma e^2/RL$$

Where,  $\sigma g^2$  = genotypic variance,  $\sigma l^2$  = location variance,  $\sigma gl^2$  = genotype by location interaction effects  $\sigma e^2$ = error variance,  $\sigma^2p$  = phenotypic variance,  $MS$ = mean square,  $R$  = number of replication and  $L$  = number of location

Table 3. Combined analysis of variance skeleton for genotypes based on randomized complete block design

Source of variation	Degree of freedom	Mean square (MS)	Expected mean square (EMS)	F-test
Genotype(G)	g-1	MS1	$\sigma_e^2 + r\sigma_{glm}^2 + rm\sigma_{gl}^2 + rl\sigma_{gm}^2 + rlm\sigma_g^2$	MS1/MS6
Location(L)	l-1	MS2	$\sigma_e^2 + r\sigma_{glm}^2 + rg\sigma_{lm}^2 + rm\sigma_{gl}^2 + rgm\sigma_l^2$	MS2/MS7
Management(M)	m-1	MS3	$\sigma_e^2 + r\sigma_{glm}^2 + rg\sigma_{lm}^2 + rl\sigma_{gm}^2 + rlg\sigma_m^2$	MS3/MS9
Replication(LM)	(r-1)lm	MS4	$\sigma_e^2 + g\sigma_r^2$	---
G x L	(g-1)(l-1)	MS5	$\sigma_e^2 + r\sigma_{glm}^2 + rm\sigma_{gl}^2$	MS5/MS8
G x M	(g-1)(m-1)	MS6	$\sigma_e^2 + r\sigma_{glm}^2 + rl\sigma_{gm}^2$	MS6/MS9
L x M	(l-1)(m-1)	MS7	$\sigma_e^2 + r\sigma_{glm}^2 + rg\sigma_{lm}^2$	MS7/MS9
G x L x M	(g-1)(l-1)(m-1)	MS8	$\sigma_e^2 + r\sigma_{glm}^2$	MS8/MS9
Pooled error	(r-1)(g-1)lm	MS9	$\sigma_e^2$	---

g = no.of genotypes; l = no. of locations; m = no.of managements; r = no. of replications.

The coefficient of variations at phenotypic and genotypic levels was estimated using the formula suggested by Singh and Chaudhury (1985) as follows:

$$\text{Phenotypic Coefficient of variation (PCV)} = \frac{\sqrt{\text{phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$\text{Genotypic Coefficient of variation (GCV)} = \frac{\sqrt{\text{Genotypic Variance}}}{\text{Grand mean}} \times 100$$

According to Johnson *et al.* (1955) PCV and GCV values were categorized as low, moderate and high values as follows: low for values ranged from 0 - 10%, moderate 10 – 20% and high for values greater than 20%.

### 3.5.2.2. Heritability and expected genetic advance

Broad sense heritability ( $H^2$ ) as the proportion of the total variability that is attributable to genetic causes or the ratio of the genetic variance to the total phenotypic variance over locations was calculated using the formula adopted by Allard (1960) as:

$$h^2 = \sigma_g^2 / [\sigma_g^2 + \sigma_{gl}^2/L + \sigma_e^2/RL] \times 100$$

Where:  $h^2$  = heritability in broad sense,  $\sigma_g^2$ =genotypic variance,  $\sigma_{gl}^2$ =genotype by location interaction effects,  $\sigma_e^2$ =error variance, R = number of replication and L = number of location. According to Robinson *et al.* (1949), heritability of a trait is considered as high

when the value is more than 60% and moderate when it ranged from 30-60% and low when it is less than 30%.

Genetic advance as part of the mean (GA) for each character was computed using the formula adopted by Johnson *et al.* (1955). According to Johnson *et al.* (1955) GA that is expected from selecting the top 5% of the tested genotypes as percentage of the mean (GAM) was categorized as of Low (0-10), Moderate (10-20), High (>20).

$$GA = k \cdot \sigma_p \cdot h^2 \quad \text{and} \quad GA \text{ (as \% of the mean)} = \frac{GA}{\bar{x}} \times 100$$

Where,  $k$  = selection differential (at 5% selection intensity with value 2.06)  $\sigma_p$  = phenotypic standard deviation,  $h^2$  = heritability;  $\bar{x}$  = Grand mean; According to Johnson *et al.* (1955) GA that is expected from selecting the top 5% of the tested genotypes as percentage of the mean (GAM) is categorized as of Low (0-10), Moderate (10-20), High (>20).

### 3.5.2.3. Genetic distance and clustering

The genetic distance of genotypes was estimated using Euclidean distance (ED) based on pooled mean data after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Sneath and Sokal (1973) as follows:

$$ED_{jk} = \sqrt{\sum_{i=1}^n (X_{ij} - X_{ik})^2}$$

Where,  $ED_{jk}$  = distance between genotypes  $j$  and  $k$ ;  $X_{ij}$  and  $X_{ik}$  = phenotype traits values of the  $i^{\text{th}}$  character for genotypes  $j$  and  $k$ , respectively; and  $n$  = number of phenotype traits used to calculate the distance.

The distance matrix from 19 traits (12 agronomic and 7 stress tolerance indices) was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis were presented in the form of dendrogram. In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other genotypes. The calculated average distance (ED) was used to estimate which genotype(s) is closest or distant to others.

### 3.5.3. Association of Traits

#### 3.5.3.1. Phenotypic and genotypic correlation coefficient analysis

Phenotypic ( $r_p$ ) and genotypic ( $r_g$ ) correlations between two traits were estimated using the formula suggested by Johnson *et al.* (1955) and Singh and Chaudhury (1985).

$$r_p = \frac{Pcov_{xy}}{\sqrt{(V_{px} \cdot V_{py})}} \quad r_g = \frac{Gcov_{xy}}{\sqrt{(V_{gx} \cdot V_{gy})}}$$

Where,  $r_p$  = Phenotypic correlation coefficient,  $r_g$  = Genotypic correlation coefficient,  $Pcov_{xy}$  = Phenotypic covariance between variables x and y,  $Gcov_{xy}$  = Genotypic covariance between variables x and y,  $V_{px}$  = Phenotypic variance of variable x,  $V_{gx}$  = Genotypic variance of variable x,  $V_{py}$  = Phenotypic variance of variable y and  $V_{gy}$  = Genotypic variance of variable y.

The calculated phenotypic correlation value was tested for its significance using t-test:

$$t = r_p / SE(r_p)$$

Where,  $r_p$  = Phenotypic correlation;  $SE(r_p)$  = Standard error of phenotypic correlation obtained using the following formula (Sharma, 1998).

$$SE(r_p) = \sqrt{\frac{1 - r_p^2}{n - 2}}$$

Where, n is the number of genotypes tested,  $r_p^2$  is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = r_{gxy} / SEr_{gxy}$$

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SEr_{gxy} = \sqrt{\frac{1 - r_{gxy}^2}{h^2x} \cdot h^2y}$$

Where,  $r_{gxy}^2$  = genotypic correlation coefficient,  $h^2x$  = Heritability of trait x and  $h^2y$  = Heritability of trait y.

### 3.5.3.2. Path coefficient analysis

Path coefficient analysis was conducted as suggested by Wright (1921) and worked out by Dewey and Lu (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$$r_{ij} = p_{ij} + \sum r_{ik}p_{kj}$$

Where,  $r_{ij}$  = Mutual association between the independent trait (i) and dependent trait, seed yield (j) as measured by the correlation coefficients,  $p_{ij}$  = Components of direct effects of the independent trait (i) as measured by the path coefficients and  $\sum r_{ik}p_{kj}$  = summation of components of indirect effect of a given independent trait (i) on a given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor will be measured as the residual effect. Residual effect (h) will be calculated using the formula given by Dewey and Lu (1959).

$$h = \sqrt{1 - R^2}$$

Where, h = residual effect and  $R^2 = \sum r_{ij}p_{ij}$

### 3.5.4. Stability Analysis

The combined general analysis of variance was conducted over environments and by considering each as one environment (six environments) for grain yield the effect of genotype by environment interaction on yield. Stability analysis was conducted for grain yield to assess the stability grain yield of faba bean genotypes under different environments.

Stability parameters such as analysis of variance from Additive Main Effects and Multiplicative Interaction (AMMI) (Zobel *et al.*, 1988) stability parameters (interaction principal component axes (IPCA) scores of genotype and environment and pooled mean values) and GGE-biplot (genotype and genotype by environment interaction) was employed for grain yield due to significant mean squares for genotype, and genotype by environment interaction. The ANOVA of AMMI model was computed for six environments viz. data from three environments for non-stressed (lime treated plots) and data from three environments for non-treated plots or soil acidity stress each considered as one environment. AMMI model ANOVA was employed to partition the total variance into its component parts (genotype, environment, genotype by environment interaction and pooled error) thereby to determine the most important component in controlling grain yield.

Different statistical software packages were used to analyze the data. Analysis of variance at individual environment and combined over environments were computed using the SAS statistical software (SAS, 2010). Windows software developed by Yan (2001) GenStat 15<sup>th</sup> edition (Genstat, 2012) statistical software was used for AMMI (Zobel *et al.*, 1988) model and GGE biplot (Yan, 2001). Since AMMI model does not make provision for a quantitative stability measure, AMMI stability value (ASV) (Purchase, 1997) measure was computed in order to quantify and rank genotypes according to their yield by using Microsoft office excel 2010.

#### 3.5.4.1. AMMI analysis

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype by environment interaction. It has proven useful for understanding complex GEI. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments. The model equation is:

$$Y_{ij} = m + G_i + E_j + \sum \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

Where  $Y_{ij}$  is the yield of the  $i^{th}$  genotype in the  $j^{th}$  environment;  $m$  is the grand mean;  $G_i$  and  $E_j$  are the genotype and environment deviations from the grand mean, respectively;  $\lambda_k$



is the eigenvalue of the PCA axis  $k$ ;  $\alpha_{ik}$  and  $\gamma_{jk}$  are the genotype and environment principal component scores for axis  $k$ ;  $n$  is the number of principal components retained in the model and  $\hat{\epsilon}_{ij}$  is the error term.

According to Gollob (1968) the df for the PC axis can be calculated as:

$$df = G + E - 1 - 2n$$

Where: G= genotype, E=environment and n=number of IPCA axis

Because the IPCA1 score contributes more to the GEI sum of squares, a weighted value (ASV) was needed, which was calculated according to the relative contribution to the interaction by IPCA1 as compared to IPCA2 (Purchase, 1997):

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

Where  $SS_{IPCA1}/SS_{IPCA2}$  = is the weight given to the IPCA1 value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares, IPCA1 score is the IPCA1 score for that specific genotype, and IPCA2 score is the IPCA2 score for that specific genotype.

To show a clear insight into specific GEI combinations and the general pattern of adaptation, a biplot of genotypes and environments (Kempton, 1984) was done for grain yield. In the biplots the first IPCA has been used as the ordinate (Y- axis) and the main effects (means of the genotypes and environments) represent abscissa (X- axis) in AMMI1 and the first IPCA will be used as the ordinate (Y-axis) and the second IPCA represent abscissa (X-axis) in AMMI 2.

#### 3.5.4.2. GGE-biplot analysis

The GGE-Biplot was used for analyzing GEI and stability of the genotypes (Yan, 2001). The GGE-Biplot approach is preferred to AMMI since only G and GEI are important and E is not important, and therefore only these components must be simultaneously considered (Yan *et al.*, 2007). GGE biplot best identifies GEI pattern of data and clearly shows which variety performs best in which environments, and thus facilitates mega-environment identification than AMMI. Otherwise, both GGE and AMMI models are

equivalent as far as their accuracy is concerned (Fekadu *et al.*, 2012). The GGE-Biplot model based on singular value decomposition (SVD) of  $t$  principal components is given as follows:

$$Y_{ij} - \mu_i - \beta_j = \sum_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where,  $Y_{ij}$  is the performance of genotype  $i$  in environment  $j$ ,  $\mu$  is the grand mean,  $\beta_j$  the main effect of environment  $j$ ,  $k$  is the number of principal components (PC),  $\lambda_k$  is singular value of the  $k^{\text{th}}$  PC,  $\alpha_{ik}$  and  $\gamma_{jk}$  are the score of  $i^{\text{th}}$  genotype and  $j^{\text{th}}$  environment, respectively for  $PC_k$ ,  $\varepsilon_{ij}$  is the residual associated with genotype  $i$  in environment  $j$ . Usually only the first two PCs are used especially if they account for the major portion of the GEI.

## 4. RESULTS AND DISCUSSION

### 4.1. Soil Chemical Properties of Test Locations

The physico-chemical properties of the soils from the three test locations showed very strong acidic condition for all test locations with the pH values of 4.66 at Holetta, 4.94 at Watebecha Minjaro and 4.49 at Jeldu (Table 4). In practical terms, soils pH between 6.6 and 7.3 are considered as neutral; 5.6 to 6.5 are moderately acid and below 5.5 strongly acid (Alemu *et al.*, 2016). It was observed little modification of pH at each location in the lime treated blocks since the soil is still under very strong acidic category. This may indicate that lime improves the chemical properties of soils but it need more time to bring to the required level. Follet *et al.* (1981) reported that lime is slow acting, of long duration. Likewise, Adane (2014) reported that applied lime may not significantly increase the grain yield compared to the control at first year. However, a significant increase in yield will be expected in the next planting season due to slow acting of lime.

The exchangeable acidity was very high at Jeldu (3.36cmol/kgsoil). The values of  $Al^{3+}$ , Mn and other micronutrients were high and low K, Ca, Mg and Na with variable amounts was observed at Jeldu. The levels of exchangeable cations were increased at lime treated plots except  $Na^+$  while decreased micronutrients (Table 4). The level of soil phosphorus was increased at harvest except at Watebecha Minjaro. As reported by Fageria *et al.* (2012) applied lime at harvest increased soil extractable P and K with the reduction of soil acidity and that might contributed to the better nutrition of beans and lead to higher growth.

At Watebecha Minjaro, the level of measured soil chemical properties before planting and at harvesting was more or less similar with minor change. The similarity in the chemical properties may be due to little pH change 4.94 to 5.08. The exchangeable  $Al^{3+}$  decreased on lime treated blocks as compared to the lime-free. Similar results were reported by Temesgen *et al.* (2017) with increase in the amounts of lime incorporated, soil pH values increased with a corresponding decrease in exchangeable  $Al^{3+}$  of the soil. The high clay content of the location leads to high buffering capacity because the buffering capacity of the soil increase as the clay content increase; as a result it needs more lime than the calculated rate to reduce acidity and increase the productivity of faba bean.

As reported by Derib (2014), soils with high clay content and cation exchange capacity (CEC) leads to high buffering capacity because the buffering capacity of the soil increase as the CEC increase; as a result high amount of lime will be required to alleviate acidity and increase the productivity of acid sensitive crops. Endalkachew *et al.* (2018) reported that lime application reduce soil acidity and Al toxicity and increase P availability which have a role in root development and high rates of energy transfer in nodule formation. Similarly, Onwonga *et al.* (2008), reported that in lime applied acid soils,  $Al^{3+}$  and  $H^+$  ions were reduced as it reacts with water leading to the production of  $OH^-$  ions to form  $Al(OH)_3$  and  $H_2O$  and the precipitation of  $Al^{3+}$  and  $H^+$  by lime causes the pH to increase which enhances microbial activity and nutrient availability. Generally, applying calcium containing lime materials improve nutrient availability, particularly phosphorus; through reduction of phosphorus fixation thereby improving soil pH where maximum availability of the nutrient may be obtained. The result agrees with the reports of Abebe and Tolera (2014).

Table 4. Results of soil chemical analysis before and after liming at three locations

Parameter	Holetta		Watebecha Minjaro		Jeldu		
	Before lime	After lime	Before lime	After lime	Before lime	After lime	
Texture (%)	Clay	47.50	---	70.00	---	40.00	---
	Silt	36.25	---	8.75	---	36.25	---
	Sand	16.25	---	13.75	---	23.75	---
pH	4.66	5.03	4.94	5.08	4.49	4.80	
TN (%)	0.14	0.14	0.14	0.21	0.29	0.30	
Avail. P	7.96	9.57	12.74	12.74	13.17	15.14	
CEC	18.18	19.04	17.38	18.80	20.24	20.42	
OC (%)	1.25	1.36	2.14	2.18	2.61	2.65	
Ex. Na (ppm)	0.03	0.03	0.03	0.03	0.02	0.03	
Ex.K (ppm)	0.57	0.58	0.53	0.54	0.14	0.23	
Ex.Mg (ppm)	2.35	2.46	1.25	1.26	0.50	0.58	
Ex.Ca (ppm)	9.43	10.89	9.30	10.95	6.35	11.82	
Ex. Al (PPm)	0.49	0.28	0.55	0.33	2.39	0.85	
Mn (ppm)	48.58	47.76	37.97	30.16	58.23	50.45	
Cu (ppm)	4.07	3.92	3.70	3.12	4.95	3.85	
Ext.Fe (ppm)	180.77	164.45	245.70	231.07	341.13	327.43	
Ext.Zn (ppm)	0.83	0.68	1.15	1.10	4.42	2.67	
Ex. Acidity	1.01	0.61	0.98	0.62	3.36	1.30	
Bulk density( $gcm^{-3}$ )	1.26	----	1.12	-----	1.05	----	

CEC= cation exchange capacity, OC= organic carbon, TN= total nitrogen, Ex. = exchangeable, Ext=extractable

## 4.2. Analysis of Variance and Mean Performances of Genotypes

### 4.2.1. Analysis of Variance

The analysis of variance (ANOVA) computed for each location with and without lime application indicated the presence of significant ( $P \leq 0.01$ ) differences among genotypes for all traits except for grain filling period at Watebecha Minjaro in plots which did not receive lime and number of seed per pod at all locations in plots treated with and without lime application (Appendix Table 1 and 2). The results of ANOVA computed for acidity stress indices showed that the genotypes had significant variations for all acidity stress indices at all locations (Appendix Table 3). The significant difference for genotypes showed the presence of sufficient genetic variation for most traits among the tested genotypes except number of seed per pod.

Gemechu *et al.* (2005) had also reported nonsignificant difference of Ethiopian faba bean germplasm accessions in number of seeds per pod. Significant genotypic differences in faba bean genotypes for days to flowering, plant height, number of pod per plant and hundred seed weight had also been reported by Kumar *et al.* (2017). The significant ( $P \leq 0.05$ ) effect of locations on hundred seed weight of faba bean has been reported (Ashenafi and Mekuria, 2015). The highly significant differences ( $P \leq 0.01$ ) for grain yield with and without lime application indicated the variations of genotypes under acid soil and lime applications. The significant difference for all stress tolerance indices indicated that the tested faba bean genotypes had different genes for stress tolerance.

The results revealed the homogeneity of error variances for all traits except hundred seeds weight and grain production efficiency without lime and days to 50% flowering with lime application (Appendix Table 4). The combined analysis of variance over three locations for each management indicated the presence of significant variations among genotypes, locations for all traits. The two way interaction of genotype by location had significant effects on all 12 traits of genotypes both under lime and without lime application except interaction of genotype by location had non-significant effect on number of pod per podding node without lime application (Table 5). The effect of genotype x location interaction being significant on most of the traits for each management over location indicated the differential performance of genotypes in different managements over locations.

The result partially agrees with the findings of Abebe and Tolera (2014) who reported significant difference for plant height and grain yield and nonsignificant difference for number of pod per plant, number of seed per pod and hundred seeds weight as a result of lime application on acid soils of western highlands of Ethiopia. Many reports also showed the presence of significant effects of  $G \times E$  interaction on grain yield in faba bean in different sets of environments in Ethiopia (Gemechu and Mussa, 2009, Million and Habtamu, 2012; Tamene *et al.*, 2015). Contrary to the current result Tamene *et al.* (2015) reported a non-significant interaction effect for chocolate spot disease resistance due to environmental variance.

The combined analysis of variance over three locations for soil acidity stress indices showed the presence of significant differences among genotypes for all indices, location and interaction of genotype by location had also significant influence on the stress indices of genotypes (Table 6) which indicated that genotypes performed differently in different locations. Previously Javed *et al.* (2011) reported that variation of stress tolerance indices across location implied genotypes have different genes controlling yield and stress tolerance indices.

The significant effects of  $G \times L$  interaction indicated that the genotypes had differential performance over locations for agronomic traits and the effects of experimental plots with lime and without lime applications also exerted differential effects over locations on the performance of genotypes. The results were supported by the significant effect of location and interaction of genotype by location on stress indices of genotypes. Due to the performance inconsistency of genotypes over locations such as with significant effects of  $G \times L$  interactions, selection of genotypes for superior performance under one set of environment may perform poorly under different environment This implies that recommendation of genotypes for all locations and managements of soil acidity is hardly possible based on better performance of genotypes at one location and management. In line with this result, Gemechu *et al.* (2015) reported that under significant  $G \times L$  selection of genotypes that perform best under all sets of environments becomes impractical.

Table 5. Mean squares from combined analysis of variance without (above) and with lime application (below) over three locations for 12 traits of 50 faba bean genotypes in 2017 main cropping season.

Trait	Without lime application					
	Rep (6)	Genotype (G) (49)	Location (L) (2)	G x L (98)	Error (294)	CV (%)
DF	11.54	22.67**	4730.67**	4.45**	1.22	2.05
DM	20.56	27.38**	4012.56**	5.20**	2.69	1.12
GFP (day)	28.59	37.51**	4401.98**	8.22**	3.69	2.09
PH (cm)	1855.06	175.01**	277083.56**	79.32**	31.67	5.06
PNPP	8.19	5.90**	242.89**	1.20**	0.78	13.49
PPP	4.62	21.55**	309.31**	2.86**	1.52	14.75
PPPN	0.11	0.09**	0.13**	0.02	0.02	11.16
HSW (g)	110.15	2395.51**	715.23**	42.72**	11.99	4.94
CS (%)	1451.75 (580.70)	482.59** (192.71)	2502.76** (1044.86)	344.07** (145.24)	143.28 (57.63)	36.29 (22.08)
GY (g)	430.05	572.51**	15788.37**	190.83**	58.96	12.20
GPE (g)	2359.41	1858.03**	113609.25**	683.50**	207.49	13.26
EGR (g/day)	490.21	700.33**	27756.57**	232.64**	72.07	12.31
With lime application						
DF	15.00	13.25**	4567.41**	4.12**	1.27	2.08
DM	15.27	23.54**	4438.82**	6.61**	2.31	1.04
GFP(day)	17.08	28.50**	5922.11**	9.26**	2.51	1.72
PH(cm)	1489.31	144.10**	243555.95**	85.82**	34.54	4.58
PNPP	3.64	6.04**	100.70**	1.33*	0.94	12.00
PPP	5.55	35.50**	237.27**	4.30**	2.24	12.84
PPPN	0.10	0.14**	3.69**	0.04**	0.02	10.15
HSW(g)	137.61	2690.63**	2305.57**	41.76**	12.96	5.01
CS (%)	873.28 (387.65)	573.40** (251.76)	9065.48** (3979.73)	357.20** (163.50)	78.09 (35.70)	32.17 (19.50)
GY(g)	376.50	1032.64**	1028.45**	281.20**	87.03	10.02
GPE(g)	2182.34	3853.17**	106043.51**	1069.63**	304.37	10.87
EGR(g/day)	347.55	1176.61**	3771.96**	330.84**	103.57	10.02

\*and\*\*, significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation. Rep= replication, CV (%) = coefficient of variation in percent, DF= days to flowering(days), DM = days to maturity(days), GFP= Grain filling period(days), PH = plant height(cm), PNPP=Number of podding node per plant, PPP= Number of Pod per Plant, PPPN= Number of pod per podding node, HSW= hundred seed weight(g), GY= Grain yield per 5 plants(g), CS= Chocolate spot disease(%),GPE= Grain production efficiency(g), EGR= Economic growth rate(g/day).

Table 6. Mean squares of combined analysis of variance over locations for soil acidity stress indices based on grain yield of 50 faba bean genotypes evaluated with and without lime application in 2017 main cropping season.

Trait	Block (6)	Genotype (G) (49)	Location ( L) (2)	G x L (98)	Error (294)	CV (%)
RYR <sup>ψ</sup>	0.01	0.04 <sup>**</sup>	2.36 <sup>**</sup>	0.03 <sup>**</sup>	0.00	16.97
YI <sup>ψ</sup>	0.09	0.12 <sup>**</sup>	3.22 <sup>**</sup>	0.04 <sup>**</sup>	0.01	12.23
STI <sup>ψ</sup>	0.43	0.61 <sup>**</sup>	4.28 <sup>**</sup>	0.15 <sup>**</sup>	0.07	21.01
SSI <sup>ψ</sup>	0.09	0.99 <sup>**</sup>	46.50 <sup>**</sup>	0.68 <sup>**</sup>	0.08	20.80
MP(g)	391.44	674.74 <sup>**</sup>	2412.78 <sup>**</sup>	148.32 <sup>**</sup>	63.13	10.18
GMP(g)	404.80	653.45 <sup>**</sup>	4661.11 <sup>**</sup>	148.77 <sup>**</sup>	62.98	10.43
HM(g)	417.88	641.25 <sup>**</sup>	7400.56 <sup>**</sup>	155.91 <sup>**</sup>	63.74	10.76

<sup>\*</sup> and <sup>\*\*</sup>, significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation. CV (%) = coefficient of variation in percent, RYR= relative yield reduction, YI= yield index, STI= stress tolerance index, SSI= stress susceptible index, MP= mean productivity (g), GMP= geometric mean productivity (g), HM= harmonic mean,  $\psi$  = unit less trait.

## 4.2.2. Mean Performances of Genotypes for Morpho-agronomic Traits

### 4.2.2.1. Phenological and growth traits

The genotypes had days to 50% flowering in the range between 51.4 days (EH09004-2) and 58.9 days (Wayu) and overall mean of 54.1 days without lime application over the three locations. Without lime application, the genotypes showed significantly early flowering (6.3 days) for EH07023-3, EH09002-1, EH06088-6, EH08035-1 and EH09004-2 compared to the late flowering Wayu and Gebelcho (Appendix Table 6a). Days to 50% flowering varied in the range between 44.7 days (EH08035-1) and 55.3 days (Wayu) at Holetta and 56.7 days (EKLS/CSR02014-2-4) and 61.0 days (Hachalu) at Watebecha Minjaro and between 53.3 (EH08035-1) and 60.0 (Wayu) at Jeldu with the application of lime over the three locations. The genotypes had days to 90% maturity in the range between 142.1 days (Degaga) and 149 days (EKLS/CSR02014-2-4) and 142.7 days (KUSE2-27-33) and 148.8 days (EH07023-3) with overall mean of 145.9 days without and with lime application over the three locations, respectively. A total of 13 genotypes including EKLS/CSR02014-2-4 took longer days to attain 90% maturity over locations without lime applications with nonsignificant difference among the mean values of genotypes and a total of nine genotypes found as early maturity significantly different from



other genotypes mean maturity days over locations (Appendix Table 6b). The genotypes had mean value of 91.8 and 91.9 days for grain filling period with the range spanning between 87.2 and 95.3 days for Wayu and EKLS/CSR02014-2-4 and 87.7 and 96 days for Wayu and EH07023-3 without and with lime, respectively over locations (Appendix Table 6c).

The observed variations among genotypes for days to flowering and maturity over locations with different management may be due to the inherent characteristics of genotypes and the influence of locations. The genotypes showed early maturity in case of without lime application to escape from stress imposed due to soil acidity. The grain filling period of the genotypes associated with days to flowering and maturity. Therefore, short grain filling period resulted from short days to flowering and maturity is an advantage if any terminal moisture stress encountered in the location(s). It was reported that faba bean genotypes took 61 to 65 days for days to 50 % flowering and 130-143 days to 90% maturity (Tewodros *et al.*, 2015). Million (2012) also reported 57-63 and 137-146 days to 50% flowering and days to 90% maturity, respectively, for eight faba genotypes evaluated at Haramaya University. This study result partially agrees with the previous findings of Million (2012) and Tekle *et al.* (2016) that grain filling period of faba bean genotypes ranged from 78-87 and 75-88 days, respectively. In contrast to this study result, Hirpa *et al.* (2013) reported that application of lime hastened flowering and maturity in common bean.

The genotypes had overall mean plant height (111.2 and 128.2 cm) with the range between 100.8 and 1119 cm for Wayu and Obse and 119 and 137.1 cm for Wayu and EH07023-3 without and with lime application, respectively over locations. A total of 24 genotypes including Obse and 15 including EH07023-3 had taller plant height over locations without and with lime, respectively with nonsignificant difference among the mean values of genotypes but significantly different from other genotypes mean values. A total of eleven and fourteen genotypes were significantly shorter from other genotypes mean plant height over locations without and with lime, respectively (Appendix Table 6d). The mean number of podding node per plant of genotypes over locations was between 5.1 and 8.3 for EH09007-4 and NC58 and between 6.6 (Numan) and 9.6 (KUSE2-27-33 and Wolki) with the mean values of 6.5 and 8.1 without and with lime, respectively. The genotypes KUSE2-27-33, Wolki, Cool-0024, Cool-0035, CS20DK and Degaga followed by other thirteen genotypes had

significantly high number of podding node per plant and EH09007-4, EH09031-4, Numan followed by fifteen other genotypes had less number of podding node per plant that are significantly different from the other genotypes with lime over locations (Appendix Table 6e).

The significant difference in plant height and number of podding node per plant of genotypes over locations and managements indicated the existing variation among the faba bean genotypes evaluated which were mainly attributed to genotype and their growing environment. Soil acidity stress reduced plant height and number of podding node per plant of genotypes as compared to lime treated plots (Appendix Table 6d and 6e). The result indicated that stressed environments hinder the growth of faba bean. In harmony with this result faba bean genotypes Siddiqui *et al.* (2015) and Tewodros *et al.* (2015) reported longer plant height under optimum environments than stress environments. Similarly, lime application improved plant height of faba bean genotypes on acid soil (Ouertatani *et al.*, 2011; Abebe and Tolera, 2014). Partially in agreement with this result a plant height of 119-137cm were reported under optimum environment (Million, 2012). As reported by Mussa and Gemechu (2006) faba bean has a problem of flower abortion consequently this reduces the number of podding node per plant.

#### 4.2.2.2. Yield components

The genotypes had mean number of pod per plant (PPP) that ranged between 5.6 (EH09007-4) and 12.7 (CS20DK) without lime and 8.4 (EH09007-4) and 16.0 (CS20DK) with lime with an overall mean value of 8.1 and 11.7, respectively. The genotypes CS20DK and NC58 without lime and Wolki, KUSE2-27-33, Cool-0024 and CS20DK with lime had high PPP that is significantly different than other genotypes over locations (Appendix Table 6f). The mean number of pod per podding node (PPPN) of genotypes ranged from 1.09 (EH09007-4) to 1.59 (CS20DK) and 1.25 (EH06070-3) to 1.72 (CS20DK) without and with lime application, respectively. The genotypes CS20DK had high number of pod per podding node significantly different from other genotypes over locations both with and without lime (Appendix Table 6g). The genotypes had different PPP as affected by management, location, genetic makeup of genotypes and the interaction of them. Both PPP and PPPN increased in case of lime application. The increase in PPP directly related with increase in grain yield. The PPP and number of pod per podding node varied over locations with different management levels due to unfavorability of test

environments. Moreover the variations in PPP under limed and stressed environments were due the sensitivity of this trait to soil acidity. The result agreed with the reports of Tamene (2008) and Million (2012) who reported 10 to 16 and 6 to 10 pods per plant, respectively; and also Tamene (2008) reported that the number of pods per node was significantly different across locations. It was reported that more PPP under limed than lime free condition in acidic soil in faba bean and common bean, respectively (Ouertatani *et al.*, 2011; Hirpa *et al.*, 2013). In contradict to this study result it was reported that no variation in PPP as a result of lime application (Abebe and Tolera, 2014) and 19 to 22 PPP (Tekle *et al.*, 2016).

The genotypes had hundred seed weight (HSW) that ranged between 36.7g (Wayu) and 98.5g (Numan) and with overall mean of 71.8g with lime application over the three locations. In case of lime application over the three locations, Numan showed larger and Wayu smaller HSW which was significantly different from other genotypes (Appendix Table 6h). Hundred seeds weight of genotypes varied in the range between 36.5g (Wayu) and 99.3g (Numan) at Holetta and 36.1g (Wayu) and 91.5g (EH09031-4) at Watebecha Minjaro and between 33.6g (Wayu) and 99.5g (Numan) at Jeldu without lime application over the three locations. The genotypes had high HSW significantly different than other genotypes EH09031-4, EH06070-3, EKLS/CSR02017-3-4, EKLS/CSR02010-4-3, EKLS/CSR02028-1-1, EH07015-7 and Numan at Holetta, EH07023-3, EH09031-4, EH06088-6, EKLS/CSR02017-3-4, and EKLS/CSR02019-2-4 at Watebecha Minjaro and EH07015-7, EH07023-3 and Numan at Jeldu. However, the genotype Wayu had significantly lower HSW at all locations (Appendix Table 6h). Based on HSW distribution Wayu was the least whereas the recently released variety Numan was the highest. The variation in HSW over location was due to the genetic potential of the genotypes rather than soil acidity of test locations because there were no rank order changes of the lowest and highest HSW of genotypes. The result implied that HSW was less affected by soil acidity stress of test sites as compared to the other traits. Tamene *et al.* (2015) reported that hundred seed weight in faba bean was less variable than grain yield. Likewise, Abebe and Tolera (2014) also reported that HSW was not changed as a response of lime application under acidic soil.

The genotypes had grain production efficiency (GPE) in the range between 92.70g (Wayu) and 201.14g (Moti) and overall mean of 160.6g with lime application over the three locations. The mean grain production efficiency of tested genotypes without lime application varied from 69.60 (Wayu) to 188.67 (EK05006-3), 74.77 (Wayu) to 129.30 (Wolki) and 37 (Wayu) to 126.33 (Obse) with the mean values of 139.49, 99.64 and 86.69 at Holetta, Watebecha Minjaro and Jeldu, respectively (Appendix Table 6j). The mean economic growth rate (EGR) varied from 46.98% (Wayu) to 90.52% (CS20DK) and 69.48% (Holetta2) to 127.88% (CS20DK) with the mean values of 68.95 and 101.59% without and with lime over locations, respectively (Appendix Table 6k). The variation in GPE over locations indicated that the variation in grain yield and grain filling period of genotypes across locations. The more the GPE of the genotype implied the more the grain yield and grain filling period and short days to 50% flowering of the genotypes. Similarly increase in EGR attributed by increase in grain yield and decrease in grain filling period. Improvement in grain yield is indirectly improvement GPE and EGR of genotypes. Accordingly, there is plenty of variability among the genotypes for selection designed for of these traits. It was reported that the highest economic growth rate was recorded for CS20DK than other genotypes (Tamene, 2008).

#### 4.2.2.3. Grain yield performance of genotypes

The genotypes had mean grain yield (GY) in the range between 40.72g (Wayu) and 79.56g (CS20DK) and overall mean of 62.93g without lime application over the three locations. In case of without lime application over the three locations, CS20DK, Obse, Wolki, Didia, Dosha, Hachalu, Numan and Moti were high yielder while Wayu was low yielder significantly different from other genotypes. Likewise, the genotypes had GY in the range between 61.6g (Wayu) and 115.1g (Moti) with the mean value of 93.13g with lime application over the three locations. The genotypes Moti, CS20DK, EKLS/CSR0200104-3 were high yielder whereas Wayu and Holetta-2 were low yielder with significantly different from other genotypes (Table 7). The grain yield of Wayu was the least under each management level, location and their interaction due to its smaller hundred seeds weight. In agreement with this result the older varieties (Kuse2-27-33, NC-58, Wayu and Selale) were consistently low yielder over environments (Tamene, 2008) and CS20DK was high yielder genotype over locations under optimum environments (Tamene *et al.*, 2015).

Jeldu was the lowest and highest yielder environment without and with lime application, respectively (Table 7). The variation in the highest and lowest yield at each location was a result of significant genotype by management interaction. The variety Wayu was the least yielding at separate and over locations. The GY varied within genotypes with different managements, location and their interaction. The soil acidity problem of test locations leads to 32.34% relative reduction in GY of genotypes and lime application improved GY for all genotypes over lime free condition (Table 7). The grain yield difference with and without lime application indicated the sensitivity of the-[\*]; genotypes to soil acidity stress and the growing environment more contributed for GY in addition to genotype. In line with this result previously reported that faba bean varieties grown on varying pH levels showed seed yield per plant was greater on soil pH 7.7 than on soil pH 4.7 suggesting that acid soil reduced grain yield (Elliott and Whittington, 2009). Similarly, previously reported that liming significantly increased grain yield (Ouertatani *et al.*, 2011) and 32% yield increment as a result of lime application reported in faba bean at pH 5.1 (Endalkachew *et al.*, 2018), 26% in common bean (Hirpa *et al.*, 2013). Furthermore, acid soil significantly affect the grain yield of faba bean in western highlands of Ethiopia (Abebe and Tolera, 2014; Asnakech *et al.*, 2017) and faba bean varieties gave lower yield compared to the national average yield in Ethiopia due to strong acidic status of the soil (pH 5.1) (Degife and Kiya, 2016). Contorary to the current result CS20DK was reported as the lowest yielder variety as compared to Gora, Walki and Geblecho (Degife and Kiya, 2016). Different authors reported that low yields in acid soil could mainly be either due to the deficiency of P, Ca and Mg and toxicity of Al, Fe and Mn (Dodd and Mallarino, 2005; Endalkachew *et al.*, 2018) while grain yield increment on lime treated soil is related to reduction of toxic levels of soil Al<sup>3+</sup> and H<sup>+</sup> ions (Fageria *et al.*, 2012). In this study generally, genotypes showed inconsistent performance in terms of seed yield across environment under both management regimes which indicated the presence of environmental influence on the performance of the genotypes.

Table 7. Mean performance of 50 faba bean genotypes for grain yield (g/5plants) evaluated without and with lime at each location and combined over three locations in 2017 main cropping season.

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	60.20 <sup>h-o</sup>	69.27 <sup>e-m</sup>	48.47 <sup>f-l</sup>	59.31 <sup>i-q</sup>	97.12 <sup>c-k</sup>	78.23 <sup>j-n</sup>	112.43 <sup>a-d</sup>	95.93 <sup>c-j</sup>
2	Wolki	96.51 <sup>a</sup>	89.40 <sup>ab</sup>	40.80 <sup>klm</sup>	75.57 <sup>abc</sup>	101.65 <sup>b-g</sup>	102.27 <sup>a-f</sup>	87.20 <sup>g-o</sup>	97.04 <sup>c-j</sup>
3	EK LS/CSR02012-2-3	66.78 <sup>f-n</sup>	61.27 <sup>k-s</sup>	56.43 <sup>b-j</sup>	61.49 <sup>g-o</sup>	99.08 <sup>c-i</sup>	87.37 <sup>f-m</sup>	109.17 <sup>a-f</sup>	98.54 <sup>b-g</sup>
4	Obse	80.80 <sup>a-g</sup>	78.70 <sup>a-f</sup>	73.17 <sup>a</sup>	77.56 <sup>ab</sup>	100.37 <sup>b-g</sup>	84.60 <sup>g-n</sup>	108.20 <sup>a-g</sup>	97.72 <sup>b-i</sup>
5	NC58	64.73 <sup>g-n</sup>	69.90 <sup>d-m</sup>	50.30 <sup>d-l</sup>	61.64 <sup>g-o</sup>	82.65 <sup>g-m</sup>	84.13 <sup>g-n</sup>	79.87 <sup>k-q</sup>	82.22 <sup>k-n</sup>
6	Ashebeka	80.60 <sup>a-g</sup>	63.20 <sup>i-s</sup>	64.23 <sup>a-e</sup>	69.34 <sup>b-h</sup>	99.25 <sup>c-i</sup>	94.53 <sup>d-i</sup>	102.63 <sup>a-j</sup>	98.81 <sup>b-g</sup>
7	Hachalu	80.23 <sup>a-g</sup>	75.60 <sup>c-h</sup>	62.90 <sup>a-f</sup>	72.91 <sup>a-e</sup>	90.74 <sup>d-l</sup>	95.97 <sup>c-i</sup>	82.45 <sup>j-q</sup>	89.73 <sup>e-k</sup>
8	Degaga	72.78 <sup>c-k</sup>	60.93 <sup>k-s</sup>	45.13 <sup>i-l</sup>	59.62 <sup>i-q</sup>	84.68 <sup>f-l</sup>	92.43 <sup>e-j</sup>	84.67 <sup>h-p</sup>	87.26 <sup>i-m</sup>
9	EH09031-4	68.93 <sup>d-m</sup>	65.50 <sup>h-r</sup>	50.37 <sup>d-l</sup>	61.60 <sup>g-o</sup>	89.43 <sup>d-l</sup>	88.07 <sup>f-m</sup>	88.30 <sup>f-o</sup>	88.60 <sup>g-l</sup>
10	Holetta-2	59.99 <sup>h-o</sup>	54.20 <sup>rs</sup>	45.57 <sup>i-l</sup>	53.25 <sup>n-r</sup>	65.15 <sup>mno</sup>	63.27 <sup>o</sup>	63.60 <sup>qr</sup>	64.01 <sup>o</sup>
11	EH09007-4	56.41 <sup>k-o</sup>	66.10 <sup>g-r</sup>	41.80 <sup>j-m</sup>	54.77 <sup>l-r</sup>	85.38 <sup>e-l</sup>	86.37 <sup>g-m</sup>	96.27 <sup>b-l</sup>	89.34 <sup>e-k</sup>
12	EH07023-3	68.06 <sup>e-n</sup>	67.73 <sup>e-o</sup>	61.43 <sup>a-h</sup>	65.74 <sup>d-k</sup>	91.62 <sup>d-l</sup>	93.53 <sup>e-i</sup>	122.73 <sup>a</sup>	102.63 <sup>bc</sup>
13	EK05006-3	93.37 <sup>ab</sup>	54.18 <sup>rs</sup>	62.47 <sup>a-g</sup>	70.01 <sup>b-g</sup>	89.33 <sup>d-l</sup>	90.77 <sup>e-k</sup>	117.07 <sup>ab</sup>	99.06 <sup>b-g</sup>
14	EK LS/CSR02014-2-4	56.86 <sup>k-o</sup>	72.00 <sup>c-l</sup>	59.43 <sup>a-i</sup>	62.76 <sup>f-l</sup>	82.78 <sup>g-m</sup>	81.17 <sup>i-n</sup>	103.03 <sup>a-j</sup>	88.99 <sup>f-l</sup>
15	Numan	86.65 <sup>a-d</sup>	72.67 <sup>c-k</sup>	58.93 <sup>a-i</sup>	72.75 <sup>a-e</sup>	84.85 <sup>f-l</sup>	78.20 <sup>j-n</sup>	110.97 <sup>a-e</sup>	91.34 <sup>d-k</sup>
16	Bulga 70	66.07 <sup>g-n</sup>	69.90 <sup>d-m</sup>	30.10 <sup>mn</sup>	55.36 <sup>l-r</sup>	86.32 <sup>e-l</sup>	90.53 <sup>e-l</sup>	90.53 <sup>e-n</sup>	89.13 <sup>e-l</sup>
17	EK05001-1	66.83 <sup>f-n</sup>	71.33 <sup>c-l</sup>	49.63 <sup>e-l</sup>	62.60 <sup>f-m</sup>	80.05 <sup>i-n</sup>	75.70 <sup>l-o</sup>	107.50 <sup>a-g</sup>	87.75 <sup>h-m</sup>
18	Dosha	85.21 <sup>a-e</sup>	66.93 <sup>f-q</sup>	70.00 <sup>ab</sup>	74.05 <sup>a-d</sup>	89.71 <sup>d-l</sup>	93.47 <sup>e-i</sup>	111.03 <sup>a-e</sup>	98.07 <sup>b-h</sup>
19	Gora	69.21 <sup>d-m</sup>	78.00 <sup>b-g</sup>	65.77 <sup>abc</sup>	70.99 <sup>b-f</sup>	96.66 <sup>d-k</sup>	92.2 <sup>e-k</sup>	110.97 <sup>a-e</sup>	99.94 <sup>b-e</sup>
20	EH08035-1	72.81 <sup>c-k</sup>	56.33 <sup>o-s</sup>	43.90 <sup>i-m</sup>	57.68 <sup>j-r</sup>	104.63 <sup>a-f</sup>	103.33 <sup>a-e</sup>	90.03 <sup>e-o</sup>	99.33 <sup>b-g</sup>
21	Wayu	43.59 <sup>o</sup>	53.27 <sup>s</sup>	25.30 <sup>n</sup>	40.72 <sup>s</sup>	58.80 <sup>o</sup>	73.97 <sup>mno</sup>	52.03 <sup>r</sup>	61.60 <sup>o</sup>
22	EK LS/CSR02023-2-1	58.35 <sup>j-o</sup>	55.17 <sup>p-s</sup>	47.77 <sup>f-l</sup>	53.76 <sup>m-r</sup>	85.28 <sup>e-l</sup>	95.38 <sup>d-i</sup>	93.77 <sup>d-m</sup>	91.48 <sup>d-k</sup>
23	Mesay	60.58 <sup>h-o</sup>	60.13 <sup>l-s</sup>	44.80 <sup>j-m</sup>	55.17 <sup>l-r</sup>	75.65 <sup>l-o</sup>	77.33 <sup>k-n</sup>	83.50 <sup>i-p</sup>	78.83 <sup>lmn</sup>
24	EH09004-2	75.38 <sup>c-j</sup>	67.87 <sup>e-o</sup>	37.23 <sup>lmn</sup>	60.16 <sup>i-q</sup>	122.95 <sup>a</sup>	96.37 <sup>c-i</sup>	78.27 <sup>l-q</sup>	99.19 <sup>b-g</sup>
25	EH06088-6	52.69 <sup>l-o</sup>	61.43 <sup>k-s</sup>	65.90 <sup>abc</sup>	60.01 <sup>i-q</sup>	96.89 <sup>d-k</sup>	87.33 <sup>f-m</sup>	103.40 <sup>a-j</sup>	95.87 <sup>c-j</sup>
	Mean	69.98a	67.66b	51.16c	62.93	92.62b	90.80b	95.96a	93.13
	Relative Reduction (%)	24.44	25.48	46.69	32.34				

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05.

