GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS IN SOYBEAN [*Glycine max* (L.) Merrill]] FOR GRAIN YIELD IN ETHIOPIA

M.Sc. Thesis

By

MESFIN HAILEMARIAM

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JIMMA, Ethiopia

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DEDICATION

I dedicated this thesis to those individuals that miss their first, second and or else third choices in their academy life.

STATEMENT OF THE AUTHOR

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BIOGRAPHICA SKETCH

The author was born in West Shewa Zone, Addis Alem town 42km west of Addis Ababa in 1990. He attended both primary and secondary schools in Addis Alem, and then he joined preparatory school at Debre Sina Preparatory School until 2007. Then he joined Debre Berhan University and graduated B.Sc. in Plant Science in July 2010. Then, he joins Jimma Agriculture Research Centre as Junior Researcher in the Pulses, Oil and Fiber Case Team, and then pursued his M.Sc. study in Plant Breeding in October 2014 in Jimma University.

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ABBREVIATIONS AND ACRONYMS

AEC	Average Environment Coordinate
AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
AON	Advanced Observation Nursery
ASV	AMMI Stability Value
b_i	Regression Slope
CSA	Central Statistical Agency
CV	Coefficient of Variation
CV_i	Francis and Kannenberg Coefficient of Variation
DMRT	Duncan Multiple Range Test
EIAR	Ethiopian Institute of Agricultural Research
FAOSTAT	Food and Agriculture Organization statistics
GEI	Genotype by Environment Interaction
GGE	Genotype by Genotype by environment
GLM	General Linear Model
JARC	Jimma Agricultural Research Centre
JRA	Joint Regression Analysis
Kg/ha	Kilograms per hectare
LSD	Least Significance difference
m.a.s.l.	Meters above sea levels
PC	Principal component
P_i	Lin and Binns cultivar superiority measure
RCBD	Randomized Complete Block Design
S^2d_i	Deviation from regression
SAS	Statistical Analysis Software
SVP	Singular Value Partition
W_i	Wricke's ecovalence
YS_i	Kang's yield stability
σ^2_i	Shukla's variance

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ABSTRACT

*Soybean (Glycine max (L.) Merrill] is that recently introduced crop in Ethiopia and also getting importance over time. However, production is affected by environment interaction and lack of stable genotypes across locations. Hence, this experiment was conducted with the objectives of estimating the genotype by environment interaction through stability parameters and to study the interrelationship among stability parameters. Twenty-four soybean genotypes were planted at six soybeans major growing agroecologies of Ethiopia (Asosa, Bako, Dimtu, Jimma, Metu and Pawe) with RCBD in three replications in 2015/2016 cropping season. Among the nine traits subjected to the combined analysis all are showed a highly significant (P < 0.01) environment, genotype and GEI that claims the need of stability analysis. Similarly, combined AMMI ANOVA for grain yield revealed that there were a very highly significant (P< 0.01) difference among genotypes, environments and genotype by environment interactions and accounted 15.3%, 47.32% and 14.24% of the total variations respectively. The high percentages of the environments are an indication that the major factor that influences the yield performance of soybean grain in Ethiopia is the environment. In addition, the first two IPCAs are significant and accounted for 70.34 form a total of interaction sum squares. Nine stability measures viz.,Additive Main Effects and Multiplicative Interactions (AMMI), AMMI stability value (ASV), Francis and Kannenberg's Coefficient of Variability (CV_i), The Environmental Variance (S^2_i), Wricke's Ecovalence Analysis (W_i), Shukla's Stability Variance (σ^2_i), Finlay and Wilkenson (b_i), Eberhart and Russell's (b_i and S^2d_i), Lin and Binns's cultivar performance measure (P_i) and Genotype plus GEI (GGE) bi-plot analysis were used to identify the high yielding and stable genotypes across the testing environments. Genotypes Hang dou No-1 and Spry were the most stable genotypes by stability measures such as ASV, Shukla's stability variance, Wricke's ecovalence, Finlay and Wilkinson's, environmental variance, Eberhart and Russell's and, Lin and Binns's cultivar performance measure. The total correspondence for significance Spearman's rank correlation was used to see the level of association among stability measures. P_i showed a positive highly significant rank correlation(r=0.97**) with mean grain yield and it did not show any correlation with other stability measures except S^2_i (r=-0.85**) and b_i (r=0.88**). From AMMI model, genotypes SCS-1, AFGAT and Clarck-63k were selected as best varieties for Asosa, AFGAT, SCS-1 and Clarck-63k for Bako; SCS-1, ks4895, and Clarck-63k for Dimtu; SCS-1, ks4895 and AGS-7-1 for Jimma; AFGAT, Clarck-63k and Motte for Metu; SCS-1, AFGAT and Clarck-63k for Pawe that suit to a specific environment. AMMI1 biplot showed Pawe is ideal environment; Bako is favorable environment; Asosa average environment; and the rest environments viz., Dimtu, Jimma, and Metu as unfavorable environments. Whereas AMMI-2 biplot analysis genotypes Prichard, Spry, Delsoy 4710 and Croton 3.9 were identified as stable genotypes. Bako and Metu were identified as the most discriminating environments this may due the effects of climate change called El Niño. Mega environments and the best yielding soybean genotypes on each mega environment were revealed by GGE bi-plots analysis model. The genotypes SCS-1 and AGS-7-1 were stable across soybean growing environments and it recommended for mega environment production.*