Table 7. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	Watebecha Minjaro	Jeldu	Mean	Holetta	Watebecha Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	68.53 <sup>d-n</sup>	61.53 <sup>k-s</sup>	49.03 <sup>e-l</sup>	59.70 <sup>i-q</sup>	94.17 <sup>d-l</sup>	95.23 <sup>d-i</sup>	113.83 <sup>a-d</sup>	101.08 <sup>bcd</sup>
27	Kasa	50.51 <sup>no</sup>	58.27 <sup>m-s</sup>	45.50 <sup>i-l</sup>	51.43 <sup>qr</sup>	80.23 <sup>h-n</sup>	74.80 <sup>mno</sup>	72.17 <sup>n-q</sup>	75.73 <sup>n</sup>
28	Cool-0025	72.95 <sup>c-k</sup>	65.50 <sup>h-r</sup>	49.00 <sup>e-l</sup>	62.48 <sup>f-m</sup>	101.37 <sup>b-g</sup>	90.33 <sup>e-l</sup>	103.80 <sup>a-i</sup>	98.50 <sup>b-g</sup>
29	EH06070-3	70.23 <sup>d-l</sup>	56.90 <sup>n-s</sup>	44.63 <sup>i-m</sup>	57.25 <sup>k-r</sup>	85.55 <sup>e-l</sup>	73.47 <sup>mno</sup>	94.40 <sup>d-m</sup>	84.47 <sup>k-n</sup>
30	EK LS/CSR02010-4-3	70.60 <sup>d-l</sup>	67.60 <sup>e-o</sup>	47.90 <sup>f-l</sup>	62.03 <sup>g-n</sup>	109.16 <sup>a-d</sup>	112.70 <sup>ab</sup>	103.57 <sup>a-i</sup>	108.47 <sup>ab</sup>
31	Cool-0031	59.10 <sup>i-o</sup>	72.10 <sup>c-l</sup>	48.60 <sup>f-l</sup>	59.93 <sup>i-q</sup>	97.57 <sup>c-k</sup>	101.93 <sup>a-f</sup>	95.77 <sup>c-l</sup>	98.42 <sup>b-h</sup>
32	Cool-0018	70.34 <sup>d-l</sup>	68.13 <sup>e-o</sup>	45.90 <sup>h-l</sup>	61.46 <sup>g-o</sup>	100.98 <sup>b-g</sup>	82.50 <sup>h-n</sup>	109.57 <sup>a-e</sup>	97.68 <sup>b-i</sup>
33	EK LS/CSR02028-1-1	77.09 <sup>b-i</sup>	72.33 <sup>c-l</sup>	44.90 <sup>i-m</sup>	64.78 <sup>e-k</sup>	94.85 <sup>d-l</sup>	87.87 <sup>f-m</sup>	113.40 <sup>a-d</sup>	98.71 <sup>b-g</sup>
34	EK 05037-4	69.13 <sup>d-m</sup>	79.67 <sup>a-e</sup>	51.50 <sup>c-l</sup>	66.76 <sup>d-i</sup>	104.96 <sup>a-e</sup>	97.17 <sup>c-h</sup>	100.50 <sup>b-k</sup>	100.87 <sup>bcd</sup>
35	Cool-0035	66.55 <sup>f-n</sup>	83.30 <sup>abc</sup>	54.77 <sup>b-k</sup>	68.21 <sup>c-i</sup>	98.27 <sup>c-i</sup>	95.63 <sup>d-i</sup>	98.17 <sup>b-l</sup>	97.36 <sup>c-j</sup>
36	KUSE2-27-33	65.09 <sup>g-n</sup>	58.30 <sup>m-s</sup>	39.97 <sup>klm</sup>	54.45 <sup>l-r</sup>	94.28 <sup>d-l</sup>	95.53 <sup>d-i</sup>	97.90 <sup>b-l</sup>	95.90 <sup>c-j</sup>
37	EH07015-7	79.17 <sup>a-g</sup>	54.77 <sup>qrs</sup>	65.07 <sup>a-d</sup>	66.34 <sup>d-j</sup>	107.09 <sup>a-d</sup>	92.97 <sup>e-j</sup>	101.87 <sup>a-j</sup>	100.64 <sup>bcd</sup>
38	Cool-0024	79.49 <sup>a-g</sup>	74.00 <sup>c-j</sup>	50.57 <sup>c-l</sup>	68.02 <sup>c-i</sup>	100.15 <sup>b-h</sup>	109.27 <sup>a-d</sup>	100.33 <sup>b-k</sup>	103.25 <sup>bc</sup>
39	Selale	51.53 <sup>mno</sup>	60.73 <sup>k-s</sup>	37.97 <sup>lmn</sup>	50.08 <sup>r</sup>	62.52 <sup>no</sup>	97.33 <sup>c-h</sup>	64.87 <sup>pqr</sup>	74.91 <sup>n</sup>
40	Moti	84.53 <sup>a-f</sup>	75.40 <sup>c-i</sup>	58.30 <sup>a-i</sup>	72.74 <sup>a-e</sup>	119.24 <sup>ab</sup>	110.50 <sup>abc</sup>	115.57 <sup>abc</sup>	115.10 <sup>a</sup>
41	EH06027-2	72.05 <sup>d-k</sup>	67.27 <sup>f-p</sup>	47.00 <sup>g-l</sup>	62.09 <sup>g-n</sup>	83.06 <sup>g-m</sup>	92.90 <sup>e-j</sup>	84.30 <sup>i-p</sup>	86.75 <sup>j-m</sup>
42	EK LS/CSR02019-2-4	73.56 <sup>c-k</sup>	69.07 <sup>e-n</sup>	57.33 <sup>b-j</sup>	66.65 <sup>d-i</sup>	107.17 <sup>a-d</sup>	89.90 <sup>e-l</sup>	96.07 <sup>b-l</sup>	97.71 <sup>b-i</sup>
43	EH09002-1	76.79 <sup>b-i</sup>	61.97 <sup>j-s</sup>	43.83 <sup>i-m</sup>	60.86 <sup>h-p</sup>	77.60 <sup>k-n</sup>	84.93 <sup>g-n</sup>	97.77 <sup>b-l</sup>	86.77 <sup>j-m</sup>
44	Tumsa	77.51 <sup>b-h</sup>	78.07 <sup>b-g</sup>	57.17 <sup>b-j</sup>	70.91 <sup>b-f</sup>	97.49 <sup>c-k</sup>	99.23 <sup>b-g</sup>	106.93 <sup>a-g</sup>	101.22 <sup>bcd</sup>
45	Gebelcho	66.59 <sup>f-n</sup>	71.83 <sup>c-l</sup>	57.23 <sup>b-j</sup>	65.22 <sup>e-k</sup>	95.03 <sup>d-l</sup>	91.33 <sup>e-k</sup>	74.40 <sup>m-q</sup>	86.92 <sup>j-m</sup>
46	EK05037-5	55.92 <sup>k-o</sup>	60.50 <sup>k-s</sup>	42.47 <sup>j-m</sup>	52.96 <sup>o-r</sup>	78.14 <sup>j-n</sup>	81.37 <sup>i-n</sup>	85.73 <sup>h-o</sup>	81.75 <sup>k-n</sup>
47	Didi'a	90.60 <sup>abc</sup>	81.97 <sup>a-d</sup>	50.90 <sup>c-l</sup>	74.49 <sup>a-d</sup>	97.93 <sup>c-j</sup>	110.37 <sup>abc</sup>	94.23 <sup>d-m</sup>	100.84 <sup>bcd</sup>
48	Cool-0034	64.18 <sup>g-n</sup>	79.77 <sup>a-e</sup>	57.17 <sup>b-j</sup>	67.04 <sup>c-i</sup>	94.49 <sup>d-l</sup>	99.17 <sup>b-g</sup>	105.60 <sup>a-h</sup>	99.75 <sup>b-f</sup>
49	CS20DK	85.81 <sup>a-e</sup>	89.97 <sup>a</sup>	62.90 <sup>a-f</sup>	79.56 <sup>a</sup>	116.57 <sup>abc</sup>	115.63 <sup>a</sup>	107.53 <sup>a-g</sup>	113.24 <sup>a</sup>
50	Tesfa	57.44 <sup>j-o</sup>	52.87 <sup>s</sup>	46.63 <sup>h-l</sup>	52.31 <sup>pqr</sup>	92.17 <sup>d-l</sup>	71.20 <sup>no</sup>	70.07 <sup>o-r</sup>	77.81 <sup>mn</sup>
Mean		69.98a	67.66b	51.16c	62.93	92.62b	90.80b	95.96a	93.13
Relative Reduction (%)		24.44	25.48	46.69	32.34				

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05.

#### 4.2.2.4. Disease reaction response of genotypes

The overall mean performances of genotypes for chocolate spot disease reaction over location with and without lime application were between 18.95 - 43.84% (for CS20DK and Cool-0031) and 26.17 - 43.69% (for Tumsa and NC58) with mean value of 30.64 and 34.39%, respectively. The genotypes CS20DK, Tumsa, Gebelcho, Numan EH06070-3, EH09002-1, EKLS/CSR02012-2-3, EH09007-4, EH07015-7, EH09031-4 and EK05037-4 showed less susceptibility to chocolate spot whereas Cool-0031, Cool-0025, Cool-0035 and EH08035-1 were susceptible with significant difference from other genotypes over locations with and without lime application (Appendix Table 6i).

The result indicated the presence of higher chance of selecting disease resistant genotypes for disease stress which is one of the faba bean production problems in the study area. Lime application brought a reduction in severity of chocolate spot which implied that stress condition aggravate disease susceptibility. Genotypes that become susceptible to chocolate spot disease gave lower grain yield as compared to genotypes relatively resistant. It was reported that soil acidity of growing environments expose faba bean to greater chocolate spot infection (Getachew *et al.*, 2005). Likewise, chocolate spot infection was higher in lower pH 4.8 than higher soil pH 7.0 thereby reduced plant vigor and consequently increased disease susceptibility (Elliott and Whittington, 2009). Furthermore, chocolate spot is the most widespread and destructive faba bean disease in Ethiopia, with estimated yield reductions of up to 68% on susceptible cultivars (Samuel *et al.*, 2010) and contributes to low productivity (Asnakech *et al.*, 2016).

#### 4.2.3. Genotypes Soil Acidity Tolerance Indices

The mean values of genotypes for all soil acidity stress tolerance indices over three locations are presented in Table 8. The mean soil acidity stress tolerance index (STI) of genotypes ranged from 0.54 to 1.86 with overall mean value of 1.22. The genotypes Wayu and Holetta-2 had significantly lower, while Moti and CS20DK had significantly higher mean soil acidity stress tolerance index than other genotypes but nonsignificant difference between mean values of these genotypes. In general, 48% of the genotypes showed lower and higher soil acidity stress tolerance index than the overall mean (Table 8). As reported by Majid *et al.* (2010) genotypes with STI values  $\geq 1$  possess a higher stress tolerance



(STI). Likewise, 82% of the genotypes had STI values  $\geq 1$  and identified as soil acidity stress tolerant genotypes.

Stress susceptible index (SSI) varied in the range between 0.48 (Holetta-2) and 2.04 (EK LS/CSR02010-4-3) with the mean values of 1.33 over locations. The genotypes KUSE2-27-33, EH08035-1, EK LS/CSR02017-3-4 and Moti had significantly high SSI from other genotypes. A total of 26 (52%) genotypes had lower stress susceptible index than the overall mean of genotypes (Table 8). The genotypes showed relative yield reduction of 0.17 to 0.43% with a mean value of 0.32% in plots without lime as compared to plots with lime application. Numan and EKLS/CSR02010-4-3 showed significantly lowest and highest yield reduction, respectively. However, other three and eight genotypes also had lower and higher yield reduction, respectively, without significant difference with the mean yield reduction of Numan and EK LS/CSR02010-4-3. Generally, 50% and 48% genotypes showed yield reduction lower and higher than the overall mean yield reduction of genotypes, respectively (Table 8).

The low values of SSI and RYR and high values of other evaluated indices indicate better performance of genotypes under stress condition. Therefore, genotypes with low SSI and RYR values were tolerant to soil acidity and that have high values may not perform best under soil acidity condition. Accordingly, genotypes Moti, EKLS/CSR02010-4-3, EH08035-1, KUSE2-27-33 and EKLS/CSR02017-3-4 might not be recommended for areas with soil acidity problem whereas Numan, Holetta-2, Hachalu, Obse, Dosh, Wolki, Gebelcho and NC58 might perform best under acidic soil condition.

The genotypes had mean yield index of 0.90 in the range between 0.58 and 1.14 for Wayu and CS20DK, respectively. CS20DK followed by Moti, Didea, Wolki, Obse, Hachalu, Numan and Dosh had significantly different high yield index than other genotypes while Wayu had significantly lower yield index than mean of other genotypes. A total of 29 (58%) and 21 (42%) genotypes had lower and higher mean YI than overall mean of genotypes, respectively. The genotypes had mean values of 78.02, 76.06 and 74.20g in the range from 51.15 to 96.40, 49.87 to 94.73 and 48.64 to 93.11g in mean productivity (MP), geometric mean productivity (GMP) and harmonic mean (HM) for Wayu and CS20DK respectively. The genotypes CS20DK and Moti had significantly higher while Wayu lower values different than other genotypes. On the other hand, 22 (44%), 23 (46%) and 25

(50%) genotypes had lower MP, GMP and HM than overall mean of genotypes, respectively (Table 8).

In most cases the mean values of genotypes for percent yield reduction and soil acidity tolerance index not coincide with mean values of genotypes for other five soil acidity stress indices. However, Moti and CS20DK had significantly higher YI, MP, GMP and HM. Moti had significantly higher while CS20DK lower mean stress susceptible index over the three locations. The genotypes EH08035-1, EK LS/CSR02017-3-4 and KUSE2-27-33 had significantly higher yield index which coincides with higher percent yield reduction, but Wolki, Obse, Hachalu and Numan had significantly higher mean yield index as opposed to the significantly lower yield reduction (Table 8).

In general, some genotypes showed similar ranks for two or more soil acidity stress indices. Accordingly, relatively similar ranks of genotypes for STI, GMP and HM were observed. Similar results were reported that genotypes showed relatively identical ranks for MP, HM, GMP and STI (Javed *et al.*, 2011) for STI, GMP and MP parameters of drought tolerance indices of Turkish oat landraces (Mevlut and Sait, 2011). Likewise similar patterns of STI and GMP were reported for drought tolerance indices of bread wheat and potato genotypes (Farshadfar *et al.*, 2012; Zerihun, 2016). Furthermore, genotypes can be categorized as tolerant or susceptible for STI, MP and GMP indices (Sabaghnia and Janmohammadi, 2014). The authors concluded that parameters that identify genotypes in a similar order were equally important for screening stress tolerant genotypes.

In this study, yield index identified CS20DK, Obse, Wolki, Didi'a, Dosha, Hachalu, Numan and Moti as the best and Wayu the least soil acidity adapted genotypes. In most cases, it is rare that the genotypes that had high yield also exhibiting good performance for stress indices. However, CS20DK and Moti had higher mean yield besides showed significantly higher STI, YI, MP, GMP and HM. This suggested that CS20DK and Moti had relatively high grain yield with and without lime application as compared to the other genotypes in spite of the high RYR of Moti. It was reported that genotypes with high STI, MP and GMP values are better yielding under both stress levels (Asrat and Blair, 2014).

Generally, based on the values of multiple indices (YI, STI, MP, GMP, HM, SSI and RYR) genotypes Wolki, Dosha, Obse, Hachalu and Numan were identified as the most desirable soil acidity tolerant genotypes whereas KUSE2-27-33 was identified as the most sensitive genotype. Moreover, the great variability of the 50 faba bean genotypes exhibited a good potential to screening large germplasm of faba bean for soil acidity tolerance and develop a cultivar that are tolerant to soil acidity in the country. It is possible to conclude that SSI and STI have inverse relationship and genotypes with high SSI mean that genotypes have low STI value. Likewise such value will have by default high RYR and low MP, GMP and HM.

Table 8. Mean performance of seven soil acidity stress indices based on grain yield of 50 faba bean genotypes evaluated with and without lime application at three locations in 2017

No.	Genotype	RYR	SSI	YI	STI	MP	GMP	HM
1	Cool-0030	0.36 <sup>d-l</sup>	1.61 <sup>b-f</sup>	0.85 <sup>j-q</sup>	1.14 <sup>g-l</sup>	77.63 <sup>d-n</sup>	74.62 <sup>h-n</sup>	71.82 <sup>i-q</sup>
2	Wolki	0.24 <sup>u-x</sup>	0.94 <sup>q-t</sup>	1.08 <sup>abc</sup>	1.54 <sup>bcd</sup>	86.29 <sup>bcd</sup>	84.73 <sup>b-f</sup>	83.26 <sup>b-f</sup>
3	EK LS/CSR02012-2-3	0.37 <sup>c-j</sup>	1.63 <sup>b-f</sup>	0.88 <sup>h-o</sup>	1.24 <sup>e-k</sup>	80.01 <sup>c-n</sup>	77.64 <sup>c-n</sup>	75.36 <sup>e-o</sup>
4	Obse	0.20 <sup>wxy</sup>	0.89 <sup>rst</sup>	1.11 <sup>ab</sup>	1.56 <sup>bc</sup>	87.63 <sup>bc</sup>	86.81 <sup>bc</sup>	86.02 <sup>abc</sup>
5	NC58	0.25 <sup>s-w</sup>	0.91 <sup>q-t</sup>	0.88 <sup>h-o</sup>	1.03 <sup>j-n</sup>	71.93 <sup>m-r</sup>	70.88 <sup>m-q</sup>	69.87 <sup>l-r</sup>
6	Ashebeka	0.30 <sup>l-u</sup>	1.30 <sup>g-o</sup>	0.99 <sup>b-i</sup>	1.40 <sup>c-g</sup>	84.06 <sup>c-g</sup>	82.52 <sup>c-i</sup>	81.02 <sup>b-i</sup>
7	Hachalu	0.19 <sup>xy</sup>	0.74 <sup>t</sup>	1.04 <sup>a-e</sup>	1.35 <sup>c-i</sup>	81.31 <sup>c-l</sup>	80.82 <sup>c-k</sup>	80.34 <sup>b-j</sup>
8	Degaga	0.31 <sup>i-r</sup>	1.22 <sup>j-q</sup>	0.85 <sup>j-q</sup>	1.07 <sup>i-n</sup>	73.44 <sup>j-q</sup>	71.77 <sup>k-p</sup>	70.17 <sup>k-r</sup>
9	EH09031-4	0.31 <sup>k-s</sup>	1.19 <sup>l-r</sup>	0.88 <sup>h-o</sup>	1.13 <sup>g-m</sup>	75.08 <sup>g-p</sup>	73.69 <sup>i-o</sup>	72.34 <sup>h-q</sup>
10	Holetta-2	0.18 <sup>y</sup>	0.48 <sup>u</sup>	0.76 <sup>n-r</sup>	0.71 <sup>op</sup>	58.62 <sup>t</sup>	58.22 <sup>s</sup>	57.84 <sup>u</sup>
11	EH09007-4	0.38 <sup>a-h</sup>	1.52 <sup>c-j</sup>	0.78 <sup>m-r</sup>	1.00 <sup>j-n</sup>	72.05 <sup>m-r</sup>	69.44 <sup>n-r</sup>	67.00 <sup>n-t</sup>
12	EH07023-3	0.34 <sup>e-m</sup>	1.63 <sup>b-f</sup>	0.94 <sup>d-l</sup>	1.37 <sup>c-h</sup>	84.18 <sup>c-g</sup>	81.78 <sup>c-j</sup>	79.49 <sup>c-j</sup>
13	EK05006-3	0.27 <sup>p-v</sup>	1.28 <sup>h-o</sup>	1.00 <sup>b-h</sup>	1.40 <sup>c-h</sup>	84.53 <sup>c-f</sup>	82.21 <sup>c-j</sup>	80.01 <sup>b-j</sup>
14	EK LS/CSR02014-2-4	0.28 <sup>n-v</sup>	1.16 <sup>m-r</sup>	0.90 <sup>f-m</sup>	1.14 <sup>g-l</sup>	75.87 <sup>f-p</sup>	74.42 <sup>h-o</sup>	73.02 <sup>h-p</sup>
15	Numan	0.17 <sup>y</sup>	0.82 <sup>st</sup>	1.04 <sup>a-e</sup>	1.34 <sup>c-i</sup>	82.04 <sup>c-j</sup>	80.64 <sup>c-l</sup>	79.32 <sup>c-k</sup>
16	Bulga 70	0.38 <sup>a-i</sup>	1.49 <sup>d-l</sup>	0.79 <sup>m-r</sup>	1.02 <sup>j-n</sup>	72.24 <sup>l-q</sup>	69.06 <sup>n-r</sup>	66.26 <sup>o-u</sup>
17	EK05001-1	0.25 <sup>r-v</sup>	1.11 <sup>n-s</sup>	0.89 <sup>f-m</sup>	1.10 <sup>h-m</sup>	75.16 <sup>g-p</sup>	73.19 <sup>j-o</sup>	71.35 <sup>j-q</sup>
	Mean	0.32	1.33	0.90	1.22	78.02	76.06	74.20

Mean values followed by similar letter(s) in each column had nonsignificant difference at  $P < 0.05$ , RYR= relative yield reduction, SSI= stress susceptible index, YI=yield index, STI =soil acidity tolerance index, MP= mean productivity, GMP= geometric mean productivity, HM= harmonic mean

Table 8. Continued

No	Genotype	RYR	SSI	YI	STI	MP	GMP	HM
18	Dosha	0.23 <sup>vwx</sup>	1.06 <sup>n-s</sup>	1.06 <sup>a-d</sup>	1.48 <sup>b-e</sup>	86.04 <sup>bcd</sup>	84.86 <sup>b-e</sup>	83.71 <sup>b-e</sup>
19	Gora	0.28 <sup>n-v</sup>	1.27 <sup>h-o</sup>	1.01 <sup>b-f</sup>	1.45 <sup>b-f</sup>	85.45 <sup>bcd</sup>	83.97 <sup>b-g</sup>	82.52 <sup>b-g</sup>
20	EH08035-1	0.43 <sup>abc</sup>	1.83 <sup>abc</sup>	0.82 <sup>k-r</sup>	1.19 <sup>e-k</sup>	78.51 <sup>c-n</sup>	75.47 <sup>f-n</sup>	72.57 <sup>h-q</sup>
21	Wayu	0.35 <sup>e-l</sup>	0.92 <sup>q-t</sup>	0.58 <sup>s</sup>	0.54 <sup>p</sup>	51.15 <sup>u</sup>	49.87 <sup>t</sup>	48.64 <sup>v</sup>
22	EK LS/CSR02023-2-1	0.41 <sup>a-d</sup>	1.66 <sup>b-e</sup>	0.77 <sup>m-r</sup>	1.01 <sup>j-n</sup>	72.62 <sup>k-q</sup>	69.91 <sup>m-q</sup>	67.34 <sup>n-t</sup>
23	Mesay	0.29 <sup>l-v</sup>	1.04 <sup>o-s</sup>	0.79 <sup>m-r</sup>	0.89 <sup>l-o</sup>	66.99 <sup>p-s</sup>	65.65 <sup>o-s</sup>	64.36 <sup>p-u</sup>
24	EH09004-2	0.40 <sup>a-e</sup>	1.72 <sup>bcd</sup>	0.86 <sup>j-q</sup>	1.28 <sup>c-k</sup>	79.67 <sup>c-n</sup>	77.0 <sup>d-n</sup>	74.45 <sup>f-o</sup>
25	EH06088-6	0.37 <sup>b-j</sup>	1.58 <sup>b-i</sup>	0.86 <sup>j-q</sup>	1.18 <sup>f-k</sup>	77.93 <sup>d-n</sup>	75.73 <sup>e-n</sup>	73.59 <sup>g-o</sup>
26	EK LS/CSR02017-3-4	0.40 <sup>a-f</sup>	1.82 <sup>abc</sup>	0.85 <sup>j-q</sup>	1.22 <sup>e-k</sup>	80.38 <sup>c-m</sup>	77.14 <sup>d-n</sup>	74.12 <sup>f-o</sup>
27	Kasa	0.32 <sup>h-q</sup>	1.07 <sup>n-s</sup>	0.73 <sup>qr</sup>	0.80 <sup>no</sup>	63.59 <sup>rst</sup>	62.24 <sup>qrs</sup>	60.94 <sup>stu</sup>
28	Cool-0025	0.36 <sup>d-k</sup>	1.59 <sup>b-h</sup>	0.89 <sup>f-m</sup>	1.26 <sup>d-k</sup>	80.48 <sup>c-m</sup>	78.00 <sup>c-n</sup>	75.65 <sup>d-n</sup>
29	EH06070-3	0.31 <sup>j-r</sup>	1.20 <sup>k-r</sup>	0.82 <sup>l-r</sup>	0.99 <sup>k-n</sup>	70.85 <sup>n-r</sup>	68.98 <sup>n-r</sup>	67.22 <sup>n-t</sup>
30	EK LS/CSR02010-4-3	0.43 <sup>a</sup>	2.04 <sup>a</sup>	0.89 <sup>g-n</sup>	1.39 <sup>c-h</sup>	85.24 <sup>cde</sup>	81.77 <sup>c-j</sup>	78.48 <sup>c-m</sup>
31	Cool-0031	0.39 <sup>a-g</sup>	1.69 <sup>bcd</sup>	0.86 <sup>j-q</sup>	1.22 <sup>e-k</sup>	79.17 <sup>c-n</sup>	76.60 <sup>e-n</sup>	74.14 <sup>f-o</sup>
32	Cool-0018	0.35 <sup>d-l</sup>	1.60 <sup>b-g</sup>	0.88 <sup>h-o</sup>	1.21 <sup>e-k</sup>	79.56 <sup>c-n</sup>	76.66 <sup>e-n</sup>	73.97 <sup>f-o</sup>
33	EK LS/CSR02028-1-1	0.32 <sup>i-q</sup>	1.49 <sup>d-l</sup>	0.93 <sup>e-l</sup>	1.29 <sup>c-j</sup>	81.73 <sup>c-k</sup>	78.78 <sup>c-m</sup>	76.12 <sup>d-n</sup>
34	EK 05037-4	0.34 <sup>g-o</sup>	1.50 <sup>d-l</sup>	0.95 <sup>d-j</sup>	1.38 <sup>c-h</sup>	83.82 <sup>c-g</sup>	81.62 <sup>c-j</sup>	79.53 <sup>c-j</sup>
35	Cool-0035	0.30 <sup>k-t</sup>	1.28 <sup>g-o</sup>	0.97 <sup>c-j</sup>	1.37 <sup>c-h</sup>	82.78 <sup>c-i</sup>	81.08 <sup>c-j</sup>	79.44 <sup>c-j</sup>
36	KUSE2-27-33	0.43 <sup>ab</sup>	1.83 <sup>abc</sup>	0.78 <sup>m-r</sup>	1.07 <sup>i-n</sup>	75.18 <sup>g-p</sup>	71.78 <sup>k-p</sup>	68.63 <sup>n-s</sup>
37	EH07015-7	0.35 <sup>e-l</sup>	1.51 <sup>d-k</sup>	0.95 <sup>d-k</sup>	1.39 <sup>c-h</sup>	83.48 <sup>c-h</sup>	81.42 <sup>c-j</sup>	79.44 <sup>c-j</sup>
38	Cool-0024	0.34 <sup>f-n</sup>	1.55 <sup>c-i</sup>	0.97 <sup>c-j</sup>	1.45 <sup>c-f</sup>	85.63 <sup>bcd</sup>	83.40 <sup>b-h</sup>	81.27 <sup>b-h</sup>
39	Selale	0.32 <sup>i-q</sup>	1.09 <sup>n-s</sup>	0.72 <sup>r</sup>	0.79 <sup>no</sup>	62.49 <sup>st</sup>	61.05 <sup>rs</sup>	59.65 <sup>tu</sup>
40	Moti	0.37 <sup>b-j</sup>	1.86 <sup>ab</sup>	1.04 <sup>a-e</sup>	1.72 <sup>ab</sup>	93.92 <sup>ab</sup>	91.22 <sup>ab</sup>	88.63 <sup>ab</sup>
41	EH06027-2	0.28 <sup>m-v</sup>	1.09 <sup>n-s</sup>	0.89 <sup>g-n</sup>	1.11 <sup>g-m</sup>	74.42 <sup>h-p</sup>	73.08 <sup>j-o</sup>	71.79 <sup>i-q</sup>
42	EK LS/CSR02019-2-4	0.31 <sup>i-r</sup>	1.37 <sup>e-n</sup>	0.95 <sup>d-j</sup>	1.34 <sup>c-i</sup>	82.17 <sup>c-j</sup>	80.54 <sup>c-l</sup>	78.96 <sup>c-l</sup>
43	EH09002-1	0.28 <sup>o-v</sup>	1.14 <sup>m-r</sup>	0.87 <sup>i-p</sup>	1.07 <sup>i-n</sup>	73.81 <sup>i-p</sup>	71.60 <sup>l-p</sup>	69.58 <sup>m-s</sup>
44	Tumsa	0.29 <sup>l-v</sup>	1.33 <sup>f-o</sup>	1.01 <sup>b-g</sup>	1.47 <sup>b-f</sup>	86.06 <sup>bcd</sup>	84.33 <sup>b-g</sup>	82.67 <sup>b-g</sup>
45	Gebelcho	0.24 <sup>t-x</sup>	0.96 <sup>p-t</sup>	0.93 <sup>e-l</sup>	1.18 <sup>f-k</sup>	76.06 <sup>e-o</sup>	75.23 <sup>g-n</sup>	74.41 <sup>f-o</sup>
46	EK05037-5	0.35 <sup>d-l</sup>	1.27 <sup>i-p</sup>	0.76 <sup>o-r</sup>	0.88 <sup>l-o</sup>	67.35 <sup>o-s</sup>	65.50 <sup>o-s</sup>	63.75 <sup>q-u</sup>
47	Didi'a	0.26 <sup>q-v</sup>	1.16 <sup>m-r</sup>	1.06 <sup>a-d</sup>	1.55 <sup>bcd</sup>	87.66 <sup>bc</sup>	86.14 <sup>bcd</sup>	84.68 <sup>bcd</sup>
48	Cool-0034	0.33 <sup>h-p</sup>	1.44 <sup>d-m</sup>	0.96 <sup>c-j</sup>	1.37 <sup>c-h</sup>	83.39 <sup>c-h</sup>	81.48 <sup>c-j</sup>	79.64 <sup>c-j</sup>
49	CS20DK	0.30 <sup>k-t</sup>	1.48 <sup>d-l</sup>	1.14 <sup>a</sup>	1.86 <sup>a</sup>	96.40 <sup>a</sup>	94.73 <sup>a</sup>	93.11 <sup>a</sup>
50	Tesfa	0.32 <sup>h-q</sup>	1.12 <sup>n-s</sup>	0.75 <sup>pqr</sup>	0.85 <sup>mno</sup>	65.06 <sup>q-t</sup>	63.73 <sup>p-s</sup>	62.43 <sup>r-u</sup>
	Mean	0.32	1.33	0.90	1.22	78.02	76.06	74.20

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05, RYR= relative yield reduction, SSI= stress suseptible index, YI=yield index, STI =soil acidity tolerance index, MP= mean productivity, GMP= geometric mean productivity, HM= harmonic mean

### 4.3. Estimates of Variability Component

#### 4.3.1. Estimates of Phenotypic and Genotypic Coefficients of Variation

The phenotypic (PCV) and genotypic (GCV) coefficients of variations, broad sense heritability ( $H^2$ ) and expected genetic advance computed without lime for 11 and with lime application for 12 agro-morphology traits over locations are presented in Table 9.

The GCV values fall in the range between 1.08 and 23.05 and 0.94 and 23.88% and PCV values between 1.20 and 23.26% and 1.11 and 24.07% without and with lime application, respectively. The lowest and highest values of GCV and PCV were calculated for days to 90% maturity and hundred seed weight, respectively, for both GCV and PCV for both without and with lime application. The differences between PCV and GCV were in the range between 0.12 to 6.78 and 0.17 to 7.04 for days to 90% maturity and chocolate spot disease for all traits without and with lime, respectively (Table 9). The differences between traits without and lime application were in the range between 0.14 and 3.54% for GCV and 0.09 and 3.8% for PCV (Table 9). The low differences between phenotypic and genotypic coefficients of variations under two managements over locations may indicate the less influence of environmental factors in the expression of traits. Similarly, narrow PCV and GCV variation in faba bean have been reported by various authors (Solieman and Ragheb, 2014; Hamza *et al.*, 2017; Mostafa *et al.*, 2017) and they stated that variability due to the genetic constitution of the genotypes was more than variability exerted by environmental factors

The values of PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%) (Johnson *et al.* 1955). Accordingly, both the PCV and GCV values were high for hundred seed weight both with and without lime applications and the values of both genetic parameters were moderate for number of podding node per plan, number of pod per plant, grain yield, grain production efficiency and economic growth rate without lime. Likewise with lime moderate for number of pod per plant, grain production efficiency and chocolate spot. Almost all the traits fell under high and moderate PCV and GCV under stress (without lime) and non-stress (with lime) over locations (Table 9). The high to moderate PCV and GCV for the mentioned traits suggested that the traits were less influenced by environmental factors and selection based on phenotypic expression of the

genotypes could be applied as breeding method. Ejigu *et al.* (2016) reported that, high phenotypic and genotypic coefficients of variation as an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding.

The PCV values were moderate and GCV values were low (<10%) for grain yield and economic growth rate with lime and for chocolate spot without lime and the values were low for both parameters for days to 50% flowering, days to 90% maturity, plant height, and grain filling period for both managements (Table 9). This implies greater influence of environmental factors for the phenotypic expression of these traits that make difficult or practically impossible to exercise selection based on phenotypic performance of the genotypes to improve the traits. This result was in close agreement with the findings of Haridy and El-Said (2016) and Sekhon *et al.* (2017) who reported high environmental variance than genotypic variance for days to 90% maturity and plant height and days to 50% flowering, days to 90% maturity and plant height, respectively. Likewise, Hamza *et al.* (2017) reported high environmental variance for days to 50% flowering and plant height.

Table 9. Estimates of phenotypic and genotypic coefficient of variation, heritability and genetic advance for 11 and 12 traits of 50 faba bean genotypes based on the analysis of variance without (above) and with lime (below) over three locations in 2017.

Traits	Without lime										
	Range	Mean	$\sigma^2_g$	$\sigma^2_p$	$\sigma^2_l$	$\sigma^2_{gl}$	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA K=5%	GAM
Days to 50% flowering	51.44-58.89	54.06	2.02	2.52	31.51	1.03	2.63	2.94	80.37	2.63	4.87
Days to 90% maturity	142.11-149.00	145.86	2.46	3.04	26.72	0.73	1.08	1.20	81.01	2.91	2.00
Grain filling period(days)	87.22-95.33	91.80	3.26	4.17	29.29	1.36	1.97	2.22	78.10	3.29	3.58
Plant height(cm)	100.78-119.00	111.24	10.63	19.45	1846.70	6.61	2.93	3.96	54.68	4.97	4.47
Number of podding node plant <sup>-1</sup>	5.11-8.33	6.54	0.52	0.66	1.61	0.11	11.06	12.38	79.74	1.33	20.37
Number of pod plant <sup>-1</sup>	5.56-12.67	8.36	2.08	2.39	2.04	0.44	17.24	18.52	86.71	2.77	33.12
Hundred seed weight(g)	35.39-93.92	70.13	261.42	266.17	4.48	9.78	23.05	23.26	98.22	33.06	47.13
Grain yield(g/5plants)	40.72-79.56	62.93	42.41	63.61	103.98	42.18	10.35	12.67	66.67	10.97	17.43
Chocolate spot disease (%)	26.17-43.69	34.39	5.27	21.41	6.00	25.80	6.68	13.46	24.63	2.35	6.84
Grain production efficiency(g)	60.46-138.01	108.61	130.50	206.45	752.84	148.32	10.52	13.23	63.21	18.74	17.25
Economic growth rate(g/day)	46.98-90.52	68.95	51.97	77.81	183.49	51.43	10.45	12.79	66.78	12.15	17.63
With lime											
Days to 50% flowering	52.33-58.11	54.05	1.01	1.47	30.42	0.90	1.86	2.24	68.88	1.72	3.19
Days to 90% maturity	142.67-148.78	145.92	1.88	2.62	29.55	1.34	0.94	1.11	71.92	2.40	1.64
Grain filling period(days)	87.67-96.00	91.87	2.14	3.17	39.42	2.20	1.59	1.94	67.50	2.48	2.70
Plant height(cm)	119.00-137.11	128.20	6.48	16.01	1623.10	9.72	1.99	3.12	40.45	3.34	2.60
Number of podding node plant <sup>-1</sup>	6.56-9.56	8.08	0.52	0.67	0.66	0.13	8.95	10.14	77.91	1.32	16.30
Number of pod plant <sup>-1</sup>	8.44-16.00	11.66	3.47	3.94	1.55	0.67	15.97	17.03	87.89	3.60	30.88
Number of pod podding nod <sup>-1</sup>	1.25-1.72	1.44	0.01	0.02	0.02	0.00	7.59	8.79	74.45	0.19	13.50
Hundred seed weight(g)	36.67-98.50	71.83	294.32	298.96	15.09	9.36	23.88	24.07	98.45	35.12	48.89
Grain yield(g/5plants)	61.60-115.10	93.13	83.49	114.74	4.98	62.80	9.81	11.50	72.77	16.08	17.27
Chocolate spot disease (%)	18.95-43.84	30.64	9.81	27.97	25.44	40.19	10.22	17.26	35.06	3.83	12.48
Grain production efficiency(g)	92.70-201.14	160.57	309.28	428.13	699.83	244.15	10.95	12.89	72.24	30.84	19.20
Economic growth rate(g/day)	69.48-127.88	101.59	93.97	130.73	22.94	74.05	9.54	11.25	71.88	16.96	16.69

$\sigma^2_g$ - Genotypic variance,  $\sigma^2_p$ - phenotypic variance,  $\sigma^2_l$ - location variance,  $\sigma^2_{gl}$ -genotype by location interaction variance, GCV-Genotypic coefficient of variation, PCV- phenotypic coefficient of variation, H<sup>2</sup> – broad sense heritability, GA-Genetic advance, GAM-Genetic advance as percentage of mean.

### 4.3.2. Estimates of Heritability and Expected Genetic Advance

The broad sense heritability ( $H^2$ ) and genetic advance as percent of mean (GAM) values ranged from 24.63 to 98.22% and 35.06 to 98.45% and 2.0 to 47.13% and 1.64 to 48.89% without and with lime, respectively, over locations (Table 9). A low and high heritability values were calculated for chocolate spot disease and hundred seed weight, respectively, under lime and without lime applications over locations. Also low and high GAM computed for days to 90% maturity and hundred seed weight, respectively, under both managements (Table 9). This result implied that  $H^2$  and GAM values were higher under stress free condition than stressed environments. In contrary to the current result Million and Habtamu (2012) reported the genetic advance as percent of the mean moderate for number of seeds per plant (12.32%) and high for seed yield (35.46%).

It was suggested that the importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much progress can be made through selection (Johnson *et al.*, 1955). Heritability values can be categorized as low (<30%), moderate (30-60%) and high (>60%) (Robinson *et al.*, 1949; Johnson *et al.*, 1955) and genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%) (Johnson *et al.*, 1955). In this study, high heritability accompanied with high to moderate genetic advance was observed for number of podding node per plant, number of pod per plant, hundred seed weight and grain yield under both managements. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the traits. PhaniKrishna *et al.* (2015) suggested that selection based on phenotypic performance of genotypes would be effective to improve traits that have high genetic advance as percent of mean coupled with high heritability estimates. The traits with high to moderate heritability, indicates that it may respond moderate to high for phenotypic selection (Singh and Ceccarelli, 1996). The high  $H^2$  and GAM value of traits indicates the high possibility of transferring traits from parents to the next progeny. Many authors (Gemechu and Mussa, 2009; Million and Habtamu, 2012; Tafere *et al.*, 2013; Bakhiet *et al.*, 2015; Sharifi, 2015; Hamza *et al.*, 2017) also reported high estimates of broad sense heritability for hundred seed weight and grain yield in faba bean genotypes at varied



environments and number of genotypes. In agreement with this result high GAM were reported for number of pod per plant (Million and Habtamu, 2012; Bakhiet *et al.*, 2015). In contradict to this finding low GAM reported for hundred seed weight and grain yield (Hamza *et al.*, 2017).

Low GAM values were calculated for days to 50% flowering, days to 90% maturity, grain filling period and plant height under lime and additionally for chocolate spot without lime applications over locations. Low heritability coupled with low GAM was calculated for chocolate spot without lime application over locations (Table 9). The result indicated that low heritability values for chocolate spot limit possibility of improvement for this trait through selection. In contradict to this result high heritability for chocolate spot disease was reported (El-Badawy *et al.*, 2012; Asnakech, 2014). The probable reason for the variation of traits low to high GAM and vice versa with this result and others were due to the difference in the genetic makeup of the evaluated genotypes.

Medium to high estimates of GCV, PCV,  $H^2$  and GAM were computed for hundred seed weight and number of pod per plant under both lime levels. Traits with high PCV, GCV,  $H^2$  and GAM indicated that these traits are controlled by genetic factor and higher chance for improvement these traits through selection. In general, the present results showed heritability and genetic advance values did not show a definite trend with and without limed applications. For most of the traits heritability under lime free condition is less than limed condition while genetic advance in contrasting direction. From previous work reports, the magnitude of heritability and genetic advance under favorable and unfavorable environment did not follow the same trend. Singh (2002) reported that favorable environment show higher estimates of heritability and genetic advance values than unfavorable environment. Heritability and genetic advance value may be masked due to a greater genotype by environment interaction under unfavorable conditions (Rosielle and Hambin, 1981). Likewise Gemechu *et al.* (2015) reported that heritability and genetic advance values varied in the presence or absence of phosphorus in chick pea. In contrary, to the current result and the reports of others Ceccarelli and Grando (1996) reported that heritability and genetic advance valued influence by the nature of the genetic material evaluated not by the growing environment.

## **4.4. Association of Traits**

### **4.4.1. Phenotypic and Genotypic Correlations of Grain Yield with Other Traits**

Grain yield showed positive and significant phenotypic association with plant height, number of podding node per plant, pod per plant and hundred seed weight under lime free condition over location. Likewise, grain yield showed positive and significant phenotypic association with days to 90% maturity, grain filling period and hundred seed weight under lime application over locations. In addition, grain yield had positive and significant association with grain production efficiency and economic growth rate under lime and without lime applications over locations (Table 10). Therefore, any improvement of traits with significant positive correlation would result in a substantial increment on grain yield. Similarly, significant positive correlation of grain yield with hundred seed weight (Singh *et al.*, 2017), with pods per plant (Gemechu and Mussa, 2002; Tofiq *et al.*, 2016) were reported by different authors.

Grain yield had positive and significant genotypic correlation with plant height, hundred seed weight, grain production efficiency and economic growth rate both with and without lime application (Table 10). The result indicated any improvement of traits with significant positive correlation would result in a substantial increment on grain yield. Similar results were reported that seed yield strongly correlated with plant height (Million, 2012; Tafere *et al.*, 2013; Birhanu, 2016; Tekle *et al.*, 2016). Likewise, recent reports on faba bean also indicated significant and positive association of yield with plant height and hundred seed weight at genotypic level (Kumar *et al.*, 2017; Singh *et al.*, 2017). In contrast to this result previously reported nonsignificant and positive correlation of plant height with seed yield per plant (Chaubey *et al.*, 2012) and negative but significant association of plant height and number of pods per plant with seed yield per plot (Tadele *et al.*, 2011).

Generally, positive and significant association of pairs of traits at phenotypic and genotypic level justified the possibility of correlated response to selection. The negative correlations prohibit the simultaneous improvement of those traits. From the correlation analysis, it can be concluded that plant height and hundred seed weight were found to be important yield

components of faba bean. Similar findings have been reported that effective yield improvement would be achieved through the traits which have significant and positive correlation with yield and other economic traits (Shrifi, 2015; Tofiq *et al.*, 2016; Singh *et al.*, 2017). Likewise, significant positive correlation was reported between seed yield and plant height, number of pod per plant and hundred seed weight (Mostafa *et al.*, 2017).

The magnitudes of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients except in rare cases, which indicate the presence of inherent or genetic association among various traits. In agreement with this finding Singh *et al.* (2017) reported higher genotypic correlation coefficients than phenotypic correlations and concluded that phenotypic expression of the correlation gets modified under the influence of environment and genotypic correlation provides measures of genetic association between traits and is more reliable than phenotypic correlation and this helps to identify the traits to be considered in breeding programme.

#### **4.4.2. Phenotypic and Genotypic Correlations among other Traits**

Days to 90% maturity was significant and positively correlated with days to 50% flowering, grain filling period and hundred seed weight at phenotypic level and with grain filling period, hundred seed weight and grain production efficiency at genotypic level without lime. With lime with days to 50% flowering, grain filling period, number of pod per podding node, hundred seed weight, grain yield, chocolate spot and grain production efficiency at phenotypic level and with grain filling period, plant height and hundred seed weight at genotypic level with lime. It had significant and negative genotypic correlation with number of podding node per plant and pod per plant with and without lime applications over locations (Table 10). The result indicated that improvement of traits that have positive and significant relation leads to improvement of days to 90% maturity indirectly whereas improvement of traits that negatively correlated hinders improvement of days to 90% maturity. Similarly Kumar *et al.* (2017) reported that, days to maturity significant and positively correlated with hundred seed weight.

Hundred seeds weight significantly and positively correlated with days to 90% maturity, grain filling period, plant height, grain production efficiency and economic growth rate whereas

significant and negatively correlated with days to 50% flowering, number of podding node per plant, number of pod per plant and chocolate spot at phenotypic level both with and without lime application. At genotypic level significant and positive association of HSW with days to 90% maturity, grain filling period, and grain production efficiency at both lime levels (Table 10). The result indicated any improvement of traits with significant positive correlation would result in a substantial increment on hundred seeds weight. Previously positive and significant genotypic correlation of hundred seed weight with days to 90% maturity were reported by different authors (Chaubey *et al.*, 2012; Tafere *et al.*, 2013; Kumar *et al.*, 2017).

#### **4.4.3. Phenotypic Direct and Indirect Effects of Traits on Grain Yield**

The result of phenotypic path analysis indicated that economic growth rate followed by grain production efficiency, grain filling period and days to 50% flowering had maximum positive direct effects on grain yield without lime, while economic growth rate followed by grain production efficiency and days to 90% maturity had maximum positive direct effects on grain yield with lime. However days to maturity under lime free and HSW under limed had negative direct effect on grain yield. Days to 90% maturity and HSW contributed to grain yield mainly *via* their highest and positive indirect effect with grain filling period and grain production efficiency under lime free and limed condition respectively. Traits like economic growth rate, grain production efficiency and days to 90% maturity under lime free and economic growth rate, grain production efficiency, grain filling period and days to 50% flowering under limed condition ultimately affects grain yield were the components that exerted a substantial direct effect on grain yield. The residual effect determines unaccounted variability of the dependent factor (grain yield). The magnitude 0.036 and 0.028 indicates that the traits included in the path analysis explained 96.4 % and 97.2% of the variation in grain yield without and with lime respectively (Table 11). Similar results were reported that negative direct effect of plant height on grain yield (Singh *et al.*, 2017) and suggested phenotypic path analysis may not provide a true picture of direct and indirect causes. Incontradict number of pod per plant and plant height had high positive direct effect at phenotypic level on seed yield per plant (Birhanu, 2016; Sekhon *et al.*, 2017).

Table 10. Phenotypic (above diagonal) and genotypic correlation coefficients (below diagonal) for 11 and 12 agronomic traits with grain yield in 50 faba bean genotypes tested without and with lime application over three locations in 2017

Trait	Without lime											
	DF	DM	GFP	PH	PNPP	PPP	HSW	GY	CS	GPE	EGR	
DF	1	0.44**	-0.55**	-0.58**	-0.11*	-0.01	-0.20**	-0.25**	-0.07	-0.68**	-0.09	
DM	0.25	1	0.51**	-0.81**	-0.62**	-0.51**	0.16**	-0.46**	0.05	-0.43**	-0.54**	
GFP	-0.56**	0.66**	1	-0.20**	-0.48**	-0.46**	0.33**	-0.18**	0.11*	0.26**	-0.42**	
PH	0.11	0.22	0.11	1	0.61**	0.48**	0.10*	0.64**	-0.12*	0.69**	0.63**	
PNPP	0.22	-0.52**	-0.61**	0.28	1	0.86**	-0.34**	0.61**	-0.12*	0.43**	0.68**	
PPP	0.36**	-0.48**	-0.70**	0.23	0.94**	1	-0.51**	0.57**	-0.07	0.36**	0.64**	
HSW	-0.30*	0.59**	0.73**	0.16	-0.77**	-0.84**	1	0.22**	-0.20**	0.31**	0.13*	
GY	0.09	0.24	0.14	0.75**	0.21	0.16	0.31*	1	-0.18**	0.86**	0.97**	
CS	-0.09	-0.23	-0.13	0.11	0.30*	0.32*	-0.38*	-0.13	1	-0.08	-0.20**	
GPE	-0.24	0.29*	0.43**	0.69**	0.03	-0.07	0.49**	0.93**	-0.11	1	0.72**	
EGR	0.18	0.12	-0.04	0.73**	0.32*	0.28	0.18	0.98**	-0.12	0.86**	1	
	With lime											
	DF	DM	GFP	PH	PNPP	PPP	PPPN	HSW	GY	CS	GPE	EGR
DF	1	0.32**	-0.56**	-0.44**	0.18**	0.39**	0.39**	-0.24**	-0.06	-0.06	-0.60**	0.16**
DM	0.24	1	0.60**	-0.83**	-0.40**	-0.05	0.39**	0.15**	0.15**	0.29**	0.12*	-0.09
GFP	-0.47**	0.75**	1	-0.36**	-0.50**	-0.37**	0.01	0.33**	0.18**	0.31**	0.61**	-0.21**
PH	-0.02	0.34*	0.32*	1	0.30**	-0.11*	-0.51**	0.12*	-0.03	-0.31**	0.09	0.11*
PNPP	0.08	-0.62**	-0.62**	0.09	1	0.72**	-0.04	-0.44**	0.06	-0.08	-0.17**	0.26**
PPP	0.29*	-0.56**	-0.71**	0.00	0.92**	1	0.65**	-0.68**	0.08	0.07	-0.21**	0.23**
PPPN	0.52**	-0.37**	-0.69**	-0.08	0.65**	0.89**	1	-0.50**	0.03	0.20**	-0.15**	0.03
HSW	-0.28*	0.61**	0.75**	0.30*	-0.76**	-0.88**	-0.84**	1	0.26**	-0.14**	0.38**	0.13**
GY	-0.18	0.16	0.27	0.58**	0.12	0.02	-0.12	0.37**	1	0.04	0.80**	0.92**
CS	-0.22	-0.25	-0.08	0.18	0.32*	0.29*	0.21	-0.32*	0.00	1	0.120*	-0.08
GPE	-0.41**	0.21	0.47	0.57**	-0.01	-0.16	-0.32*	0.50**	0.96**	0.04	1	0.55**
EGR	-0.10	0.03	0.10	0.54**	0.24	0.15	0.01	0.24	0.98**	0.01	0.91**	1

\*, \*\* = significant at  $P < 0.05$  and  $P < 0.01$  respectively, DF = days to 50% flowering, DM = days to 90% maturity, GFP = grain filling period, PH = plant height, PNPP = number of podding node per plant, PPP = number of pod per plant, PPPN = number of pod per podding node, HSW = hundred seed weight, GY = grain yield, CS = chocolate spot, GPE = grain production efficiency, EGR = economic growth rate

Table 11. Phenotypic direct (bold diagonal) and indirect (off diagonal) effects on grain yield in 50 faba bean genotypes tested without and with lime application over locations

Without lime											
Trait	DF	DM	PLH	PNPP	PPP	HSW	CS	GFP	GPE	EGR	r <sub>p</sub>
DF	<b>0.152</b>	-0.017	-0.003	0.000	0.000	-0.001	0.000	-0.093	-0.221	-0.072	-0.255*
DM	0.066	<b>-0.038</b>	-0.004	-0.002	-0.004	0.001	0.000	0.087	-0.138	-0.426	-0.458*
PLH	-0.088	0.031	<b>0.005</b>	0.002	0.003	0.000	0.000	-0.034	0.221	0.500	0.641*
PNPP	-0.016	0.024	0.003	<b>0.003</b>	0.006	-0.001	0.000	-0.081	0.138	0.536	0.611*
PPP	-0.002	0.020	0.002	0.003	<b>0.007</b>	-0.002	0.000	-0.079	0.117	0.507	0.572*
HSW	-0.030	-0.006	0.000	-0.001	-0.004	<b>0.004</b>	-0.001	0.057	0.101	0.100	0.221*
CS	-0.011	-0.002	-0.001	0.000	0.000	-0.001	<b>0.003</b>	0.019	-0.027	-0.155	-0.176*
GFP	-0.083	-0.020	-0.001	-0.001	-0.003	0.001	0.000	<b>0.170</b>	0.082	-0.329	-0.184*
GPE	-0.104	0.016	0.004	0.001	0.003	0.001	0.000	0.043	<b>0.322</b>	0.570	0.856**
EGR	-0.014	0.021	0.003	0.002	0.004	0.001	-0.001	-0.070	0.232	<b>0.791</b>	0.969**
With lime											
Trait	DM	HSW	GFP	GPE	EGR	r <sub>p</sub>					
DM	<b>0.158</b>	-0.001	0.020	0.041	-0.067	0.151*					
HSW	0.024	<b>-0.005</b>	0.011	0.133	0.098	0.262*					
GFP	0.095	-0.002	<b>0.032</b>	0.213	-0.160	0.179					
GPE	0.019	-0.002	0.020	<b>0.348</b>	0.414	0.799**					
EGR	-0.014	-0.001	-0.007	0.192	<b>0.751</b>	0.921**					

Residual effect = 0.028 (without) and 0.036 (with), DF = days to 50% flowering, DM = days to 90% maturity, PH = plant height, PNPP= number of podding node per plant, PPP = number of pod per plant, HSW = hundred seed weight, CS= chocolate spot, GPE=grain production efficiency, EGR= economic growth rate

#### 4.4.4. Genotypic Direct and Indirect Effects of Traits on Grain Yield

The genotypic path coefficient analysis was done on the basis significance correlation at genotypic levels. Therefore, based on their correlation coefficient, at genotypic level 4 traits that have significant relationship with grain yield at both lime levels were included in the path analysis. The genotypic correlations were partitioned in to direct and indirect effects using grain yield as a dependent variable (Table 12). The genotypic path analysis indicated that economic growth rate followed by grain production efficiency, hundred seed weight and plant height exerted positive direct effect on grain yield over locations with and without lime. Similar results were reported by Sekhon *et al.* (2017) and Birhanu (2016) that plant height had high positive direct effect on seed yield per plant while in contradict high and negative direct effect of hundred seeds weight on seed yield per plant at genotypic level.

The residual effect 0.058 and 0.59 indicates that traits which are included in the genotypic path analysis explained 94% of the total variation in grain yield at both lime levels. The path analysis indicated that hundred seed weight should be used as direct selection criteria for better grain yield. Therefore, selecting genotypes having high hundred seed weight should be used to improve seed yield in faba bean. In harmony with this result, different authors reported that hundred seed weight had positive and direct effects on seed yield and suggested that selection based on hundred seed weight helps for improvement of grain yield in faba bean (Tadele *et al.*, 2011; Verma *et al.*, 2013; Shrifi, 2015; Kumar *et al.*, 2017)

Table 12. Genotypic direct (bold diagonal) and indirect effect (off diagonal) of four traits on grain yield in 50 faba bean genotypes tested without and with lime application over locations.

Without lime					
Trait	PLH	HSW	GPE	EGR	$r_g$
PLH	<b>0.026</b>	0.007	0.182	0.535	0.750 <sup>**</sup>
HSW	0.004	<b>0.044</b>	0.131	0.135	0.314 <sup>*</sup>
GPE	0.017	0.022	<b>0.266</b>	0.625	0.930 <sup>**</sup>
EGR	0.019	0.008	0.228	<b>0.728</b>	0.983 <sup>**</sup>
With lime					
Trait	PLH	HSW	GPE	EGR	$r_g$
PLH	<b>0.030</b>	0.012	0.173	0.368	0.584 <sup>**</sup>
HSW	0.009	<b>0.041</b>	0.152	0.164	0.367 <sup>*</sup>
GPE	0.017	0.020	<b>0.306</b>	0.616	0.960 <sup>**</sup>
EGR	0.016	0.010	0.277	<b>0.681</b>	0.984 <sup>**</sup>

Residual effect = 0.058 (without) and 0.059 (with), PH = plant height, HSW = hundred seed weight, GPE=grain production efficiency, EGR= economic growth rate

## 4.5. Genetic Divergence

### 4.5.1. Genetic Distances among Genotypes

The genetic distance estimated by Euclidean distances (ED) from 12 traits for all possible pairs of 50 faba bean genotypes showed wide differences in the range between 1.23 and 11.52 and 1.04 and 11.06 under lime and without lime application over locations, respectively (Appendix Table 7 and 8). The highest ED over three locations with lime applications was calculated between G21 and G12 (11.52) followed by G30 and G21 (10.80), G40 and G21 (10.65), while the lowest ED was registered between G23 and G5 (1.23) followed by G13 and G1 (1.42) (Appendix Table 7). Without lime application, the highest ED was calculated

between G4 and G21 (11.06) followed by G12 and G21 (10.24), G11 and G49 (10.09), G18 and G21 (10.03) and G21 and G49 (9.97), while the lowest ED was registered between G16 and G23 (1.04) followed by G14 and G33 (1.21) and G17 and G30 (1.28) (Appendix Table 8). Genotypes with minimum distance were not genetically diverse or there was little genetic diversity between these genotypes. Increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F<sub>2</sub> and F<sub>3</sub> generation following a cross of distantly related parents; the greater will be the opportunities for the effective selection for yield factors (Ghaderi *et al.*, 1984).

The result suggested that, maximum genetic recombination is expected from the hybridization of the parents selected from divergent genotypes. Conversely, crossing of parents selected from similar genotypes could not give higher heterotic value in F<sub>1</sub> and will result in narrow range of variability in the segregating F<sub>2</sub> generation. However, the breeder must specify their objectives in order to make best use of the traits where the traits are divergent. This finding is parallel with the reports of Million (2012) maximum genetic segregation and genetic recombination is expected from crosses that involve parents from the clusters characterized by significant distances, Gemechu *et al.* (2005) on evaluation 144 faba bean landraces and Million and Habtamu (2012) on evaluation of 25 elite faba bean genotypes.

Generally, higher inter genotype distances between genotypes were obtained when the genotypes grown under non-stressed condition (lime treated plots) compared to stressed condition (without lime). It is generally believed that more conducive environments may be expected to result in better expression of the genetic potential of the genotypes for the trait evaluated (Rosielle and Hamblin, 1981; Gemechu, 2012) despite the controversy that there is no interrelationship between the growing environment and magnitude of genetic variation (Ceccarelli and Grando, 1996).



#### 4.5.2. Clustering of Genotypes

Based on ED matrix, the 50 faba bean genotypes were grouped into 10 distinct clusters with and without lime application over locations using 3.2 as cutting point (mean ED - SD) (Figure 1 and 2). This implied the presence of wide variability among the tested genotypes. Likewise, Million (2012) reported the grouping of 8 released faba bean varieties into 3 clusters. Their differences were mainly attributed to the variation on thousand seed weight. Similarly, Birhanu (2016) reported the grouping of 36 faba bean genotypes into 7 clusters based on 8 yield traits. The disparity in the number of clusters is attributed to the variation in tested genotypes and the number of parameters considered.

Cluster I was the largest cluster containing 12 (24%) genotypes. Clusters I, II, VI and VII together accounted for 72% containing 36 genotypes each having 12, 9, 9 and 6 genotypes, respectively. Cluster III and IV constituted 8 genotypes (16%) with 5 and 3 genotypes, respectively. Cluster V and IX contain 2 genotypes each and VIII and X were solitary clusters. The five larger clusters (I, II, III, VI and VII) together accounted for 82% containing 41 genotypes without lime application (Figure 2; Table 14).

Similarly, under limed condition, cluster VI was the largest that contained 12 (24%) of the tested genotypes. The four larger clusters (I, V, VI and VII) together accounted (74%) containing 37 genotypes. Cluster II and VIII constituted 9 genotypes (18%) with 6 and 3 genotypes, respectively. Cluster III, IV, IX and X were solitary clusters. Cluster IX had outstanding performance than any other genotypes tested in this study (Figure 1; Table 13).

The two genotypes CS20DK in cluster VIII with and IX without and Wayu in cluster X under both lime levels were clustered as solitary which implied the significant variation to the other genotypes. In harmony with this result Million (2012) reported solitary cluster among eight genotypes in a previous study.

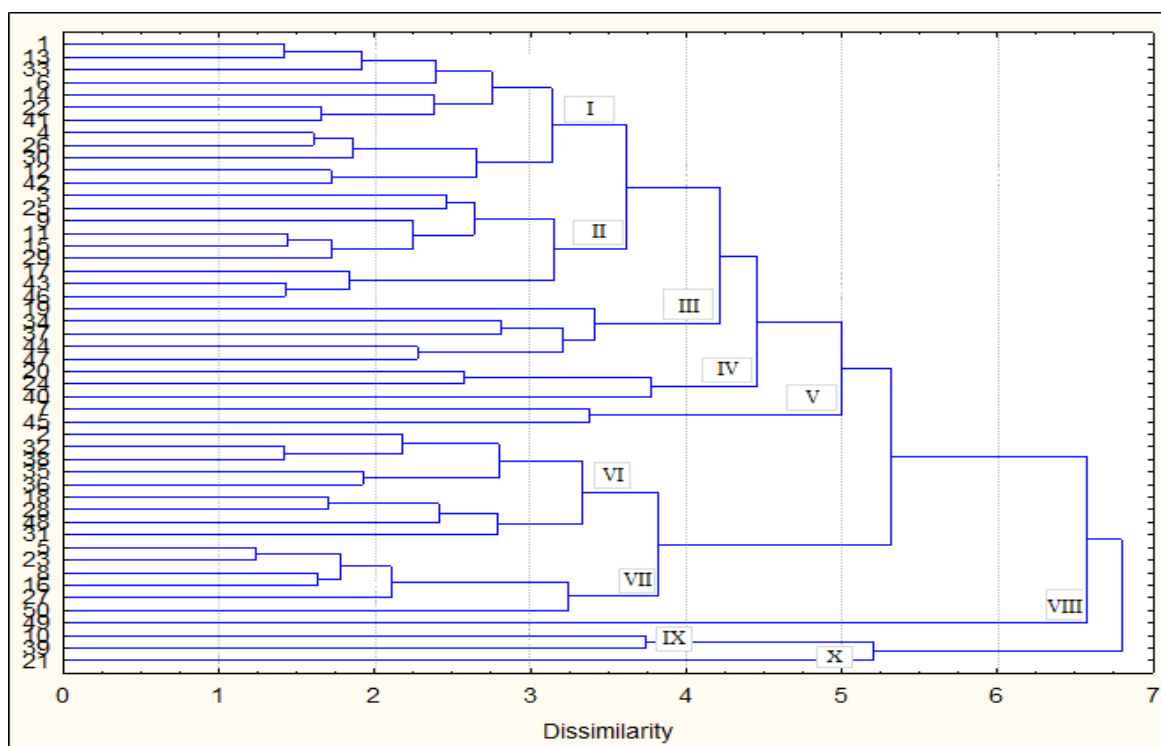


Figure 1. Dendrogram of 50 faba bean genotypes developed based on Euclidian distance using mean of 12 agronomic traits with lime application

Table 13. Distribution of 50 faba bean genotypes in to ten clusters using mean of 12 agronomic traits with lime application

Cluster	Number of genotype	Genotypes
I	8	Cool-0030(1), Cool-0025(28), Cool-0031(31), Cool-0035(35), Cool-0024(38), Cool-0034(48), Moti (40), Dosha (18)
II	6	Tumsa(44), Gebelcho(45), Wolki(2), Ashebeka(6), Hachalu(7), Didi'a(47)
III	1	Obse(4)
IV	1	NC58(5)
V	9	Cool-0018(32), Degaga(8), Holetta-2(10), Bulga 70(16), Mesay (23), Kasa (27), KUSE2-27-33(36), Selale(39), Tesfa (50)
VI	12	EK LS/CSR 02012-2-3(3), EH07023-3(12), EK05006-3(13) EK LS/CSR 02014-2-4(14), EK05001-1(17), EK LS/CSR 02010-4-3(30), EK LS/CSR 02028-1-1(33), EH07015-7(37), EH06027-2(41), EK LS/CSR 02019-2-4(42), Numan (15), Gora(19)
VII	8	EH09031-4(9), EH09007-4(11), EH08035-1(20), EK LS/CSR 02023-2-1 (22), EH09004-2(24), EK LS/CSR 02017-3-4(26), EH06070-3 (29), EH09002-1(43)
VIII	3	EH06088-6(25), EK 05037-4(34), EK05037-5(46)
IX	1	CS20DK(49)
X	1	Wayu(21)

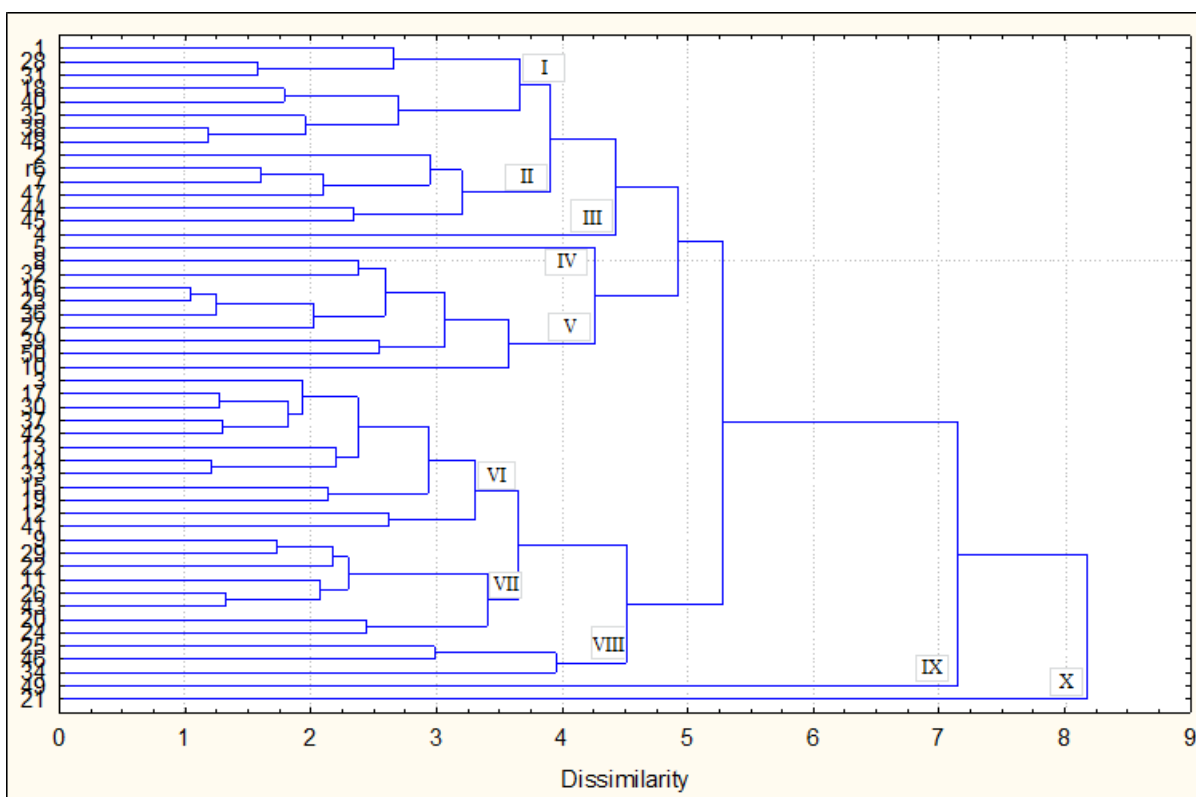


Figure 2. Dendrogram of 50 faba bean genotypes developed based on Euclidian distance using mean of 12 agronomic traits without lime application

Table 14. Distribution of 50 faba bean genotypes in to ten clusters using mean of 12 agronomic traits without lime application

Cluster	Number of genotype	Genotypes
I	12	Cool-0030 (1), EH07023-3 (12), EK05006-3(13), EK LS/CSR 02014-2-4(14), EK LS/CSR 02023-2-1 (22), EK LS/CSR 02017-3-4 (26), EK LS/CSR 02010-4-3(30), EK LS/CSR02028-1-1 (33), EH06027-2 (41), EK LS/CSR 02019-2-4 (42), Obse (4), Ashebeka (6)
II	9	EK LS/CSR 02012-2-3(3), EH09007-4(11), EH09031-4(9), EK05001-1(17), EH06070-3 (29), EH06088-6 (25), EH09002-1(43), EK05037-5 (46), Numan (15)
III	5	EK 05037-4(34), EH07015-7 (37), Gora (19), Tumsa (44), Didi'a(47)
IV	3	EH08035-1(20), EH09004-2(24), Moti(40)
V	2	Hachalu(7), Gebelcho (45)
VI	9	Cool-0025(28), Cool-0031(31), Cool-0018(32), Cool-0035(35), Cool-0024(38), Cool-0034(48), Wolki(2), Dosha (18), KUSE2-27-33(36)
VII	6	NC58(5), Degaga(8), Bulga 70(16), Mesay (23), Kasa (27), Tesfa (50)
VIII	1	CS20DK(49)
IX	2	Holetta-2(10), Selale(39)
X	1	Wayu(21)

### 4.5.3. Cluster Mean Analysis

The mean value of the 12 quantitative traits in each cluster over three locations with and without lime application is presented in Table 15. Cluster I consisted of twelve and eight genotypes having the characteristic of high hundred seeds weight, late maturity and grain filling period and also high grain yield and susceptible to chocolate spot disease followed by cluster IV and moderate to the other traits without and with lime, respectively.

Cluster II considered as long grain filling period, less in number of pod per plant and high hundred seeds weight without lime and late maturity with lime. The rest traits were intermediate to this cluster. Cluster III consisted of five and one genotype having the characteristic of late maturity and early flowering and grain filling period without and with lime application, respectively. Three and one genotypes were included in cluster IV and this cluster characterized by early flowering and maturity both without and with lime application, respectively (Table 15).

Cluster V consisted of two and nine genotypes characterized by long plant height without lime and intermediate with lime application. Cluster VI consisted of nine and twelve genotypes without and with lime, respectively, with a characteristic feature of late days to 90% maturity, long grain filling period and high hundred seeds weight in case of lime. Cluster VII contained six released varieties and eight pipeline genotypes with a feature of early in days to 90% maturity and with less number of pods per plant and high hundred seeds weight without and with lime application, respectively (Table 15).

Cluster VIII constituted by one and three genotypes without and with lime, respectively. Cluster VIII had short grain filling period, less susceptible to chocolate spot, high grain yield and pod per plant under lime free condition. Cluster IX characterized with less hundred seeds weight and grain yield without lime and with high number of pod per plant, high grain yield, low hundred seeds weight and resistant to chocolate spot with lime application and the rest traits were intermediate to this cluster as compared to the other clusters and this cluster was found as best of all the other clusters in all traits performance under lime. Cluster X constituted by single genotype under both lime levels and had late days to 50% flowering and

short grain filling period and plant height, low hundred seed weight and grain yield and susceptible to chocolate spot under both lime levels (Table 15).

Generally, under lime free condition, cluster III, VI and VII showed intermediate results of all traits without maximum and minimum values of each trait considered in this study. Cluster VIII was found as best of all the other clusters. Under limed condition, cluster II, V and VIII showed intermediate results of all traits without maximum and minimum values of each trait considered in this study. Cluster VIII without lime and IX with lime constructed by single genotype CS20DK that found best performing under both lime levels. Two genotypes Wayu and CS20DK constructed single cluster under both stress levels which implied these genotypes were distinct in their features than other evaluated genotypes.

Table 15. Mean performances of different clusters for 12 agronomic traits in 50 faba bean genotypes evaluated without (above) and with lime application (below) over locations in 2017 main cropping season.

Traits	Cluster (without)									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Days to 50% flowering(days)	53.88	53.33	54.56	52.15	57.33	54.12	53.81	55.78	54.06	58.89
Days to 90% maturity(days)	147.35	146.37	147.18	143.37	147.00	145.19	143.13	144.33	145.83	146.11
Plant height(cm)	112.10	109.42	114.04	110.30	115.83	113.17	109.46	112.11	105.44	100.78
Grain filling period(days)	93.47	93.02	92.62	91.22	89.67	91.06	89.31	88.56	91.78	87.22
Number of podding node plant <sup>-1</sup>	6.04	5.68	6.60	6.30	6.56	7.32	7.46	8.00	6.61	6.44
Number of pod plant <sup>-1</sup>	7.34	6.70	8.18	7.59	8.94	9.77	10.00	12.67	8.83	9.56
Number of pod podding nod <sup>-1</sup>	1.22	1.19	1.24	1.22	1.39	1.35	1.35	1.59	1.35	1.46
Hundred seed weight(g)	82.26	84.83	79.94	77.15	73.06	55.61	48.82	51.89	49.05	35.39
Grain yield(g/5plants)	64.48	60.48	69.90	63.53	69.06	65.69	55.92	79.56	51.66	40.72
Chocolate spot disease (%)	33.96	31.10	32.41	37.06	31.70	36.86	38.25	27.63	33.07	40.12
Grain production efficiency(g)	113.87	107.44	120.27	113.72	108.95	111.81	94.12	127.46	88.88	60.46
Economic growth rate(g/day)	69.31	65.38	76.03	70.07	77.34	72.70	62.92	90.52	56.52	46.98
With lime										
Days to 50% flowering(days)	54.03	56.09	52.78	53.33	53.88	53.78	53.10	53.07	55.44	58.11
Days to 90% maturity(days)	145.63	147.02	145.89	143.89	144.23	147.15	145.94	145.85	144.56	145.78
Plant height(cm)	129.60	131.28	132.22	130.33	125.27	130.47	125.83	126.30	125.33	119.00
Grain filling period(days)	91.60	90.93	93.11	90.56	90.36	93.37	92.85	92.78	89.11	87.67
Number of podding node plant <sup>-1</sup>	8.83	8.15	7.11	9.11	8.72	7.44	7.38	8.04	9.33	7.89
Number of pod plant <sup>-1</sup>	13.29	12.30	9.78	14.22	13.40	10.03	9.61	10.67	16.00	12.89
Number of pod podding nod <sup>-1</sup>	1.52	1.51	1.36	1.59	1.54	1.36	1.30	1.34	1.72	1.68
Hundred seed weight(g)	60.74	73.10	77.50	45.23	50.80	87.95	87.97	79.87	51.83	36.67
Grain yield(g/5plants)	100.80	95.76	97.72	82.22	82.36	96.71	92.53	92.67	113.24	61.60
Chocolate spot disease (%)	36.19	26.11	32.36	34.98	32.58	30.38	28.48	27.53	18.95	31.17
Grain production efficiency(g)	173.18	156.34	175.69	141.16	139.37	170.64	164.31	164.97	183.12	92.70
Economic growth rate(g/day)	110.31	105.73	104.74	91.02	91.56	103.61	100.01	100.00	127.85	70.73

#### 4.6. Principal Component Analysis

The principal component analysis indicated that the first principal component accounted for 37.20 and 39.23% of the total multi-trait standardized variations over locations whereas the second principal component was accounted for 29.10 and 25.25% without and with lime application, respectively. The first and second PCs together accounted for 66.30 and 64.49% of the total variation and the first three PCs accounted 77.35 and 77.57% of the total variation without and with lime application over locations, respectively (Table 16). Similarly previously reported that, the first four PCs explained 83.7% of the total variation in which PC1 explained the most variability (36.1%), PC2 (22.3%) and PC3 (15.4%) (Birhanu, 2016).

The top important traits responsible for genetic divergence in the major axis (PC1) include hundred seed weight, plant height, number of pod per plant, number of podding node per plant and chocolate spot under both lime levels. Days to 50% flowering and days to 90% maturity were also important. The least contributors were grain filling period, number of pod per podding node and economic growth rate. In PC2, the observed variations (29.10% and 25.25%) were caused mainly by grain filling period, number of pod per podding node, grain production efficiency and economic growth rate under both with and without lime application (Table 16). In line with this result, it was reported that the variance explained by PC1 was mostly due to traits related to days to 90% maturity and hundred seed weight whereas PC2 was mostly related to grain yield, plant height and number of pod per plant (Birhanu, 2016).

It is normally assumed that traits with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). Accordingly, many traits contributed to the total variation and, therefore, the differentiation of the genotypes into different clusters was rather dictated by the cumulative effects of a number of traits. Due to more variation explained by the PC1 its scores could effectively represent the genotype effect (Ali *et al.*, 2011; Birhanu, 2016). In this experiment, the PC analysis ultimately showed the amount of variability for the traits that could be used for the improvement of faba bean genotypes.

Table 16. The first three PCs explained for 12 traits of 50 faba bean genotypes evaluated without lime (left) and with lime application (right) in 2017 at three locations of central Ethiopia.

No.	Traits	Without lime			With lime		
		Eigenvectors			Eigenvectors		
		PC1	PC2	PC3	PC1	PC2	PC3
1	Days to 50% flowering	0.20	0.08	0.71	-0.17	-0.06	0.63
2	Days to 90% maturity	-0.28	0.10	0.45	0.30	-0.10	0.39
3	Grain filling period(days)	-0.01	0.44	-0.05	0.17	0.34	0.14
4	Plant height(cm)	0.38	0.18	-0.18	-0.32	0.32	-0.11
5	Number of podding node plant <sup>-1</sup>	0.42	0.16	-0.05	-0.37	0.27	0.04
6	Number of pod plant <sup>-1</sup>	0.39	0.09	0.18	-0.37	0.15	0.24
7	Number of pod podding nod <sup>-1</sup>	-0.07	0.50	0.00	0.20	0.47	0.07
8	Hundred seed weight(g)	-0.43	0.08	0.06	0.42	-0.06	0.02
9	Grain yield(g/5plants)	0.17	-0.01	-0.40	-0.11	0.15	-0.33
10	Chocolate spot disease (%)	-0.39	0.03	-0.17	0.39	-0.05	-0.07
11	Grain production efficiency(g)	-0.18	0.45	-0.19	0.27	0.42	-0.07
12	Economic growth rate(g/day)	0.00	0.50	0.03	0.14	0.50	0.08
	Eigenvalue	4.84	3.78	1.44	5.10	3.28	1.70
	% variance explained	37.20	29.10	11.06	39.23	25.25	13.09
	Cumulative % of variance	37.20	66.30	77.35	39.23	64.49	77.57

PC= principal component



## **4.7. Genotype x Location x Management Interaction and Yield Stability of Genotypes**

The genotypes showed differential performance across all environments of the testing sites, which means the genotypes reacted differently to different environmental conditions resulted in performance variation of the genotypes thereby showed Genotype by Environment Interaction (GEI). When the expression of the genetic potential of the genotype is influenced by the environmental factors, screening of genotypes with higher stability is very important breeding strategy.

### **4.7.1. Analysis of Variance from AMMI Model**

The result of analysis of variance from AMMI model showed that environments (E), genotypes (G) and genotype x environment interaction (GEI) had significant effect on grain yield of 50 faba bean genotypes. This model has been regarded as a powerful analytical tool while dealing with large GEI data sets and it provide the relative contribution of factors to the total sum squares (Gauch, 1992). Accordingly, the environment accounted for 58.05% of the total sum of squares while the genotype and GEI accounted for 16.08% and 14.28%, respectively (Table 17). The magnitude of environment was 4.1 times greater than the GEI. From this result, the large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in seed yield and influence faba bean production. The high contribution of environment (48 to 88%) to grain yield variability of faba bean in Ethiopia have been reported by other authors (Mulusew *et al.*, 2008; Tamene, 2015; Teklay *et al.*, 2015; Asnakech *et al.*, 2017). Therefore, different genotypes need to be evaluated over locations to determine their performance across environments.

The AMMI analysis of variance indicated that the mean squares of the first four IPCA scores and residual were significant ( $P \leq 0.01$ ). The first principal component axis (IPCA1) of the interaction captured 37.81% of the interaction sum of squares. The IPCA2, IPCA3 and IPCA4 explained 22.26, 15.64 and 13.99% of GEI sum of squares, respectively. The first two IPCAs (IPCA1 and IPCA2) together contributed 60.07% of the total GEI sum of squares (Table 17). It has been reported that 50 to 77% of the first IPCA score contribution in faba bean genotypes (Mulusew *et al.*, 2008; Teklay *et al.*, 2015; Asnakech *et al.*, 2017). Tamene (2015) also reported 66.6% of contribution of the

first two IPCAs to GEI sum square. The IPCA scores of genotypes in the AMMI analysis are an indication of stability or adaptability over environments. The greater the IPCA scores, the more specific adapted is a genotype to certain environments. The more the IPCA scores approximate to zero regardless of the positive or negative signs, the more stable or adapted the genotype is over all the environments (Purchase, 1997; Rashidi *et al.*, 2013).

The GEI mean squares highly significant ( $P \leq 0.01$ ) indicated the yield of genotypes varied over environments. Therefore, apart to the effects of environments and genotypes the GEI also attributed for the differential yield performance of genotypes over environments. It was reported in grain yield of checkpea that AMMI analysis showed significant ( $p \leq 0.01$ ) GEI indicating the presence of genetic variation and possible selection of stable entries (Rashidi *et al.*, 2013).

Table 17. AMMI analysis of variance for grain yield (g/5plants) of 50 faba bean genotypes tested at six environments (three locations with and without lime applications) in 2017

Source of variation	DF	SS	MS	% Variance Explained	% Cumulative
Total	899	411475	458		
Treatment	299	363728	1216**		
Genotype	49	66124	1349**	16.08	
Environment	5	238846	47769**	58.05	
Block	12	4836	403**		
Interaction	245	58758	240**	14.28	
IPCA1	53	22214	419**	37.81	
IPCA2	51	13082	257**	22.26	60.07
IPCA3	49	9191	188**	15.64	75.71
IPCA4	47	8219	175**	13.99	89.70
Residuals	45	6052	134**		
Error	588	42911	73		

\*\* Significant difference at ( $P \leq 0.01$ ), DF= degree of freedom, SS= sum of square, MS= mean squares

#### 4.7.2. Yield Stability of Genotypes from AMMI Model

According to AMMI model, genotypes with large IPCA scores regardless of their positive or negative sign is an indication of instability of the genotypes or their specific adaptability whereas the small scores close to zero have small interactions and are stable (Zobel *et al.*, 1988). Accordingly, ten genotypes (G48, G44, G9, G37, G8, G42, G3, G39, G45 and G1) that had small IPCA scores close to zero indicated that, these genotypes were more stable for yield whereas seven genotypes (G2, G32, G24, G20, G4, G30 and G15) had high IPCA scores showing their unstability over locations and soil acidity managements. Previously Rashidi *et al.* (2013) reported that genotypes with means greater than grand mean and IPCA score nearly zero are considered as generally adaptable to all environment whereas genotypes with larger IPCA scores are adapted to specific environments.

In this model, genotype with least ASV or have smallest distance from the origin are considered as the most stable, where as those which have highest ASV are considered as unstable (Purchase, 1997). The finding in this research shown that different genotypes were evaluated by using AMMI stability model and gave different stability results based on their ASV values for different locations with different soil managements. Accordingly, genotypes, G44, G48, G9, G39, G3, G37, G45, G42, G1 and G8 had smaller ASV ranked as the 1<sup>st</sup> to 10<sup>th</sup> indicating the genotypes were most stable whereas G49, G2, G17, G13, G24, G6, G15, G23, G18 and G25 with their higher ASV considered as the least stable for grain yield performance across the testing environments (Table 18).

Based on genotypes that had grain yield greater than the overall mean and lower values of IPCAs and ASV genotypes G44, G48, G3, G37 and G42 were stable while G2, G15 G24 and G49 unstable. Stable genotypes more or less show similar yield performance over environments whereas unstable genotypes perform differently.

Table 18. Stability parameters for grain yield (g/5plants) of 50 faba bean genotypes from AMMI model analyses at six environments (three locations with and without lime) in 2017

Geno	Pooled mean	AMMI model stability			Geno	Pooled mean	AMMI model stability		
		IPCA1	IPCA2	ASV			IPCA1	IPCA2	ASV
G1	77.62(30)	-0.61	0.42	0.61(42)	G26	80.39(23)	-0.30	1.06	1.05(30)
G2	86.30(5)	4.38	-2.08	6.00(2)	G27	63.58(47)	-0.59	-0.32	0.88(36)
G3	80.02(24)	-0.40	0.26	0.43(46)	G28	80.49(22)	-0.20	0.95	0.95(34)
G4	87.64(4)	-1.54	-1.44	2.15(15)	G29	70.86(43)	-0.99	-0.22	2.13(16)
G5	71.93(42)	-0.06	-1.01	1.01(31)	G30	85.25(10)	1.13	2.35	2.48(12)
G6	84.08(13)	-1.10	0.09	3.78(6)	G31	79.18(27)	1.16	0.83	1.61(24)
G7	81.32(21)	1.15	-2.30	2.15(14)	G32	79.57(26)	-1.55	1.72	0.88(37)
G8	73.44(38)	0.27	-0.05	0.64(40)	G33	81.74(20)	0.57	-0.19	0.96(33)
G9	75.10(35)	-0.16	-0.17	0.23(48)	G34	83.82(14)	0.21	1.01	1.01(32)
G10	58.63(49)	-1.19	-2.10	2.28(13)	G35	82.78(17)	0.59	-0.23	0.92(35)
G11	72.06(41)	-0.18	0.65	0.64(41)	G36	75.18(33)	1.61	0.70	2.53(11)
G12	84.19(12)	0.53	-1.24	1.19(26)	G37	83.49(15)	-0.26	0.06	0.51(44)
G13	84.53(11)	-1.96	-0.34	4.73(4)	G38	85.64(8)	0.84	0.94	1.23(25)
G14	75.88(32)	-0.41	-1.65	1.67(20)	G39	62.49(48)	-0.32	0.46	0.37(47)
G15	82.05(19)	0.31	-3.19	3.19(7)	G40	93.92(2)	0.98	1.43	1.65(22)
G16	72.24(40)	0.01	1.65	1.65(23)	G41	74.42(36)	-0.94	0.50	1.19(27)
G17	75.17(34)	-2.02	-0.37	4.74(3)	G42	82.18(18)	0.29	0.08	0.57(43)
G18	86.06(7)	-1.89	-0.90	2.88(9)	G43	73.82(37)	0.14	-1.07	1.07(29)
G19	85.47(9)	1.10	-2.06	1.90(18)	G44	86.07(6)	0.12	-0.14	0.08(50)
G20	78.51(28)	1.33	1.70	2.07(17)	G45	76.07(31)	0.24	-0.54	0.51(45)
G21	51.16(50)	-0.53	0.25	0.73(39)	G46	67.36(44)	-1.25	0.60	1.70(19)
G22	72.62(39)	-0.70	1.28	1.17(28)	G47	87.67(3)	0.51	0.55	0.74(38)
G23	67.00(45)	-1.30	-0.22	3.17(8)	G48	83.40(16)	0.09	0.04	0.15(49)
G24	79.68(25)	2.94	1.69	4.23(5)	G49	96.40(1)	2.4	-0.28	7.02(1)
G25	77.94(29)	-1.22	0.22	2.84(10)	G50	65.06(46)	-1.22	0.59	1.66(21)

Geno = genotype, AMMI= Additive main effect and multiplicative interaction, IPCA= interaction principal component axis, ASV= AMMI stability value, number in parenthesis are ranks of genotypes.

The average grain yield for the genotypes over environments ranged from 51.15g (Jeldu without lime, E5) to 95.95g (Jeldu with lime application, E6). The genotype G49 was selected as first ranking selection at E3 and E4 (Watebecha Minjaro with and without lime application) and third ranking selection at E2 (Holetta with lime). The genotype G2 also identified as first ranking at E1 (Holetta with lime) of AMMI the first four selection, second and third ranking selection at E4 (Watebecha Minjaro with lime) and E3 (Watebecha Minjaro without lime), respectively. The genotype, G40 also identified as first and third ranking at three environments (E2, E4 and E6) and G47 identified 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> ranking selection at E3, E1 and E4, respectively (Table 19). The AMMI first four ranking selections over six environments indicated that G49, G2, G40 and G47 genotypes were better performing at half of the environments than others and these genotypes were performed good both under lime and without lime application except G40.

Table 19. The first four AMMI selections for grain yield (g/5plants) per environment.

Environment ID	Environment	Mean GY	1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>	4 <sup>th</sup>
E1	Holetta unlimed	69.98	G2	G13	G47	G15
E2	Holetta limed	92.62	G40	G24	G49	G30
E3	Watebecha Minjaro unlimed	67.64	G49	G47	G2	G48
E4	Watebecha Minjaro limed	90.79	G49	G2	G40	G47
E5	Jeldu unlimed	51.15	G4	G18	G19	G25
E6	Jeldu limed	95.95	G12	G13	G40	G26

GY= grain yield

The stability of genotypes for yield over locations alone may not allow making a decision as the genotypes are worth for production. For instances, only genotype G44 had six ranking mean grain yield among the first 10 stable genotypes identified by low IPCA1 and IPCA2 scores, and among the first 10 stable genotypes identified by low ASV. Therefore, it is necessary to consider all the stability parameters along with the mean grain yield. Considering the IPCAs scores, ASV and the first four AMMI selections along with mean grain yield, G49, G40, G47 and G2 had high mean grain yield with 1-5<sup>th</sup> ranks and identified as the first four selections of AMMI each at three environments with contrasting managements (lime and without lime applications) except G40. In addition, G48 and G44 had 16<sup>th</sup> and 6<sup>th</sup> ranking mean yield and identified as the first two most stable genotypes by ASV and IPCA1 and IPCA2 scores. G18 was the 7<sup>th</sup> and 9<sup>th</sup> ranking for mean grain yield and stable genotype identified by ASV, respectively. G48 was identified among the first four AMMI selections at one environment; however, G44 was not identified among the first four AMMI selections. The genotype G4 had the 4<sup>th</sup> ranking mean grain yield, identified as one of the first four AMMI selections over six environments at one environment but not identified among the first 10 stable genotypes by IPCAs scores and ASV. In contrast, the genotypes G9, G3 and G45 identified as 3<sup>rd</sup>, 5<sup>th</sup> and 6<sup>th</sup> stable genotypes, respectively, by ASV and IPCAs scores while G37 and G42 identified as 7<sup>th</sup> and 8<sup>th</sup> ranking stable genotypes by ASV. However, the genotypes had mean grain yield in the rank between 15 and 35 among 50 faba bean genotypes (Table 18 and Table 19).

In choosing superior genotypes, a low or minimal genotype x environment interaction must exist (Cotes *et al.*, 2002). However, if genotypes had varied stability for yield, it is necessary to consider the stability parameters along with high performance but the varieties can be responsive to changing environments (dynamic stability) (Yan and Kang, 2003). Therefore, G49, G40, G47, G2, G48, G44, G18 and G4 may be considered as worthy

genotypes for high yield over environments than G9, G3, G45, G37 and G42 identified stable genotypes with lower yield than the former genotypes.

#### 4.7.3. “Which-Won-Where” Patterns and Stability of Genotypes

A polygon view of the GGE biplot for grain yield resulted in eight vertex genotypes with both positive (high yielding) and negative (low yielding) PCA1 scores. The eight genotypes G21 (Wayu), G24 (EH09004-2), G2 (Wolki), G49 (CS20DK), G40 (Moti), G12 (EH07023-3), G17 (EK05001-1) and G10 (Holetta-2) that located on the vertices of the polygon performed either the best or the poorest in one or more environments (Figure 3). The GGE biplot analysis provided a visual interpretation of the relationship among the genotypes and test environments. As stated by Asnakech *et al.* (2017) when the environments fell in different sectors of the polygon view of the GGE biplot it indicated the best genotype at one environment may not perform best at another environment. Likewise, the environments fell in two different sectors of the polygon view.

Environments with large PC1 scores are those environments that better discriminate among genotypes and those with PC2 scores near zero are more representative of an average environment (Yan, 2001). In this study the environments, E2 and E6 had larger PC1 scores and well discriminated among the genotypes. According to Yan (2001) genotypes at the apex of each sector are the best performing at environments included in that sector if the GGE is sufficiently approximated by PC1 and PC2. As shown in Figure 3, PC1 and PC2 accounted 73.53% of the variation of the total PCs for grain yield over six environments showing that they had sufficiently explained the GGE. Accordingly, genotypes G40 (Moti), G49 (CS20DK) and G2 (Wolki) were the best performers at Holetta and Watebecha Minjaro at both lime levels and G12 (EH07023-3) was the best performer at Jeldu whereas the other four vertex genotypes G24, G21, G10 and G17 fell in sectors with no environment markers. Therefore, genotypes with environmental markers can be recommended for adaptation to those specific environments. However, stability of the genotypes over environments should first be considered.

Large positive PC1 scores for genotypes indicated that those genotypes had higher average yield and PC2 scores near zero indicated that those genotypes were more stable (Yan, 2001; Fekadu *et al.* 2012). Accordingly, genotypes G49, G40, G44, G48, G47, G30, G42, G6, G37 and G38 were high yielding genotypes. On the other hand, genotypes G21, G10, G39, G27, G50, G23 and G46 were with large negative PC1 scores and they were low yielding genotypes. Genotypes with relatively low PC2 scores such as G44, G48, G28, G42, G6, G37, G22, G36, G9, G46, G27, G50 and G10 can be considered relatively stable. However, among these genotypes, only G44, G48, G28, G42, G6 and G37 were high yielding and should be considered as stable for recommendation (Figure 3).

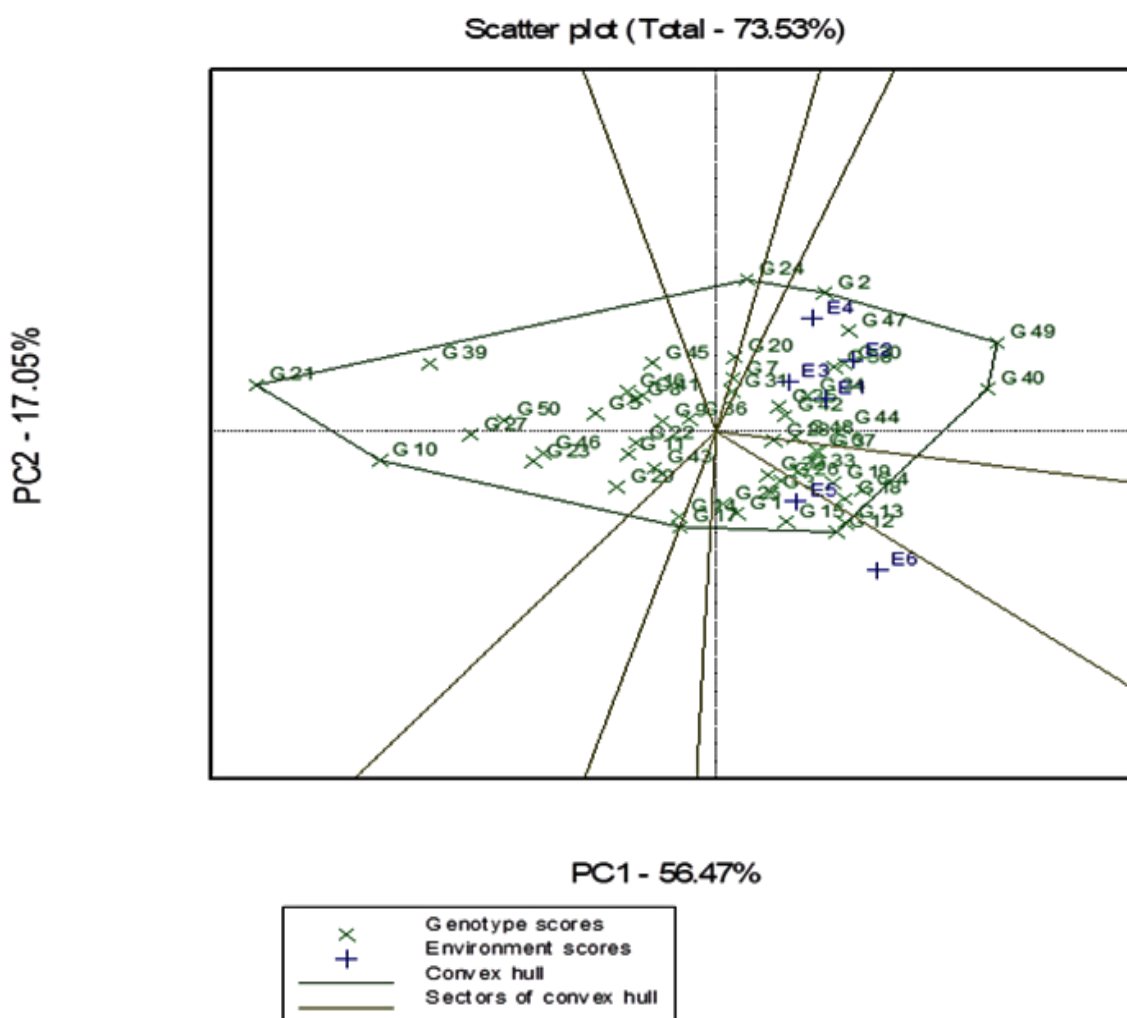


Figure 3. GGE-Biplot showing environments and their respective faba bean genotypes. (G= genotype and G1-G50 listed in Table 1, E= environment and E1-E6 listed in Table 19)

#### **4.7.4. Evaluation of Environments and Ranking of Genotypes over Environments**

The GGE biplots showing the discriminating ability and representativeness of the test environments were presented in Figure 4. The average environment is represented by the small circle at the end of the arrow and contains the average coordinates of all test environments (Yan and Tinker, 2005). As suggested by Yan (2001) environments with short vector length have the smallest angle with the “Average-Environment Coordinate” (AEC) indicating that it is more representative of the test environments. The concentric circles aid in the visualization of the length of the environment vectors. E6 had the longest vector from the biplot origin indicating it was the most discriminating of the test environments.

In general based on the representativeness of test environments, E1 was the most representative of the environments for grain yield followed by E2, E3 and E4. In contrast, E5 and E6 were the least representative environments. However, E6 was the best discriminating (informative) of the genotypes and it was the least representative of the test environments. An ideal test environment should effectively discriminate genotypes and represent the environments (Yan and Kang, 2002). According to Yan and Tinker (2005), environments that give little information on genotypes (Non-discriminating) should not be used as test environments. Thus, in this study among all the six environments, E2 represented the ideal test environment (in the first concentric circle) with moderate discriminating ability of the genotypes and representativeness of the test environment for faba bean grain yield. This environment can be used for selecting generally adapted genotypes (Figure 4).