Key Words: AMMI Model, ASV, GGE, Mega-environment, Rank correlation, Stability Analysis.

1. INTRODUCTION

Soybean [(*Glycine max* (L.) Merrill] belongs to a family Fabaceae of the genus Glycine. The genus Glycine has two subgenera – Soja and Glycine. The subgenus Soja consists of two species: G. max (2n =2x = 40), the cultivated species, and Glycine soja (L.) Sieb or G. ussuriensis (2n=2x=40), a wild species. These two species are cross fertile. Many other species in Glycine have been identified, but the exact classification of most of them is still in doubt. There are 15 wild species of soybean in which G.tabacinia and Glycine have polyploidy forms including 2n=4x=80 (Acquaah, 2007).

Soybean is considered among the oldest cultivated crops. The first record of the crop is contained in a 2838 BC. Chinese book in which Emperor Cheng-ung described the plant. Soybean was a WuKu", one of the sacred five grains (the others being rice, wheat, barley, and millet) considered essential for the existence of Chinese civilization. Cultivated soybean is believed to have derived from a wild progenitor, *Glycine ussuriensis*, which occur in eastern Asia (Korea, Taiwan, Japan, Yangtze Valley of Central China, Northeastern provinces of China, adjacent areas of Russia). The plant was first domesticated in the Eastern half of Northern China in the 11th Century BC (Acquaah,2007). Then after, it spread to several other countries developing landraces, and forming secondary gene center in Japan, Indonesia, Philippines, Vietnam, Thailand, Malaysia, Myanmar, Nepal, and North India (Hymowitz, 2004). The crop was introduced into Ethiopia in the 1950s, and it has been growing in different agro-ecologies of the country (Hammer and Haraldson, 1975; Atnaf *et al*., 2013; Amare, 1987). Nowadays, nationally mandated soybean research coordinator is Pawe Agricultural Research Centre, but other research like Jimma, Bako and Asosa Agricultural Research Centers are undertaking the different soybean research in their specific agroecology's. In addition, Jimma Agricultural Research Centre, introduces soybean germplasms from different institution abroad and also since 2010, is the only Centre in engaging in hybridization program. The genetic stock of the program introduction of materials from abroad i.e. more than 500 soybean germplasm (both commercial and accessions) from the United States Genetic Resource Centre and other sources and also Pawe agricultural research Centre is also introduces 15-30 genotypes every year from International Institute of Tropical Agriculture (Tesfaye *et al.*, unpublished).

From the commercial point of view, soybean has a high commercial value and contains all the amino acids required by the human body except methionine, usually found in cereals such as maize (Osho, 1995). Of all the grain legumes, soybean has the highest concentration of protein, i.e. about 40% protein (Greenberg and Hartung, 1998). While most other grain legumes contain only about 20% proteins by volume. It is important to note that beef and fish contain about 18% protein. Soybean products are cholesterol free and high in calcium, phosphorus, and fiber (Greenberg and Hartung, 1998). Soybean provides more protein and lower levels of saturated fat than most other vegetable grains. In addition, it serves as human diet, livestock, aquaculture, and soybean also serves as a biofuel feedstock (Masuda *et al*., 2009).