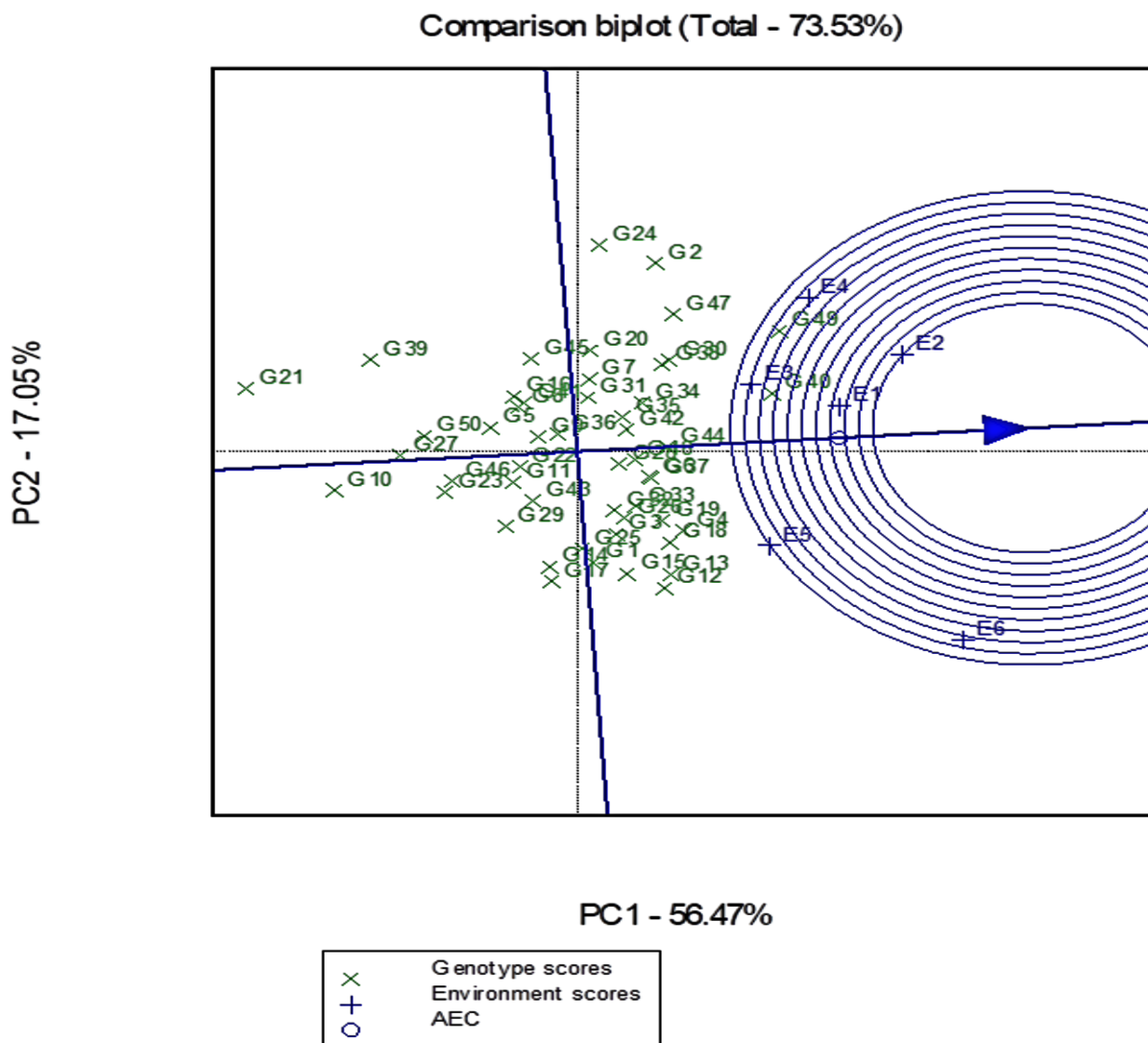


Figure 4. Comparison of environments based on discriminating ability and representativeness. (G= genotype and G1-G50 listed in Table 1, E= environment and E1-E6 listed in Table 19)

The ranking biplot containing the mean yield performance and stability of genotypes over environments is presented in Figure 5. The line that passes through the biplot origin is called the average environment coordinate (AEC), and it shows the stability of the genotypes (Yan, 2001). The stability of the genotypes is measured by their projection to the AEC y-axis (A line). That means, the greater the absolute length of the projection of a genotype, the less stable it is or the shorter the absolute length, the more stable it is (Yan, 2001; Fekadu *et al.*, 2012; Asnakech *et al.*, 2017). The A line separates genotypes with yield below the mean and above the mean. Those genotypes to the right of this line were high yielders while those to the left were low yielders. The single-arrow on the AEC points to higher mean yield. Accordingly, G49 had the highest yield, followed by G40 while G21

is the poorest genotype for grain yield. The double-headed line is the AEC ordinate that points in either direction to greater variability (least stability). Accordingly, G44, G6, G37, G28, G48, G31, G35, G42, G34, G9, G36, G22, G46, G27, G50 and G10 were the most stable genotypes but only G44, G6, G37, G28, G48, G31, G35, G42 and G34 with above average performance while genotypes G24, G2, G47, G15, G12 and G13 were the least stable but high yielding (Figure 5).

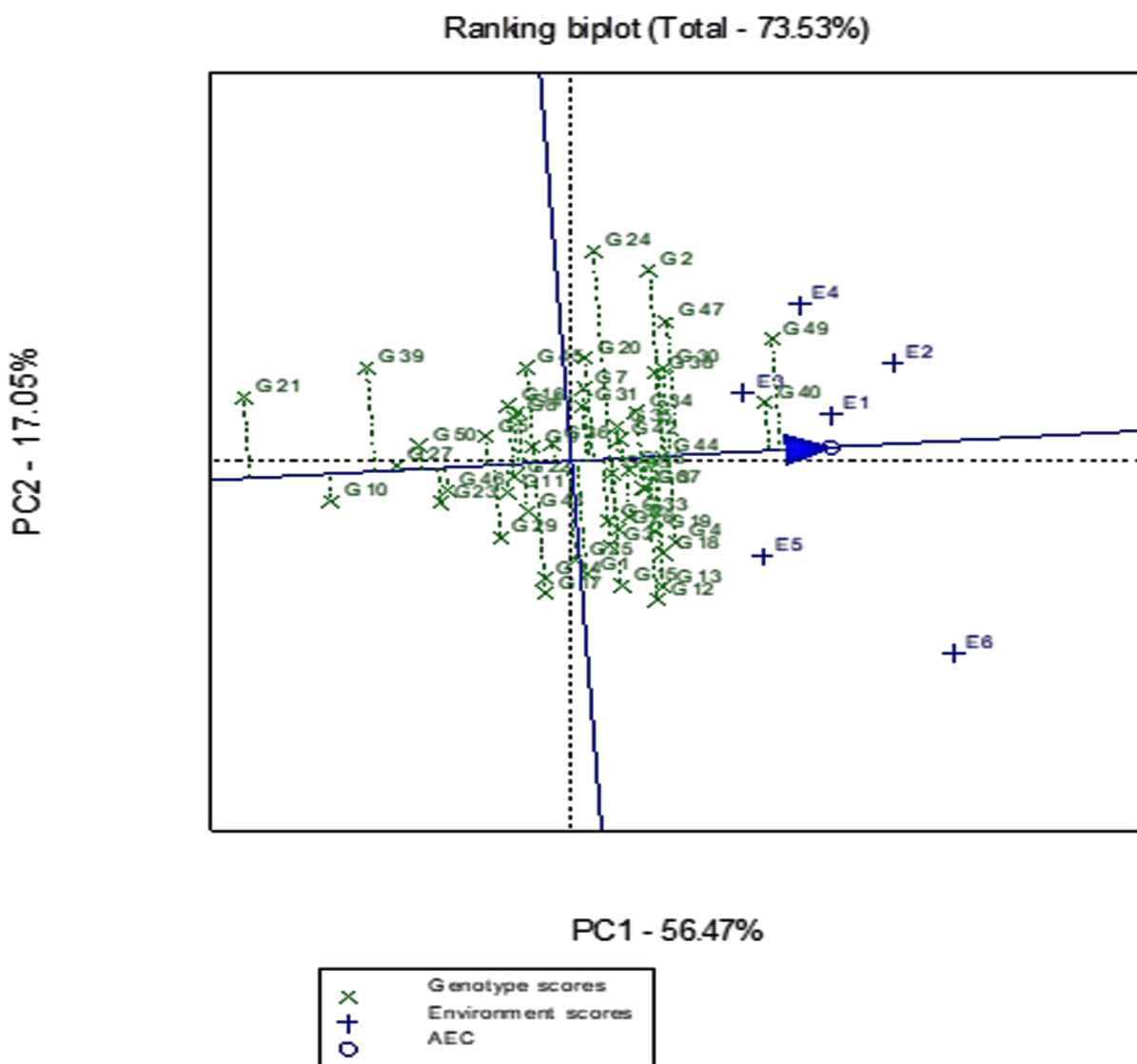


Figure 5. Mean yield performance and stability of genotypes over environments.

(G= genotype and G1-G50 listed in Table 13, E= environment and E1-E6 listed in Table 19)

#### 4.7.5. Stability, Mean Yield, and Stress Tolerance of Genotypes

A total of 28 genotypes had mean yield greater than overall mean yield of genotypes (>78.02 g/5plants) of which 18 genotypes had yield advantage of 0.16 to 17.49% over the recently released variety (Numan, G15) of which eight were released varieties. The two varieties CS20DK (G49) and Moti (G40) released in 1977 and 2006 had the highest yield advantages of 17.49 and 14.47%, respectively and also had better stress tolerance index. The genotypes yield performance and yield stability judged by AMMI and GGE biplot parameters match each other. The genotypes, G44 and G49 were identified as most stable and unstable, respectively, by ASV and GGE biplot parameters, but G49 and G44 had first and sixth ranking high mean yield with 17.49 and 4.9% advantages over the recently released variety, respectively. In addition, G49 was identified among the first four AMMI selections at three environments both under lime and without lime applications over two locations but G44 not identified among the first four AMMI selections. The other two genotypes, G48 and G2 were identified as 2<sup>nd</sup> most stable and unstable genotypes, respectively, by ASV and GGE biplot parameters, however, G2 and G48 had 5<sup>th</sup> and 16<sup>th</sup> ranking mean yield with 5.18 and 1.65% yield advantages over the recently released variety, respectively. In addition, G2 was identified among the first four AMMI selections at three environments both under lime and without lime applications over two locations but G48 was identified among the first four AMMI selections at one location (Watebecha Minjaro) without lime application (Table 19). The yield rank performances of genotypes were inconsistent. Similarly, it was reported that no single cultivar that showed superior performance over all environments (Tamene, 2015).

The three genotypes, G40, G47 and G4 not identified among the first 10 stable genotypes by AMMI and GGE biplot parameters, but had mean yield advantages of 14.47, 6.85 and 6.81%, respectively, over recently released variety. The mean yield rank of G40 and G47 was 2<sup>nd</sup> and 3<sup>rd</sup>, respectively, whereas G4 had the 4<sup>th</sup> rank among 50 genotypes. G40 and G47 are identified among the first four AMMI selections at three environments under lime and both under lime and without lime applications over three and two locations, respectively, while G4 identified among the first four AMMI selections at one location (Jeldu) without lime applications. The two genotypes, G37 and G42 were identified as 7<sup>th</sup> and 8<sup>th</sup> stable genotypes, respectively, by ASV and had relatively low value of IPC2 of GGE biplot indicating the genotypes were stable for yield. These two genotypes, G37 and

G42 had 15<sup>th</sup> and 18<sup>th</sup> mean yield rank with 1.76 and 0.16% yield advantages, respectively, over recently released variety.

Low or minimal genotype x environment interaction must exist to identify superior genotypes (Cotes *et al.*, 2002), however, if genotypes yield stability and mean yield rank varied, it is necessary to consider both the stability parameters and high performance over environments but they can be responsive to changing environments (Yan and Kang, 2003). The main problem with stability statistics is that a single model cannot provide an accurate picture because of the genotype's multivariate response to varying environments (Lin *et al.*, 1986). Therefore, it is necessary simultaneous consideration of mean yield, stability of genotypes evaluated by two or more stability parameters of different models and stress tolerant indices. Accordingly, G49, G40 G47 and G2 could be recommended as high yielding genotypes over locations and soil acidity managements whereas G4, G18 and G19 as better performing genotypes at specific location (Jeldu) and G48 at Watebecha Minjaro without lime application could be considered as high yielding. In addition, G13 could be considered for yield and stability over locations and soil acidity managements though the yield advantage was 3.02% over the recently released variety. The two genotypes, G30 and G12 also could be considered as good yielder at Holetta and Jeldu, respectively, with lime applications.

Generally, based on AMMI and GGE biplot stability parameters among the evaluated 50 faba bean genotypes Tumsa (G44), Cool-0034 (G48), EH07015-7 (G37) and EKLS/CSR02019-2-4 (G42) were identified as the four most stable or relatively stable and productive genotypes. These genotypes may perform more or less similarly across environments thereby considered as wide adaptable whereas G2, G15, G24 and G49 had a combination of high yield, dynamic response to environments. Therefore, the pipeline genotypes G48, G37 and G42 will be recommended for commercial release considering their stability, better yield performance and relatively better tolerance to soil acidity stress. In line with this result, based on AMMI stability model Tumsa (G44) was reported as high yielding and the most stable variety across environments (Tamene, 2015).

Table 20. List of 28 genotypes with mean yield greater the overall mean yield of genotypes, stability and stress tolerance indices

No.	Genotype	Yield	% advantage over		AMMI			GGE biplot			AEC point	double- arrow	STI
			Mean	Numan	IPCA1	IPCA2	ASV	AMMI Selec.	PC1	PC2			
1	G49	96.40(1)	23.56	17.49	2.4	-0.28	7.02(1)	3	Positive	relatively high	to the right	above	1.86
2	G40	93.92(2)	20.38	14.47	0.98	1.43	1.65(22)	3	Positive	relatively low	to the right	above	1.72
3	G47	87.67(3)	12.37	6.85	0.51	0.55	0.74(38)	3	Positive	relatively high	to the right	above	1.55
4	G4	87.64(4)	12.33	6.81	-1.54	-1.44	2.15(15)	1	Positive	relatively low	to the right	above	1.56
5	G2	86.30(5)	10.61	5.18	4.38	-2.08	6.00(2)	3	Positive	relatively high	to the right	below	1.54
6	G44	86.07(6)	10.32	4.90	0.12	-0.14	0.08(50)	no	Positive	relatively low	to the right	above	1.47
7	G18	86.06(7)	10.31	4.89	-1.89	-0.9	2.88(9)	1	Positive	relatively low	to the right	below	1.48
8	G38	85.64(8)	9.77	4.38	0.84	0.94	1.23(25)	no	Positive	relatively low	to the right	above	1.45
9	G19	85.47(9)	9.55	4.17	1.1	-2.06	1.90(18)	1	Positive	relatively low	to the right	below	1.45
10	G30	85.25(10)	9.27	3.90	1.13	2.35	2.48(12)	1	Positive	relatively low	to the right	above	1.39
11	G13	84.53(11)	8.34	3.02	-1.96	-0.34	4.73(4)	2	Positive	relatively high	to the right	below	1.40
12	G12	84.19(12)	7.91	2.61	0.53	-1.24	1.19(26)	1	Positive	relatively high	to the right	below	1.37
13	G6	84.08(13)	7.77	2.47	-1.1	0.09	3.78(6)	no	Positive	relatively low	to the right	above	1.40
14	G34	83.82(14)	7.43	2.16	0.21	1.01	1.01(32)	no	Positive	relatively low	to the right	above	1.38
15	G37	83.49(15)	7.01	1.76	-0.26	0.06	0.51(44)	no	Positive	relatively low	to the right	below	1.39
16	G48	83.40(16)	6.90	1.65	0.09	0.04	0.15(49)	1	Positive	relatively low	to the right	below	1.37
17	G35	82.78(17)	6.10	0.89	0.59	-0.23	0.92(35)	no	Positive	relatively low	to the right	above	1.37
18	G42	82.18(18)	5.33	0.16	0.29	0.08	0.57(43)	no	Positive	relatively low	to the right	above	1.34
19	G15	82.05(19)	5.17	0.00	0.31	-3.19	3.19(7)	1	Positive	relatively high	to the right	below	1.34
20	G33	81.74(20)	4.77	-0.38	0.57	-0.19	0.96(33)	no	Positive	relatively low	to the right	above	1.29
21	G7	81.32(21)	4.23	-0.89	1.15	-2.3	2.15(14)	no	Positive	relatively low	to the right	above	1.35
22	G28	80.49(22)	3.17	-1.90	-0.2	0.95	0.95(34)	no	Positive	relatively low	to the right	below	1.26
23	G26	80.39(23)	3.04	-2.02	-0.3	1.06	1.05(30)	1	Positive	relatively low	to the right	below	1.22
24	G3	80.02(24)	2.56	-2.47	-0.4	0.26	0.43(46)	no	Positive	relatively low	to the right	below	1.24
25	G24	79.68(25)	2.13	-2.89	2.94	1.69	4.23(5)	1	Positive	relatively high	to the right	above	1.28
26	G32	79.57(26)	1.99	-3.02	-1.55	1.72	0.88(37)	no	Positive	relatively low	to the right	below	1.21
27	G31	79.18(27)	1.49	-3.50	1.16	0.83	1.61(24)	no	Positive	relatively low	to the right	above	1.22
28	G20	78.51(28)	0.63	-4.31	1.33	1.7	2.07(17)	no	Positive	relatively low	to the right	above	1.19

AMMI= Additive main effect and multiplicative interaction, ASV= Ammi stability value, IPCA= interaction principal component axis, STI= stress tolerance index,

## 5. SUMMARY AND CONCLUSION

Faba bean is an important legume crop in Ethiopia mainly cultivated in the mid to high altitude areas with elevations 1800-3000 meter above sea level. It is a major source of protein for those who cannot afford animal products and also improves soil fertility. However, the highlands of Ethiopia are characterized by high soil acidity. Soil acidity is one of the major production constraints of faba bean in the highlands of Ethiopia. Therefore, this research was conducted to estimate genetic variability in faba bean genotypes under soil acidity stress and non-stress conditions, determine association among characters and the direct and indirect effects of characters on yield of faba bean genotypes and assess effect of genotype x environment x management interaction on grain yield of faba bean and determine stability of genotypes for yield. A total of 50 faba bean genotypes were evaluated in randomized complete block design with three replications at Holetta, Watebecha Minjaro and Jeldu with out and with lime application in 2017.

The analysis of variance (ANOVA) for each management at each location and combined ANOVA over locations showed the presence of significant ( $P \leq 0.01$ ) differences among genotypes for all agronomic traits except number of seeds per pod. Similarly, the mean squares due to genotype x location were significant for all traits except number of pod per podding node under lime free condition. The ANOVA from AMMI model showed that environment, genotype and genotype x environment interaction contributed 58.05, 16.08 and 14.28%, to total sum square of grain yield, respectively. The results indicated the presence of genetic variability in the faba bean genotypes for most of agromorphology traits and soil acidity stress tolerance indices that could be exploited in breeding programs. The significant differences among locations, the significant effects of G x L interactions on grain yield and other traits showed the differential response of genotypes over locations and managements and the test locations were different each other.

The higher mean grain yield of 115.1 and 113.24 g/5 plants obtained from Moti and CS20DK, respectively over locations with lime while 79.56 g/5 plants obtained from CS20DK without lime. A total of eighteen genotypes had mean yield advantage of 0.16 to 17.49% over the recently released variety (Numan, G15, 2016) of which eight were released varieties. The genotypes had the lowest and highest overall mean yield at Jeldu without and with lime applications, respectively. Soil acidity caused an overall mean yield reduction of 32.34% though varied number of genotypes produced higher mean grain yield

under lime and without lime application over locations. The results indicated the yield reduction due to soil acidity stress was high and it suggested the importance of lime application to obtain higher yield in each locations. Considering all stress indices, genotypes Wolki, Dosha, Obse, Hachalu and Numan were identified as relatively tolerant to soil acidity whereas KUSE2-27-33 was the most sensitive genotype. Moreover, the great variability of the 50 faba bean genotypes indicated a good potential to screening genotypes for soil acidity and to develop tolerant cultivar.

The computed genotypic coefficient of variations (GCV) ranged between 1.08-23.05 and 0.94-23.88% and phenotypic coefficient of variations (PCV) between 1.20-23.26% and 1.11-24.07% without and with lime, respectively. Whereas heritability ( $H^2$ ) 24.63- 98.22% and 35.06 - 98.45% and genetic advance as percent of the mean (GAM) ranged from 2.0 - 47.13% and 1.64 - 48.89%, respectively. All the highest values for all components obtained for hundred seeds weight while all lowest values except for  $H^2$  obtained for days to 90% maturity. Under both lime levels the medium to high estimates of GCV, PCV,  $H^2$  and GAM computed for hundred seeds weight, number of pod per plant and grain production efficiency suggested the selection based on phenotypic expression of genotypes is possible to improve the traits. Plant height and hundred seeds weight had positive and significant associations with grain yield at genotypic level and these traits also exerted positive direct effect on grain yield with and without lime application over locations. This suggested that the two traits will have practical importance in selection of faba bean genotypes for high grain yield.

Euclidean distances (ED) of genotypes estimated from 12 agromorphology traits over locations indicated the wide genetic distances among genotypes that ranged between 1.23-11.50 and 1.04-11.06 with and without lime. The 50 faba bean genotypes were grouped into 10 distinct clusters by Unweighted Pair group Method with Arithmetic Means clustering method based on ED matrix estimated from overall mean of 12 traits over locations for both lime levels. Cluster IV and I consisted of 12 (24%) genotypes with and without lime, respectively. Cluster V with and cluster II and VII without lime were constructed each by 9 genotypes. The two genotypes CS20DK in cluster VIII with and IX without and Wayu in cluster X under both lime levels were clustered as solitary which implied they have significant variation to the other genotypes and found as the best and least performing genotypes, respectively. Under lime free condition, cluster III, VI and VII

showed intermediate results of all traits without maximum and minimum values of each trait considered in this study. Cluster VIII was found as best of all the other clusters having a characteristics of short grain filling period, less susceptible to chocolate spot, high number of pod per plant and grain yield. Under limed condition, cluster II, V and VIII showed intermediate results of all traits considered in this study. Cluster VIII without lime and IX with lime constructed by single genotype CS20DK that found best performing under both lime levels suggested selection of genotypes from these clusters for traits of interest is possible. The first three principal components (PCs) accounted for 77.35 and 77.57% of which PC1 constituted 37.20 and 39.23% and PC2 29.10 and 25.25% the total variation among 50 faba bean genotypes without and with lime application, respectively. Hundred seed weight, plant height, number of pod per plant, number of podding node per plant and chocolate spot had relatively higher contribution in PC1 under both lime levels.

Considering stability parameters from AMMI model and GGE-biplot and mean grain yield G49 (CS20DK), G40 (Moti), G47 (Didea) and G2 (Wolki) were identified as responsive to environments, high yielding over locations and managements whereas G44 (Tumsa), G48 (Cool-0034), G42 (EKLS/CSR02019- 2-4) and G37 (EH07015-7) were relatively stable for yield. The G4 (Obse), G18 (Dosha) and G19 (Gora) specific to Jeldu without lime application, G30 (EKLS/CSR02010-4-3) and G12 (EH07023-3) at Holetta and Jeldu, respectively, with lime applications were identified as good performing genotypes. Therefore, it was an indication to obtain genotypes better performing at specific location and management or over locations and managements. This result suggested evaluating further the above 13 and other 5 a total of 18 genotypes that had mean grain yield greater than the recently released variety.

The research results, allowed to conclude that the presence of variability in faba genotypes with wide genetic distance is a good opportunity to identify genotypes of interest both under lime and without lime application. The lime application was a good management to increase yield of faba bean, however, the differential performance of genotypes over locations for both managements suggested the evaluation of genotypes over locations with and without lime application in a future breeding activity to identify genotypes tolerant to acid soils. The experiment was conducted for one season and the possible effect of season on yield of genotypes was not assessed. Therefore, it needs to evaluate at least for one more seasons to make a reliable and conclusive recommendation.



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## 7. APPENDICES

Appendix Table 1. Mean squares from analysis of variance for 13 traits of 50 faba bean genotypes evaluated without lime application at Holetta, Watebecha Minjaro and Jeldu in 2017 main cropping season

Trait	Holetta				Watebecha Minjaro				Jeldu			
	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)
DF	15.86	20.20 <sup>**</sup>	1.27	2.37	3.12	4.10 <sup>**</sup>	1.56	2.15	15.65	7.27 <sup>**</sup>	0.84	1.62
DM	29.73	15.64 <sup>**</sup>	3.74	1.36	15.86	5.37 <sup>**</sup>	2.17	1.03	16.08	16.76 <sup>**</sup>	2.15	0.97
GFP(day)	3.73	25.73 <sup>**</sup>	3.43	1.96	18.61	7.12	4.82	2.57	63.45	21.09 <sup>**</sup>	2.81	1.76
PH(cm)	3795.21	91.72 <sup>**</sup>	31.98	3.81	915.98	172.70 <sup>**</sup>	29.93	4.51	854.00	69.22 <sup>**</sup>	33.08	8.97
PNPP	1.53	1.93 <sup>**</sup>	0.80	12.72	21.45	4.04 <sup>**</sup>	0.78	11.79	1.61	2.31 <sup>**</sup>	0.76	17.07
PPP	4.82	6.33 <sup>**</sup>	1.19	12.33	5.79	12.62 <sup>**</sup>	1.77	14.04	3.26	8.33 <sup>**</sup>	1.59	18.73
PPPN	0.01	0.03 <sup>**</sup>	0.01	8.86	0.29	0.05 <sup>**</sup>	0.03	12.45	0.03	0.06 <sup>**</sup>	0.02	11.77
SPP	0.02	0.02	0.02	4.75	0.02	0.01	0.01	3.83	0.01	0.03	0.03	5.53
HSW(g)	314.25	897.94 <sup>**</sup>	17.66	5.79	10.17	667.53 <sup>**</sup>	12.69	5.20	6.03	915.47 <sup>**</sup>	5.61	3.42
GY(g)	910.13	397.89 <sup>**</sup>	80.53	12.82	164.63	260.56 <sup>**</sup>	37.33	9.03	215.39	295.73 <sup>**</sup>	59.01	15.01
CS (%)	1789.61	401.14 <sup>**</sup>	148.59	35.61	630.14	355.89 <sup>**</sup>	142.69	42.03	1935.50	413.70 <sup>**</sup>	138.56	32.43
	(720.62)	(158.29)	(58.17)	(21.64)	(250.24)	(161.70)	(59.58)	(24.56)	(771.25)	(163.19)	(55.14)	(20.35)
GPE(g)	5159.39	1727.24 <sup>**</sup>	338.95	13.20	375.30 <sup>*</sup>	497.64 <sup>**</sup>	96.89	9.88	1543.53	1000.17 <sup>**</sup>	186.62	15.76
EGR(g/day)	1045.04	472.86 <sup>**</sup>	94.57	13.12	316.49 <sup>**</sup>	402.97 <sup>**</sup>	58.91	9.69	109.09	289.77 <sup>**</sup>	62.74	14.80

<sup>\*\*</sup>and<sup>\*</sup>, significant at P<0.05 and P<0.01, respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation and angular transformed values. Rep= replication, CV (%) = coefficient of variation in percent, DF= days to flowering(days), DM = days to maturity(days), GFP= Grain filling period(days), PH = plant height(cm), PNPP= Number of podding node per plant, PPP= Number of Pod per Plant, PPPN= Number of pod per podding node, SPP= Number of seed per pod, HSW= hundred seed weight(g), GY= Grain yield per 5 plants(g), CS= Chocolate spot disease(%),GPE= Grain production efficiency(g), EGR= Economic growth rate(g/day).



Appendix Table 2. Mean squares from analysis of variance for 13 traits of 50 faba bean genotypes evaluated with lime application at Holetta, Watebecha Minjaro and Jeldu in 2017 main cropping season

Trait	Holetta				Watebecha				Jeldu			
	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)
DF	15.86	13.35**	1.47	2.54	27.85	3.19**	1.81	2.30	1.29	4.95**	0.52	1.30
DM	18.69	14.16**	3.24	1.26	5.81	5.92**	2.02	0.99	21.33	16.68**	1.67	0.85
GFP(day)	1.45	21.08**	2.80	1.77	16.85	7.18**	2.83	1.99	32.94	18.77**	1.90	1.43
PH(cm)	2265.69	84.93**	46.93	4.29	1550.41	106.93**	28.24	3.74	651.84	123.86**	28.45	6.45
PNPP	4.35	2.60**	1.03	12.87	2.06	3.22**	1.01	11.20	4.50	2.90**	0.78	11.96
PPP	11.34	9.53**	2.62	15.74	1.29	16.70**	2.42	12.21	4.02	17.87**	1.68	10.86
PPPN	0.01	0.04**	0.02	9.83	0.09	0.06**	0.03	12.07	0.21	0.123**	0.02	8.51
SPP	0.03	0.01	0.01	3.83	0.09	0.04	0.05	7.25	0.03	0.03	0.03	6.17
HSW(g)	356.86	992.85**	19.92	5.86	16.71	759.43**	9.94	4.60	39.27	1021.88**	9.02	4.24
CS (%)	1567.89 (656.24)	463.57** (209.20)	76.00 (32.39)	32.68 (18.81)	370.67 (236.41)	259.94** (135.43)	79.80 (42.48)	44.38 (25.37)	681.29 (270.31)	564.28** (234.12)	78.46 (32.24)	24.87 (15.78)
GY(g)	805.56	507.32**	96.85	10.63	71.37	377.66**	56.09	8.25	50.55	712.10**	113.11	11.09
GPE(g)	4488.75	2600.03**	425.80	11.22	795.15	700.78**	164.17	9.74	456.14	2709.11**	359.59	11.41
EGR(g/day)	806.59	592.22**	114.07	10.90	30.87	591.69**	77.05	8.18	40.93	656.77**	120.86	11.06

\*and\*\*, significant at  $P < 0.05$  and  $P < 0.01$ , respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation and angular transformed values. Rep= replication, CV (%) = coefficient of variation in percent, DF= days to flowering(days), DM = days to maturity(days), GFP= Grain filling period(days), PH = plant height(cm), PNPP=Number of podding node per plant, PPP= Number of Pod per Plant, PPPN= Number of pod per podding node, SPP= Number of seed per pod, HSW= hundred seed weight(g), GY= Grain yield per 5 plants(g), CS= Chocolate spot disease(%), GPE= Grain production efficiency(g), EGR= Economic growth rate(g/day).

Appendix Table 3. Mean squares from analysis of variance for soil acidity stress indices of 50 faba bean genotypes at Holetta, Watebecha Minjaro and Jeldu with and without lime application in 2017 main cropping season

Index	Holetta				Watebecha Minjaro				Jeldu				F-ratio
	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)	Rep (2)	Genotype (49)	Error (98)	CV (%)	
RYR $\psi$	0.02	0.04**	0.002	20.52	0.01	0.03**	0.002	17.48	0.01	0.03*	0.004	14.30	2.00
YI $\psi$	0.18	0.08**	0.017	12.87	0.03	0.05**	0.008	9.03	0.05	0.06**	0.012	15.05	2.13
STI $\psi$	0.94	0.36**	0.099	23.29	0.14	0.26**	0.044	16.50	0.22	0.28**	0.053	22.41	2.25
SSI $\psi$	0.20	0.83**	0.052	22.97	0.04	0.61**	0.040	19.67	0.03	0.91**	0.137	18.74	3.43
MP(g)	832.52	346.07**	81.92	11.13	112.18	240.41**	41.508	8.13	229.61	384.91**	65.950	11.04	1.97
GMP(g)	855.54	343.94**	82.14	11.29	122.44	238.91**	41.396	8.23	236.41	368.15**	65.420	11.60	1.98
HM(g)	878.92	345.40**	82.71	11.48	132.89	241.12**	41.47	8.34	241.84	366.56**	67.06	12.37	1.99

\*and\*\*, significant at  $P < 0.05$  and  $P < 0.01$ , respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation. Rep= replication, CV (%) = coefficient of variation in percent, RYR= relative yield reduction, YI= yield index, STI= soil acidity tolerance index, SSI= soil acidity susceptible index, MP= mean productivity (g), GMP= geometric mean productivity (g), HM= harmonic mean,  $\psi$  = unit less trait.

Appendix Table 4. Error variances ratio (F-values) used for homogeneity test in experiments conducted over locations and lime and without lime managements in 2017 main cropping season

Trait	Without and with lime at each location			Without lime at three locations	With lime at three locations	Without and with lime at three locations (Six environments)
	Holetta	Watebecha Minjaro	Jeldu			
Days to flowering	1.16	1.16	1.62	1.86	3.48	3.48
Days to maturity	1.15	1.07	1.29	1.74	1.94	2.24
Grain filling period(days)	1.23	1.70	1.48	1.72	1.49	2.54
Plant height(cm)	1.47	1.06	1.16	1.11	1.66	1.66
Number of podding node plant <sup>-1</sup>	1.29	1.29	1.03	1.05	1.32	1.36
Number of pod plant <sup>-1</sup>	2.20	1.37	1.06	1.49	1.56	2.20
Number of pod podding nod <sup>-1</sup>	2.00	1.00	1.00	3.00	1.50	3.00
Hundred seed weight(g)	1.13	1.28	1.61	3.15	2.21	3.55
Chocolate spot disease	1.80	1.40	1.71	1.08	1.32	1.85
Grain yield(g/5plants)	1.20	1.50	1.92	2.16	2.02	3.03
Grain production efficiency(g)	1.26	1.69	1.93	3.50	2.59	4.39
Economic growth rate(g/day)	1.21	1.31	1.93	1.61	1.57	2.05

The error variances ratio was computed by dividing the higher error variance by the smaller error variance as per Gomez and Gomez (1984).

Appendix Table 5. Mean squares from combined analysis of variance over locations with and without lime application (six environments) for 12 traits of 50 faba bean genotypes in 2017 main cropping season

Trait	Block (12)	Genotype (G) (49)	Location (L) (2)	Management (M) (1)	G x M (49)	L x M (2)	G x L (98)	G x L x M (98)	Error (588)	CV (%)
DF(day)	13.27	33.78**	9273.74**	0.03	2.14*	24.34**	6.83**	1.74*	1.25	2.06
DM(day)	17.91	47.21**	8435.08**	0.87	3.71*	16.30**	8.49**	3.32*	2.50	1.08
GFP (day)	22.84	59.68**	10253.34**	1.28	6.33**	70.74**	12.45**	5.03**	3.10	1.92
PH (cm)	1672.19	279.19**	518731.50**	64736.32**	39.92	1908.01**	116.91**	48.23**	33.10	4.81
PNPP	5.91	11.06**	304.55**	533.61**	0.88	39.04**	1.42**	1.11*	0.86	12.68
PPP	5.09	53.82**	281.41**	2450.25**	3.23**	265.17**	4.11**	3.05**	1.88	13.70
PPPN	0.11	0.22**	2.61**	6.02**	0.02	1.22**	0.03**	0.03	0.02	10.58
HSW (g)	123.88	5049.13**	2777.22**	649.62**	37.01**	243.58**	54.42**	30.06**	12.47	4.98
GY (g)	403.27	1349.87**	4815.28**	205123.39**	255.29**	12001.40**	296.64**	175.41**	73.00	10.95
CS (%)	1162.51 (484.18)	930.00** (388.81)	10248.74** (4428.38)	6833.78** (3161.40)	125.98 (55.66)	1319.50** (596.20)	483.58** (212.62)	217.68** (96.12)	110.68 (46.67)	34.81 (21.01)
GPE (g)	2270.87	4852.72**	174044.10**	607391.62**	858.49**	45608.66**	1179.80**	573.33**	255.93	11.89
EGR (g/day)	418.88	1569.20**	21292.41**	239647.13**	307.73**	10236.12**	349.49**	214.00**	87.82	10.99

\* and \*\*, significant at  $P < 0.05$  and  $P < 0.01$ , respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation and angular transformed values for CS. CV (%) = coefficient of variation in percent, DF= days to 50% flowering, DM = days to 90% maturity, GFP= Grain filling period, PH = plant height, PNPP=Number of podding node per plant, PPP= Number of Pod per Plant, PPPN= Number of pod per podding node, HSW= hundred seed weight, GY= Grain yield in gram per 5 plants, CS= Chocolate spot disease, GPE= Grain production efficiency, EGR= Economic growth rate.

Appendix Table 6. Mean performance of 50 faba bean genotypes for 11 agronomic traits evaluated with and without lime application at three locations in 2017 main cropping season

6a. Days to 50% flowering

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	48.3 <sup>e-h</sup>	59.7 <sup>a-d</sup>	59.3 <sup>bc</sup>	55.8 <sup>ef</sup>	48.3 <sup>c-h</sup>	58.7 <sup>a-e</sup>	56.0 <sup>f-j</sup>	54.3
2	Wolki	52.3 <sup>bc</sup>	58.3 <sup>b-h</sup>	57.7 <sup>c-f</sup>	56.1 <sup>de</sup>	50.0 <sup>b-e</sup>	59.3 <sup>a-e</sup>	56.3 <sup>e-i</sup>	55.2
3	EK LS/CSR02012-2-3	45.7 <sup>j-m</sup>	58.0 <sup>b-h</sup>	55.3 <sup>h-l</sup>	53.0 <sup>o-r</sup>	46.3 <sup>g-k</sup>	58.0 <sup>b-e</sup>	55.3 <sup>h-l</sup>	53.2
4	Obse	45.3 <sup>klm</sup>	57.7 <sup>c-h</sup>	56.0 <sup>f-j</sup>	53.0 <sup>o-r</sup>	46.3 <sup>g-k</sup>	57.3 <sup>cde</sup>	54.7 <sup>j-m</sup>	52.8
5	NC58	46.0 <sup>i-m</sup>	57.7 <sup>c-h</sup>	56.7 <sup>e-i</sup>	53.4 <sup>k-r</sup>	46.7 <sup>g-k</sup>	57.0 <sup>de</sup>	56.3 <sup>e-i</sup>	53.3
6	Ashebeka	52.7 <sup>b</sup>	59.3 <sup>a-e</sup>	59.3 <sup>bc</sup>	57.1 <sup>cd</sup>	51.0 <sup>b</sup>	59.3 <sup>a-e</sup>	57.3 <sup>b-f</sup>	55.9
7	Hachalu	50.7 <sup>cd</sup>	59.0 <sup>a-f</sup>	58.7 <sup>bcd</sup>	56.1 <sup>de</sup>	50.7 <sup>bc</sup>	61.0 <sup>a</sup>	57.3 <sup>b-f</sup>	56.3
8	Degaga	47.3 <sup>f-k</sup>	58.0 <sup>b-h</sup>	57.7 <sup>c-f</sup>	54.3 <sup>h-n</sup>	47.3 <sup>f-j</sup>	58.0 <sup>b-e</sup>	55.7 <sup>g-k</sup>	53.7
9	EH09031-4	46.0 <sup>i-m</sup>	58.0 <sup>b-h</sup>	56.0 <sup>f-j</sup>	53.3 <sup>l-r</sup>	47.0 <sup>f-k</sup>	57.0 <sup>de</sup>	55.0 <sup>i-l</sup>	53.0
10	Holetta-2	48.0 <sup>e-i</sup>	57.7 <sup>c-h</sup>	55.0 <sup>i-l</sup>	53.6 <sup>j-r</sup>	47.7 <sup>e-i</sup>	58.3 <sup>a-e</sup>	55.0 <sup>i-l</sup>	53.7
11	EH09007-4	46.3 <sup>h-m</sup>	56.7 <sup>fgh</sup>	55.0 <sup>i-l</sup>	52.7 <sup>p-s</sup>	47.0 <sup>f-k</sup>	57.3 <sup>cde</sup>	55.3 <sup>h-l</sup>	53.2
12	EH07023-3	45.3 <sup>klm</sup>	56.7 <sup>fgh</sup>	55.7 <sup>g-k</sup>	52.6 <sup>q-t</sup>	46.0 <sup>h-k</sup>	57.7 <sup>b-e</sup>	54.7 <sup>j-m</sup>	52.8
13	EK05006-3	47.7 <sup>f-j</sup>	57.3 <sup>d-h</sup>	56.0 <sup>f-j</sup>	53.7 <sup>i-q</sup>	48.0 <sup>d-i</sup>	59.7 <sup>a-d</sup>	57.3 <sup>b-f</sup>	55.0
14	EK LS/CSR02014-2-4	47.0 <sup>g-l</sup>	58.0 <sup>b-h</sup>	56.0 <sup>f-j</sup>	53.7 <sup>i-q</sup>	49.3 <sup>b-f</sup>	56.7 <sup>e</sup>	56.0 <sup>f-j</sup>	54.0
15	Numan	47.3 <sup>f-k</sup>	59.3 <sup>a-e</sup>	57.3 <sup>d-g</sup>	54.7 <sup>f-k</sup>	47.7 <sup>e-i</sup>	58.0 <sup>b-e</sup>	55.3 <sup>h-l</sup>	53.7
16	Bulga 70	45.7 <sup>j-m</sup>	57.0 <sup>e-h</sup>	56.7 <sup>e-i</sup>	53.1 <sup>n-r</sup>	46.7 <sup>g-k</sup>	58.7 <sup>a-e</sup>	55.3 <sup>h-l</sup>	53.6
17	EK05001-1	45.3 <sup>klm</sup>	59.0 <sup>a-f</sup>	55.3 <sup>h-l</sup>	53.2 <sup>m-r</sup>	45.7 <sup>ijk</sup>	58.0 <sup>b-e</sup>	54.3 <sup>klm</sup>	52.7
18	Dosha	47.3 <sup>f-k</sup>	57.7 <sup>c-h</sup>	55.3 <sup>h-l</sup>	53.4 <sup>k-r</sup>	48.3 <sup>c-h</sup>	60.3 <sup>ab</sup>	55.3 <sup>h-l</sup>	54.7
19	Gora	47.0 <sup>g-l</sup>	58.7 <sup>a-g</sup>	57.0 <sup>d-h</sup>	54.2 <sup>h-o</sup>	47.0 <sup>f-k</sup>	58.0 <sup>b-e</sup>	57.7 <sup>b-e</sup>	54.2
20	EH08035-1	44.3 <sup>m</sup>	57.0 <sup>e-h</sup>	53.7 <sup>l</sup>	51.7 <sup>st</sup>	44.7 <sup>k</sup>	59.0 <sup>a-e</sup>	53.3 <sup>m</sup>	52.3
21	Wayu	55.3 <sup>a</sup>	60.0 <sup>abc</sup>	61.3 <sup>a</sup>	58.9 <sup>a</sup>	55.3 <sup>a</sup>	59.0 <sup>a-e</sup>	60.0 <sup>a</sup>	58.1
22	EK LS/CSR02023-2-1	45.7 <sup>j-m</sup>	57.0 <sup>e-h</sup>	55.3 <sup>h-l</sup>	52.7 <sup>p-s</sup>	46.3 <sup>g-k</sup>	59.0 <sup>a-e</sup>	55.0 <sup>i-l</sup>	53.4
23	Mesay	47.3 <sup>f-k</sup>	57.3 <sup>d-h</sup>	55.3 <sup>h-l</sup>	53.3 <sup>l-r</sup>	47.3 <sup>f-j</sup>	58.0 <sup>b-e</sup>	55.0 <sup>i-l</sup>	53.4
24	EH09004-2	44.3 <sup>m</sup>	56.0 <sup>h</sup>	54.0 <sup>kl</sup>	51.4 <sup>t</sup>	45.0 <sup>jk</sup>	58.3 <sup>a-e</sup>	54.0 <sup>lm</sup>	52.4
25	EH06088-6	45.0 <sup>lm</sup>	57.3 <sup>d-h</sup>	54.7 <sup>jkl</sup>	52.3 <sup>rst</sup>	46.0 <sup>h-k</sup>	59.0 <sup>a-e</sup>	54.3 <sup>klm</sup>	53.1
	Mean	47.6c	58.0a	56.5b	54.1	47.9c	58.5a	55.9b	54.1

Appendix Table 6a. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	45.3 <sup>klm</sup>	57.0 <sup>e-h</sup>	55.7 <sup>g-k</sup>	52.7 <sup>p-s</sup>	46.0 <sup>h-k</sup>	60.0 <sup>abc</sup>	54.3 <sup>klm</sup>	53.4
27	Kasa	48.0 <sup>e-i</sup>	57.0 <sup>e-h</sup>	56.0 <sup>f-j</sup>	53.7 <sup>i-q</sup>	48.0 <sup>d-i</sup>	57.7 <sup>b-e</sup>	55.3 <sup>h-l</sup>	53.7
28	Cool-0025	47.7 <sup>f-j</sup>	59.3 <sup>a-e</sup>	56.3 <sup>f-j</sup>	54.4 <sup>g-m</sup>	47.7 <sup>e-i</sup>	59.7 <sup>a-d</sup>	55.3 <sup>h-l</sup>	54.2
29	EH06070-3	47.0 <sup>g-l</sup>	60.3 <sup>ab</sup>	57.3 <sup>d-g</sup>	54.9 <sup>f-i</sup>	48.3 <sup>c-h</sup>	57.7 <sup>b-e</sup>	56.3 <sup>e-i</sup>	54.1
30	EK LS/CSR02010-4-3	46.0 <sup>i-m</sup>	57.7 <sup>c-h</sup>	56.3 <sup>f-j</sup>	53.3 <sup>l-r</sup>	45.7 <sup>ijk</sup>	58.7 <sup>a-e</sup>	55.0 <sup>i-l</sup>	53.1
31	Cool-0031	50.0 <sup>de</sup>	59.0 <sup>a-f</sup>	57.7 <sup>c-f</sup>	55.6 <sup>efg</sup>	48.7 <sup>c-g</sup>	57.3 <sup>cde</sup>	56.7 <sup>d-h</sup>	54.2
32	Cool-0018	47.7 <sup>f-j</sup>	57.3 <sup>d-h</sup>	56.7 <sup>e-i</sup>	53.9 <sup>h-p</sup>	48.3 <sup>c-h</sup>	57.3 <sup>cde</sup>	56.0 <sup>f-j</sup>	53.9
33	EK LS/CSR02028-1-1	48.0 <sup>e-i</sup>	56.3 <sup>gh</sup>	56.7 <sup>e-i</sup>	53.7 <sup>i-q</sup>	47.3 <sup>f-j</sup>	58.3 <sup>a-e</sup>	56.7 <sup>d-h</sup>	54.1
34	EK 05037-4	46.3 <sup>h-m</sup>	58.0 <sup>b-h</sup>	54.7 <sup>jkl</sup>	53.0 <sup>o-r</sup>	46.0 <sup>h-k</sup>	58.0 <sup>b-e</sup>	55.0 <sup>i-l</sup>	53.0
35	Cool-0035	47.0 <sup>g-l</sup>	57.0 <sup>e-h</sup>	56.3 <sup>f-j</sup>	53.4 <sup>k-r</sup>	47.7 <sup>e-i</sup>	58.7 <sup>a-e</sup>	56.0 <sup>f-j</sup>	54.1
36	KUSE2-27-33	46.3 <sup>h-m</sup>	56.7 <sup>fgh</sup>	56.0 <sup>f-j</sup>	53.0 <sup>o-r</sup>	47.0 <sup>f-k</sup>	59.3 <sup>a-e</sup>	55.0 <sup>i-l</sup>	53.8
37	EH07015-7	46.7 <sup>g-l</sup>	57.0 <sup>e-h</sup>	56.0 <sup>f-j</sup>	53.2 <sup>m-r</sup>	47.0 <sup>f-k</sup>	60.0 <sup>abc</sup>	56.7 <sup>d-h</sup>	54.6
38	Cool-0024	46.7 <sup>g-l</sup>	57.7 <sup>c-h</sup>	55.7 <sup>g-k</sup>	53.3 <sup>l-r</sup>	46.7 <sup>g-k</sup>	58.7 <sup>a-e</sup>	55.7 <sup>g-k</sup>	53.7
39	Selale	48.3 <sup>e-h</sup>	56.0 <sup>h</sup>	59.3 <sup>bc</sup>	54.6 <sup>g-l</sup>	47.3 <sup>f-j</sup>	57.7 <sup>b-e</sup>	58.0 <sup>bcd</sup>	54.3
40	Moti	46.3 <sup>h-m</sup>	58.0 <sup>b-h</sup>	55.7 <sup>g-k</sup>	53.3 <sup>l-r</sup>	46.3 <sup>g-k</sup>	58.3 <sup>a-e</sup>	55.7 <sup>g-k</sup>	53.4
41	EH06027-2	48.7 <sup>d-g</sup>	59.3 <sup>a-e</sup>	56.7 <sup>e-i</sup>	54.9 <sup>f-i</sup>	48.7 <sup>c-g</sup>	57.3 <sup>cde</sup>	57.0 <sup>c-g</sup>	54.3
42	EK LS/CSR02019-2-4	46.3 <sup>h-m</sup>	58.0 <sup>b-h</sup>	56.3 <sup>f-j</sup>	53.6 <sup>j-r</sup>	47.0 <sup>f-k</sup>	58.7 <sup>a-e</sup>	55.3 <sup>h-l</sup>	53.7
43	EH09002-1	45.3 <sup>klm</sup>	57.7 <sup>c-h</sup>	54.7 <sup>jkl</sup>	52.6 <sup>q-t</sup>	46.3 <sup>g-k</sup>	57.3 <sup>cde</sup>	54.7 <sup>j-m</sup>	52.8
44	Tumsa	53.3 <sup>b</sup>	61.0 <sup>a</sup>	58.3 <sup>b-e</sup>	57.6 <sup>bc</sup>	50.0 <sup>b-e</sup>	60.3 <sup>ab</sup>	58.3 <sup>bc</sup>	56.2
45	Gebelcho	56.0 <sup>a</sup>	60.0 <sup>abc</sup>	59.7 <sup>b</sup>	58.6 <sup>ab</sup>	54.3 <sup>a</sup>	60.0 <sup>abc</sup>	58.7 <sup>b</sup>	57.7
46	EK05037-5	45.7 <sup>j-m</sup>	57.7 <sup>c-h</sup>	56.7 <sup>e-i</sup>	53.3 <sup>l-r</sup>	46.7 <sup>g-k</sup>	57.3 <sup>cde</sup>	55.3 <sup>h-l</sup>	53.1
47	Didi'a	48.3 <sup>e-h</sup>	59.3 <sup>a-e</sup>	56.7 <sup>e-i</sup>	54.8 <sup>f-j</sup>	51.0 <sup>b</sup>	57.7 <sup>b-e</sup>	57.0 <sup>c-g</sup>	55.2
48	Cool-0034	47.7 <sup>f-j</sup>	57.7 <sup>c-h</sup>	56.3 <sup>f-j</sup>	53.9 <sup>h-p</sup>	48.3 <sup>c-h</sup>	57.0 <sup>de</sup>	55.3 <sup>h-l</sup>	53.6
49	CS20DK	49.3 <sup>def</sup>	59.3 <sup>a-e</sup>	58.7 <sup>bcd</sup>	55.8 <sup>ef</sup>	50.3 <sup>bcd</sup>	59.7 <sup>a-d</sup>	56.3 <sup>e-i</sup>	55.4
50	Tesfa	50.7 <sup>cd</sup>	59.3 <sup>a-e</sup>	55.0 <sup>i-l</sup>	55.0 <sup>e-h</sup>	50.7 <sup>bc</sup>	59.0 <sup>a-e</sup>	55.0 <sup>i-l</sup>	54.9
	Mean	47.6 <sup>c</sup>	58.0 <sup>a</sup>	56.5 <sup>b</sup>	54.1	47.9 <sup>c</sup>	58.5 <sup>a</sup>	55.9 <sup>b</sup>	54.1

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6b. Mean performance of 50 faba bean genotypes for days to 90% maturity

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	144.3 <sup>a-e</sup>	144.7 <sup>a-f</sup>	153.0 <sup>b-h</sup>	147.3 <sup>a-g</sup>	143.3 <sup>a-e</sup>	144.3 <sup>a-h</sup>	154.3 <sup>b-f</sup>	147.3 <sup>a-h</sup>
2	Wolki	141.7 <sup>c-k</sup>	142.7 <sup>c-g</sup>	151.0 <sup>f-l</sup>	145.1 <sup>h-n</sup>	141.7 <sup>c-h</sup>	142.3 <sup>f-i</sup>	149.3 <sup>m-p</sup>	144.4 <sup>m-r</sup>
3	EK LS/CSR02012-2-3	142.7 <sup>a-i</sup>	144.7 <sup>a-f</sup>	153.7 <sup>b-f</sup>	147.0 <sup>b-h</sup>	143.7 <sup>a-e</sup>	146.0 <sup>abc</sup>	154.3 <sup>b-f</sup>	148.0 <sup>a-d</sup>
4	Obse	141.7 <sup>c-k</sup>	142.7 <sup>c-g</sup>	152.7 <sup>b-i</sup>	145.7 <sup>g-m</sup>	142.3 <sup>b-g</sup>	143.3 <sup>c-i</sup>	152.0 <sup>f-l</sup>	145.9 <sup>g-n</sup>
5	NC58	139.7 <sup>h-n</sup>	141.3 <sup>g</sup>	148.7 <sup>l-o</sup>	143.2 <sup>o-r</sup>	141.0 <sup>d-h</sup>	142.0 <sup>ghi</sup>	148.7 <sup>op</sup>	143.9 <sup>p-s</sup>
6	Ashebeka	145.3 <sup>abc</sup>	144.3 <sup>a-g</sup>	153.0 <sup>b-h</sup>	147.6 <sup>a-g</sup>	144.0 <sup>a-e</sup>	147.0 <sup>a</sup>	154.3 <sup>b-f</sup>	148.4 <sup>ab</sup>
7	Hachalu	145.0 <sup>a-d</sup>	143.0 <sup>b-g</sup>	152.3 <sup>c-j</sup>	146.8 <sup>c-i</sup>	143.3 <sup>a-e</sup>	145.0 <sup>a-f</sup>	150.7 <sup>j-o</sup>	146.3 <sup>d-k</sup>
8	Degaga	136.3 <sup>n</sup>	141.7 <sup>fg</sup>	148.3 <sup>l-o</sup>	142.1 <sup>r</sup>	138.3 <sup>hi</sup>	142.7 <sup>e-i</sup>	150.0 <sup>l-p</sup>	143.7 <sup>p-s</sup>
9	EH09031-4	144.0 <sup>a-f</sup>	145.7 <sup>abc</sup>	153.3 <sup>b-g</sup>	147.7 <sup>a-f</sup>	142.7 <sup>a-g</sup>	145.7 <sup>a-d</sup>	153.7 <sup>b-h</sup>	147.3 <sup>a-h</sup>
10	Holetta-2	142.3 <sup>a-j</sup>	145.7 <sup>abc</sup>	151.7 <sup>c-k</sup>	146.6 <sup>c-j</sup>	143.7 <sup>a-e</sup>	142.7 <sup>e-i</sup>	152.0 <sup>f-l</sup>	146.1 <sup>f-m</sup>
11	EH09007-4	141.7 <sup>c-k</sup>	143.3 <sup>b-g</sup>	152.0 <sup>d-k</sup>	145.7 <sup>g-m</sup>	141.7 <sup>c-h</sup>	143.7 <sup>c-i</sup>	153.7 <sup>b-h</sup>	146.3 <sup>d-k</sup>
12	EH07023-3	142.0 <sup>b-k</sup>	143.0 <sup>b-g</sup>	157.0 <sup>a</sup>	147.3 <sup>a-g</sup>	143.0 <sup>a-f</sup>	143.3 <sup>c-i</sup>	160.0 <sup>a</sup>	148.8 <sup>a</sup>
13	EK05006-3	144.0 <sup>a-f</sup>	146.0 <sup>ab</sup>	155.3 <sup>ab</sup>	148.4 <sup>abc</sup>	144.3 <sup>a-d</sup>	144.3 <sup>a-h</sup>	154.0 <sup>b-g</sup>	147.6 <sup>a-g</sup>
14	EK LS/CSR02014-2-4	145.3 <sup>abc</sup>	146.7 <sup>a</sup>	155.0 <sup>abc</sup>	149.0 <sup>a</sup>	143.3 <sup>a-e</sup>	143.7 <sup>c-i</sup>	154.3 <sup>b-f</sup>	147.1 <sup>a-h</sup>
15	Numan	141.7 <sup>c-k</sup>	144.7 <sup>a-f</sup>	154.0 <sup>b-e</sup>	146.8 <sup>c-i</sup>	143.0 <sup>a-f</sup>	146.7 <sup>ab</sup>	152.0 <sup>f-l</sup>	147.2 <sup>a-h</sup>
16	Bulga 70	139.3 <sup>i-n</sup>	142.7 <sup>c-g</sup>	149.7 <sup>j-n</sup>	143.9 <sup>m-r</sup>	141.0 <sup>d-h</sup>	142.3 <sup>f-i</sup>	150.3 <sup>k-p</sup>	144.6 <sup>l-r</sup>
17	EK05001-1	142.7 <sup>a-i</sup>	144.0 <sup>a-g</sup>	154.3 <sup>a-e</sup>	147.0 <sup>b-h</sup>	142.0 <sup>b-g</sup>	142.0 <sup>ghi</sup>	149.3 <sup>m-p</sup>	144.4 <sup>m-r</sup>
18	Dosha	141.0 <sup>e-l</sup>	142.3 <sup>d-g</sup>	153.7 <sup>b-f</sup>	145.7 <sup>g-m</sup>	143.0 <sup>a-f</sup>	144.7 <sup>a-g</sup>	151.7 <sup>g-m</sup>	146.4 <sup>c-k</sup>
19	Gora	144.0 <sup>a-f</sup>	144.3 <sup>a-g</sup>	154.3 <sup>a-e</sup>	147.6 <sup>a-g</sup>	143.7 <sup>a-e</sup>	142.3 <sup>f-i</sup>	153.0 <sup>d-j</sup>	146.3 <sup>d-k</sup>
20	EH08035-1	138.3 <sup>k-n</sup>	143.3 <sup>b-g</sup>	150.0 <sup>i-m</sup>	143.9 <sup>m-r</sup>	139.7 <sup>f-i</sup>	142.3 <sup>f-i</sup>	150.0 <sup>l-p</sup>	144.0 <sup>p-s</sup>
21	Wayu	143.7 <sup>a-g</sup>	144.3 <sup>a-g</sup>	150.3 <sup>h-m</sup>	146.1 <sup>e-k</sup>	143.7 <sup>a-e</sup>	142.7 <sup>e-i</sup>	151.0 <sup>i-o</sup>	145.8 <sup>h-o</sup>
22	EK LS/CSR02023-2-1	143.7 <sup>a-g</sup>	144.7 <sup>a-f</sup>	152.0 <sup>d-k</sup>	146.8 <sup>c-i</sup>	145.3 <sup>abc</sup>	143.0 <sup>d-i</sup>	153.3 <sup>c-i</sup>	147.2 <sup>a-h</sup>
23	Mesay	137.3 <sup>lmn</sup>	143.3 <sup>b-g</sup>	148.0 <sup>mno</sup>	142.9 <sup>pqr</sup>	139.7 <sup>f-i</sup>	142.7 <sup>e-i</sup>	150.3 <sup>k-p</sup>	144.2 <sup>n-s</sup>
24	EH09004-2	137.0 <sup>mn</sup>	141.3 <sup>g</sup>	148.7 <sup>l-o</sup>	142.3 <sup>qr</sup>	138.3 <sup>hi</sup>	141.3 <sup>i</sup>	149.0 <sup>nop</sup>	142.9 <sup>rs</sup>
25	EH06088-6	142.3 <sup>a-j</sup>	142.7 <sup>c-g</sup>	152.0 <sup>d-k</sup>	145.7 <sup>g-m</sup>	142.0 <sup>b-g</sup>	143.3 <sup>c-i</sup>	152.7 <sup>d-k</sup>	146.0 <sup>g-m</sup>
	Mean	142.2 <sup>c</sup>	143.6 <sup>b</sup>	151.8 <sup>a</sup>	145.9	142.5 <sup>c</sup>	143.1 <sup>b</sup>	142.2 <sup>a</sup>	145.9

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6b. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	142.0 <sup>b-k</sup>	145.0 <sup>a-e</sup>	150.7 <sup>g-m</sup>	145.9 <sup>f-l</sup>	142.0 <sup>b-g</sup>	144.0 <sup>b-i</sup>	153.7 <sup>b-h</sup>	146.6 <sup>c-k</sup>
27	Kasa	139.3 <sup>i-n</sup>	142.7 <sup>c-g</sup>	146.3 <sup>o</sup>	142.8 <sup>pqr</sup>	141.3 <sup>d-h</sup>	141.3 <sup>i</sup>	148.0 <sup>p</sup>	143.6 <sup>qrs</sup>
28	Cool-0025	143.0 <sup>a-i</sup>	142.7 <sup>c-g</sup>	151.7 <sup>e-k</sup>	145.8 <sup>f-l</sup>	141.3 <sup>d-h</sup>	143.0 <sup>d-i</sup>	150.3 <sup>k-p</sup>	144.9 <sup>k-q</sup>
29	EH06070-3	144.0 <sup>a-f</sup>	145.3 <sup>a-d</sup>	154.3 <sup>a-e</sup>	147.9 <sup>a-e</sup>	145.3 <sup>abc</sup>	145.0 <sup>a-f</sup>	153.3 <sup>c-i</sup>	147.9 <sup>a-e</sup>
30	EK LS/CSR02010-4-3	143.3 <sup>a-h</sup>	143.0 <sup>b-g</sup>	153.3 <sup>b-g</sup>	146.6 <sup>c-j</sup>	143.7 <sup>a-e</sup>	142.7 <sup>e-i</sup>	152.7 <sup>d-k</sup>	146.3 <sup>d-k</sup>
31	Cool-0031	143.7 <sup>a-g</sup>	144.7 <sup>a-f</sup>	153.3 <sup>b-g</sup>	147.2 <sup>a-g</sup>	143.7 <sup>a-e</sup>	141.7 <sup>hi</sup>	154.7 <sup>b-e</sup>	146.7 <sup>c-j</sup>
32	Cool-0018	138.7 <sup>j-n</sup>	142.3 <sup>d-g</sup>	150.3 <sup>h-m</sup>	143.8 <sup>n-r</sup>	139.3 <sup>ghi</sup>	142.0 <sup>ghi</sup>	151.0 <sup>i-o</sup>	144.1 <sup>o-s</sup>
33	EK LS/CSR02028-1-1	145.7 <sup>ab</sup>	145.7 <sup>abc</sup>	155.0 <sup>abc</sup>	148.8 <sup>ab</sup>	145.7 <sup>ab</sup>	142.3 <sup>f-i</sup>	155.7 <sup>bc</sup>	147.9 <sup>a-e</sup>
34	EK 05037-4	143.3 <sup>a-h</sup>	144.7 <sup>a-f</sup>	152.0 <sup>d-k</sup>	146.7 <sup>c-i</sup>	144.0 <sup>a-e</sup>	142.0 <sup>ghi</sup>	154.0 <sup>b-g</sup>	146.7 <sup>c-j</sup>
35	Cool-0035	141.7 <sup>c-k</sup>	142.0 <sup>efg</sup>	151.0 <sup>f-l</sup>	144.9 <sup>i-o</sup>	139.7 <sup>f-i</sup>	141.3 <sup>i</sup>	150.0 <sup>l-p</sup>	143.7 <sup>p-s</sup>
36	KUSE2-27-33	141.3 <sup>d-k</sup>	142.7 <sup>c-g</sup>	148.3 <sup>l-o</sup>	144.1 <sup>l-q</sup>	136.7 <sup>i</sup>	142.0 <sup>ghi</sup>	149.3 <sup>m-p</sup>	142.7 <sup>s</sup>
37	EH07015-7	144.7 <sup>a-e</sup>	145.0 <sup>a-e</sup>	154.7 <sup>a-d</sup>	148.1 <sup>a-d</sup>	145.7 <sup>ab</sup>	144.0 <sup>b-i</sup>	151.0 <sup>i-o</sup>	146.9 <sup>b-i</sup>
38	Cool-0024	141.7 <sup>c-k</sup>	143.7 <sup>b-g</sup>	150.3 <sup>h-m</sup>	145.2 <sup>h-n</sup>	141.0 <sup>d-h</sup>	142.7 <sup>e-i</sup>	150.0 <sup>l-p</sup>	144.6 <sup>l-r</sup>
39	Selale	144.0 <sup>a-f</sup>	141.3 <sup>g</sup>	150.0 <sup>i-m</sup>	145.1 <sup>h-n</sup>	146.0 <sup>a</sup>	142.3 <sup>f-i</sup>	150.3 <sup>k-p</sup>	146.2 <sup>e-l</sup>
40	Moti	140.0 <sup>g-n</sup>	142.0 <sup>efg</sup>	149.7 <sup>j-n</sup>	143.9 <sup>m-r</sup>	141.7 <sup>c-h</sup>	141.3 <sup>i</sup>	152.3 <sup>e-l</sup>	145.1 <sup>j-q</sup>
41	EH06027-2	144.7 <sup>a-e</sup>	143.7 <sup>b-g</sup>	152.0 <sup>d-k</sup>	146.8 <sup>c-i</sup>	144.0 <sup>a-e</sup>	143.7 <sup>c-i</sup>	153.7 <sup>b-h</sup>	147.1 <sup>a-h</sup>
42	EK LS/CSR02019-2-4	146.0 <sup>a</sup>	144.7 <sup>a-f</sup>	153.7 <sup>b-f</sup>	148.1 <sup>a-d</sup>	144.7 <sup>a-d</sup>	143.7 <sup>c-i</sup>	156.0 <sup>b</sup>	148.1 <sup>abc</sup>
43	EH09002-1	141.0 <sup>e-l</sup>	144.0 <sup>a-g</sup>	149.7 <sup>j-n</sup>	144.9 <sup>i-o</sup>	142.0 <sup>b-g</sup>	142.7 <sup>e-i</sup>	151.3 <sup>h-n</sup>	145.3 <sup>i-p</sup>
44	Tumsa	143.7 <sup>a-g</sup>	144.0 <sup>a-g</sup>	154.3 <sup>a-e</sup>	147.3 <sup>a-g</sup>	143.7 <sup>a-e</sup>	145.3 <sup>a-e</sup>	154.7 <sup>b-e</sup>	147.9 <sup>a-e</sup>
45	Gebelcho	143.3 <sup>a-h</sup>	144.3 <sup>a-g</sup>	154.0 <sup>b-e</sup>	147.2 <sup>a-g</sup>	144.7 <sup>a-d</sup>	143.7 <sup>c-i</sup>	155.0 <sup>bcd</sup>	147.8 <sup>a-f</sup>
46	EK05037-5	142.3 <sup>a-j</sup>	142.7 <sup>c-g</sup>	149.3 <sup>k-n</sup>	144.8 <sup>j-o</sup>	140.3 <sup>e-h</sup>	143.0 <sup>d-i</sup>	151.3 <sup>h-n</sup>	144.9 <sup>k-q</sup>
47	Didi'a	143.7 <sup>a-g</sup>	142.7 <sup>c-g</sup>	152.3 <sup>c-j</sup>	146.2 <sup>d-j</sup>	146.0 <sup>a</sup>	143.0 <sup>d-i</sup>	152.7 <sup>d-k</sup>	147.2 <sup>a-h</sup>
48	Cool-0034	141.7 <sup>c-k</sup>	142.0 <sup>efg</sup>	151.0 <sup>f-l</sup>	144.9 <sup>i-o</sup>	143.3 <sup>a-e</sup>	141.7 <sup>hi</sup>	154.0 <sup>b-g</sup>	146.3 <sup>d-k</sup>
49	CS20DK	140.3 <sup>f-m</sup>	142.0 <sup>efg</sup>	150.7 <sup>g-m</sup>	144.3 <sup>k-p</sup>	139.3 <sup>ghi</sup>	141.7 <sup>hi</sup>	152.7 <sup>d-k</sup>	144.6 <sup>l-r</sup>
50	Tesfa	140.3 <sup>f-m</sup>	144.3 <sup>a-g</sup>	147.0 <sup>no</sup>	143.9 <sup>m-r</sup>	139.7 <sup>f-i</sup>	141.3 <sup>i</sup>	148.0 <sup>p</sup>	143.0 <sup>ts</sup>
	Mean	142.2 <sup>c</sup>	143.6 <sup>b</sup>	151.8 <sup>a</sup>	145.9	142.5 <sup>c</sup>	143.1 <sup>b</sup>	142.2 <sup>a</sup>	145.9

Mean values followed by similar letter(s) in each column had nonsignificant difference at  $P < 0.05$



Appendix Table 6c. Mean performance of 50 faba bean genotypes for grain filling period

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	96.0 <sup>a-f</sup>	85.0 <sup>a-e</sup>	93.7 <sup>g-m</sup>	91.6 <sup>g-l</sup>	95.0 <sup>c-m</sup>	85.7 <sup>a-h</sup>	98.3 <sup>b-f</sup>	93.0 <sup>b-h</sup>
2	Wolki	89.3 <sup>ijkl</sup>	84.3 <sup>b-e</sup>	93.3 <sup>h-n</sup>	89.0 <sup>m-r</sup>	91.7 <sup>m-q</sup>	83.0 <sup>f-i</sup>	93.0 <sup>l-o</sup>	89.2 <sup>r-v</sup>
3	EK LS/CSR02012-2-3	97.0 <sup>a-e</sup>	86.7 <sup>a-e</sup>	98.3 <sup>a-e</sup>	94.0 <sup>a-f</sup>	97.3 <sup>a-f</sup>	88.0 <sup>ab</sup>	99.0 <sup>bcd</sup>	94.8 <sup>ab</sup>
4	Obse	96.3 <sup>a-f</sup>	85.0 <sup>a-e</sup>	96.7 <sup>b-h</sup>	92.7 <sup>c-j</sup>	96.0 <sup>a-j</sup>	86.0 <sup>a-g</sup>	97.3 <sup>c-h</sup>	93.1 <sup>b-h</sup>
5	NC58	93.7 <sup>e-i</sup>	83.7 <sup>cde</sup>	92.0 <sup>l-o</sup>	89.8 <sup>k-q</sup>	94.3 <sup>e-m</sup>	85.0 <sup>b-i</sup>	92.3 <sup>no</sup>	90.6 <sup>l-t</sup>
6	Ashebeka	92.7 <sup>f-j</sup>	85.0 <sup>a-e</sup>	93.7 <sup>g-m</sup>	90.4 <sup>j-p</sup>	93.0 <sup>i-o</sup>	87.7 <sup>abc</sup>	97.0 <sup>c-i</sup>	92.6 <sup>d-j</sup>
7	Hachalu	94.3 <sup>c-h</sup>	84.0 <sup>cde</sup>	93.7 <sup>g-m</sup>	90.7 <sup>j-p</sup>	92.7 <sup>j-p</sup>	84.0 <sup>d-i</sup>	93.3 <sup>k-o</sup>	90.0 <sup>p-t</sup>
8	Degaga	89.0 <sup>kl</sup>	83.7 <sup>cde</sup>	90.7 <sup>mno</sup>	87.8 <sup>qr</sup>	91.0 <sup>n-r</sup>	84.7 <sup>b-i</sup>	94.3 <sup>i-n</sup>	90.0 <sup>p-t</sup>
9	EH09031-4	98.0 <sup>abc</sup>	87.7 <sup>a-d</sup>	97.3 <sup>b-f</sup>	94.3 <sup>a-d</sup>	95.7 <sup>a-k</sup>	88.7 <sup>a</sup>	98.7 <sup>b-e</sup>	94.3 <sup>bcd</sup>
10	Holetta-2	94.3 <sup>c-h</sup>	88.0 <sup>abc</sup>	96.7 <sup>b-h</sup>	93.0 <sup>b-i</sup>	96.0 <sup>a-j</sup>	84.3 <sup>c-i</sup>	97.0 <sup>c-i</sup>	92.4 <sup>e-k</sup>
11	EH09007-4	95.3 <sup>b-f</sup>	86.7 <sup>a-e</sup>	97.0 <sup>b-g</sup>	93.0 <sup>b-i</sup>	94.7 <sup>d-m</sup>	86.3 <sup>a-f</sup>	98.3 <sup>b-f</sup>	93.1 <sup>b-h</sup>
12	EH07023-3	96.7 <sup>a-e</sup>	86.3 <sup>a-e</sup>	101.3 <sup>a</sup>	94.8 <sup>abc</sup>	97.0 <sup>a-g</sup>	85.7 <sup>a-h</sup>	105.3 <sup>a</sup>	96.0 <sup>a</sup>
13	EK05006-3	96.3 <sup>a-f</sup>	88.7 <sup>ab</sup>	99.3 <sup>ab</sup>	94.8 <sup>abc</sup>	96.3 <sup>a-i</sup>	84.7 <sup>b-i</sup>	96.7 <sup>c-j</sup>	92.6 <sup>d-j</sup>
14	EK LS/CSR02014-2-4	98.3 <sup>ab</sup>	88.7 <sup>ab</sup>	99.0 <sup>abc</sup>	95.3 <sup>a</sup>	94.0 <sup>f-n</sup>	87.0 <sup>a-e</sup>	98.3 <sup>b-f</sup>	93.1 <sup>b-h</sup>
15	Numan	94.3 <sup>c-h</sup>	85.3 <sup>a-e</sup>	96.7 <sup>b-h</sup>	92.1 <sup>e-j</sup>	95.3 <sup>b-l</sup>	88.7 <sup>a</sup>	96.7 <sup>c-j</sup>	93.6 <sup>b-g</sup>
16	Bulga 70	93.7 <sup>e-i</sup>	85.7 <sup>a-e</sup>	93.0 <sup>i-n</sup>	90.8 <sup>j-o</sup>	94.33 <sup>e-m</sup>	83.7 <sup>e-i</sup>	95.0 <sup>h-n</sup>	91.0 <sup>i-r</sup>
17	EK05001-1	97.3 <sup>a-e</sup>	84.7 <sup>b-e</sup>	99.0 <sup>abc</sup>	93.7 <sup>a-g</sup>	96.3 <sup>a-i</sup>	84.0 <sup>d-i</sup>	95.0 <sup>h-n</sup>	91.8 <sup>g-p</sup>
18	Dosha	93.7 <sup>e-i</sup>	84.7 <sup>b-e</sup>	98.3 <sup>a-e</sup>	92.2 <sup>d-j</sup>	94.7 <sup>d-m</sup>	84.3 <sup>c-i</sup>	96.3 <sup>d-j</sup>	91.8 <sup>g-p</sup>
19	Gora	97.0 <sup>a-e</sup>	85.7 <sup>a-e</sup>	97.3 <sup>b-f</sup>	93.3 <sup>a-h</sup>	96.7 <sup>a-h</sup>	84.3 <sup>c-i</sup>	95.3 <sup>g-m</sup>	92.1 <sup>e-m</sup>
20	EH08035-1	94.0 <sup>d-h</sup>	86.3 <sup>a-e</sup>	96.3 <sup>b-i</sup>	92.2 <sup>d-j</sup>	95.0 <sup>c-m</sup>	83.3 <sup>f-i</sup>	96.7 <sup>c-j</sup>	91.7 <sup>h-q</sup>
21	Wayu	88.3 <sup>kl</sup>	84.3 <sup>b-e</sup>	89.0 <sup>o</sup>	87.2 <sup>r</sup>	88.3 <sup>f</sup>	83.7 <sup>e-i</sup>	91.0 <sup>o</sup>	87.7 <sup>v</sup>
22	EK LS/CSR02023-2-1	98.0 <sup>abc</sup>	87.7 <sup>a-d</sup>	96.7 <sup>b-h</sup>	94.1 <sup>a-e</sup>	99.00 <sup>a</sup>	84.0 <sup>d-i</sup>	98.3 <sup>b-f</sup>	93.8 <sup>b-e</sup>
23	Mesay	90.0 <sup>ijkl</sup>	86.0 <sup>a-e</sup>	92.7 <sup>j-n</sup>	89.6 <sup>l-q</sup>	92.3 <sup>k-p</sup>	84.7 <sup>b-i</sup>	95.3 <sup>g-m</sup>	90.8 <sup>j-s</sup>
24	EH09004-2	92.7 <sup>f-j</sup>	85.3 <sup>a-e</sup>	94.7 <sup>f-l</sup>	90.9 <sup>i-n</sup>	93.3 <sup>h-o</sup>	83.0 <sup>f-i</sup>	95.0 <sup>h-n</sup>	90.4 <sup>m-t</sup>
25	EH06088-6	97.3 <sup>a-e</sup>	85.3 <sup>a-e</sup>	97.3 <sup>b-f</sup>	93.3 <sup>a-h</sup>	96.0 <sup>a-j</sup>	84.3 <sup>c-i</sup>	98.3 <sup>b-f</sup>	92.9 <sup>c-h</sup>
	Mean	94.57b	85.55c	95.27a	91.8	94.59b	84.69c	96.34a	91.87

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6c. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	96.7 <sup>a-e</sup>	88.0 <sup>abc</sup>	95.0 <sup>e-l</sup>	93.2 <sup>a-h</sup>	96.0 <sup>a-j</sup>	84.0 <sup>d-i</sup>	99.3 <sup>bc</sup>	93.1 <sup>b-h</sup>
27	Kasa	91.3 <sup>g-k</sup>	85.7 <sup>a-e</sup>	90.3 <sup>no</sup>	89.1 <sup>m-r</sup>	93.3 <sup>h-o</sup>	83.7 <sup>e-i</sup>	92.7 <sup>mno</sup>	89.9 <sup>q-t</sup>
28	Cool-0025	95.3 <sup>b-f</sup>	83.3 <sup>de</sup>	95.3 <sup>d-l</sup>	91.3 <sup>h-l</sup>	93.7 <sup>g-n</sup>	83.3 <sup>f-i</sup>	95.0 <sup>h-n</sup>	90.7 <sup>k-s</sup>
29	EH06070-3	97.0 <sup>a-e</sup>	85.0 <sup>a-e</sup>	97.0 <sup>b-g</sup>	93.0 <sup>b-i</sup>	97.0 <sup>a-g</sup>	87.3 <sup>a-d</sup>	97.0 <sup>c-i</sup>	93.8 <sup>b-e</sup>
30	EK LS/CSR02010-4-3	97.3 <sup>a-e</sup>	85.3 <sup>a-e</sup>	97.0 <sup>b-g</sup>	93.2 <sup>a-h</sup>	98.0 <sup>a-d</sup>	84.0 <sup>d-i</sup>	97.7 <sup>c-h</sup>	93.2 <sup>b-h</sup>
31	Cool-0031	93.7 <sup>e-i</sup>	85.7 <sup>a-e</sup>	95.7 <sup>c-k</sup>	91.7 <sup>g-l</sup>	95.0 <sup>c-m</sup>	84.3 <sup>c-i</sup>	98.0 <sup>b-g</sup>	92.4 <sup>e-k</sup>
32	Cool-0018	91.0 <sup>h-k</sup>	85.0 <sup>a-e</sup>	93.7 <sup>g-m</sup>	89.9 <sup>k-q</sup>	91.0 <sup>n-r</sup>	84.7 <sup>b-i</sup>	95.0 <sup>h-n</sup>	90.2 <sup>n-t</sup>
33	EK LS/CSR02028-1-1	97.7 <sup>a-d</sup>	89.3 <sup>a</sup>	98.3 <sup>a-e</sup>	95.1 <sup>ab</sup>	98.3 <sup>abc</sup>	84.0 <sup>d-i</sup>	99.0 <sup>bcd</sup>	93.8 <sup>b-e</sup>
34	EK 05037-4	97.0 <sup>a-e</sup>	86.7 <sup>a-e</sup>	97.3 <sup>b-f</sup>	93.7 <sup>a-g</sup>	98.0 <sup>a-d</sup>	84.0 <sup>d-i</sup>	99.0 <sup>bcd</sup>	93.7 <sup>b-f</sup>
35	Cool-0035	94.7 <sup>b-g</sup>	85.0 <sup>a-e</sup>	94.7 <sup>f-l</sup>	91.4 <sup>g-l</sup>	92.0 <sup>l-q</sup>	82.7 <sup>ghi</sup>	94.0 <sup>j-n</sup>	89.6 <sup>r-u</sup>
36	KUSE2-27-33	95.0 <sup>b-f</sup>	86.0 <sup>a-e</sup>	92.3 <sup>k-n</sup>	91.1 <sup>h-m</sup>	89.7 <sup>pqr</sup>	82.7 <sup>ghi</sup>	94.3 <sup>i-n</sup>	88.9 <sup>tuv</sup>
37	EH07015-7	98.0 <sup>abc</sup>	88.0 <sup>abc</sup>	98.7 <sup>a-d</sup>	94.9 <sup>ab</sup>	98.7 <sup>ab</sup>	84.0 <sup>d-i</sup>	94.3 <sup>i-n</sup>	92.3 <sup>e-l</sup>
38	Cool-0024	95.0 <sup>b-f</sup>	86.0 <sup>a-e</sup>	94.7 <sup>f-l</sup>	91.9 <sup>f-k</sup>	94.3 <sup>e-m</sup>	84.0 <sup>d-i</sup>	94.3 <sup>i-n</sup>	90.9 <sup>j-s</sup>
39	Selale	95.7 <sup>b-f</sup>	85.3 <sup>a-e</sup>	90.7 <sup>mno</sup>	90.6 <sup>j-p</sup>	98.7 <sup>ab</sup>	84.7 <sup>b-i</sup>	92.3 <sup>no</sup>	91.9 <sup>f-o</sup>
40	Moti	93.7 <sup>e-i</sup>	84.0 <sup>cde</sup>	94.0 <sup>f-l</sup>	90.6 <sup>j-p</sup>	95.3 <sup>b-l</sup>	83.0 <sup>f-i</sup>	96.7 <sup>c-j</sup>	91.7 <sup>h-q</sup>
41	EH06027-2	96.0 <sup>a-f</sup>	84.3 <sup>b-e</sup>	95.3 <sup>d-l</sup>	91.9 <sup>f-k</sup>	95.3 <sup>b-l</sup>	86.3 <sup>a-f</sup>	96.7 <sup>c-j</sup>	92.8 <sup>c-i</sup>
42	EK LS/CSR02019-2-4	99.7 <sup>a</sup>	86.7 <sup>a-e</sup>	97.3 <sup>b-f</sup>	94.6 <sup>abc</sup>	97.7 <sup>a-e</sup>	85.0 <sup>b-i</sup>	100.7 <sup>b</sup>	94.44 <sup>bc</sup>
43	EH09002-1	95.7 <sup>b-f</sup>	86.3 <sup>a-e</sup>	95.0 <sup>e-l</sup>	92.3 <sup>d-j</sup>	95.7 <sup>a-k</sup>	85.3 <sup>b-i</sup>	96.7 <sup>c-j</sup>	92.6 <sup>d-j</sup>
44	Tumsa	90.3 <sup>i-l</sup>	83.0 <sup>e</sup>	96.0 <sup>b-j</sup>	89.8 <sup>k-q</sup>	93.7 <sup>g-n</sup>	85.0 <sup>b-i</sup>	96.3 <sup>d-j</sup>	91.7 <sup>h-q</sup>
45	Gebelcho	87.3 <sup>l</sup>	84.3 <sup>b-e</sup>	94.3 <sup>f-l</sup>	88.7 <sup>o-r</sup>	90.3 <sup>o-r</sup>	83.7 <sup>e-i</sup>	96.3 <sup>d-j</sup>	90.1 <sup>o-t</sup>
46	EK05037-5	96.7 <sup>a-e</sup>	85.0 <sup>a-e</sup>	92.7 <sup>j-n</sup>	91.4 <sup>g-l</sup>	93.7 <sup>g-n</sup>	85.7 <sup>a-h</sup>	96.0 <sup>e-k</sup>	91.8 <sup>g-p</sup>
47	Didi'a	95.3 <sup>b-f</sup>	83.3 <sup>de</sup>	95.7 <sup>c-k</sup>	91.4 <sup>g-l</sup>	95.0 <sup>c-m</sup>	85.3 <sup>b-i</sup>	95.7 <sup>f-k</sup>	92.0 <sup>e-n</sup>
48	Cool-0034	94.0 <sup>d-h</sup>	84.3 <sup>b-e</sup>	94.7 <sup>f-l</sup>	91.0 <sup>i-n</sup>	95.0 <sup>c-m</sup>	84.7 <sup>b-i</sup>	98.7 <sup>b-e</sup>	92.8 <sup>c-i</sup>
49	CS20DK	91.0 <sup>h-k</sup>	82.7 <sup>e</sup>	92.0 <sup>l-o</sup>	88.6 <sup>pqr</sup>	89.0 <sup>qr</sup>	82.0 <sup>i</sup>	96.3 <sup>d-j</sup>	89.1 <sup>s-v</sup>
50	Tesfa	89.7 <sup>jkl</sup>	85.0 <sup>a-e</sup>	92.0 <sup>l-o</sup>	88.9 <sup>n-r</sup>	89.0 <sup>qr</sup>	82.3 <sup>hi</sup>	93.0 <sup>l-o</sup>	88.1 <sup>uv</sup>
	Mean	94.57b	85.55c	95.27a	91.8	94.59b	84.69c	96.34a	91.87

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6d. Mean performance of 50 faba bean genotypes for plant height

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	152.3 <sup>a-g</sup>	121.3 <sup>b-l</sup>	62.7 <sup>a-f</sup>	112.1 <sup>b-l</sup>	160.7 <sup>a-h</sup>	133.0 <sup>no</sup>	89.3 <sup>bc</sup>	127.7 <sup>c-m</sup>
2	Wolki	152.0 <sup>a-g</sup>	124.7 <sup>a-j</sup>	65.3 <sup>a-f</sup>	114.0 <sup>a-h</sup>	164.7 <sup>a-f</sup>	142.0 <sup>c-n</sup>	83.3 <sup>b-f</sup>	130.0 <sup>b-k</sup>
3	EK LS/CSR02012-2-3	152.0 <sup>a-g</sup>	131.3 <sup>abc</sup>	68.7 <sup>a-e</sup>	117.3 <sup>ab</sup>	166.0 <sup>a-f</sup>	134.0 <sup>mno</sup>	86.0 <sup>b-f</sup>	128.7 <sup>b-l</sup>
4	Obse	155.3 <sup>a-d</sup>	128.3 <sup>a-g</sup>	73.3 <sup>ab</sup>	119.0 <sup>a</sup>	168.7 <sup>a</sup>	137.7 <sup>h-o</sup>	90.3 <sup>bc</sup>	132.2 <sup>a-g</sup>
5	NC58	149.3 <sup>a-i</sup>	131.7 <sup>ab</sup>	66.0 <sup>a-f</sup>	115.7 <sup>a-e</sup>	166.7 <sup>a-e</sup>	146.7 <sup>a-j</sup>	77.7 <sup>e-k</sup>	130.3 <sup>b-j</sup>
6	Ashebeka	160.3 <sup>a</sup>	128.0 <sup>a-g</sup>	68.3 <sup>a-e</sup>	118.9 <sup>a</sup>	167.7 <sup>abc</sup>	142.3 <sup>b-n</sup>	93.7 <sup>b</sup>	134.6 <sup>abc</sup>
7	Hachalu	158.3 <sup>ab</sup>	130.0 <sup>a-e</sup>	68.3 <sup>a-e</sup>	118.9 <sup>a</sup>	163.7 <sup>a-g</sup>	150.7 <sup>a-d</sup>	83.3 <sup>b-f</sup>	132.6 <sup>a-e</sup>
8	Degaga	145.0 <sup>d-j</sup>	109.7 <sup>nop</sup>	64.0 <sup>a-f</sup>	106.2 <sup>k-p</sup>	161.3 <sup>a-h</sup>	139.7 <sup>e-o</sup>	80.7 <sup>c-j</sup>	127.2 <sup>d-m</sup>
9	EH09031-4	146.0 <sup>c-i</sup>	114.7 <sup>i-p</sup>	61.0 <sup>c-f</sup>	107.2 <sup>i-o</sup>	158.0 <sup>a-h</sup>	135.0 <sup>l-o</sup>	80.7 <sup>c-j</sup>	124.6 <sup>h-o</sup>
10	Holetta-2	142.3 <sup>f-j</sup>	110.3 <sup>m-p</sup>	67.7 <sup>a-f</sup>	106.8 <sup>j-p</sup>	152.3 <sup>fgh</sup>	137.3 <sup>h-o</sup>	70.7 <sup>ijk</sup>	120.1 <sup>no</sup>
11	EH09007-4	139.0 <sup>ij</sup>	110.0 <sup>nop</sup>	63.0 <sup>a-f</sup>	104.0 <sup>nop</sup>	157.3 <sup>a-h</sup>	130.3 <sup>o</sup>	82.0 <sup>c-g</sup>	123.2 <sup>k-o</sup>
12	EH07023-3	145.0 <sup>d-j</sup>	122.7 <sup>b-k</sup>	73.3 <sup>ab</sup>	113.7 <sup>a-i</sup>	164.3 <sup>a-f</sup>	142.7 <sup>b-n</sup>	104.3 <sup>a</sup>	137.1 <sup>a</sup>
13	EK05006-3	154.7 <sup>a-d</sup>	108.0 <sup>op</sup>	65.3 <sup>a-f</sup>	109.3 <sup>d-o</sup>	158.0 <sup>a-h</sup>	137.3 <sup>h-o</sup>	93.7 <sup>b</sup>	129.7 <sup>b-k</sup>
14	EK LS/CSR02014-2-4	144.0 <sup>d-j</sup>	128.0 <sup>a-g</sup>	61.7 <sup>b-f</sup>	111.2 <sup>b-m</sup>	155.3 <sup>a-h</sup>	148.0 <sup>a-h</sup>	82.7 <sup>c-f</sup>	128.7 <sup>b-l</sup>
15	Numan	154.0 <sup>a-e</sup>	119.3 <sup>e-n</sup>	70.0 <sup>a-d</sup>	114.4 <sup>a-g</sup>	155.3 <sup>a-h</sup>	138.0 <sup>g-o</sup>	89.0 <sup>bcd</sup>	127.4 <sup>d-m</sup>
16	Bulga 70	145.3 <sup>c-j</sup>	128.3 <sup>a-g</sup>	57.7 <sup>ef</sup>	110.4 <sup>c-n</sup>	157.0 <sup>a-h</sup>	142.7 <sup>b-n</sup>	76.7 <sup>e-k</sup>	125.4 <sup>f-o</sup>
17	EK05001-1	148.7 <sup>b-i</sup>	127.7 <sup>a-g</sup>	65.0 <sup>a-f</sup>	113.8 <sup>a-i</sup>	159.0 <sup>a-h</sup>	142.7 <sup>b-n</sup>	87.0 <sup>b-e</sup>	129.6 <sup>b-k</sup>
18	Dosha	156.7 <sup>abc</sup>	125.3 <sup>a-j</sup>	74.3 <sup>a</sup>	118.8 <sup>a</sup>	161.7 <sup>a-h</sup>	146.7 <sup>a-j</sup>	81.7 <sup>c-h</sup>	130.0 <sup>b-k</sup>
19	Gora	146.3 <sup>c-i</sup>	131.7 <sup>ab</sup>	65.7 <sup>a-f</sup>	114.6 <sup>a-f</sup>	159.0 <sup>a-h</sup>	147.7 <sup>a-h</sup>	87.0 <sup>b-e</sup>	131.2 <sup>a-h</sup>
20	EH08035-1	141.0 <sup>g-j</sup>	120.3 <sup>c-n</sup>	56.3 <sup>f</sup>	105.9 <sup>l-p</sup>	154.3 <sup>b-h</sup>	139.3 <sup>f-o</sup>	79.7 <sup>c-j</sup>	124.4 <sup>h-o</sup>
21	Wayu	134.3 <sup>j</sup>	121.0 <sup>b-m</sup>	47.0 <sup>g</sup>	100.8 <sup>p</sup>	149.0 <sup>h</sup>	140.3 <sup>d-o</sup>	67.7 <sup>k</sup>	119.0 <sup>o</sup>
22	EK LS/CSR02023-2-1	146.3 <sup>c-i</sup>	117.7 <sup>g-o</sup>	63.3 <sup>a-f</sup>	109.1 <sup>e-o</sup>	162.3 <sup>a-h</sup>	146.3 <sup>a-k</sup>	84.7 <sup>b-f</sup>	131.1 <sup>a-h</sup>
23	Mesay	142.3 <sup>f-j</sup>	126.3 <sup>a-h</sup>	64.7 <sup>a-f</sup>	111.1 <sup>b-m</sup>	160.0 <sup>a-h</sup>	148.7 <sup>a-g</sup>	77.7 <sup>e-k</sup>	128.8 <sup>b-l</sup>
24	EH09004-2	149.3 <sup>a-i</sup>	121.0 <sup>b-m</sup>	57.0 <sup>ef</sup>	109.1 <sup>e-o</sup>	152.7 <sup>e-h</sup>	141.7 <sup>c-n</sup>	76.7 <sup>e-k</sup>	123.7 <sup>j-o</sup>
25	EH06088-6	140.0 <sup>h-j</sup>	118.0 <sup>f-o</sup>	60.7 <sup>c-f</sup>	106.2 <sup>k-p</sup>	149.3 <sup>h</sup>	136.0 <sup>j-o</sup>	81.7 <sup>c-h</sup>	122.3 <sup>l-o</sup>
	Mean	148.3a	121.3b	64.1c	111.2	159.6a	142.3b	82.6c	128.2

Mean values followed by similar letter(s) in each column had nonsignificant difference at  $P < 0.05$

Appendix Table 6d. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	147.0 <sup>b-i</sup>	111.0 <sup>l-p</sup>	63.0 <sup>a-f</sup>	107.0 <sup>j-p</sup>	164.7 <sup>a-f</sup>	142.0 <sup>c-n</sup>	85.0 <sup>b-f</sup>	130.6 <sup>a-j</sup>
27	Kasa	142.0 <sup>f-j</sup>	127.7 <sup>a-g</sup>	60.0 <sup>c-f</sup>	109.9 <sup>c-o</sup>	164.7 <sup>a-f</sup>	140.7 <sup>d-o</sup>	71.7 <sup>g-k</sup>	125.7 <sup>e-n</sup>
28	Cool-0025	158.3 <sup>ab</sup>	118.3 <sup>f-o</sup>	65.7 <sup>a-f</sup>	114.1 <sup>a-h</sup>	164.7 <sup>a-f</sup>	144.0 <sup>a-m</sup>	81.3 <sup>c-h</sup>	130.0 <sup>b-k</sup>
29	EH06070-3	149.3 <sup>a-i</sup>	108.3 <sup>op</sup>	67.7 <sup>a-f</sup>	108.4 <sup>f-o</sup>	158.3 <sup>a-h</sup>	133.3 <sup>mno</sup>	81.3 <sup>c-h</sup>	124.3 <sup>h-o</sup>
30	EK LS/CSR02010-4-3	152.0 <sup>a-g</sup>	124.3 <sup>a-j</sup>	61.7 <sup>b-f</sup>	112.7 <sup>a-k</sup>	166.7 <sup>a-e</sup>	147.3 <sup>a-i</sup>	83.0 <sup>b-f</sup>	132.3 <sup>a-f</sup>
31	Cool-0031	145.7 <sup>c-i</sup>	130.7 <sup>a-d</sup>	67.7 <sup>a-f</sup>	114.7 <sup>a-f</sup>	159.0 <sup>a-h</sup>	147.0 <sup>a-i</sup>	84.3 <sup>b-f</sup>	130.1 <sup>b-k</sup>
32	Cool-0018	149.7 <sup>a-i</sup>	115.7 <sup>h-o</sup>	60.0 <sup>c-f</sup>	108.4 <sup>f-o</sup>	168.3 <sup>ab</sup>	140.3 <sup>d-o</sup>	85.0 <sup>b-f</sup>	131.2 <sup>a-h</sup>
33	EK LS/CSR02028-1-1	147.0 <sup>b-i</sup>	114.3 <sup>j-p</sup>	59.3 <sup>def</sup>	106.9 <sup>j-p</sup>	161.3 <sup>a-h</sup>	130.7 <sup>o</sup>	86.7 <sup>b-e</sup>	126.2 <sup>d-n</sup>
34	EK 05037-4	151.3 <sup>a-h</sup>	124.0 <sup>b-k</sup>	64.3 <sup>a-f</sup>	112.9 <sup>a-j</sup>	165.3 <sup>a-f</sup>	146.3 <sup>a-k</sup>	86.3 <sup>b-e</sup>	132.7 <sup>a-d</sup>
35	Cool-0035	152.3 <sup>a-g</sup>	120.3 <sup>c-n</sup>	66.3 <sup>a-f</sup>	113.0 <sup>a-j</sup>	159.3 <sup>a-h</sup>	145.7 <sup>a-l</sup>	84.7 <sup>b-f</sup>	129.9 <sup>b-k</sup>
36	KUSE2-27-33	153.3 <sup>a-f</sup>	110.0 <sup>nop</sup>	60.3 <sup>c-f</sup>	107.9 <sup>g-o</sup>	164.0 <sup>a-g</sup>	135.7 <sup>k-o</sup>	83.0 <sup>b-f</sup>	127.6 <sup>d-m</sup>
37	EH07015-7	150.0 <sup>a-i</sup>	119.7 <sup>d-n</sup>	71.3 <sup>abc</sup>	113.7 <sup>a-i</sup>	163.0 <sup>a-h</sup>	138.0 <sup>g-o</sup>	82.3 <sup>c-f</sup>	127.8 <sup>c-m</sup>
38	Cool-0024	151.0 <sup>a-h</sup>	128.7 <sup>a-g</sup>	63.7 <sup>a-f</sup>	114.4 <sup>a-g</sup>	163.0 <sup>a-h</sup>	149.0 <sup>a-f</sup>	81.3 <sup>c-h</sup>	131.1 <sup>a-h</sup>
39	Selale	145.3 <sup>c-j</sup>	104.7 <sup>p</sup>	62.3 <sup>b-f</sup>	104.1 <sup>nop</sup>	153.3 <sup>d-h</sup>	139.0 <sup>f-o</sup>	71.3 <sup>h-k</sup>	121.2 <sup>mno</sup>
40	Moti	155.3 <sup>a-d</sup>	126.3 <sup>a-h</sup>	66.0 <sup>a-f</sup>	115.9 <sup>a-d</sup>	159.0 <sup>a-h</sup>	147.7 <sup>a-h</sup>	85.7 <sup>b-f</sup>	130.8 <sup>a-i</sup>
41	EH06027-2	146.0 <sup>c-i</sup>	125.7 <sup>a-i</sup>	63.0 <sup>a-f</sup>	111.6 <sup>b-m</sup>	160.7 <sup>a-h</sup>	153.7 <sup>a</sup>	81.0 <sup>c-i</sup>	131.8 <sup>a-g</sup>
42	EK LS/CSR02019-2-4	150.7 <sup>a-h</sup>	124.0 <sup>b-k</sup>	66.7 <sup>a-f</sup>	113.8 <sup>a-i</sup>	167.0 <sup>a-d</sup>	152.0 <sup>abc</sup>	86.7 <sup>b-e</sup>	135.2 <sup>ab</sup>
43	EH09002-1	144.3 <sup>d-j</sup>	113.3 <sup>k-p</sup>	59.0 <sup>def</sup>	105.6 <sup>m-p</sup>	153.0 <sup>d-h</sup>	136.7 <sup>i-o</sup>	84.7 <sup>b-f</sup>	124.8 <sup>h-o</sup>
44	Tumsa	150.0 <sup>a-i</sup>	120.0 <sup>d-n</sup>	68.0 <sup>a-f</sup>	112.7 <sup>a-k</sup>	159.0 <sup>a-h</sup>	140.0 <sup>d-o</sup>	89.0 <sup>bcd</sup>	129.3 <sup>b-k</sup>
45	Gebelcho	147.3 <sup>b-i</sup>	124.7 <sup>a-j</sup>	66.3 <sup>a-f</sup>	112.8 <sup>a-j</sup>	154.7 <sup>a-h</sup>	152.3 <sup>abc</sup>	83.7 <sup>b-f</sup>	130.2 <sup>b-j</sup>
46	EK05037-5	144.0 <sup>d-j</sup>	118.3 <sup>f-o</sup>	60.3 <sup>c-f</sup>	107.8 <sup>h-o</sup>	154.0 <sup>c-h</sup>	142.3 <sup>b-n</sup>	75.3 <sup>f-k</sup>	123.9 <sup>i-o</sup>
47	Didi'a	153.0 <sup>a-f</sup>	135.3 <sup>a</sup>	61.0 <sup>c-f</sup>	116.4 <sup>abc</sup>	155.3 <sup>a-h</sup>	153.0 <sup>ab</sup>	84.7 <sup>b-f</sup>	131.0 <sup>a-h</sup>
48	Cool-0034	147.7 <sup>b-i</sup>	129.0 <sup>a-f</sup>	63.0 <sup>a-f</sup>	113.2 <sup>a-j</sup>	153.0 <sup>d-h</sup>	150.3 <sup>a-e</sup>	78.3 <sup>d-j</sup>	127.2 <sup>d-m</sup>
49	CS20DK	142.0 <sup>e-j</sup>	126.3 <sup>a-h</sup>	67.3 <sup>a-f</sup>	112.1 <sup>b-l</sup>	150.0 <sup>gh</sup>	142.3 <sup>b-n</sup>	83.7 <sup>b-f</sup>	125.3 <sup>g-o</sup>
50	Tesfa	138.7 <sup>ij</sup>	110.0 <sup>nop</sup>	61.7 <sup>b-f</sup>	103.4 <sup>op</sup>	153.7 <sup>c-h</sup>	136.7 <sup>i-o</sup>	70.3 <sup>jk</sup>	120.2 <sup>no</sup>
	Mean	148.3a	121.3b	64.1c	111.2	159.6a	142.3b	82.6c	128.2

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6e. Mean performance of 50 faba bean genotypes for number of podding node per plant

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	6.7 <sup>c-f</sup>	6.7 <sup>e-i</sup>	4.7 <sup>b-e</sup>	6.0 <sup>i-p</sup>	7.3 <sup>b-f</sup>	9.7 <sup>a-f</sup>	8.7 <sup>abc</sup>	8.6 <sup>a-g</sup>
2	Wolki	8.3 <sup>abc</sup>	9.7 <sup>ab</sup>	5.3 <sup>b-e</sup>	7.8 <sup>abc</sup>	9.7 <sup>a</sup>	11.0 <sup>ab</sup>	8.0 <sup>a-e</sup>	9.6 <sup>a</sup>
3	EK LS/CSR02012-2-3	6.7 <sup>c-f</sup>	6.7 <sup>e-i</sup>	4.7 <sup>b-e</sup>	6.0 <sup>i-p</sup>	7.0 <sup>c-f</sup>	7.3 <sup>gh</sup>	7.7 <sup>a-f</sup>	7.3 <sup>h-l</sup>
4	Obse	7.0 <sup>b-f</sup>	6.0 <sup>ghi</sup>	6.3 <sup>ab</sup>	6.4 <sup>e-m</sup>	6.7 <sup>def</sup>	7.7 <sup>fgh</sup>	7.0 <sup>c-h</sup>	7.1 <sup>i-l</sup>
5	NC58	8.0 <sup>a-d</sup>	9.7 <sup>ab</sup>	7.3 <sup>a</sup>	8.3 <sup>a</sup>	8.3 <sup>a-e</sup>	11.3 <sup>a</sup>	7.7 <sup>a-f</sup>	9.1 <sup>ab</sup>
6	Ashebeka	8.0 <sup>a-d</sup>	7.0 <sup>d-i</sup>	5.7 <sup>a-d</sup>	6.9 <sup>c-j</sup>	7.7 <sup>a-f</sup>	9.0 <sup>b-g</sup>	7.7 <sup>a-f</sup>	8.1 <sup>b-i</sup>
7	Hachalu	7.3 <sup>a-f</sup>	7.3 <sup>c-h</sup>	6.0 <sup>abc</sup>	6.9 <sup>c-j</sup>	8.0 <sup>a-f</sup>	9.0 <sup>b-g</sup>	7.0 <sup>c-h</sup>	8.0 <sup>b-j</sup>
8	Degaga	9.0 <sup>a</sup>	8.0 <sup>b-f</sup>	5.7 <sup>a-d</sup>	7.6 <sup>a-d</sup>	9.0 <sup>abc</sup>	10.0 <sup>a-e</sup>	8.7 <sup>abc</sup>	9.2 <sup>a</sup>
9	EH09031-4	6.7 <sup>c-f</sup>	5.3 <sup>i</sup>	3.7 <sup>e</sup>	5.2 <sup>op</sup>	7.7 <sup>a-f</sup>	7.7 <sup>fgh</sup>	4.7 <sup>i</sup>	6.7 <sup>kl</sup>
10	Holetta-2	6.7 <sup>c-f</sup>	6.0 <sup>ghi</sup>	5.7 <sup>a-d</sup>	6.1 <sup>h-p</sup>	7.3 <sup>b-f</sup>	9.0 <sup>b-g</sup>	7.3 <sup>b-g</sup>	7.9 <sup>c-j</sup>
11	EH09007-4	6.0 <sup>ef</sup>	5.7 <sup>hi</sup>	3.7 <sup>e</sup>	5.1 <sup>p</sup>	6.7 <sup>def</sup>	8.0 <sup>e-h</sup>	5.3 <sup>hi</sup>	6.7 <sup>kl</sup>
12	EH07023-3	6.3 <sup>def</sup>	6.0 <sup>ghi</sup>	4.7 <sup>b-e</sup>	5.7 <sup>k-p</sup>	8.3 <sup>a-e</sup>	8.0 <sup>e-h</sup>	6.7 <sup>d-h</sup>	7.7 <sup>e-l</sup>
13	EK05006-3	7.3 <sup>a-f</sup>	6.0 <sup>ghi</sup>	5.3 <sup>b-e</sup>	6.2 <sup>g-o</sup>	7.0 <sup>c-f</sup>	9.3 <sup>a-g</sup>	7.7 <sup>a-f</sup>	8.0 <sup>b-j</sup>
14	EK LS/CSR02014-2-4	6.0 <sup>ef</sup>	7.0 <sup>d-i</sup>	5.0 <sup>b-e</sup>	6.0 <sup>i-p</sup>	7.0 <sup>c-f</sup>	7.7 <sup>fgh</sup>	7.0 <sup>c-h</sup>	7.2 <sup>i-l</sup>
15	Numan	6.3 <sup>def</sup>	5.7 <sup>hi</sup>	4.0 <sup>de</sup>	5.3 <sup>nop</sup>	6.7 <sup>def</sup>	6.7 <sup>h</sup>	6.3 <sup>e-h</sup>	6.6 <sup>l</sup>
16	Bulga 70	7.7 <sup>a-e</sup>	9.0 <sup>abc</sup>	4.7 <sup>b-e</sup>	7.1 <sup>b-h</sup>	8.0 <sup>a-f</sup>	10.3 <sup>a-d</sup>	8.3 <sup>a-d</sup>	8.9 <sup>a-d</sup>
17	EK05001-1	6.7 <sup>c-f</sup>	8.0 <sup>b-f</sup>	5.3 <sup>b-e</sup>	6.7 <sup>d-k</sup>	7.7 <sup>a-f</sup>	7.7 <sup>fgh</sup>	8.7 <sup>abc</sup>	8.0 <sup>b-j</sup>
18	Dosha	7.3 <sup>a-f</sup>	7.3 <sup>c-h</sup>	6.3 <sup>ab</sup>	7.0 <sup>b-i</sup>	8.3 <sup>a-e</sup>	9.7 <sup>a-f</sup>	8.0 <sup>a-e</sup>	8.7 <sup>a-f</sup>
19	Gora	5.7 <sup>f</sup>	7.0 <sup>d-i</sup>	5.3 <sup>b-e</sup>	6.0 <sup>i-p</sup>	6.0 <sup>f</sup>	8.7 <sup>c-h</sup>	6.3 <sup>e-h</sup>	7.0 <sup>i-l</sup>
20	EH08035-1	6.3 <sup>def</sup>	6.0 <sup>ghi</sup>	4.0 <sup>de</sup>	5.4 <sup>m-p</sup>	7.7 <sup>a-f</sup>	9.0 <sup>b-g</sup>	7.3 <sup>b-g</sup>	8.0 <sup>b-j</sup>
21	Wayu	6.7 <sup>c-f</sup>	8.0 <sup>b-f</sup>	4.7 <sup>b-e</sup>	6.4 <sup>e-m</sup>	8.0 <sup>a-f</sup>	9.3 <sup>a-g</sup>	6.3 <sup>e-h</sup>	7.9 <sup>c-j</sup>
22	EK LS/CSR02023-2-1	6.0 <sup>ef</sup>	7.0 <sup>d-i</sup>	4.0 <sup>de</sup>	5.7 <sup>k-p</sup>	7.7 <sup>a-f</sup>	7.7 <sup>fgh</sup>	6.7 <sup>d-h</sup>	7.3 <sup>h-l</sup>
23	Mesay	7.3 <sup>a-f</sup>	8.7 <sup>a-d</sup>	6.0 <sup>abc</sup>	7.3 <sup>b-f</sup>	9.3 <sup>ab</sup>	9.7 <sup>a-f</sup>	8.0 <sup>a-e</sup>	9.0 <sup>abc</sup>
24	EH09004-2	7.3 <sup>a-f</sup>	7.3 <sup>c-h</sup>	3.7 <sup>e</sup>	6.1 <sup>h-p</sup>	7.7 <sup>a-f</sup>	9.3 <sup>a-g</sup>	7.3 <sup>b-g</sup>	8.1 <sup>b-i</sup>
25	EH06088-6	5.7 <sup>f</sup>	6.3 <sup>f-i</sup>	4.7 <sup>b-e</sup>	5.6 <sup>l-p</sup>	8.3 <sup>a-e</sup>	8.0 <sup>e-h</sup>	6.7 <sup>d-h</sup>	7.7 <sup>e-l</sup>
	Mean	7.0 <sup>b</sup>	7.5 <sup>a</sup>	5.1 <sup>c</sup>	6.5	7.9 <sup>b</sup>	9.0 <sup>a</sup>	7.4 <sup>c</sup>	8.1

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6e. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	6.0 <sup>ef</sup>	6.3 <sup>f-i</sup>	4.0 <sup>de</sup>	5.4 <sup>m-p</sup>	6.3 <sup>ef</sup>	9.0 <sup>b-g</sup>	7.0 <sup>c-h</sup>	7.4 <sup>g-l</sup>
27	Kasa	7.3 <sup>a-f</sup>	9.0 <sup>abc</sup>	6.0 <sup>abc</sup>	7.4 <sup>a-e</sup>	9.0 <sup>abc</sup>	9.3 <sup>a-g</sup>	7.0 <sup>c-h</sup>	8.4 <sup>a-h</sup>
28	Cool-0025	7.7 <sup>a-e</sup>	7.3 <sup>c-h</sup>	6.0 <sup>abc</sup>	7.0 <sup>b-i</sup>	8.0 <sup>a-f</sup>	9.3 <sup>a-g</sup>	8.0 <sup>a-e</sup>	8.4 <sup>a-h</sup>
29	EH06070-3	6.0 <sup>ef</sup>	6.7 <sup>e-i</sup>	4.0 <sup>de</sup>	5.6 <sup>l-p</sup>	6.7 <sup>def</sup>	7.3 <sup>gh</sup>	6.7 <sup>d-h</sup>	6.9 <sup>jkl</sup>
30	EK LS/CSR02010-4-3	6.0 <sup>ef</sup>	7.3 <sup>c-h</sup>	4.3 <sup>cde</sup>	5.9 <sup>j-p</sup>	6.3 <sup>ef</sup>	8.0 <sup>e-h</sup>	7.3 <sup>b-g</sup>	7.2 <sup>i-l</sup>
31	Cool-0031	6.7 <sup>c-f</sup>	8.0 <sup>b-f</sup>	5.0 <sup>b-e</sup>	6.6 <sup>d-l</sup>	9.0 <sup>abc</sup>	9.3 <sup>a-g</sup>	8.7 <sup>abc</sup>	9.0 <sup>abc</sup>
32	Cool-0018	8.0 <sup>a-d</sup>	7.7 <sup>c-g</sup>	6.0 <sup>abc</sup>	7.2 <sup>b-g</sup>	8.7 <sup>a-d</sup>	9.3 <sup>a-g</sup>	9.3 <sup>a</sup>	9.1 <sup>ab</sup>
33	EK LS/CSR02028-1-1	7.3 <sup>a-f</sup>	6.7 <sup>e-i</sup>	4.3 <sup>cde</sup>	6.1 <sup>h-p</sup>	7.0 <sup>c-f</sup>	8.0 <sup>e-h</sup>	7.0 <sup>c-h</sup>	7.3 <sup>h-l</sup>
34	EK 05037-4	7.0 <sup>b-f</sup>	8.3 <sup>a-e</sup>	6.0 <sup>abc</sup>	7.1 <sup>b-h</sup>	9.0 <sup>abc</sup>	9.0 <sup>b-g</sup>	8.3 <sup>a-d</sup>	8.8 <sup>a-e</sup>
35	Cool-0035	7.0 <sup>b-f</sup>	9.0 <sup>abc</sup>	6.0 <sup>abc</sup>	7.3 <sup>b-f</sup>	9.0 <sup>abc</sup>	10.7 <sup>abc</sup>	8.3 <sup>a-d</sup>	9.3 <sup>a</sup>
36	KUSE2-27-33	8.3 <sup>abc</sup>	8.7 <sup>a-d</sup>	5.7 <sup>a-d</sup>	7.6 <sup>a-d</sup>	9.0 <sup>abc</sup>	10.3 <sup>a-d</sup>	9.3 <sup>a</sup>	9.6 <sup>a</sup>
37	EH07015-7	7.3 <sup>a-f</sup>	7.3 <sup>c-h</sup>	4.3 <sup>cde</sup>	6.3 <sup>f-n</sup>	8.0 <sup>a-f</sup>	7.3 <sup>gh</sup>	7.3 <sup>b-g</sup>	7.6 <sup>f-l</sup>
38	Cool-0024	8.0 <sup>a-d</sup>	10.0 <sup>a</sup>	6.0 <sup>abc</sup>	8.0 <sup>ab</sup>	9.3 <sup>ab</sup>	10.3 <sup>a-d</sup>	9.0 <sup>ab</sup>	9.6 <sup>a</sup>
39	Selale	7.3 <sup>a-f</sup>	9.0 <sup>abc</sup>	5.0 <sup>b-e</sup>	7.1 <sup>b-h</sup>	7.0 <sup>c-f</sup>	9.3 <sup>a-g</sup>	7.0 <sup>c-h</sup>	7.8 <sup>d-k</sup>
40	Moti	8.3 <sup>abc</sup>	8.3 <sup>a-e</sup>	5.3 <sup>b-e</sup>	7.3 <sup>b-f</sup>	8.0 <sup>a-f</sup>	9.7 <sup>a-f</sup>	7.7 <sup>a-f</sup>	8.4 <sup>a-h</sup>
41	EH06027-2	6.7 <sup>c-f</sup>	6.7 <sup>e-i</sup>	4.7 <sup>b-e</sup>	6.0 <sup>i-p</sup>	7.0 <sup>c-f</sup>	9.3 <sup>a-g</sup>	6.0 <sup>f-i</sup>	7.4 <sup>g-l</sup>
42	EK LS/CSR02019-2-4	6.3 <sup>def</sup>	7.0 <sup>d-i</sup>	5.0 <sup>b-e</sup>	6.1 <sup>h-p</sup>	8.0 <sup>a-f</sup>	8.3 <sup>d-h</sup>	7.7 <sup>a-f</sup>	8.0 <sup>b-j</sup>
43	EH09002-1	6.7 <sup>c-f</sup>	7.0 <sup>d-i</sup>	4.3 <sup>cde</sup>	6.0 <sup>i-p</sup>	7.3 <sup>b-f</sup>	9.0 <sup>b-g</sup>	7.3 <sup>b-g</sup>	7.9 <sup>c-j</sup>
44	Tumsa	7.0 <sup>b-f</sup>	8.0 <sup>b-f</sup>	5.7 <sup>a-d</sup>	6.9 <sup>c-j</sup>	8.7 <sup>a-d</sup>	8.7 <sup>c-h</sup>	6.7 <sup>d-h</sup>	8.0 <sup>b-j</sup>
45	Gebelcho	7.0 <sup>b-f</sup>	7.3 <sup>c-h</sup>	4.3 <sup>cde</sup>	6.2 <sup>g-o</sup>	7.7 <sup>a-f</sup>	8.7 <sup>c-h</sup>	5.7 <sup>ghi</sup>	7.3 <sup>h-l</sup>
46	EK05037-5	6.0 <sup>ef</sup>	7.3 <sup>c-h</sup>	3.7 <sup>e</sup>	5.7 <sup>k-p</sup>	7.3 <sup>b-f</sup>	9.0 <sup>b-g</sup>	6.7 <sup>d-h</sup>	7.7 <sup>e-l</sup>
47	Didi'a	7.3 <sup>a-f</sup>	8.0 <sup>b-f</sup>	4.7 <sup>b-e</sup>	6.7 <sup>d-k</sup>	7.3 <sup>b-f</sup>	9.7 <sup>a-f</sup>	6.7 <sup>d-h</sup>	7.9 <sup>c-j</sup>
48	Cool-0034	7.3 <sup>a-f</sup>	9.0 <sup>abc</sup>	6.0 <sup>abc</sup>	7.4 <sup>a-e</sup>	8.3 <sup>a-e</sup>	9.3 <sup>a-g</sup>	8.3 <sup>a-d</sup>	8.7 <sup>a-f</sup>
49	CS20DK	8.7 <sup>ab</sup>	9.0 <sup>abc</sup>	6.3 <sup>ab</sup>	8.0 <sup>ab</sup>	9.7 <sup>a</sup>	10.3 <sup>a-d</sup>	8.0 <sup>a-e</sup>	9.3 <sup>a</sup>
50	Tesfa	7.0 <sup>b-f</sup>	8.3 <sup>a-e</sup>	5.7 <sup>a-d</sup>	7.0 <sup>b-i</sup>	9.0 <sup>abc</sup>	9.7 <sup>a-f</sup>	7.0 <sup>c-h</sup>	8.6 <sup>a-g</sup>
	Mean	7.0b	7.5a	5.1c	6.5	7.9b	9.0a	7.4c	8.1

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6f. Mean performance of 50 faba bean genotypes for number of pod per plant

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	8.0 <sup>fj</sup>	9.3 <sup>e-l</sup>	6.3 <sup>c-i</sup>	7.9 <sup>h-o</sup>	9.7 <sup>f-k</sup>	12.7 <sup>f-k</sup>	14.0 <sup>b-f</sup>	12.1 <sup>f-l</sup>
2	Wolki	11.7 <sup>ab</sup>	13.3 <sup>ab</sup>	6.3 <sup>c-i</sup>	10.4 <sup>b</sup>	13.7 <sup>abc</sup>	17.0 <sup>ab</sup>	14.0 <sup>b-f</sup>	14.9 <sup>abc</sup>
3	EK LS/CSR02012-2-3	7.7 <sup>g-j</sup>	8.3 <sup>g-m</sup>	5.3 <sup>f-i</sup>	7.1 <sup>l-r</sup>	8.3 <sup>ijk</sup>	10.3 <sup>j-m</sup>	10.0 <sup>j-n</sup>	9.6 <sup>qrs</sup>
4	Obse	8.3 <sup>e-j</sup>	8.0 <sup>h-m</sup>	8.0 <sup>b-e</sup>	8.1 <sup>f-m</sup>	8.0 <sup>jk</sup>	10.3 <sup>j-m</sup>	11.0 <sup>h-m</sup>	9.8 <sup>p-s</sup>
5	NC58	10.7 <sup>bcd</sup>	13.7 <sup>a</sup>	11.7 <sup>a</sup>	12.0 <sup>a</sup>	11.0 <sup>b-j</sup>	16.0 <sup>a-e</sup>	15.7 <sup>abc</sup>	14.2 <sup>bcd</sup>
6	Ashebeka	10.0 <sup>b-f</sup>	9.3 <sup>e-l</sup>	6.3 <sup>c-i</sup>	8.6 <sup>d-k</sup>	10.0 <sup>e-k</sup>	13.0 <sup>e-k</sup>	12.0 <sup>f-k</sup>	11.7 <sup>g-o</sup>
7	Hachalu	10.0 <sup>b-f</sup>	9.3 <sup>e-l</sup>	8.3 <sup>bcd</sup>	9.2 <sup>b-h</sup>	10.0 <sup>e-k</sup>	13.7 <sup>c-i</sup>	11.7 <sup>f-l</sup>	11.8 <sup>g-n</sup>
8	Degaga	10.7 <sup>bcd</sup>	10.0 <sup>d-j</sup>	7.3 <sup>b-g</sup>	9.3 <sup>b-g</sup>	12.0 <sup>a-h</sup>	13.7 <sup>c-i</sup>	15.0 <sup>b-e</sup>	13.6 <sup>c-f</sup>
9	EH09031-4	7.3 <sup>hij</sup>	6.3 <sup>m</sup>	4.7 <sup>hi</sup>	6.1 <sup>rs</sup>	8.0 <sup>jk</sup>	10.3 <sup>j-m</sup>	7.3 <sup>o</sup>	8.6 <sup>rs</sup>
10	Holetta-2	8.7 <sup>d-i</sup>	8.0 <sup>h-m</sup>	8.3 <sup>bcd</sup>	8.3 <sup>e-l</sup>	10.0 <sup>e-k</sup>	11.7 <sup>h-l</sup>	11.3 <sup>g-l</sup>	11.0 <sup>j-q</sup>
11	EH09007-4	6.3 <sup>j</sup>	6.3 <sup>m</sup>	4.0 <sup>i</sup>	5.6 <sup>s</sup>	8.0 <sup>jk</sup>	9.3 <sup>lm</sup>	8.0 <sup>no</sup>	8.4 <sup>s</sup>
12	EH07023-3	7.0 <sup>ij</sup>	6.3 <sup>m</sup>	6.7 <sup>c-h</sup>	6.7 <sup>n-s</sup>	9.0 <sup>h-k</sup>	10.3 <sup>j-m</sup>	10.7 <sup>h-m</sup>	10.0 <sup>o-s</sup>
13	EK05006-3	9.3 <sup>c-h</sup>	7.3 <sup>j-m</sup>	7.3 <sup>b-g</sup>	8.0 <sup>g-n</sup>	9.0 <sup>h-k</sup>	12.7 <sup>f-k</sup>	11.7 <sup>f-l</sup>	11.1 <sup>i-q</sup>
14	EK LS/CSR02014-2-4	7.0 <sup>ij</sup>	8.0 <sup>h-m</sup>	5.3 <sup>f-i</sup>	6.8 <sup>m-s</sup>	8.0 <sup>jk</sup>	10.0 <sup>klm</sup>	10.7 <sup>h-m</sup>	9.6 <sup>qrs</sup>
15	Numan	7.7 <sup>g-j</sup>	8.0 <sup>h-m</sup>	4.7 <sup>hi</sup>	6.8 <sup>m-s</sup>	8.3 <sup>ijk</sup>	8.0 <sup>m</sup>	9.3 <sup>l-o</sup>	8.6 <sup>rs</sup>
16	Bulga 70	9.7 <sup>b-g</sup>	12.0 <sup>a-e</sup>	6.7 <sup>c-h</sup>	9.4 <sup>b-f</sup>	10.3 <sup>d-k</sup>	15.7 <sup>a-f</sup>	16.3 <sup>ab</sup>	14.1 <sup>bcd</sup>
17	EK05001-1	8.0 <sup>f-j</sup>	9.0 <sup>f-m</sup>	6.3 <sup>c-i</sup>	7.8 <sup>i-p</sup>	9.3 <sup>g-k</sup>	10.0 <sup>klm</sup>	11.7 <sup>f-l</sup>	10.3 <sup>m-q</sup>
18	Dosha	8.7 <sup>d-i</sup>	8.3 <sup>g-m</sup>	8.7 <sup>bc</sup>	8.6 <sup>d-k</sup>	10.7 <sup>c-k</sup>	12.7 <sup>f-k</sup>	13.7 <sup>c-g</sup>	12.3 <sup>e-k</sup>
19	Gora	7.0 <sup>ij</sup>	9.3 <sup>e-l</sup>	6.7 <sup>c-h</sup>	7.7 <sup>i-p</sup>	8.3 <sup>ijk</sup>	11.3 <sup>i-l</sup>	9.3 <sup>l-o</sup>	9.7 <sup>qrs</sup>
20	EH08035-1	7.3 <sup>hij</sup>	6.7 <sup>lm</sup>	4.7 <sup>hi</sup>	6.2 <sup>qrs</sup>	9.3 <sup>g-k</sup>	12.0 <sup>g-l</sup>	11.0 <sup>h-m</sup>	10.8 <sup>k-q</sup>
21	Wayu	9.7 <sup>b-g</sup>	12.7 <sup>abc</sup>	6.3 <sup>c-i</sup>	9.6 <sup>b-e</sup>	12.3 <sup>a-g</sup>	14.7 <sup>b-h</sup>	11.7 <sup>f-l</sup>	12.9 <sup>d-h</sup>
22	EK LS/CSR02023-2-1	7.0 <sup>ij</sup>	7.7 <sup>i-m</sup>	4.7 <sup>hi</sup>	6.4 <sup>p-s</sup>	10.0 <sup>e-k</sup>	10.7 <sup>i-m</sup>	9.3 <sup>l-o</sup>	10.0 <sup>o-s</sup>
23	Mesay	9.3 <sup>c-h</sup>	11.7 <sup>a-f</sup>	8.0 <sup>b-e</sup>	9.7 <sup>b-e</sup>	13.3 <sup>a-d</sup>	13.3 <sup>d-j</sup>	14.0 <sup>b-f</sup>	13.6 <sup>c-f</sup>
24	EH09004-2	8.7 <sup>d-i</sup>	9.0 <sup>f-m</sup>	5.0 <sup>ghi</sup>	7.6 <sup>j-q</sup>	9.7 <sup>f-k</sup>	12.0 <sup>g-l</sup>	9.7 <sup>k-o</sup>	10.4 <sup>l-q</sup>
25	EH06088-6	7.0 <sup>ij</sup>	7.3 <sup>j-m</sup>	6.0 <sup>d-i</sup>	6.8 <sup>m-s</sup>	9.7 <sup>f-k</sup>	9.3 <sup>lm</sup>	10.3 <sup>i-n</sup>	9.8 <sup>p-s</sup>
	Mean	8.8b	9.5a	6.7c	8.36	10.3c	12.8a	11.9b	11.7

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6f. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	7.3 <sup>hij</sup>	7.0 <sup>klm</sup>	5.0 <sup>ghi</sup>	6.4 <sup>p-s</sup>	7.7 <sup>k</sup>	11.7 <sup>h-l</sup>	9.3 <sup>l-o</sup>	9.6 <sup>qrs</sup>
27	Kasa	10.3 <sup>b-e</sup>	11.7 <sup>a-f</sup>	9.7 <sup>ab</sup>	10.6 <sup>b</sup>	12.0 <sup>a-h</sup>	15.0 <sup>b-g</sup>	13.0 <sup>d-h</sup>	13.3 <sup>c-g</sup>
28	Cool-0025	11.3 <sup>abc</sup>	10.7 <sup>c-h</sup>	7.7 <sup>b-f</sup>	9.9 <sup>bcd</sup>	11.3 <sup>a-i</sup>	13.0 <sup>e-k</sup>	14.0 <sup>b-f</sup>	12.8 <sup>d-i</sup>
29	EH06070-3	7.3 <sup>hij</sup>	7.0 <sup>klm</sup>	5.3 <sup>f-i</sup>	6.6 <sup>o-s</sup>	7.7 <sup>k</sup>	9.3 <sup>lm</sup>	8.7 <sup>mno</sup>	8.6 <sup>rs</sup>
30	EK LS/CSR02010-4-3	7.3 <sup>hij</sup>	9.3 <sup>e-l</sup>	5.0 <sup>ghi</sup>	7.2 <sup>k-r</sup>	8.3 <sup>ijk</sup>	12.0 <sup>g-l</sup>	9.3 <sup>l-o</sup>	9.9 <sup>p-s</sup>
31	Cool-0031	9.3 <sup>c-h</sup>	12.0 <sup>a-e</sup>	7.3 <sup>b-g</sup>	9.6 <sup>b-e</sup>	12.7 <sup>a-f</sup>	13.3 <sup>d-j</sup>	15.7 <sup>abc</sup>	13.9 <sup>b-e</sup>
32	Cool-0018	10.3 <sup>b-e</sup>	9.7 <sup>e-k</sup>	8.0 <sup>b-e</sup>	9.3 <sup>b-g</sup>	12.7 <sup>a-f</sup>	13.0 <sup>e-k</sup>	16.3 <sup>ab</sup>	14.0 <sup>b-e</sup>
33	EK LS/CSR02028-1-1	9.3 <sup>c-h</sup>	7.3 <sup>j-m</sup>	5.0 <sup>ghi</sup>	7.2 <sup>k-r</sup>	9.0 <sup>h-k</sup>	11.3 <sup>i-l</sup>	12.3 <sup>f-j</sup>	10.9 <sup>k-q</sup>
34	EK 05037-4	7.7 <sup>g-j</sup>	11.3 <sup>a-f</sup>	7.0 <sup>c-h</sup>	8.7 <sup>d-j</sup>	10.7 <sup>c-k</sup>	12.0 <sup>g-l</sup>	12.7 <sup>e-i</sup>	11.8 <sup>g-n</sup>
35	Cool-0035	10.0 <sup>b-f</sup>	10.7 <sup>c-h</sup>	8.7 <sup>bc</sup>	9.8 <sup>bcd</sup>	12.3 <sup>a-g</sup>	15.7 <sup>a-f</sup>	14.0 <sup>b-f</sup>	14.0 <sup>b-e</sup>
36	KUSE2-27-33	10.7 <sup>bcd</sup>	11.0 <sup>b-g</sup>	8.0 <sup>b-e</sup>	9.9 <sup>bcd</sup>	12.0 <sup>a-h</sup>	16.3 <sup>a-d</sup>	17.7 <sup>a</sup>	15.3 <sup>ab</sup>
37	EH07015-7	8.3 <sup>e-j</sup>	8.0 <sup>h-m</sup>	5.7 <sup>e-i</sup>	7.3 <sup>j-r</sup>	9.0 <sup>h-k</sup>	10.3 <sup>j-m</sup>	9.7 <sup>k-o</sup>	9.7 <sup>qrs</sup>
38	Cool-0024	10.0 <sup>b-f</sup>	13.3 <sup>ab</sup>	7.7 <sup>b-f</sup>	10.3 <sup>bc</sup>	14.3 <sup>a</sup>	16.7 <sup>abc</sup>	15.0 <sup>b-e</sup>	15.3 <sup>ab</sup>
39	Selale	9.3 <sup>c-h</sup>	11.7 <sup>a-f</sup>	7.0 <sup>c-h</sup>	9.3 <sup>b-g</sup>	10.0 <sup>e-k</sup>	17.0 <sup>ab</sup>	12.0 <sup>f-k</sup>	13.0 <sup>d-h</sup>
40	Moti	9.7 <sup>b-g</sup>	10.7 <sup>c-h</sup>	6.7 <sup>c-h</sup>	9.0 <sup>c-i</sup>	10.3 <sup>d-k</sup>	13.7 <sup>c-i</sup>	12.0 <sup>f-k</sup>	12.0 <sup>f-m</sup>
41	EH06027-2	8.3 <sup>e-j</sup>	8.0 <sup>h-m</sup>	5.7 <sup>e-i</sup>	7.3 <sup>j-r</sup>	9.0 <sup>h-k</sup>	13.7 <sup>c-i</sup>	10.0 <sup>j-n</sup>	10.9 <sup>k-q</sup>
42	EK LS/CSR02019-2-4	8.0 <sup>f-j</sup>	8.7 <sup>g-m</sup>	5.7 <sup>e-i</sup>	7.4 <sup>j-r</sup>	10.7 <sup>c-k</sup>	10.3 <sup>j-m</sup>	9.7 <sup>k-o</sup>	10.2 <sup>n-r</sup>
43	EH09002-1	7.7 <sup>g-j</sup>	8.0 <sup>h-m</sup>	5.3 <sup>f-i</sup>	7.0 <sup>l-r</sup>	9.3 <sup>g-k</sup>	11.0 <sup>i-m</sup>	11.3 <sup>g-l</sup>	10.6 <sup>l-q</sup>
44	Tumsa	9.0 <sup>d-i</sup>	9.3 <sup>e-l</sup>	7.7 <sup>b-f</sup>	8.7 <sup>d-j</sup>	11.3 <sup>a-i</sup>	13.0 <sup>e-k</sup>	12.0 <sup>f-k</sup>	12.1 <sup>f-l</sup>
45	Gebelcho	9.7 <sup>b-g</sup>	9.7 <sup>e-k</sup>	6.7 <sup>c-h</sup>	8.7 <sup>d-j</sup>	10.0 <sup>e-k</sup>	13.3 <sup>d-j</sup>	11.0 <sup>h-m</sup>	11.4 <sup>h-p</sup>
46	EK05037-5	7.0 <sup>ij</sup>	8.3 <sup>g-m</sup>	4.7 <sup>hi</sup>	6.7 <sup>n-s</sup>	9.3 <sup>g-k</sup>	12.3 <sup>g-l</sup>	9.7 <sup>k-o</sup>	10.4 <sup>l-q</sup>
47	Didi'a	9.3 <sup>c-h</sup>	9.7 <sup>e-k</sup>	6.7 <sup>c-h</sup>	8.6 <sup>d-k</sup>	9.7 <sup>f-k</sup>	15.0 <sup>b-g</sup>	11.0 <sup>h-m</sup>	11.9 <sup>f-n</sup>
48	Cool-0034	10.0 <sup>b-f</sup>	12.3 <sup>a-d</sup>	8.0 <sup>b-e</sup>	10.1 <sup>bc</sup>	11.7 <sup>a-h</sup>	14.7 <sup>b-h</sup>	15.3 <sup>a-d</sup>	13.9 <sup>b-e</sup>
49	CS20DK	13.0 <sup>a</sup>	13.3 <sup>ab</sup>	11.7 <sup>a</sup>	12.7 <sup>a</sup>	14.0 <sup>ab</sup>	18.3 <sup>a</sup>	15.7 <sup>abc</sup>	16.0 <sup>a</sup>
50	Tesfa	9.0 <sup>d-i</sup>	10.3 <sup>c-i</sup>	7.7 <sup>b-f</sup>	9.0 <sup>c-i</sup>	13.0 <sup>a-e</sup>	14.7 <sup>b-h</sup>	10.3 <sup>i-n</sup>	12.7 <sup>d-j</sup>
	Mean	8.8b	9.5a	6.7c	8.36	10.3c	12.8a	11.9b	11.7

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05



Appendix Table 6g. Mean performance of 50 faba bean genotypes for number of pod poding node<sup>-1</sup>

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	1.22 <sup>d-j</sup>	1.42 <sup>a-f</sup>	1.33 <sup>b-g</sup>	1.33 <sup>b-j</sup>	1.33 <sup>a-h</sup>	1.31 <sup>c-h</sup>	1.62 <sup>d-l</sup>	1.42 <sup>f-p</sup>
2	Wolki	1.42 <sup>a-e</sup>	1.38 <sup>a-g</sup>	1.20 <sup>d-g</sup>	1.33 <sup>b-i</sup>	1.41 <sup>a-f</sup>	1.55 <sup>a-f</sup>	1.72 <sup>b-j</sup>	1.56 <sup>a-i</sup>
3	EK LS/CSR02012-2-3	1.16 <sup>f-j</sup>	1.26 <sup>b-h</sup>	1.23 <sup>d-g</sup>	1.22 <sup>e-l</sup>	1.19 <sup>e-i</sup>	1.42 <sup>c-h</sup>	1.33 <sup>nop</sup>	1.31 <sup>m-p</sup>
4	Obse	1.20 <sup>e-j</sup>	1.37 <sup>a-h</sup>	1.27 <sup>d-g</sup>	1.28 <sup>c-k</sup>	1.20 <sup>d-i</sup>	1.34 <sup>c-h</sup>	1.54 <sup>g-o</sup>	1.36 <sup>k-p</sup>
5	NC58	1.35 <sup>a-h</sup>	1.42 <sup>a-f</sup>	1.63 <sup>ab</sup>	1.47 <sup>ab</sup>	1.31 <sup>a-h</sup>	1.42 <sup>c-h</sup>	2.03 <sup>a</sup>	1.59 <sup>a-f</sup>
6	Ashebeka	1.26 <sup>b-j</sup>	1.33 <sup>a-h</sup>	1.17 <sup>d-g</sup>	1.25 <sup>e-l</sup>	1.30 <sup>b-h</sup>	1.46 <sup>b-h</sup>	1.54 <sup>g-o</sup>	1.43 <sup>e-o</sup>
7	Hachalu	1.38 <sup>a-f</sup>	1.28 <sup>a-h</sup>	1.37 <sup>b-f</sup>	1.34 <sup>b-g</sup>	1.24 <sup>c-i</sup>	1.52 <sup>a-h</sup>	1.72 <sup>b-j</sup>	1.49 <sup>c-l</sup>
8	Degaga	1.18 <sup>f-j</sup>	1.25 <sup>b-h</sup>	1.30 <sup>c-g</sup>	1.25 <sup>e-l</sup>	1.34 <sup>a-h</sup>	1.36 <sup>c-h</sup>	1.74 <sup>b-i</sup>	1.48 <sup>d-m</sup>
9	EH09031-4	1.10 <sup>ij</sup>	1.20 <sup>b-h</sup>	1.33 <sup>b-g</sup>	1.21 <sup>e-l</sup>	1.04 <sup>i</sup>	1.35 <sup>c-h</sup>	1.47 <sup>i-p</sup>	1.29 <sup>nop</sup>
10	Holetta-2	1.30 <sup>a-i</sup>	1.33 <sup>a-h</sup>	1.40 <sup>b-f</sup>	1.34 <sup>b-g</sup>	1.37 <sup>a-g</sup>	1.30 <sup>c-h</sup>	1.52 <sup>h-o</sup>	1.39 <sup>i-p</sup>
11	EH09007-4	1.05 <sup>j</sup>	1.11 <sup>e-h</sup>	1.10 <sup>fg</sup>	1.09 <sup>l</sup>	1.20 <sup>c-i</sup>	1.19 <sup>gh</sup>	1.40 <sup>k-p</sup>	1.27 <sup>op</sup>
12	EH07023-3	1.11 <sup>ij</sup>	1.06 <sup>gh</sup>	1.37 <sup>b-f</sup>	1.18 <sup>g-l</sup>	1.08 <sup>hi</sup>	1.28 <sup>c-h</sup>	1.61 <sup>d-m</sup>	1.33 <sup>l-p</sup>
13	EK05006-3	1.28 <sup>a-i</sup>	1.24 <sup>b-h</sup>	1.37 <sup>b-f</sup>	1.30 <sup>c-k</sup>	1.29 <sup>b-i</sup>	1.35 <sup>c-h</sup>	1.59 <sup>e-n</sup>	1.41 <sup>h-p</sup>
14	EK LS/CSR02014-2-4	1.17 <sup>f-j</sup>	1.18 <sup>c-h</sup>	1.13 <sup>efg</sup>	1.16 <sup>ijkl</sup>	1.13 <sup>ghi</sup>	1.30 <sup>c-h</sup>	1.54 <sup>g-o</sup>	1.33 <sup>l-p</sup>
15	Numan	1.21 <sup>d-j</sup>	1.43 <sup>a-e</sup>	1.17 <sup>d-g</sup>	1.27 <sup>d-k</sup>	1.25 <sup>c-i</sup>	1.21 <sup>fgh</sup>	1.52 <sup>h-o</sup>	1.33 <sup>l-p</sup>
16	Bulga 70	1.26 <sup>b-j</sup>	1.34 <sup>a-h</sup>	1.47 <sup>bcd</sup>	1.36 <sup>b-f</sup>	1.28 <sup>b-i</sup>	1.52 <sup>a-h</sup>	1.99 <sup>ab</sup>	1.59 <sup>a-e</sup>
17	EK05001-1	1.20 <sup>e-j</sup>	1.12 <sup>e-h</sup>	1.23 <sup>d-g</sup>	1.18 <sup>g-l</sup>	1.22 <sup>c-i</sup>	1.32 <sup>c-h</sup>	1.41 <sup>k-p</sup>	1.31 <sup>m-p</sup>
18	Dosha	1.19 <sup>f-j</sup>	1.14 <sup>d-h</sup>	1.37 <sup>b-f</sup>	1.23 <sup>e-l</sup>	1.28 <sup>b-i</sup>	1.31 <sup>c-h</sup>	1.73 <sup>b-j</sup>	1.44 <sup>e-n</sup>
19	Gora	1.25 <sup>c-j</sup>	1.34 <sup>a-h</sup>	1.20 <sup>d-g</sup>	1.26 <sup>d-k</sup>	1.39 <sup>a-g</sup>	1.34 <sup>c-h</sup>	1.52 <sup>g-o</sup>	1.42 <sup>g-p</sup>
20	EH08035-1	1.17 <sup>f-j</sup>	1.12 <sup>e-h</sup>	1.20 <sup>d-g</sup>	1.16 <sup>i-l</sup>	1.22 <sup>c-i</sup>	1.34 <sup>c-h</sup>	1.46 <sup>j-p</sup>	1.34 <sup>l-p</sup>
21	Wayu	1.46 <sup>abc</sup>	1.59 <sup>a</sup>	1.33 <sup>B-g</sup>	1.46 <sup>ab</sup>	1.57 <sup>a</sup>	1.58 <sup>a-d</sup>	1.88 <sup>a-d</sup>	1.68 <sup>ab</sup>
22	EK LS/CSR02023-2-1	1.17 <sup>f-j</sup>	1.11 <sup>e-h</sup>	1.20 <sup>d-g</sup>	1.16 <sup>ijkl</sup>	1.30 <sup>b-h</sup>	1.40 <sup>c-h</sup>	1.39 <sup>l-p</sup>	1.36 <sup>k-p</sup>
23	Mesay	1.28 <sup>b-i</sup>	1.34 <sup>a-h</sup>	1.33 <sup>B-g</sup>	1.32 <sup>b-k</sup>	1.43 <sup>a-e</sup>	1.37 <sup>c-h</sup>	1.76 <sup>b-h</sup>	1.52 <sup>b-k</sup>
24	EH09004-2	1.19 <sup>f-j</sup>	1.23 <sup>b-h</sup>	1.27 <sup>d-g</sup>	1.23 <sup>e-l</sup>	1.27 <sup>c-i</sup>	1.28 <sup>c-h</sup>	1.30 <sup>op</sup>	1.29 <sup>nop</sup>
25	EH06088-6	1.25 <sup>c-j</sup>	1.16 <sup>c-h</sup>	1.20 <sup>d-g</sup>	1.20 <sup>e-l</sup>	1.16 <sup>f-i</sup>	1.18 <sup>h</sup>	1.55 <sup>f-o</sup>	1.30 <sup>nop</sup>
	Mean	1.26b	1.27b	1.31a	1.28	1.30c	1.42b	1.61a	1.44

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6g. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	1.22 <sup>d-j</sup>	1.11 <sup>e-h</sup>	1.27 <sup>d-g</sup>	1.20 <sup>e-l</sup>	1.21 <sup>c-i</sup>	1.32 <sup>c-h</sup>	1.29 <sup>op</sup>	1.27 <sup>nop</sup>
27	Kasa	1.43 <sup>a-d</sup>	1.28 <sup>a-h</sup>	1.60 <sup>abc</sup>	1.44 <sup>bc</sup>	1.34 <sup>a-h</sup>	1.61 <sup>abc</sup>	1.80 <sup>a-g</sup>	1.58 <sup>a-g</sup>
28	Cool-0025	1.48 <sup>ab</sup>	1.45 <sup>a-d</sup>	1.33 <sup>B-g</sup>	1.42 <sup>bcd</sup>	1.41 <sup>a-f</sup>	1.39 <sup>c-h</sup>	1.76 <sup>b-h</sup>	1.52 <sup>b-k</sup>
29	EH06070-3	1.22 <sup>d-j</sup>	1.05 <sup>h</sup>	1.37 <sup>b-f</sup>	1.21 <sup>e-l</sup>	1.16 <sup>f-i</sup>	1.31 <sup>c-h</sup>	1.29 <sup>op</sup>	1.25 <sup>p</sup>
30	EK LS/CSR02010-4-3	1.22 <sup>d-j</sup>	1.28 <sup>a-h</sup>	1.03 <sup>g</sup>	1.18 <sup>g-l</sup>	1.32 <sup>a-h</sup>	1.52 <sup>a-h</sup>	1.31 <sup>op</sup>	1.38 <sup>j-p</sup>
31	Cool-0031	1.42 <sup>a-e</sup>	1.50 <sup>ab</sup>	1.47 <sup>bcd</sup>	1.46 <sup>ab</sup>	1.41 <sup>a-f</sup>	1.46 <sup>b-h</sup>	1.82 <sup>a-f</sup>	1.56 <sup>a-h</sup>
32	Cool-0018	1.30 <sup>a-i</sup>	1.27 <sup>b-h</sup>	1.37 <sup>b-f</sup>	1.31 <sup>b-k</sup>	1.46 <sup>abc</sup>	1.40 <sup>c-h</sup>	1.84 <sup>a-e</sup>	1.57 <sup>a-h</sup>
33	EK LS/CSR02028-1-1	1.27 <sup>b-j</sup>	1.13 <sup>e-h</sup>	1.17 <sup>d-g</sup>	1.19 <sup>f-l</sup>	1.29 <sup>b-i</sup>	1.42 <sup>c-h</sup>	1.73 <sup>b-j</sup>	1.48 <sup>d-m</sup>
34	EK 05037-4	1.09 <sup>ij</sup>	1.39 <sup>a-f</sup>	1.17 <sup>d-g</sup>	1.22 <sup>e-l</sup>	1.18 <sup>e-i</sup>	1.33 <sup>c-h</sup>	1.54 <sup>g-o</sup>	1.35 <sup>k-p</sup>
35	Cool-0035	1.43 <sup>a-d</sup>	1.19 <sup>b-h</sup>	1.40 <sup>b-f</sup>	1.34 <sup>b-g</sup>	1.40 <sup>a-f</sup>	1.49 <sup>a-h</sup>	1.67 <sup>d-k</sup>	1.52 <sup>b-k</sup>
36	KUSE2-27-33	1.29 <sup>a-i</sup>	1.29 <sup>a-h</sup>	1.43 <sup>b-e</sup>	1.34 <sup>b-h</sup>	1.32 <sup>a-h</sup>	1.59 <sup>a-d</sup>	1.96 <sup>abc</sup>	1.62 <sup>a-d</sup>
37	EH07015-7	1.14 <sup>hij</sup>	1.10 <sup>fgh</sup>	1.27 <sup>d-g</sup>	1.17 <sup>h-l</sup>	1.13 <sup>ghi</sup>	1.42 <sup>c-h</sup>	1.34 <sup>m-p</sup>	1.30 <sup>nop</sup>
38	Cool-0024	1.25 <sup>c-j</sup>	1.36 <sup>a-h</sup>	1.37 <sup>b-f</sup>	1.33 <sup>j</sup>	1.53 <sup>ab</sup>	1.62 <sup>abc</sup>	1.71 <sup>c-j</sup>	1.62 <sup>a-d</sup>
39	Selale	1.28 <sup>b-i</sup>	1.32 <sup>a-h</sup>	1.47 <sup>bcd</sup>	1.36 <sup>b-f</sup>	1.43 <sup>a-e</sup>	1.83 <sup>a</sup>	1.70 <sup>c-j</sup>	1.65 <sup>abc</sup>
40	Moti	1.17 <sup>f-j</sup>	1.28 <sup>a-h</sup>	1.33 <sup>B-g</sup>	1.26 <sup>d-k</sup>	1.30 <sup>b-h</sup>	1.41 <sup>c-h</sup>	1.59 <sup>e-n</sup>	1.43 <sup>e-o</sup>
41	EH06027-2	1.25 <sup>c-j</sup>	1.20 <sup>b-h</sup>	1.23 <sup>d-g</sup>	1.23 <sup>e-l</sup>	1.30 <sup>b-h</sup>	1.47 <sup>b-h</sup>	1.67 <sup>d-k</sup>	1.48 <sup>d-m</sup>
42	EK LS/CSR02019-2-4	1.26 <sup>b-j</sup>	1.26 <sup>b-h</sup>	1.13 <sup>efg</sup>	1.22 <sup>e-l</sup>	1.33 <sup>a-h</sup>	1.25 <sup>d-h</sup>	1.24 <sup>p</sup>	1.27 <sup>nop</sup>
43	EH09002-1	1.15 <sup>g-j</sup>	1.15 <sup>d-h</sup>	1.17 <sup>d-g</sup>	1.15 <sup>kl</sup>	1.27 <sup>c-i</sup>	1.22 <sup>e-h</sup>	1.49 <sup>h-p</sup>	1.33 <sup>l-p</sup>
44	Tumsa	1.29 <sup>a-i</sup>	1.17 <sup>c-h</sup>	1.40 <sup>b-f</sup>	1.29 <sup>c-k</sup>	1.31 <sup>b-h</sup>	1.53 <sup>a-h</sup>	1.80 <sup>a-g</sup>	1.54 <sup>b-j</sup>
45	Gebelcho	1.37 <sup>a-g</sup>	1.33 <sup>a-h</sup>	1.60 <sup>abc</sup>	1.43 <sup>bc</sup>	1.31 <sup>b-h</sup>	1.54 <sup>a-g</sup>	1.85 <sup>a-e</sup>	1.57 <sup>a-h</sup>
46	EK05037-5	1.17 <sup>f-j</sup>	1.18 <sup>c-h</sup>	1.20 <sup>d-g</sup>	1.18 <sup>g-l</sup>	1.25 <sup>c-i</sup>	1.38 <sup>c-h</sup>	1.48 <sup>h-p</sup>	1.37 <sup>k-p</sup>
47	Didi'a	1.27 <sup>b-j</sup>	1.22 <sup>b-h</sup>	1.27 <sup>d-g</sup>	1.25 <sup>e-l</sup>	1.32 <sup>a-h</sup>	1.55 <sup>a-f</sup>	1.60 <sup>d-n</sup>	1.49 <sup>c-l</sup>
48	Cool-0034	1.37 <sup>a-h</sup>	1.30 <sup>a-h</sup>	1.37 <sup>b-f</sup>	1.37 <sup>b-e</sup>	1.40 <sup>a-f</sup>	1.57 <sup>a-e</sup>	1.88 <sup>a-d</sup>	1.62 <sup>a-d</sup>
49	CS20DK	1.50 <sup>a</sup>	1.48 <sup>abc</sup>	1.80 <sup>a</sup>	1.59 <sup>a</sup>	1.45 <sup>a-d</sup>	1.78 <sup>ab</sup>	1.94 <sup>abc</sup>	1.72 <sup>a</sup>
50	Tesfa	1.28 <sup>a-i</sup>	1.24 <sup>b-h</sup>	1.33 <sup>b-g</sup>	1.29 <sup>c-k</sup>	1.45 <sup>a-d</sup>	1.51 <sup>a-h</sup>	1.45 <sup>j-p</sup>	1.47 <sup>d-m</sup>
	Mean	1.26b	1.27b	1.31a	1.28	1.30c	1.42b	1.61a	1.44

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6h. Mean performance of 50 faba bean genotypes for hundred seeds weight

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	69.7 <sup>m</sup>	68.0 <sup>mn</sup>	67.7 <sup>pq</sup>	68.5	74.9 <sup>lm</sup>	65.5 <sup>o</sup>	66.6 <sup>no</sup>	69.0 <sup>o</sup>
2	Wolki	60.9 <sup>n</sup>	57.8 <sup>op</sup>	59.3 <sup>r</sup>	59.2	65.3 <sup>n</sup>	56.3 <sup>pq</sup>	57.7 <sup>p</sup>	59.8 <sup>p</sup>
3	EK LS/CSR02012-2-3	89.2 <sup>c-f</sup>	78.1 <sup>e-i</sup>	85.7 <sup>e-i</sup>	84.3	92.5 <sup>b-e</sup>	81.9 <sup>fgh</sup>	85.9 <sup>efg</sup>	86.8 <sup>efg</sup>
4	Obse	81.3 <sup>g-k</sup>	75.8 <sup>g-l</sup>	78.0 <sup>klm</sup>	78.4	83.8 <sup>f-k</sup>	71.2 <sup>l-o</sup>	77.5 <sup>i-l</sup>	77.5 <sup>jkl</sup>
5	NC58	51.9 <sup>o-r</sup>	49.0 <sup>qrs</sup>	42.0 <sup>w</sup>	47.7	50.0 <sup>qr</sup>	45.4 <sup>tuv</sup>	40.3 <sup>vw</sup>	45.2 <sup>x</sup>
6	Ashebeka	79.6 <sup>i-l</sup>	77.1 <sup>f-k</sup>	81.4 <sup>ijk</sup>	79.4	89.0 <sup>d-i</sup>	85.9 <sup>b-f</sup>	79.1 <sup>h-k</sup>	84.7 <sup>fgh</sup>
7	Hachalu	72.3 <sup>lm</sup>	71.5 <sup>i-n</sup>	68.9 <sup>pq</sup>	70.9	78.0 <sup>j-m</sup>	70.8 <sup>l-o</sup>	71.9 <sup>lm</sup>	73.6 <sup>mn</sup>
8	Degaga	54.3 <sup>n-r</sup>	53.3 <sup>pqr</sup>	51.7 <sup>tu</sup>	53.1	58.7 <sup>nop</sup>	52.1 <sup>qrs</sup>	51.2 <sup>q-t</sup>	54.0 <sup>rst</sup>
9	EH09031-4	97.6 <sup>ab</sup>	91.5 <sup>a</sup>	90.5 <sup>cd</sup>	93.2	99.8 <sup>b</sup>	89.1 <sup>a-d</sup>	92.1 <sup>bcd</sup>	93.6 <sup>bc</sup>
10	Holetta-2	55.0 <sup>n-q</sup>	54.4 <sup>o-r</sup>	51.1 <sup>tu</sup>	53.5	59.6 <sup>no</sup>	52.2 <sup>qrs</sup>	52.2 <sup>p-t</sup>	54.7 <sup>q-t</sup>
11	EH09007-4	90.5 <sup>b-f</sup>	82.3 <sup>b-g</sup>	81.8 <sup>h-k</sup>	84.8	97.2 <sup>bcd</sup>	84.0 <sup>d-g</sup>	93.9 <sup>abc</sup>	91.7 <sup>bcd</sup>
12	EH07023-3	88.4 <sup>d-h</sup>	88.2 <sup>ab</sup>	95.7 <sup>ab</sup>	90.8	97.8 <sup>bc</sup>	90.1 <sup>abc</sup>	95.4 <sup>abc</sup>	94.4 <sup>b</sup>
13	EK05006-3	73.5 <sup>klm</sup>	70.4 <sup>k-n</sup>	78.3 <sup>kl</sup>	74.1	83.6 <sup>g-k</sup>	75.1 <sup>j-m</sup>	81.1 <sup>ghi</sup>	79.9 <sup>ij</sup>
14	EK LS/CSR02014-2-4	89.0 <sup>c-g</sup>	82.2 <sup>b-g</sup>	82.6 <sup>g-j</sup>	84.6	90.9 <sup>c-h</sup>	78.3 <sup>g-k</sup>	84.0 <sup>fgh</sup>	84.4 <sup>gh</sup>
15	Numan	99.3 <sup>a</sup>	83.0 <sup>b-f</sup>	99.5 <sup>a</sup>	93.9	109.0 <sup>a</sup>	90.8 <sup>ab</sup>	95.7 <sup>abc</sup>	98.5 <sup>a</sup>
16	Bulga 70	48.9 <sup>pqr</sup>	49.0 <sup>qrs</sup>	45.0 <sup>vw</sup>	47.6	48.7 <sup>r</sup>	43.2 <sup>uv</sup>	44.2 <sup>uv</sup>	45.4 <sup>x</sup>
17	EK05001-1	77.9 <sup>i-l</sup>	77.2 <sup>f-j</sup>	71.1 <sup>opq</sup>	75.4	82.3 <sup>h-l</sup>	65.5 <sup>o</sup>	79.3 <sup>hij</sup>	75.7 <sup>klm</sup>
18	Dosha	76.7 <sup>i-m</sup>	67.2 <sup>n</sup>	67.2 <sup>q</sup>	70.4	73.6 <sup>m</sup>	73.5 <sup>k-n</sup>	64.6 <sup>o</sup>	70.6 <sup>no</sup>
19	Gora	90.9 <sup>b-e</sup>	80.7 <sup>c-h</sup>	83.3 <sup>f-i</sup>	84.9	88.6 <sup>d-i</sup>	84.3 <sup>c-f</sup>	96.8 <sup>ab</sup>	89.9 <sup>cde</sup>
20	EH08035-1	84.0 <sup>e-i</sup>	84.5 <sup>b-e</sup>	86.2 <sup>efg</sup>	84.9	90.3 <sup>c-h</sup>	84.0 <sup>d-g</sup>	83.4 <sup>fgh</sup>	85.9 <sup>fgh</sup>
21	Wayu	36.5 <sup>s</sup>	36.1 <sup>t</sup>	33.6 <sup>y</sup>	35.4	40.4 <sup>s</sup>	35.1 <sup>w</sup>	34.5 <sup>x</sup>	36.7 <sup>y</sup>
22	EK LS/CSR02023-2-1	84.5 <sup>e-i</sup>	83.2 <sup>b-f</sup>	86.1 <sup>e-h</sup>	84.6	97.2 <sup>bcd</sup>	82.9 <sup>efg</sup>	90.8 <sup>cde</sup>	90.3 <sup>cde</sup>
23	Mesay	49.5 <sup>pqr</sup>	51.4 <sup>p-s</sup>	47.8 <sup>uv</sup>	49.5	58.2 <sup>n-q</sup>	54.0 <sup>pqr</sup>	55.2 <sup>pqr</sup>	55.8 <sup>qrs</sup>
24	EH09004-2	74.9 <sup>j-m</sup>	74.1 <sup>h-m</sup>	78.3 <sup>kl</sup>	75.8	85.2 <sup>e-k</sup>	78.2 <sup>g-k</sup>	73.7 <sup>klm</sup>	79.0 <sup>ijk</sup>
25	EH06088-6	88.2 <sup>d-h</sup>	87.4 <sup>abc</sup>	94.1 <sup>bc</sup>	89.9	90.3 <sup>c-h</sup>	89.1 <sup>a-d</sup>	90.1 <sup>cde</sup>	89.8 <sup>cde</sup>
	Mean	72.6a	68.6b	69.2b	70.1	76.1a	68.5c	70.9b	71.8

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6h. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	93.8 <sup>a-d</sup>	87.0 <sup>abc</sup>	76.1 <sup>lm</sup>	85.7	96.4 <sup>bcd</sup>	92.4 <sup>a</sup>	90.8 <sup>cde</sup>	93.2 <sup>bc</sup>
27	Kasa	46.2 <sup>r</sup>	45.0 <sup>s</sup>	43.9 <sup>vw</sup>	45.0	52.3 <sup>o-r</sup>	41.8 <sup>v</sup>	47.9 <sup>tu</sup>	47.3 <sup>wx</sup>
28	Cool-0025	54.3 <sup>n-r</sup>	55.2 <sup>opq</sup>	56.5 <sup>rs</sup>	55.3	59.1 <sup>nop</sup>	56.2 <sup>pq</sup>	54.7 <sup>p-s</sup>	56.7 <sup>pqr</sup>
29	EH06070-3	93.5 <sup>a-d</sup>	77.8 <sup>e-i</sup>	88.7 <sup>de</sup>	86.7	92.0 <sup>b-g</sup>	84.4 <sup>c-f</sup>	86.4 <sup>efg</sup>	87.6 <sup>efg</sup>
30	EK LS/CSR02010-4-3	92.1 <sup>a-e</sup>	76.7 <sup>f-k</sup>	87.4 <sup>def</sup>	85.4	97.8 <sup>bc</sup>	88.5 <sup>a-e</sup>	98.8 <sup>a</sup>	95.0 <sup>b</sup>
31	Cool-0031	48.1 <sup>qr</sup>	46.2 <sup>s</sup>	51.5 <sup>tu</sup>	48.6	50.8 <sup>pqr</sup>	49.1 <sup>rst</sup>	49.1 <sup>stu</sup>	49.7 <sup>uvw</sup>
32	Cool-0018	57.8 <sup>no</sup>	55.1 <sup>opq</sup>	51.7 <sup>tu</sup>	54.9	56.8 <sup>o-r</sup>	54.3 <sup>pqr</sup>	50.2 <sup>rst</sup>	53.8 <sup>rst</sup>
33	EK LS/CSR02028-1-1	94.2 <sup>a-d</sup>	85.4 <sup>a-d</sup>	77.0 <sup>lm</sup>	85.5	94.8 <sup>bcd</sup>	75.0 <sup>j-m</sup>	86.2 <sup>efg</sup>	85.3 <sup>fgh</sup>
34	EK 05037-4	79.4 <sup>i-l</sup>	75.9 <sup>g-l</sup>	78.8 <sup>ijkl</sup>	78.0	79.8 <sup>j-m</sup>	72.9 <sup>k-n</sup>	74.3 <sup>j-m</sup>	75.7 <sup>klm</sup>
35	Cool-0035	55.7 <sup>n-q</sup>	55.8 <sup>opq</sup>	59.9 <sup>f</sup>	57.1	54.4 <sup>o-r</sup>	58.9 <sup>p</sup>	56.0 <sup>pq</sup>	56.4 <sup>pqr</sup>
36	KUSE2-27-33	49.9 <sup>o-r</sup>	48.0 <sup>rs</sup>	43.0 <sup>w</sup>	47.0	53.9 <sup>o-r</sup>	44.3 <sup>uv</sup>	46.7 <sup>tu</sup>	48.3 <sup>vw</sup>
37	EH07015-7	96.6 <sup>abc</sup>	82.5 <sup>b-g</sup>	95.7 <sup>ab</sup>	91.6	97.8 <sup>bc</sup>	75.7 <sup>i-l</sup>	91.5 <sup>b-e</sup>	88.3 <sup>def</sup>
38	Cool-0024	56.8 <sup>nop</sup>	51.8 <sup>p-s</sup>	49.4 <sup>tu</sup>	52.7	53.9 <sup>o-r</sup>	47.8 <sup>stu</sup>	51.1 <sup>q-t</sup>	51.0 <sup>t-w</sup>
39	Selale	51.0 <sup>o-r</sup>	45.0 <sup>s</sup>	37.8 <sup>x</sup>	44.6	53.9 <sup>o-r</sup>	46.8 <sup>s-v</sup>	36.8 <sup>wx</sup>	45.8 <sup>x</sup>
40	Moti	76.6 <sup>i-m</sup>	67.2 <sup>n</sup>	68.6 <sup>pq</sup>	70.8	81.3 <sup>i-m</sup>	69.3 <sup>mno</sup>	73.6 <sup>klm</sup>	74.7 <sup>lm</sup>
41	EH06027-2	82.9 <sup>f-j</sup>	82.3 <sup>b-g</sup>	82.9 <sup>g-j</sup>	82.7	92.2 <sup>b-f</sup>	76.7 <sup>h-l</sup>	87.3 <sup>def</sup>	85.4 <sup>fgh</sup>
42	EK LS/CSR02019-2-4	91.2 <sup>b-e</sup>	88.1 <sup>ab</sup>	83.8 <sup>f-i</sup>	87.7	99.7 <sup>b</sup>	80.9 <sup>f-j</sup>	94.4 <sup>abc</sup>	91.6 <sup>bcd</sup>
43	EH09002-1	80.5 <sup>h-k</sup>	79.3 <sup>d-h</sup>	75.6 <sup>lmn</sup>	78.5	86.2 <sup>e-j</sup>	81.2 <sup>f-i</sup>	79.4 <sup>hij</sup>	82.3 <sup>hi</sup>
44	Tumsa	74.9 <sup>j-m</sup>	69.8 <sup>lmn</sup>	70.6 <sup>opq</sup>	71.8	77.6 <sup>klm</sup>	68.1 <sup>no</sup>	70.0 <sup>mn</sup>	71.9 <sup>mno</sup>
45	Gebelcho	81.0 <sup>h-k</sup>	71.0 <sup>j-n</sup>	73.6 <sup>mno</sup>	75.2	78.0 <sup>j-m</sup>	78.3 <sup>g-k</sup>	76.7 <sup>i-l</sup>	77.7 <sup>ijkl</sup>
46	EK05037-5	79.0 <sup>i-l</sup>	79.3 <sup>d-h</sup>	71.7 <sup>nop</sup>	76.7	72.8 <sup>m</sup>	76.0 <sup>h-l</sup>	73.5 <sup>lm</sup>	74.1 <sup>lmn</sup>
47	Didi'a	73.9 <sup>klm</sup>	69.9 <sup>lmn</sup>	76.3 <sup>lm</sup>	73.4	73.1 <sup>m</sup>	68.0 <sup>no</sup>	71.9 <sup>lm</sup>	71.0 <sup>no</sup>
48	Cool-0034	52.9 <sup>n-r</sup>	60.2 <sup>o</sup>	53.1 <sup>st</sup>	55.4	59.0 <sup>nop</sup>	58.2 <sup>op</sup>	56.2 <sup>pq</sup>	57.8 <sup>pq</sup>
49	CS20DK	53.6 <sup>n-r</sup>	51.1 <sup>p-s</sup>	50.9 <sup>tu</sup>	51.9	56.7 <sup>o-r</sup>	49.4 <sup>rst</sup>	49.4 <sup>stu</sup>	51.8 <sup>tuv</sup>
50	Tesfa	51.4 <sup>o-r</sup>	49.0 <sup>qrs</sup>	49.5 <sup>tu</sup>	50.0	51.7 <sup>o-r</sup>	50.1 <sup>rst</sup>	54.6 <sup>p-s</sup>	52.1 <sup>stu</sup>
	Mean	72.6a	68.6b	69.2b	70.1	76.1a	68.5c	70.9b	71.8

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6i. Mean performance of 50 faba bean genotypes for chocolate spot disease

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	29.74 <sup>cde</sup>	41.07 <sup>ab</sup>	41.07 <sup>abc</sup>	37.29 <sup>a-g</sup>	26.26 <sup>d-g</sup>	41.07 <sup>a</sup>	26.26 <sup>cd</sup>	31.20 <sup>e-i</sup>
2	Wolki	29.74 <sup>cde</sup>	33.67 <sup>a-d</sup>	26.26 <sup>cd</sup>	29.89 <sup>e-i</sup>	26.26 <sup>d-g</sup>	26.26 <sup>b-e</sup>	26.26 <sup>cd</sup>	26.26 <sup>h-k</sup>
3	EKLS/CSR02012-2-3	26.26 <sup>de</sup>	33.21 <sup>a-d</sup>	26.26 <sup>cd</sup>	28.58 <sup>ghi</sup>	26.26 <sup>d-g</sup>	26.26 <sup>b-e</sup>	22.79 <sup>cd</sup>	25.11 <sup>i-l</sup>
4	Obse	33.21 <sup>cde</sup>	33.67 <sup>a-d</sup>	41.07 <sup>abc</sup>	35.98 <sup>a-h</sup>	37.14 <sup>bcd</sup>	26.26 <sup>b-e</sup>	33.67 <sup>abc</sup>	32.36 <sup>d-h</sup>
5	NC58	41.07 <sup>a-d</sup>	45.00 <sup>a</sup>	45.00 <sup>ab</sup>	43.69 <sup>a</sup>	37.14 <sup>bcd</sup>	22.79 <sup>cde</sup>	45.00 <sup>a</sup>	34.98 <sup>b-f</sup>
6	Ashebeka	37.14 <sup>b-e</sup>	22.79 <sup>cde</sup>	41.07 <sup>abc</sup>	33.67 <sup>b-i</sup>	22.79 <sup>efg</sup>	26.26 <sup>b-e</sup>	41.07 <sup>ab</sup>	30.04 <sup>e-i</sup>
7	Hachalu	33.21 <sup>cde</sup>	29.74 <sup>a-e</sup>	41.07 <sup>abc</sup>	34.67 <sup>b-i</sup>	26.26 <sup>d-g</sup>	26.26 <sup>b-e</sup>	41.07 <sup>ab</sup>	31.20 <sup>e-i</sup>
8	Degaga	37.14 <sup>b-e</sup>	37.14 <sup>abc</sup>	41.07 <sup>abc</sup>	38.45 <sup>a-f</sup>	37.14 <sup>bcd</sup>	19.04 <sup>de</sup>	37.60 <sup>ab</sup>	31.26 <sup>e-i</sup>
9	EH09031-4	29.74 <sup>cde</sup>	33.21 <sup>a-d</sup>	26.26 <sup>cd</sup>	29.74 <sup>f-i</sup>	15.29 <sup>g</sup>	22.51 <sup>cde</sup>	29.74 <sup>bcd</sup>	22.51 <sup>jkl</sup>
10	Holetta-2	26.26 <sup>de</sup>	37.14 <sup>abc</sup>	29.74 <sup>cd</sup>	31.05 <sup>d-i</sup>	29.74 <sup>c-f</sup>	29.74 <sup>a-d</sup>	26.26 <sup>cd</sup>	28.58 <sup>f-j</sup>
11	EH09007-4	26.26 <sup>de</sup>	37.60 <sup>abc</sup>	22.79 <sup>d</sup>	28.88 <sup>ghi</sup>	15.29 <sup>g</sup>	37.14 <sup>ab</sup>	22.79 <sup>cd</sup>	25.07 <sup>i-l</sup>
12	EH07023-3	29.74 <sup>cde</sup>	33.67 <sup>a-d</sup>	26.26 <sup>cd</sup>	29.89 <sup>e-i</sup>	26.26 <sup>d-g</sup>	37.14 <sup>ab</sup>	41.07 <sup>ab</sup>	34.82 <sup>b-f</sup>
13	EK05006-3	26.26 <sup>de</sup>	41.07 <sup>ab</sup>	41.07 <sup>abc</sup>	36.13 <sup>a-h</sup>	26.26 <sup>d-g</sup>	29.74 <sup>a-d</sup>	41.07 <sup>ab</sup>	32.36 <sup>d-h</sup>
14	EKLS/CSR02014-2-4	37.60 <sup>a-e</sup>	29.74 <sup>a-e</sup>	45.00 <sup>ab</sup>	37.44 <sup>a-g</sup>	26.26 <sup>d-g</sup>	29.74 <sup>a-d</sup>	41.07 <sup>ab</sup>	32.36 <sup>d-h</sup>
15	Numan	30.19 <sup>cde</sup>	45.00 <sup>a</sup>	30.19 <sup>bcd</sup>	35.13 <sup>a-i</sup>	26.26 <sup>d-g</sup>	26.26 <sup>b-e</sup>	22.79 <sup>cd</sup>	25.11 <sup>i-l</sup>
16	Bulga 70	37.14 <sup>b-e</sup>	33.67 <sup>a-d</sup>	37.60 <sup>a-d</sup>	36.13 <sup>a-h</sup>	37.14 <sup>bcd</sup>	26.26 <sup>b-e</sup>	41.07 <sup>ab</sup>	34.82 <sup>b-f</sup>
17	EK05001-1	41.07 <sup>a-d</sup>	22.79 <sup>cde</sup>	41.07 <sup>abc</sup>	34.98 <sup>a-i</sup>	29.74 <sup>c-f</sup>	19.04 <sup>de</sup>	41.07 <sup>ab</sup>	29.95 <sup>e-i</sup>
18	Dosha	41.07 <sup>a-d</sup>	37.14 <sup>abc</sup>	45.00 <sup>ab</sup>	41.07 <sup>abc</sup>	37.14 <sup>bcd</sup>	37.14 <sup>ab</sup>	41.07 <sup>ab</sup>	38.45 <sup>a-d</sup>
19	Gora	45.00 <sup>abc</sup>	37.14 <sup>abc</sup>	45.00 <sup>ab</sup>	42.38 <sup>ab</sup>	26.26 <sup>d-g</sup>	29.74 <sup>a-d</sup>	45.00 <sup>a</sup>	33.67 <sup>c-g</sup>
20	EH08035-1	41.07 <sup>a-d</sup>	33.67 <sup>a-d</sup>	45.00 <sup>ab</sup>	39.91 <sup>a-d</sup>	37.14 <sup>bcd</sup>	37.14 <sup>ab</sup>	45.00 <sup>a</sup>	39.76 <sup>abc</sup>
21	Wayu	48.93 <sup>ab</sup>	19.04 <sup>de</sup>	52.40 <sup>a</sup>	40.12 <sup>abc</sup>	37.14 <sup>bcd</sup>	15.29 <sup>e</sup>	41.07 <sup>ab</sup>	31.17 <sup>e-i</sup>
22	EKLS/CSR02023-2-1	33.67 <sup>b-e</sup>	37.60 <sup>abc</sup>	29.74 <sup>cd</sup>	33.67 <sup>b-i</sup>	22.79 <sup>efg</sup>	26.26 <sup>b-e</sup>	41.07 <sup>ab</sup>	30.04 <sup>e-i</sup>
23	Mesay	41.07 <sup>a-d</sup>	29.74 <sup>a-e</sup>	41.07 <sup>abc</sup>	37.29 <sup>a-g</sup>	37.14 <sup>bcd</sup>	15.29 <sup>e</sup>	45.00 <sup>a</sup>	32.48 <sup>d-h</sup>
24	EH09004-2	33.67 <sup>b-e</sup>	30.19 <sup>a-e</sup>	37.60 <sup>a-d</sup>	33.82 <sup>b-i</sup>	19.04 <sup>fg</sup>	41.07 <sup>a</sup>	22.79 <sup>cd</sup>	27.63 <sup>g-j</sup>
25	EH06088-6	29.74 <sup>cde</sup>	33.21 <sup>a-d</sup>	37.60 <sup>a-d</sup>	33.51 <sup>b-i</sup>	26.26 <sup>d-g</sup>	19.04 <sup>de</sup>	41.07 <sup>ab</sup>	28.79 <sup>f-j</sup>
	Mean	35.24a	31.43b	36.49a	34.39	30.25b	25.69c	35.97a	30.64

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6i. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	33.67 <sup>b-e</sup>	19.04 <sup>de</sup>	33.67 <sup>bcd</sup>	28.79 <sup>ghi</sup>	26.26 <sup>d-g</sup>	33.67 <sup>abc</sup>	45.00 <sup>a</sup>	34.98 <sup>b-f</sup>
27	Kasa	52.86 <sup>a</sup>	26.26 <sup>b-e</sup>	45.00 <sup>ab</sup>	41.37 <sup>abc</sup>	45.00 <sup>ab</sup>	19.04 <sup>de</sup>	45.00 <sup>a</sup>	36.35 <sup>b-e</sup>
28	Cool-0025	41.07 <sup>a-d</sup>	41.07 <sup>ab</sup>	45.00 <sup>ab</sup>	42.38 <sup>ab</sup>	45.00 <sup>ab</sup>	33.67 <sup>abc</sup>	45.00 <sup>a</sup>	41.22 <sup>ab</sup>
29	EH06070-3	22.79 <sup>e</sup>	37.60 <sup>abc</sup>	26.26 <sup>cd</sup>	28.88 <sup>ghi</sup>	22.79 <sup>efg</sup>	26.26 <sup>b-e</sup>	19.04 <sup>d</sup>	22.70 <sup>jkl</sup>
30	EK LS/CSR02010-4-3	41.07 <sup>a-d</sup>	37.14 <sup>abc</sup>	26.26 <sup>cd</sup>	34.82 <sup>b-i</sup>	26.26 <sup>d-g</sup>	29.74 <sup>a-d</sup>	41.07 <sup>ab</sup>	32.36 <sup>d-h</sup>
31	Cool-0031	41.07 <sup>a-d</sup>	41.07 <sup>ab</sup>	41.07 <sup>abc</sup>	41.07 <sup>abc</sup>	52.86 <sup>a</sup>	33.67 <sup>abc</sup>	45.00 <sup>a</sup>	43.84 <sup>a</sup>
32	Cool-0018	37.14 <sup>b-e</sup>	29.74 <sup>a-e</sup>	26.26 <sup>cd</sup>	31.05 <sup>d-i</sup>	37.14 <sup>bcd</sup>	19.04 <sup>de</sup>	41.07 <sup>ab</sup>	32.42 <sup>d-h</sup>
33	EK LS/CSR02028-1-1	37.60 <sup>a-e</sup>	37.14 <sup>abc</sup>	37.60 <sup>a-d</sup>	37.44 <sup>a-g</sup>	37.14 <sup>bcd</sup>	15.29 <sup>e</sup>	45.00 <sup>a</sup>	32.48 <sup>d-h</sup>
34	EK 05037-4	33.67 <sup>b-e</sup>	26.26 <sup>b-e</sup>	37.60 <sup>a-d</sup>	32.51 <sup>c-i</sup>	26.26 <sup>d-g</sup>	19.04 <sup>de</sup>	30.19 <sup>bcd</sup>	25.17 <sup>i-l</sup>
35	Cool-0035	45.00 <sup>abc</sup>	33.67 <sup>a-d</sup>	45.00 <sup>ab</sup>	41.22 <sup>abc</sup>	41.07 <sup>bc</sup>	29.74 <sup>a-d</sup>	45.00 <sup>a</sup>	38.60 <sup>a-d</sup>
36	KUSE2-27-33	48.93 <sup>ab</sup>	26.26 <sup>b-e</sup>	41.07 <sup>abc</sup>	38.75 <sup>a-e</sup>	37.14 <sup>bcd</sup>	15.29 <sup>e</sup>	45.00 <sup>a</sup>	32.48 <sup>d-h</sup>
37	EH07015-7	26.26 <sup>de</sup>	37.14 <sup>abc</sup>	26.26 <sup>cd</sup>	29.89 <sup>e-i</sup>	26.26 <sup>d-g</sup>	22.51 <sup>cde</sup>	26.26 <sup>cd</sup>	25.01 <sup>i-l</sup>
38	Cool-0024	41.07 <sup>a-d</sup>	22.79 <sup>cde</sup>	37.60 <sup>a-d</sup>	33.82 <sup>b-i</sup>	29.74 <sup>c-f</sup>	22.79 <sup>cde</sup>	45.00 <sup>a</sup>	32.51 <sup>d-h</sup>
39	Selale	45.00 <sup>abc</sup>	15.29 <sup>e</sup>	45.00 <sup>ab</sup>	35.10 <sup>a-i</sup>	41.07 <sup>bc</sup>	26.26 <sup>b-e</sup>	41.07 <sup>ab</sup>	36.13 <sup>b-e</sup>
40	Moti	41.07 <sup>a-d</sup>	33.67 <sup>a-d</sup>	37.60 <sup>a-d</sup>	37.44 <sup>a-g</sup>	29.74 <sup>c-f</sup>	19.04 <sup>de</sup>	41.07 <sup>ab</sup>	29.95 <sup>e-i</sup>
41	EH06027-2	29.74 <sup>cde</sup>	26.26 <sup>b-e</sup>	26.26 <sup>cd</sup>	27.42 <sup>hi</sup>	22.79 <sup>efg</sup>	22.79 <sup>cde</sup>	41.07 <sup>ab</sup>	28.88 <sup>f-j</sup>
42	EK LS/CSR02019-2-4	30.19 <sup>cde</sup>	37.14 <sup>abc</sup>	37.60 <sup>a-d</sup>	34.98 <sup>a-i</sup>	33.67 <sup>b-e</sup>	22.79 <sup>cde</sup>	41.07 <sup>ab</sup>	32.51 <sup>d-h</sup>
43	EH09002-1	30.19 <sup>cde</sup>	22.79 <sup>cde</sup>	30.19 <sup>bcd</sup>	27.73 <sup>hi</sup>	26.26 <sup>d-g</sup>	22.79 <sup>cde</sup>	26.26 <sup>cd</sup>	25.11 <sup>i-l</sup>
44	Tumsa	22.51 <sup>e</sup>	29.74 <sup>a-e</sup>	26.26 <sup>cd</sup>	26.17 <sup>i</sup>	19.04 <sup>fg</sup>	22.51 <sup>cde</sup>	26.26 <sup>cd</sup>	22.61 <sup>jkl</sup>
45	Gebelcho	26.26 <sup>de</sup>	33.67 <sup>a-d</sup>	26.26 <sup>cd</sup>	28.73 <sup>ghi</sup>	19.04 <sup>fg</sup>	22.79 <sup>cde</sup>	19.04 <sup>d</sup>	20.29 <sup>kl</sup>
46	EK05037-5	33.67 <sup>b-e</sup>	26.26 <sup>b-e</sup>	37.60 <sup>a-d</sup>	32.51 <sup>c-i</sup>	37.14 <sup>bcd</sup>	22.51 <sup>cde</sup>	26.26 <sup>cd</sup>	28.64 <sup>f-j</sup>
47	Didi'a	37.14 <sup>b-e</sup>	19.04 <sup>de</sup>	37.14 <sup>bcd</sup>	31.11 <sup>d-i</sup>	26.26 <sup>d-g</sup>	26.26 <sup>b-e</sup>	26.26 <sup>cd</sup>	26.26 <sup>h-k</sup>
48	Cool-0034	37.60 <sup>a-e</sup>	22.79 <sup>cde</sup>	37.14 <sup>bcd</sup>	32.51 <sup>c-i</sup>	41.07 <sup>bc</sup>	19.04 <sup>de</sup>	41.07 <sup>ab</sup>	33.73 <sup>c-g</sup>
49	CS20DK	22.79 <sup>e</sup>	19.04 <sup>de</sup>	41.07 <sup>abc</sup>	27.63 <sup>hi</sup>	15.29 <sup>g</sup>	19.04 <sup>de</sup>	22.51 <sup>cd</sup>	18.95 <sup>l</sup>
50	Tesfa	37.60 <sup>a-e</sup>	22.51 <sup>cde</sup>	37.60 <sup>a-d</sup>	32.57 <sup>c-i</sup>	33.67 <sup>b-e</sup>	26.26 <sup>b-e</sup>	26.26 <sup>cd</sup>	28.73 <sup>f-j</sup>
	Mean	35.24a	31.43b	36.49a	34.39	30.25b	25.69c	35.97a	30.64

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6j. Mean performance of 50 genotypes for grain production efficiency

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	119.76 <sup>h-l</sup>	98.77 <sup>e-o</sup>	76.67 <sup>g-l</sup>	98.40	190.63 <sup>d-j</sup>	114.13 <sup>i-o</sup>	197.33 <sup>bcd</sup>	167.37 <sup>d-m</sup>
2	Wolki	164.55 <sup>a-f</sup>	129.30 <sup>a</sup>	66.33 <sup>klm</sup>	120.06	187.90 <sup>d-k</sup>	143.10 <sup>a-h</sup>	144.00 <sup>i-o</sup>	158.33 <sup>g-q</sup>
3	EK LS/CSR02012-2-3	141.87 <sup>b-j</sup>	91.67 <sup>h-q</sup>	100.00 <sup>a-h</sup>	111.18	208.10 <sup>b-f</sup>	132.50 <sup>d-l</sup>	195.00 <sup>bcd</sup>	178.53 <sup>b-g</sup>
4	Obse	172.06 <sup>a-d</sup>	115.63 <sup>a-e</sup>	126.33 <sup>a</sup>	138.01	207.33 <sup>b-f</sup>	127.07 <sup>f-m</sup>	192.67 <sup>b-e</sup>	175.69 <sup>b-i</sup>
5	NC58	131.94 <sup>e-l</sup>	101.57 <sup>d-n</sup>	82.00 <sup>f-l</sup>	105.17	169.07 <sup>f-m</sup>	125.40 <sup>f-m</sup>	131.00 <sup>l-p</sup>	141.16 <sup>q-t</sup>
6	Ashebeka	141.93 <sup>b-j</sup>	90.50 <sup>i-q</sup>	101.67 <sup>a-g</sup>	111.36	180.93 <sup>f-k</sup>	140.13 <sup>a-i</sup>	173.33 <sup>b-j</sup>	164.80 <sup>d-n</sup>
7	Hachalu	149.53 <sup>b-i</sup>	107.60 <sup>b-j</sup>	100.67 <sup>a-h</sup>	119.27	166.50 <sup>f-m</sup>	132.53 <sup>d-l</sup>	134.33 <sup>k-p</sup>	144.46 <sup>o-s</sup>
8	Degaga	136.88 <sup>c-k</sup>	87.83 <sup>j-q</sup>	71.00 <sup>i-m</sup>	98.57	162.73 <sup>g-m</sup>	135.17 <sup>c-k</sup>	143.67 <sup>i-o</sup>	147.19 <sup>n-r</sup>
9	EH09031-4	147.12 <sup>b-j</sup>	99.00 <sup>e-o</sup>	87.67 <sup>e-k</sup>	111.26	182.00 <sup>e-k</sup>	137.07 <sup>b-j</sup>	158.33 <sup>e-l</sup>	159.13 <sup>f-q</sup>
10	Holetta-2	118.15 <sup>h-l</sup>	82.57 <sup>n-q</sup>	79.67 <sup>f-l</sup>	93.46	131.67 <sup>lm</sup>	91.47 <sup>o</sup>	112.33 <sup>op</sup>	111.82 <sup>u</sup>
11	EH09007-4	116.09 <sup>i-l</sup>	101.10 <sup>d-n</sup>	73.33 <sup>h-m</sup>	96.84	172.17 <sup>f-l</sup>	130.37 <sup>f-m</sup>	171.33 <sup>c-j</sup>	157.96 <sup>h-q</sup>
12	EH07023-3	144.52 <sup>b-j</sup>	103.13 <sup>d-m</sup>	111.67 <sup>a-e</sup>	119.77	193.10 <sup>d-j</sup>	138.97 <sup>a-i</sup>	236.33 <sup>a</sup>	189.47 <sup>abc</sup>
13	EK05006-3	188.67 <sup>a</sup>	83.80 <sup>m-q</sup>	111.33 <sup>a-e</sup>	127.93	179.27 <sup>f-k</sup>	129.73 <sup>f-m</sup>	197.67 <sup>bcd</sup>	168.89 <sup>d-l</sup>
14	EK LS/CSR02014-2-4	118.77 <sup>h-l</sup>	110.13 <sup>b-i</sup>	105.33 <sup>a-f</sup>	111.41	157.03 <sup>i-m</sup>	124.93 <sup>f-m</sup>	181.00 <sup>b-h</sup>	154.32 <sup>j-r</sup>
15	Numan	172.48 <sup>abc</sup>	104.97 <sup>c-k</sup>	99.33 <sup>b-h</sup>	125.59	169.53 <sup>f-m</sup>	119.27 <sup>h-n</sup>	193.67 <sup>b-e</sup>	160.82 <sup>f-q</sup>
16	Bulga 70	135.46 <sup>c-k</sup>	105.40 <sup>c-j</sup>	49.00 <sup>mn</sup>	96.62	175.10 <sup>f-k</sup>	129.70 <sup>f-m</sup>	155.67 <sup>f-m</sup>	153.49 <sup>k-r</sup>
17	EK05001-1	143.35 <sup>b-j</sup>	102.43 <sup>d-n</sup>	89.00 <sup>d-k</sup>	111.59	169.07 <sup>f-m</sup>	109.90 <sup>k-o</sup>	188.00 <sup>b-f</sup>	155.66 <sup>i-q</sup>
18	Dosha	168.76 <sup>a-e</sup>	98.07 <sup>e-o</sup>	124.67 <sup>ab</sup>	130.50	175.40 <sup>f-k</sup>	131.07 <sup>e-m</sup>	193.67 <sup>b-e</sup>	166.71 <sup>d-n</sup>
19	Gora	143.03 <sup>b-j</sup>	113.83 <sup>a-g</sup>	112.33 <sup>a-e</sup>	123.06	198.30 <sup>c-i</sup>	134.10 <sup>c-l</sup>	183.67 <sup>b-g</sup>	172.02 <sup>c-k</sup>
20	EH08035-1	154.19 <sup>a-h</sup>	85.30 <sup>k-q</sup>	79.00 <sup>f-l</sup>	106.16	222.73 <sup>a-e</sup>	146.03 <sup>a-g</sup>	163.33 <sup>d-l</sup>	177.37 <sup>b-h</sup>
21	Wayu	69.60 <sup>m</sup>	74.77 <sup>q</sup>	37.00 <sup>n</sup>	60.46	93.90 <sup>n</sup>	105.53 <sup>mno</sup>	78.67 <sup>q</sup>	92.70 <sup>v</sup>
22	EK LS/CSR02023-2-1	124.97 <sup>g-l</sup>	85.07 <sup>k-q</sup>	83.33 <sup>f-l</sup>	97.79	182.33 <sup>e-k</sup>	135.80 <sup>c-k</sup>	168.00 <sup>c-k</sup>	162.04 <sup>e-p</sup>
23	Mesay	115.07 <sup>i-l</sup>	90.17 <sup>i-q</sup>	74.67 <sup>g-m</sup>	93.30	147.60 <sup>klm</sup>	112.57 <sup>j-o</sup>	145.00 <sup>h-o</sup>	135.06 <sup>rst</sup>
24	EH09004-2	157.66 <sup>a-g</sup>	103.23 <sup>d-m</sup>	65.33 <sup>klm</sup>	108.74	255.33 <sup>a</sup>	137.30 <sup>b-j</sup>	137.67 <sup>j-o</sup>	176.77 <sup>b-h</sup>
25	EH06088-6	113.93 <sup>i-l</sup>	91.30 <sup>h-q</sup>	117.67 <sup>abc</sup>	107.63	202.40 <sup>c-g</sup>	124.97 <sup>f-m</sup>	187.33 <sup>b-f</sup>	171.57 <sup>c-k</sup>
	Mean	139.49 <sup>a</sup>	99.64 <sup>b</sup>	86.69 <sup>c</sup>	108.61	183.89 <sup>a</sup>	131.61 <sup>c</sup>	166.20 <sup>b</sup>	160.57

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6j. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	146.46 <sup>b-j</sup>	94.77 <sup>g-p</sup>	83.33 <sup>f-l</sup>	108.19	196.80 <sup>c-j</sup>	133.60 <sup>c-l</sup>	208.33 <sup>ab</sup>	179.58 <sup>b-f</sup>
27	Kasa	96.13 <sup>lm</sup>	87.63 <sup>j-q</sup>	74.00 <sup>g-m</sup>	85.92	155.93 <sup>j-m</sup>	108.60 <sup>l-o</sup>	121.00 <sup>m-p</sup>	128.51 <sup>stu</sup>
28	Cool-0025	145.93 <sup>b-j</sup>	91.83 <sup>h-q</sup>	83.00 <sup>f-l</sup>	106.92	199.77 <sup>c-h</sup>	126.63 <sup>f-m</sup>	178.00 <sup>b-i</sup>	168.13 <sup>d-m</sup>
29	EH06070-3	145.23 <sup>b-j</sup>	80.17 <sup>opq</sup>	75.67 <sup>g-l</sup>	100.35	171.93 <sup>f-l</sup>	111.53 <sup>j-o</sup>	162.67 <sup>d-l</sup>	148.71 <sup>l-r</sup>
30	EK LS/CSR02010-4-3	149.07 <sup>b-j</sup>	100.13 <sup>d-n</sup>	82.67 <sup>f-l</sup>	110.62	234.63 <sup>abc</sup>	161.57 <sup>ab</sup>	184.00 <sup>b-g</sup>	193.40 <sup>ab</sup>
31	Cool-0031	111.87 <sup>ijkl</sup>	104.70 <sup>d-l</sup>	80.67 <sup>f-l</sup>	99.08	190.60 <sup>d-j</sup>	149.77 <sup>a-f</sup>	165.67 <sup>c-l</sup>	168.68 <sup>d-m</sup>
32	Cool-0018	135.00 <sup>d-k</sup>	100.80 <sup>d-n</sup>	76.00 <sup>g-l</sup>	103.93	190.13 <sup>d-j</sup>	121.93 <sup>g-n</sup>	186.00 <sup>b-f</sup>	166.02 <sup>d-n</sup>
33	EK LS/CSR02028-1-1	157.90 <sup>a-g</sup>	114.87 <sup>a-f</sup>	78.67 <sup>f-l</sup>	117.14	197.90 <sup>c-j</sup>	127.30 <sup>f-m</sup>	197.33 <sup>bcd</sup>	174.18 <sup>b-j</sup>
34	EK 05037-4	145.00 <sup>b-j</sup>	119.13 <sup>a-d</sup>	92.33 <sup>c-k</sup>	118.82	223.43 <sup>a-e</sup>	140.77 <sup>a-h</sup>	181.00 <sup>b-h</sup>	181.73 <sup>b-e</sup>
35	Cool-0035	133.96 <sup>e-k</sup>	124.27 <sup>abc</sup>	92.67 <sup>c-k</sup>	116.96	189.73 <sup>d-j</sup>	134.63 <sup>c-l</sup>	165.00 <sup>c-l</sup>	163.12 <sup>d-o</sup>
36	KUSE2-27-33	133.58 <sup>e-k</sup>	88.23 <sup>j-q</sup>	66.33 <sup>klm</sup>	96.05	179.77 <sup>f-k</sup>	133.43 <sup>c-l</sup>	168.00 <sup>c-k</sup>	160.40 <sup>f-q</sup>
37	EH07015-7	166.78 <sup>a-f</sup>	84.80 <sup>l-q</sup>	115.00 <sup>a-d</sup>	122.19	225.10 <sup>a-d</sup>	130.07 <sup>f-m</sup>	169.67 <sup>c-k</sup>	174.94 <sup>b-i</sup>
38	Cool-0024	162.24 <sup>a-g</sup>	110.60 <sup>a-h</sup>	86.00 <sup>e-k</sup>	119.61	202.47 <sup>c-g</sup>	156.43 <sup>a-e</sup>	170.33 <sup>c-j</sup>	176.41 <sup>b-h</sup>
39	Selale	102.20 <sup>kl</sup>	92.67 <sup>h-q</sup>	58.00 <sup>lmn</sup>	84.29	130.33 <sup>m</sup>	142.80 <sup>a-h</sup>	103.67 <sup>pq</sup>	125.60 <sup>tu</sup>
40	Moti	171.47 <sup>a-d</sup>	108.97 <sup>b-i</sup>	98.33 <sup>b-i</sup>	126.26	245.13 <sup>ab</sup>	157.63 <sup>a-d</sup>	200.67 <sup>bc</sup>	201.14 <sup>a</sup>
41	EH06027-2	142.17 <sup>b-j</sup>	95.37 <sup>f-p</sup>	79.00 <sup>f-l</sup>	105.51	162.80 <sup>g-m</sup>	139.67 <sup>a-i</sup>	143.00 <sup>i-o</sup>	148.49 <sup>m-r</sup>
42	EK LS/CSR02019-2-4	158.74 <sup>a-g</sup>	103.17 <sup>d-m</sup>	99.00 <sup>b-h</sup>	120.30	223.17 <sup>a-e</sup>	130.63 <sup>em</sup>	174.67 <sup>b-i</sup>	176.16 <sup>b-h</sup>
43	EH09002-1	162.04 <sup>a-g</sup>	92.63 <sup>h-q</sup>	76.00 <sup>g-l</sup>	110.22	160.40 <sup>g-m</sup>	126.43 <sup>f-m</sup>	173.00 <sup>b-j</sup>	153.28 <sup>k-r</sup>
44	Tumsa	131.07 <sup>f-l</sup>	106.53 <sup>b-j</sup>	94.33 <sup>c-j</sup>	110.65	183.60 <sup>e-k</sup>	140.40 <sup>a-h</sup>	176.67 <sup>b-i</sup>	166.89 <sup>d-n</sup>
45	Gebelcho	103.90 <sup>kl</sup>	101.67 <sup>d-n</sup>	90.33 <sup>d-k</sup>	98.63	158.27 <sup>h-m</sup>	127.27 <sup>f-m</sup>	121.33 <sup>m-p</sup>	135.62 <sup>rst</sup>
46	EK05037-5	118.41 <sup>h-l</sup>	88.97 <sup>j-q</sup>	69.33 <sup>j-m</sup>	92.24	156.77 <sup>i-m</sup>	121.73 <sup>g-n</sup>	148.67 <sup>g-n</sup>	142.39 <sup>p-t</sup>
47	Didi'a	178.82 <sup>a-b</sup>	115.33 <sup>a-e</sup>	85.67 <sup>e-k</sup>	126.61	182.47 <sup>e-k</sup>	163.33 <sup>a</sup>	157.67 <sup>e-l</sup>	167.82 <sup>d-m</sup>
48	Cool-0034	126.65 <sup>g-l</sup>	116.53 <sup>a-e</sup>	96.33 <sup>c-j</sup>	113.17	186.33 <sup>d-k</sup>	147.40 <sup>a-g</sup>	188.33 <sup>b-f</sup>	174.02 <sup>b-j</sup>
49	CS20DK	158.05 <sup>a-g</sup>	125.67 <sup>ab</sup>	98.67 <sup>b-i</sup>	127.46	206.23 <sup>b-f</sup>	158.80 <sup>abc</sup>	184.00 <sup>b-g</sup>	183.01 <sup>bcd</sup>
50	Tesfa	101.68 <sup>kl</sup>	75.67 <sup>pq</sup>	78.00 <sup>f-l</sup>	85.11	162.40 <sup>g-m</sup>	99.37 <sup>no</sup>	118.33 <sup>nop</sup>	126.70 <sup>stu</sup>
	Mean	139.49 <sup>a</sup>	99.64 <sup>b</sup>	86.69 <sup>c</sup>	108.61	183.89 <sup>a</sup>	131.61 <sup>c</sup>	166.20 <sup>b</sup>	160.57

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05



Appendix Table 6k. Mean performance of 50 genotypes for economic growth rate

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
1	Cool-0030	62.74 <sup>l-o</sup>	81.47 <sup>d-l</sup>	52.00 <sup>e-o</sup>	65.40 <sup>j-s</sup>	102.30 <sup>c-k</sup>	91.50 <sup>l-q</sup>	114.33 <sup>a-d</sup>	102.71 <sup>d-j</sup>
2	Wolki	108.31 <sup>a</sup>	105.93 <sup>ab</sup>	43.67 <sup>l-p</sup>	85.97 <sup>ab</sup>	110.79 <sup>bcd</sup>	123.27 <sup>b-f</sup>	93.70 <sup>d-k</sup>	109.25 <sup>c-g</sup>
3	EK LS/CSR02012-2-3	68.79 <sup>h-n</sup>	70.63 <sup>i-o</sup>	57.33 <sup>b-n</sup>	65.58 <sup>i-s</sup>	101.87 <sup>c-k</sup>	99.30 <sup>h-p</sup>	110.37 <sup>a-f</sup>	103.85 <sup>d-j</sup>
4	Obse	83.86 <sup>b-i</sup>	92.90 <sup>b-f</sup>	76.00 <sup>a</sup>	84.25 <sup>abc</sup>	104.69 <sup>b-i</sup>	98.40 <sup>i-p</sup>	111.17 <sup>a-e</sup>	104.75 <sup>d-j</sup>
5	NC58	69.11 <sup>h-n</sup>	83.47 <sup>c-k</sup>	54.67 <sup>c-o</sup>	69.08 <sup>h-o</sup>	87.62 <sup>f-l</sup>	98.97 <sup>i-p</sup>	86.57 <sup>h-l</sup>	91.05 <sup>k-n</sup>
6	Ashebeka	86.97 <sup>b-h</sup>	74.33 <sup>i-o</sup>	68.67 <sup>abc</sup>	76.66 <sup>c-h</sup>	106.76 <sup>b-g</sup>	107.77 <sup>e-l</sup>	105.90 <sup>a-h</sup>	106.81 <sup>c-i</sup>
7	Hachalu	85.10 <sup>b-h</sup>	90.03 <sup>c-h</sup>	67.00 <sup>a-g</sup>	80.71 <sup>b-e</sup>	97.92 <sup>c-k</sup>	114.13 <sup>d-j</sup>	88.33 <sup>f-l</sup>	100.13 <sup>e-k</sup>
8	Degaga	81.78 <sup>b-j</sup>	72.97 <sup>i-o</sup>	49.67 <sup>i-o</sup>	68.14 <sup>h-q</sup>	93.14 <sup>c-k</sup>	109.20 <sup>e-k</sup>	89.73 <sup>e-l</sup>	97.36 <sup>g-l</sup>
9	EH09031-4	70.45 <sup>h-n</sup>	74.63 <sup>h-o</sup>	51.67 <sup>f-o</sup>	65.58 <sup>i-s</sup>	93.55 <sup>c-k</sup>	99.30 <sup>h-p</sup>	89.47 <sup>e-l</sup>	94.11 <sup>j-m</sup>
10	Holetta-2	63.71 <sup>j-o</sup>	61.70 <sup>o</sup>	47.00 <sup>i-p</sup>	57.47 <sup>st</sup>	67.82 <sup>lmn</sup>	75.10 <sup>q</sup>	65.53 <sup>mn</sup>	69.48 <sup>o</sup>
11	EH09007-4	59.22 <sup>k-o</sup>	76.30 <sup>g-o</sup>	43.00 <sup>m-p</sup>	59.51 <sup>o-t</sup>	90.26 <sup>c-k</sup>	99.97 <sup>h-p</sup>	97.90 <sup>b-j</sup>	96.04 <sup>i-l</sup>
12	EH07023-3	70.75 <sup>g-n</sup>	78.43 <sup>f-n</sup>	60.67 <sup>a-k</sup>	69.95 <sup>g-m</sup>	94.50 <sup>c-k</sup>	109.20 <sup>e-k</sup>	116.57 <sup>abc</sup>	106.76 <sup>c-i</sup>
13	EK05006-3	96.98 <sup>ab</sup>	61.20 <sup>o</sup>	62.67 <sup>a-i</sup>	73.61 <sup>d-k</sup>	92.68 <sup>c-k</sup>	107.07 <sup>e-m</sup>	121.07 <sup>a</sup>	106.94 <sup>c-i</sup>
14	EK LS/CSR02014-2-4	57.89 <sup>l-o</sup>	81.30 <sup>d-l</sup>	59.67 <sup>b-l</sup>	66.29 <sup>i-s</sup>	88.22 <sup>e-l</sup>	93.27 <sup>k-p</sup>	104.77 <sup>a-h</sup>	95.42 <sup>i-m</sup>
15	Numan	91.81 <sup>a-e</sup>	85.07 <sup>c-j</sup>	60.67 <sup>a-k</sup>	79.18 <sup>b-g</sup>	89.13 <sup>d-k</sup>	88.30 <sup>n-q</sup>	114.97 <sup>a-d</sup>	97.46 <sup>g-l</sup>
16	Bulga 70	70.53 <sup>g-n</sup>	81.60 <sup>d-l</sup>	32.33 <sup>pq</sup>	61.49 <sup>m-t</sup>	91.48 <sup>c-k</sup>	108.03 <sup>e-l</sup>	95.23 <sup>c-k</sup>	98.25 <sup>f-l</sup>
17	EK05001-1	68.75 <sup>h-n</sup>	84.30 <sup>c-j</sup>	50.00 <sup>i-o</sup>	67.68 <sup>h-r</sup>	83.01 <sup>i-m</sup>	90.03 <sup>m-q</sup>	113.23 <sup>a-d</sup>	95.42 <sup>i-m</sup>
18	Dosha	90.87 <sup>a-f</sup>	79.20 <sup>d-m</sup>	71.00 <sup>ab</sup>	80.36 <sup>b-e</sup>	94.95 <sup>c-k</sup>	110.77 <sup>e-k</sup>	115.27 <sup>a-d</sup>	107.00 <sup>c-i</sup>
19	Gora	71.37 <sup>f-n</sup>	91.13 <sup>c-g</sup>	67.33 <sup>a-f</sup>	76.61 <sup>c-h</sup>	100.05 <sup>c-k</sup>	109.27 <sup>e-k</sup>	116.37 <sup>abc</sup>	108.56 <sup>c-h</sup>
20	EH08035-1	77.58 <sup>c-l</sup>	65.30 <sup>mno</sup>	45.67 <sup>k-p</sup>	62.85 <sup>l-t</sup>	110.11 <sup>bcd</sup>	123.97 <sup>b-e</sup>	93.13 <sup>d-k</sup>	109.07 <sup>c-h</sup>
21	Wayu	49.36 <sup>o</sup>	63.23 <sup>no</sup>	28.33 <sup>q</sup>	46.98 <sup>u</sup>	66.58 <sup>mn</sup>	88.37 <sup>n-q</sup>	57.23 <sup>n</sup>	70.73 <sup>o</sup>
22	EK LS/CSR02023-2-1	59.68 <sup>k-o</sup>	62.93 <sup>o</sup>	49.33 <sup>i-o</sup>	57.32 <sup>st</sup>	86.14 <sup>g-m</sup>	113.57 <sup>d-j</sup>	95.30 <sup>c-k</sup>	98.34 <sup>f-l</sup>
23	Mesay	67.39 <sup>h-o</sup>	70.03 <sup>j-o</sup>	48.33 <sup>i-o</sup>	61.92 <sup>m-t</sup>	81.92 <sup>j-n</sup>	91.53 <sup>l-q</sup>	87.60 <sup>g-l</sup>	87.02 <sup>lmn</sup>
24	EH09004-2	81.31 <sup>b-j</sup>	79.67 <sup>d-m</sup>	39.00 <sup>opq</sup>	66.66 <sup>i-s</sup>	131.71 <sup>a</sup>	116.03 <sup>d-i</sup>	82.43 <sup>i-m</sup>	110.06 <sup>c-f</sup>
25	EH06088-6	54.16 <sup>mno</sup>	72.13 <sup>i-o</sup>	67.67 <sup>a-e</sup>	64.65 <sup>j-t</sup>	100.93 <sup>c-k</sup>	103.47 <sup>g-o</sup>	105.10 <sup>a-h</sup>	103.16 <sup>d-j</sup>
	Mean	74.10 <sup>b</sup>	79.23 <sup>a</sup>	53.53 <sup>c</sup>	68.95	98.01 <sup>b</sup>	107.32 <sup>a</sup>	99.44 <sup>b</sup>	101.59

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 6k. Continued

S.N	Genotype	Without lime				With lime			
		Holetta	W/Minjaro	Jeldu	Mean	Holetta	W/Minjaro	Jeldu	Mean
26	EK LS/CSR02017-3-4	70.78 <sup>g-n</sup>	70.03 <sup>j-o</sup>	51.67 <sup>f-o</sup>	64.16 <sup>k-t</sup>	98.03 <sup>c-k</sup>	113.40 <sup>d-j</sup>	114.57 <sup>a-d</sup>	108.67 <sup>c-h</sup>
27	Kasa	55.35 <sup>mno</sup>	68.07 <sup>k-o</sup>	50.33 <sup>h-o</sup>	57.92 <sup>rst</sup>	85.92 <sup>g-m</sup>	89.47 <sup>n-q</sup>	77.83 <sup>j-m</sup>	84.41 <sup>mn</sup>
28	Cool-0025	76.59 <sup>c-l</sup>	78.80 <sup>e-m</sup>	51.33 <sup>g-o</sup>	68.91 <sup>h-o</sup>	108.25 <sup>b-f</sup>	108.27 <sup>e-l</sup>	109.40 <sup>a-g</sup>	108.64 <sup>c-h</sup>
29	EH06070-3	72.26 <sup>f-n</sup>	67.10 <sup>l-o</sup>	45.67 <sup>k-p</sup>	61.67 <sup>m-t</sup>	88.10 <sup>e-l</sup>	84.07 <sup>pq</sup>	97.50 <sup>b-j</sup>	89.89 <sup>k-n</sup>
30	EK LS/CSR02010-4-3	72.69 <sup>e-n</sup>	79.13 <sup>e-m</sup>	49.00 <sup>i-o</sup>	66.94 <sup>h-s</sup>	111.36 <sup>bc</sup>	134.23 <sup>ab</sup>	105.97 <sup>a-h</sup>	117.19 <sup>bc</sup>
31	Cool-0031	63.00 <sup>j-o</sup>	84.10 <sup>c-j</sup>	51.00 <sup>h-o</sup>	66.03 <sup>i-s</sup>	102.66 <sup>c-k</sup>	120.90 <sup>b-g</sup>	97.60 <sup>b-j</sup>	107.05 <sup>c-i</sup>
32	Cool-0018	77.25 <sup>c-l</sup>	80.27 <sup>d-m</sup>	49.33 <sup>i-o</sup>	68.95 <sup>h-o</sup>	111.07 <sup>bc</sup>	97.47 <sup>j-p</sup>	115.27 <sup>a-d</sup>	107.93 <sup>c-h</sup>
33	EK LS/CSR02028-1-1	78.85 <sup>b-k</sup>	80.93 <sup>d-l</sup>	45.67 <sup>k-p</sup>	68.48 <sup>h-p</sup>	96.34 <sup>c-k</sup>	104.40 <sup>g-n</sup>	114.70 <sup>a-d</sup>	105.15 <sup>d-j</sup>
34	EK 05037-4	71.34 <sup>f-n</sup>	91.97 <sup>b-f</sup>	52.67 <sup>d-o</sup>	71.99 <sup>e-l</sup>	107.21 <sup>b-g</sup>	115.70 <sup>d-i</sup>	101.50 <sup>a-i</sup>	108.14 <sup>c-h</sup>
35	Cool-0035	70.35 <sup>h-n</sup>	98.03 <sup>abc</sup>	57.67 <sup>b-n</sup>	75.35 <sup>c-i</sup>	106.93 <sup>b-g</sup>	115.80 <sup>d-i</sup>	104.33 <sup>a-i</sup>	109.02 <sup>c-h</sup>
36	KUSE2-27-33	68.51 <sup>h-o</sup>	68.00 <sup>k-o</sup>	43.00 <sup>m-p</sup>	59.84 <sup>n-t</sup>	105.19 <sup>b-h</sup>	115.50 <sup>d-i</sup>	103.80 <sup>a-i</sup>	108.16 <sup>c-h</sup>
37	EH07015-7	80.69 <sup>b-j</sup>	62.20 <sup>o</sup>	66.00 <sup>a-h</sup>	69.63 <sup>h-n</sup>	108.53 <sup>b-f</sup>	110.70 <sup>e-k</sup>	107.97 <sup>a-h</sup>	109.07 <sup>c-h</sup>
38	Cool-0024	83.75 <sup>b-i</sup>	85.97 <sup>c-i</sup>	53.67 <sup>c-o</sup>	74.46 <sup>d-j</sup>	106.21 <sup>b-g</sup>	130.13 <sup>a-d</sup>	106.20 <sup>a-h</sup>	114.18 <sup>cd</sup>
39	Selale	53.84 <sup>no</sup>	71.17 <sup>i-o</sup>	41.67 <sup>n-q</sup>	55.56 <sup>t</sup>	63.36 <sup>n</sup>	115.10 <sup>d-j</sup>	70.20 <sup>mn</sup>	82.89 <sup>n</sup>
40	Moti	90.15 <sup>b-g</sup>	89.93 <sup>c-h</sup>	62.00 <sup>a-j</sup>	80.70 <sup>b-e</sup>	125.39 <sup>ab</sup>	133.10 <sup>abc</sup>	119.53 <sup>ab</sup>	126.01 <sup>ab</sup>
41	EH06027-2	75.06 <sup>d-l</sup>	79.90 <sup>d-m</sup>	49.00 <sup>i-o</sup>	67.99 <sup>h-q</sup>	87.15 <sup>f-l</sup>	107.77 <sup>e-l</sup>	87.27 <sup>g-l</sup>	94.06 <sup>j-m</sup>
42	EK LS/CSR02019-2-4	73.75 <sup>e-m</sup>	79.70 <sup>d-m</sup>	58.67 <sup>b-m</sup>	70.71 <sup>f-m</sup>	109.69 <sup>b-e</sup>	105.70 <sup>f-n</sup>	95.50 <sup>c-k</sup>	103.63 <sup>d-j</sup>
43	EH09002-1	80.33 <sup>b-j</sup>	71.87 <sup>i-o</sup>	46.33 <sup>j-p</sup>	66.18 <sup>i-s</sup>	81.09 <sup>k-n</sup>	99.53 <sup>h-p</sup>	101.10 <sup>a-i</sup>	93.91 <sup>j-m</sup>
44	Tumsa	85.89 <sup>b-h</sup>	93.97 <sup>b-e</sup>	59.33 <sup>b-l</sup>	79.73 <sup>b-f</sup>	104.07 <sup>c-i</sup>	116.83 <sup>c-h</sup>	111.03 <sup>a-e</sup>	110.65 <sup>cde</sup>
45	Gebelcho	76.22 <sup>c-l</sup>	85.03 <sup>c-j</sup>	60.67 <sup>a-k</sup>	73.97 <sup>d-k</sup>	105.12 <sup>b-h</sup>	109.20 <sup>e-k</sup>	77.33 <sup>j-m</sup>	97.22 <sup>h-l</sup>
46	EK05037-5	57.87 <sup>l-o</sup>	71.40 <sup>j-o</sup>	46.00 <sup>j-p</sup>	58.42 <sup>q-t</sup>	83.45 <sup>h-m</sup>	94.97 <sup>k-p</sup>	89.33 <sup>e-l</sup>	89.25 <sup>k-n</sup>
47	Didi'a	95.12 <sup>abc</sup>	98.40 <sup>abc</sup>	53.00 <sup>c-o</sup>	82.17 <sup>a-d</sup>	103.09 <sup>c-j</sup>	129.40 <sup>a-d</sup>	98.67 <sup>b-j</sup>	110.39 <sup>cde</sup>
48	Cool-0034	68.38 <sup>h-o</sup>	94.63 <sup>bcd</sup>	60.33 <sup>b-k</sup>	74.45 <sup>d-j</sup>	99.47 <sup>c-k</sup>	117.10 <sup>c-h</sup>	106.93 <sup>a-h</sup>	107.83 <sup>c-h</sup>
49	CS20DK	94.41 <sup>a-d</sup>	108.83 <sup>a</sup>	68.33 <sup>a-d</sup>	90.52 <sup>a</sup>	131.04 <sup>a</sup>	141.07 <sup>a</sup>	111.53 <sup>a-e</sup>	127.88 <sup>a</sup>
50	Tesfa	64.17 <sup>i-o</sup>	62.17 <sup>o</sup>	50.67 <sup>h-o</sup>	59.00 <sup>p-t</sup>	103.65 <sup>c-i</sup>	86.43 <sup>opq</sup>	75.40 <sup>k-n</sup>	88.50 <sup>lmn</sup>
	Mean	74.10 <sup>b</sup>	79.23 <sup>a</sup>	53.53 <sup>c</sup>	68.95	98.01 <sup>b</sup>	107.32 <sup>a</sup>	99.44 <sup>b</sup>	101.59

Mean values followed by similar letter(s) in each column had nonsignificant difference at P<0.05

Appendix Table 7. ED of 50 faba bean genotypes evaluated with lime application over three locations measured from 12 traits in 2017

Geno	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25
G1	0.00	3.85	3.07	2.99	4.17	2.57	3.15	3.50	4.62	5.56	4.07	4.24	1.42	3.24	3.85	3.35	3.04	1.82	4.73	3.70	7.97	2.64	3.84	4.08	2.94
G2		0.00	6.27	5.58	3.48	4.54	3.49	2.60	7.34	6.97	6.72	7.26	4.34	6.00	6.64	3.15	4.75	3.66	6.47	5.48	7.45	5.68	3.66	4.89	5.65
G3			0.00	2.43	6.56	3.60	5.01	5.86	2.93	6.54	2.68	3.09	2.83	3.11	2.02	5.91	3.57	4.30	4.68	4.45	9.91	1.84	6.03	4.44	2.46
G4				0.00	5.29	3.60	4.26	4.83	3.99	6.51	3.32	3.12	2.63	2.91	2.87	4.89	2.42	3.28	4.07	3.12	9.53	1.77	5.02	3.64	2.82
G5					0.00	5.56	4.13	1.71	7.18	5.18	6.55	7.23	4.99	5.57	6.66	1.73	3.99	3.86	6.71	5.11	6.62	5.43	1.23	5.30	5.78
G6						0.00	2.62	5.11	5.31	7.04	4.99	3.90	1.67	3.75	4.10	5.20	4.33	2.79	4.65	5.23	8.64	2.98	5.29	5.57	4.43
G7							0.00	3.71	5.83	5.83	5.16	5.89	2.75	4.00	4.72	4.06	3.89	2.87	5.06	5.17	6.49	3.85	3.80	5.23	4.79
G8								0.00	6.48	5.08	5.69	7.00	4.33	5.09	5.97	1.63	3.26	3.38	6.23	4.29	6.72	4.98	1.58	3.97	4.74
G9									0.00	5.71	2.18	5.25	4.53	2.62	2.25	6.66	4.11	5.79	4.27	5.35	9.41	3.19	6.40	5.03	3.14
G10										0.00	5.16	8.38	6.27	5.32	5.79	5.22	4.90	6.37	7.73	6.71	5.36	5.70	4.18	6.56	5.61
G11											0.00	5.25	3.93	3.00	1.44	5.96	3.17	5.10	5.09	4.31	8.78	2.69	5.74	3.91	1.95
G12												0.00	3.75	4.36	4.32	6.90	4.92	4.55	5.14	5.17	11.52	3.09	7.02	6.16	4.73
G13													0.00	2.95	3.38	4.29	3.33	1.86	4.17	3.77	8.34	2.26	4.67	4.30	3.02
G14														0.00	2.70	5.21	3.08	3.80	2.87	4.20	8.32	2.21	4.95	4.66	3.07
G15															0.00	6.18	3.40	4.84	4.65	4.65	9.08	1.87	5.93	4.53	2.50
G16																0.00	3.91	3.21	6.26	4.32	6.69	5.10	2.11	4.58	4.91
G17																	0.00	3.43	4.85	3.06	8.23	2.57	3.34	2.79	2.70
G18																		0.00	4.70	3.31	8.10	3.43	3.85	4.33	3.86
G19																			0.00	4.98	9.78	4.22	6.46	5.44	4.74
G20																				0.00	9.48	3.90	4.91	2.57	2.83
G21																					0.00	8.91	6.19	9.30	8.94
G22																						0.00	4.86	4.34	2.60
G23																							0.00	4.92	5.14
G24																								0.00	2.71
G25																									0.00

Geno= genotype, G1-G25 genotypes list given in Table1.

Appendix Table 7. Continued

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G1	3.06	4.81	3.08	4.13	3.69	3.68	3.31	2.11	3.05	4.23	5.07	3.30	3.83	4.97	3.71	2.59	3.07	3.04	4.66	5.05	3.45	2.73	2.23	5.78	5.29
G2	5.92	4.54	3.57	6.92	6.00	4.66	1.95	5.38	4.86	3.23	2.93	5.47	2.41	5.88	4.43	4.89	6.08	5.12	5.26	5.28	5.19	4.04	3.46	3.44	4.44
G3	2.43	6.96	5.44	2.89	2.80	6.06	5.71	2.31	3.25	6.61	7.41	2.73	6.20	6.81	4.40	3.11	2.41	3.10	5.49	5.98	4.13	3.79	4.58	7.55	7.24
G4	1.61	5.79	3.87	4.06	2.04	5.00	4.46	2.57	3.33	5.26	6.28	3.24	5.18	6.28	3.66	2.80	2.43	3.14	5.76	6.16	3.67	3.69	3.92	7.31	6.54
G5	6.07	1.91	3.25	6.76	6.59	4.12	2.56	5.58	5.51	3.32	3.34	6.40	3.49	4.10	5.94	4.59	6.20	4.74	6.67	6.37	4.15	5.23	3.57	6.29	3.78
G6	3.40	6.28	4.15	4.74	3.69	4.70	4.43	2.96	3.72	5.28	6.32	3.51	4.92	6.40	4.26	2.63	2.73	4.59	4.40	4.28	5.02	2.60	3.95	6.40	6.71
G7	4.47	4.42	3.47	5.03	5.03	4.66	3.60	3.97	4.85	4.34	5.14	4.30	4.63	5.07	5.11	2.68	4.52	4.36	4.71	3.38	4.12	3.17	4.07	6.05	4.66
G8	5.39	2.45	3.04	6.04	5.94	4.31	2.07	5.03	4.85	2.95	2.92	5.42	3.18	4.42	5.05	4.32	5.78	3.82	6.07	5.89	3.44	4.60	3.30	5.42	2.97
G9	4.14	7.04	6.71	2.30	4.81	7.01	6.94	3.88	4.39	7.25	7.86	3.00	7.68	6.20	6.34	3.88	4.48	3.18	5.41	5.70	3.83	4.57	6.05	8.76	6.99
G10	7.04	4.04	6.73	4.70	8.17	7.26	6.75	6.18	7.22	7.22	7.34	6.80	7.75	3.74	8.70	5.03	7.19	4.30	7.80	6.47	3.28	6.84	6.44	9.30	4.16
G11	3.41	6.26	5.93	1.65	4.30	6.96	6.28	3.34	4.85	6.95	7.57	3.31	7.15	6.15	5.76	3.42	4.26	2.18	6.24	5.89	2.76	4.82	5.56	8.26	6.04
G12	2.84	8.05	5.65	5.42	2.84	5.84	6.30	3.66	3.93	6.97	8.22	4.57	6.54	8.11	4.81	4.27	1.72	5.32	6.66	7.51	6.09	4.90	5.25	8.80	9.05
G13	2.35	5.51	3.26	4.04	2.94	4.09	3.87	1.72	3.31	4.63	5.70	2.80	4.46	5.63	3.54	2.34	2.53	3.51	4.49	4.71	3.93	2.45	3.05	6.14	5.89
G14	2.97	5.57	4.73	3.10	4.01	4.92	5.38	2.92	3.61	5.35	6.42	2.50	6.24	4.94	5.40	2.57	3.28	3.09	4.52	4.80	3.25	3.27	4.72	8.04	6.03
G15	2.94	6.60	5.83	1.80	3.64	6.76	6.21	2.82	4.47	6.98	7.74	2.99	7.02	6.43	5.49	2.69	3.41	2.76	5.80	5.40	3.42	4.29	5.41	8.20	6.67
G16	5.51	2.41	2.59	6.30	5.94	3.52	2.17	4.66	5.09	3.01	3.01	5.72	2.88	3.75	5.08	4.45	5.93	4.30	6.06	6.15	3.85	4.61	2.40	5.36	3.61
G17	3.10	4.24	3.86	3.82	4.00	5.20	3.89	3.66	3.71	4.63	5.35	3.74	4.96	5.35	4.58	2.80	3.69	1.73	6.03	5.90	1.95	4.19	4.08	7.14	4.72
G18	3.17	4.61	1.71	5.40	3.77	2.81	2.75	2.94	3.80	3.26	4.58	4.06	3.34	5.25	3.54	3.28	3.49	4.11	5.17	5.57	4.19	3.24	2.37	5.91	5.41
G19	4.03	6.98	5.22	5.55	4.19	4.95	5.84	4.26	3.87	5.16	6.29	2.90	6.43	6.24	5.18	4.51	4.58	5.18	3.67	5.33	5.44	3.22	5.44	7.88	7.40
G20	2.91	5.32	3.37	5.47	3.52	4.78	4.29	3.66	4.60	4.42	5.45	4.40	4.91	6.19	3.81	4.59	4.47	3.65	6.76	7.44	3.86	5.00	3.95	7.14	5.81
G21	9.94	5.31	8.00	8.31	10.80	8.57	7.96	8.72	10.06	8.16	7.93	9.28	8.88	5.06	10.65	7.59	10.20	8.01	8.73	6.45	6.90	8.40	8.27	9.35	4.66
G22	2.03	5.75	4.52	2.87	2.90	5.32	4.97	2.10	3.42	5.77	6.73	2.99	5.73	5.86	4.62	1.66	1.99	2.62	5.44	5.36	3.23	3.55	4.18	7.64	6.38
G23	5.71	1.67	3.68	5.86	6.43	4.59	3.08	5.22	5.28	3.81	3.90	5.90	4.14	3.75	6.08	3.97	5.83	3.88	6.46	5.86	3.21	5.04	3.82	6.60	3.19
G24	3.81	5.51	4.41	5.11	4.15	6.01	4.26	4.44	4.38	4.83	5.20	3.99	5.01	6.63	3.75	4.83	5.15	2.98	6.44	6.94	3.52	4.85	4.55	6.22	5.10
G25	2.56	5.79	4.71	3.00	3.41	5.75	5.09	2.52	3.91	5.70	6.40	2.85	5.78	5.94	4.31	3.47	3.73	1.94	5.79	6.12	2.80	4.18	4.25	7.08	5.67

Geno= genotype, G1-G50 genotypes list given in Table1

Appendix Table 7. Continued

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G26	0.00	6.50	4.16	4.13	1.69	5.18	5.02	2.43	3.56	5.53	6.77	2.95	5.64	6.85	3.62	3.30	2.00	3.56	5.85	6.39	4.22	3.91	4.36	7.61	6.99
G27		0.00	4.04	6.48	7.25	5.04	3.91	5.85	6.52	4.26	4.24	6.71	4.97	3.16	6.95	4.83	6.93	4.70	7.14	6.32	3.63	5.88	4.54	7.17	2.67
G28			0.00	6.45	4.48	2.63	2.11	3.99	4.68	2.50	3.76	5.07	2.80	5.15	3.78	4.23	4.81	4.80	5.82	6.24	4.59	4.03	2.45	5.70	5.13
G29				0.00	5.12	7.20	6.71	3.68	5.08	7.45	8.07	3.65	7.58	6.05	6.54	3.24	4.30	2.75	6.10	5.32	3.18	4.87	5.92	8.62	6.25
G30					0.00	5.49	5.08	2.82	3.56	5.79	6.86	3.33	5.44	7.62	2.78	3.97	2.69	4.42	5.82	6.74	5.21	3.92	4.37	7.09	7.77
G31						0.00	3.52	4.62	4.57	2.76	4.09	5.49	3.56	4.88	4.90	5.07	5.29	5.86	5.22	6.54	5.74	4.09	2.94	6.46	6.37
G32							0.00	4.71	4.31	2.33	2.60	5.26	1.42	5.44	3.69	4.44	5.34	4.68	5.59	5.99	4.67	3.94	2.40	4.38	4.68
G33								0.00	3.76	5.46	6.35	3.06	5.18	5.51	4.02	2.60	2.97	3.38	4.96	5.35	3.85	3.16	3.19	6.69	6.35
G34									0.00	4.70	5.44	2.81	4.55	6.56	3.53	3.93	3.18	3.91	4.12	5.84	4.83	2.73	3.86	6.32	6.96
G35										0.00	1.93	5.44	2.82	5.22	4.55	5.36	6.04	5.49	5.33	6.34	5.31	4.27	3.53	5.43	5.02
G36											0.00	6.28	2.87	5.34	5.27	6.13	7.27	5.91	5.73	6.62	5.71	4.98	4.00	4.60	4.64
G37												0.00	5.88	6.36	4.12	3.53	3.49	3.49	3.57	4.65	4.25	2.42	4.75	6.74	6.49
G38													0.00	6.20	3.59	5.34	5.82	5.58	5.89	6.78	5.75	4.40	2.37	3.88	5.77
G39														0.00	7.72	4.96	7.16	5.18	6.06	5.59	4.22	5.49	4.91	7.85	4.17
G40															0.00	5.11	4.34	5.07	5.59	6.98	5.81	3.84	3.53	4.89	7.20
G41																0.00	3.08	2.86	5.00	4.18	2.99	3.21	3.92	7.11	5.50
G42																	0.00	4.11	5.80	6.27	4.86	3.92	4.61	7.99	7.66
G43																		0.00	5.85	5.62	1.43	4.26	4.29	7.09	4.67
G44																			0.00	3.49	6.18	2.28	5.22	5.98	7.00
G45																				0.00	5.51	3.62	6.03	6.78	5.85
G46																					0.00	4.68	4.48	7.42	3.73
G47																						0.00	3.50	5.37	6.07
G48																							0.00	4.83	5.50
G49																								0.00	6.64
G50																									0.00

Geno= genotype, G26-G50 genotypes list given in Table1.

Appendix Table 8. ED of 50 faba bean genotypes evaluated without lime application over three locations measured from 12 traits in 2017

Geno	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25
G1	0.00	5.07	3.56	5.40	5.52	3.22	3.61	4.61	3.85	2.90	4.76	4.61	3.51	3.36	3.74	3.48	2.82	4.47	3.38	4.31	6.32	3.54	3.98	4.30	5.44
G2		0.00	5.80	4.75	4.97	3.42	2.59	4.78	6.84	6.15	7.83	6.50	5.18	6.61	5.09	5.07	5.12	4.15	5.26	7.26	8.98	7.28	5.11	5.74	7.68
G3			0.00	4.58	7.04	4.00	4.35	6.26	2.68	3.95	4.01	2.56	3.42	2.81	3.33	4.86	1.99	4.37	3.75	4.35	9.30	2.85	5.40	3.96	5.03
G4				0.00	6.51	4.37	3.60	6.65	5.67	6.66	7.17	5.60	3.96	5.13	3.43	6.16	4.22	2.66	3.46	6.07	11.06	6.32	6.46	5.30	7.93
G5					0.00	5.92	5.11	4.07	8.24	6.00	8.74	8.00	6.52	7.45	7.20	3.53	5.88	5.13	6.22	7.07	7.71	7.53	3.32	5.77	8.26
G6						0.00	1.61	5.53	5.21	5.42	6.52	4.98	4.12	4.51	3.38	5.19	3.55	3.53	3.49	6.21	8.49	5.55	5.37	5.55	6.69
G7							0.00	5.38	5.63	5.54	7.08	5.20	3.85	4.98	3.36	4.93	3.80	2.78	3.32	6.36	8.86	6.08	5.16	5.40	6.89
G8								0.00	6.65	4.75	6.24	7.02	6.12	6.53	6.33	2.71	5.06	5.44	6.00	4.97	6.42	5.90	2.06	3.75	6.73
G9									0.00	3.91	2.57	2.82	3.28	2.48	3.47	5.64	3.07	5.62	4.10	3.58	9.05	2.23	6.26	4.23	4.42
G10										0.00	4.01	5.00	4.34	4.25	5.49	2.83	3.55	6.01	5.30	4.29	6.13	3.16	3.68	3.96	5.31
G11											0.00	4.29	5.24	4.05	5.28	5.60	4.16	6.89	5.80	3.01	8.57	2.12	6.00	3.88	4.61
G12												0.00	3.48	3.09	3.46	5.98	3.05	4.81	3.93	4.53	10.24	3.59	6.52	4.60	3.26
G13													0.00	2.48	2.89	5.09	2.51	3.49	2.24	4.67	9.21	4.16	5.77	4.75	5.34
G14														0.00	3.48	5.44	2.04	4.47	2.81	3.94	9.03	2.59	6.02	4.83	4.94
G15															0.00	5.86	3.29	3.40	2.14	4.64	9.76	4.62	6.24	4.58	5.50
G16																0.00	3.92	5.06	5.35	4.57	6.18	4.67	1.04	3.34	6.08
G17																	0.00	3.28	2.74	3.67	8.57	2.75	4.42	3.51	4.87
G18																		0.00	2.46	5.40	10.03	5.76	5.26	4.73	6.53
G19																			0.00	4.51	9.37	4.55	5.75	4.79	5.66
G20																				0.00	8.45	2.72	4.81	2.44	4.50
G21																					0.00	8.12	6.18	8.41	9.41
G22																						0.00	5.19	3.67	4.41
G23																							0.00	3.47	6.46
G24																								0.00	4.87
G25																									0.00

Geno= genotype, G1-G25 genotypes list given in Table1.

Appendix Table 8. Continued

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G1	3.79	4.79	2.89	2.95	2.79	2.44	3.61	3.51	5.36	3.71	3.93	4.06	4.32	4.31	4.53	3.37	3.29	4.12	3.86	3.41	3.88	4.01	3.70	7.19	4.05
G2	6.47	6.17	4.36	6.44	5.64	4.99	3.69	6.32	5.91	3.63	5.49	5.75	2.94	6.50	3.13	5.31	5.54	5.89	2.82	4.09	6.96	2.84	2.60	3.23	5.76
G3	2.63	6.80	4.96	2.74	1.85	5.08	4.58	3.37	4.73	4.85	5.48	1.78	4.61	6.21	4.58	2.94	2.11	3.15	4.60	5.28	4.11	3.58	4.39	8.05	5.90
G4	5.66	7.69	5.05	6.17	4.45	5.82	5.54	5.08	6.82	4.10	6.63	4.29	4.29	8.51	3.13	6.14	3.90	5.61	5.19	6.27	7.41	2.90	4.41	6.57	7.66
G5	7.62	3.06	2.89	7.79	6.55	3.99	4.21	7.32	6.93	3.09	3.42	7.48	3.52	5.41	4.40	7.13	6.84	7.20	6.57	6.47	7.19	5.91	3.54	5.56	5.39
G6	5.29	6.49	4.00	4.56	3.86	4.09	4.45	4.70	5.34	4.01	5.70	4.07	3.97	6.40	3.65	3.90	3.66	5.28	2.30	3.12	5.78	2.40	3.65	6.11	5.87
G7	5.61	6.20	3.38	5.29	4.23	3.76	4.18	4.99	5.28	3.13	5.46	4.40	3.13	6.49	2.80	4.42	3.85	5.52	2.71	3.50	6.24	1.80	2.83	4.93	6.07
G8	5.69	3.07	3.93	6.04	5.29	4.79	2.38	6.26	6.48	3.65	2.70	6.65	4.15	3.98	4.23	5.62	6.24	4.91	5.48	5.62	4.98	5.44	3.66	6.57	2.65
G9	1.43	7.48	5.86	1.73	2.24	5.87	5.22	2.41	5.39	5.78	6.06	2.47	5.96	6.29	5.76	3.19	2.61	2.54	5.23	5.68	3.78	4.75	5.56	8.94	5.93
G10	3.32	4.48	4.08	3.15	3.65	3.77	3.28	4.20	5.71	4.67	3.20	4.65	4.68	3.25	5.69	3.89	4.40	3.43	5.21	5.02	3.44	5.39	4.10	7.76	3.17
G11	1.87	7.29	6.75	2.66	3.36	6.83	5.33	4.10	6.32	6.66	5.95	4.33	6.86	5.93	6.67	4.04	4.55	2.28	6.38	6.73	2.96	6.18	6.41	10.09	5.24
G12	3.09	7.88	5.90	3.55	2.71	6.14	5.55	3.31	3.26	5.53	6.45	2.32	5.51	6.57	5.15	2.62	2.58	3.59	5.40	6.25	3.98	4.19	5.38	8.66	6.85
G13	3.74	6.84	4.12	3.85	2.78	4.41	4.70	1.91	4.66	3.73	5.32	2.52	4.05	6.24	4.08	4.02	1.76	4.02	4.52	5.35	5.30	3.23	4.02	7.06	6.19
G14	3.16	7.16	4.96	2.84	1.91	5.01	5.41	1.21	5.00	4.91	5.64	2.18	5.31	6.29	5.20	3.83	1.57	3.81	5.34	5.97	4.46	4.44	5.27	8.96	6.23
G15	3.83	7.47	4.88	3.96	2.76	5.20	5.17	3.43	5.24	4.47	6.41	3.01	5.02	7.21	3.82	3.76	2.38	4.24	4.10	4.73	5.28	2.64	4.65	7.27	6.72
G16	4.76	2.20	2.70	5.03	4.34	3.24	1.95	5.37	5.76	3.09	1.08	5.61	3.30	3.03	4.29	4.85	5.17	4.35	5.37	5.27	4.25	5.07	2.80	6.59	2.61
G17	2.92	5.81	3.75	3.04	1.28	4.16	3.76	2.36	4.27	3.44	4.27	2.01	3.55	5.36	3.58	3.19	1.61	3.02	4.38	5.22	3.93	3.18	3.54	7.57	5.09
G18	5.50	6.46	3.65	5.85	3.81	4.65	4.71	4.48	5.01	2.52	5.39	4.12	3.16	7.04	1.79	5.17	3.42	5.34	4.87	5.90	6.24	2.50	3.50	6.40	6.73
G19	4.47	6.78	3.81	4.48	2.73	4.29	5.15	2.79	5.02	3.47	5.64	3.25	4.44	6.77	3.51	4.44	2.06	4.81	4.81	5.37	5.48	3.14	4.38	7.44	6.60
G20	2.84	5.94	5.29	4.00	2.93	5.85	4.73	3.84	5.95	5.03	4.78	4.61	5.91	5.62	5.21	4.69	4.19	2.98	6.67	6.88	3.21	5.67	5.57	9.37	5.07
G21	8.61	5.34	6.90	7.74	8.59	6.16	6.85	8.94	9.96	8.15	6.04	9.95	8.63	4.84	9.50	8.24	9.41	8.55	8.25	6.83	7.32	9.62	7.91	9.97	4.75
G22	1.92	6.35	5.39	2.13	2.13	5.42	4.87	2.97	5.52	5.53	4.97	3.33	5.83	5.32	5.85	3.63	3.26	2.69	5.98	6.20	2.81	5.48	5.52	9.53	5.05
G23	5.30	1.86	3.06	5.58	4.79	3.77	2.14	5.98	6.12	3.32	1.42	6.16	3.62	3.31	4.31	5.26	5.74	4.77	5.62	5.52	4.53	5.37	3.14	6.71	2.57
G24	3.03	4.94	4.58	4.39	3.17	5.40	3.06	4.70	5.45	4.04	3.85	4.56	4.44	5.09	3.88	4.25	4.38	2.50	5.71	6.10	3.40	4.63	3.99	7.65	4.22
G25	4.19	7.48	6.53	4.73	4.44	6.80	5.91	4.83	3.26	6.35	6.34	5.08	6.69	5.47	6.42	3.42	4.99	4.41	6.83	7.14	2.98	6.22	6.38	9.53	6.41

Geno= genotype, G1-G50 genotypes list given in Table1.

Appendix Table 8. Continued

Geno	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50
G26	0.00	6.65	5.53	1.98	2.12	5.72	4.31	3.08	5.26	5.34	5.24	2.92	5.46	5.59	5.28	3.02	3.11	1.33	5.18	5.65	2.98	4.65	5.00	8.58	5.00
G27		0.00	3.45	6.74	6.15	3.90	3.59	7.08	7.25	4.25	2.02	7.56	4.78	3.43	5.63	6.56	6.99	6.29	6.78	6.18	5.65	6.76	4.30	7.14	3.24
G28			0.00	5.42	4.29	1.57	3.32	4.89	5.58	1.78	2.90	5.34	2.88	4.49	3.50	5.10	4.46	5.46	4.87	4.66	5.44	4.20	2.55	5.82	4.52
G29				0.00	2.41	5.17	4.66	3.01	5.50	5.67	5.48	3.05	5.74	5.38	5.84	2.65	3.11	2.76	4.50	4.65	3.27	4.78	5.22	8.68	4.91
G30					0.00	4.61	4.12	2.24	4.60	4.09	4.77	2.04	4.46	5.61	4.04	2.92	1.60	2.57	4.60	5.19	3.42	3.52	4.20	8.06	5.20
G31						0.00	3.97	5.07	6.04	3.18	3.54	5.61	3.87	4.39	4.72	5.10	4.73	5.86	4.84	4.18	5.54	4.76	3.40	6.36	4.62
G32							0.00	5.15	5.35	3.04	2.50	5.06	2.76	3.67	3.53	4.13	4.86	3.58	4.02	4.42	4.30	3.99	1.98	5.50	2.59
G33								0.00	4.93	4.67	5.48	2.39	5.12	6.13	5.03	3.91	1.80	3.56	5.20	5.89	4.58	4.35	5.06	8.52	6.03
G34									0.00	5.11	5.99	4.52	4.90	5.68	5.01	3.42	4.49	5.14	5.68	6.57	4.64	4.76	4.98	7.75	6.71
G35										0.00	3.25	4.91	1.92	5.17	2.07	5.09	4.18	5.00	4.73	5.25	5.60	3.37	1.98	5.38	4.92
G36											0.00	6.01	3.58	2.91	4.68	5.41	5.54	4.79	5.91	5.87	4.65	5.64	3.29	6.93	2.71
G37												0.00	4.70	6.79	4.55	3.30	1.30	3.31	4.57	5.69	4.81	3.36	4.69	8.06	6.51
G38													0.00	5.32	2.42	4.94	4.40	4.93	4.24	5.22	5.92	3.09	1.19	4.72	5.03
G39														0.00	6.39	4.90	6.43	5.29	6.17	5.74	3.90	6.71	4.79	7.85	2.55
G40															0.00	4.93	4.10	4.81	4.39	5.42	5.87	2.36	2.52	5.37	5.79
G41																0.00	3.41	3.18	3.75	4.25	2.88	3.86	4.41	7.56	5.02
G42																	0.00	3.61	4.52	5.34	4.69	3.14	4.35	7.81	6.26
G43																		0.00	4.93	5.70	3.08	4.42	4.51	8.07	4.43
G44																			0.00	2.34	5.89	2.78	3.63	5.28	5.38
G45																				0.00	5.87	4.28	4.31	5.72	5.07
G46																					0.00	5.77	5.39	9.10	4.11
G47																						0.00	2.92	5.39	6.13
G48																							0.00	4.37	4.32
G49																								0.00	7.39
G50																									0.00

Geno= genotype, G26-G50 genotypes list given in Table1