Among the major oilseed crops in the world, soybean is the largest source of edible oils. The major U.S.A. oilseed crops are soybeans, cotton seed, sunflower-seed, canola, rapeseed and peanuts Chianu Jonas N *et al*., (2008). Similarly, as stated by (Tesfaye, 2012). Soybean is one of the world's most important pulse crops with an annual worldwide production of 223,184,884 tons in 2009 (FAOSTAT, 2014). It is the leading oil seed crop and contributed about 35% of the world's vegetable oil production in 2001 (Wilcox, 2004; Berma and Specht, 2004). It is also the world's primary livestock feed supplement (Berma and Specht, 2004). In 2016, the leading soybean producing countries were U.S. A with 108.0 million metric tons with 34%, and Brazil with 86.8 million metric tons 30 % of the world's total production (FAOSTAT, 2016).

According to recent FAO statistics, major global producers in order of importance include the United States of America, Brazil, Argentina, and China. The 10 largest soybean producers in the world (USA, Brazil, Argentina, China, India, Paraguay, Canada, Ukraine, Bolivia, and Uruguay) together produced about 313.01 million metric tons in 2015. According to the estimated by United States department of agriculture in 2016 there is 333.22 million tons could represent an increase of 20.21 million tons or a 6.46% in soybean production around the globe. World soybean trade is a big business amounting to nearly US$13 billion in 2014.

Compared to the USA, South /Latin America and Asia, Africa is a very small producer of soybean. During the last decade or so, Africa accounted for 0.4– 1% of total world production of soybean. The main producers within the continent include Nigeria, South Africa, Uganda, and Zimbabwe. Nigeria, which contributed nearly 50% of Africa's output, accounted for a mere 0.3% of the world soybean output in 2013. About 19 African countries were recorded in the world soybean production statistics compiled by FAO. These African soybeans producing countries and the proportion (%) of African soybean production that each account for: Nigeria (48.9%), Uganda (16.8%), South Africa (14.9%), Zimbabwe (8.4%), Ethiopia (2.7%), Rwanda (2.0%), Egypt (1.7%), and Democratic Republic of Congo (1.4%) (Chianu Jonas *et al*., 2008).

In Sub-Saharan Africa, fertile land in Southern and Western Africa, combined with continued investment in corporate farms by private equity firms, international development organizations and banks, is expected to continue boosting production growth (Sopov, M. *et al,* 2015). In 2011, soybean was planted on 1.1 million hectares which accounts only 1 % of arable lands. Currently, there are a total product 1.4 million metric tonnes per year with the production of 2.5 million by 2025. These means soybean grows to a total of 4.1% compound annual growth rate (Sopov, *et al,* 2015).

The study that conducted in our country identified that the total hectare of land under soybean production during the last 10 years has increased by ten folds; while the total volume of production during the same period increased by 21 folds (CSA 2002-2011). The productivity level of soybean is 1.06 tone/hectare and this level is very low compared to its potential which could go up to 4ton/ha if improved varieties are used (Hailu *et al*., 2014). The country imports 15 million Kilograms of soybean products and spend 11 million USD for importing various soybean products every year. The average volume of soybean export is 1.4 million kilograms with trade deficit of 138 million kilograms annually.

Despite the early introduction soybean, it was not easy to achieve wider dissemination and production of soybean; especially among the small-scale farmers and also its production has not yet spread over compared to the country's potential (Atnaf *et al*., 2013; Tesfaye, 2012). These are due to lack of improved and stable varieties suited for different growing ecologies in the country and lack of popularization and market linkages (Asfaw *et al*.,2006). And the soybean scaling-up effort has not been consistent, weak market linkage between producers, processors, exporters and consumers, limited use of improved varieties, limited knowledge in use of soybean in cropping systems. Beside these, Tesfaye (2012) the constraints in support of the above authors by mentioning main limitations for this were: lack of knowhow by the local farmers on how to utilize the crop, unavailability of an attractive market for the produce, and lack of a systematic approach for popularizing the crop through training female farmers on how to prepare different meals from soybean.

On supporting the above authors**,** Bekabil (2015) suggest that lack or no market information system effective agricultural marketing. Consequently, the proportion of land in the country in which soybean was grown remained low for several years.

Soybean is an intermediate altitude crop, which performs well in areas with an altitudinal and annual rainfall range of 1300-1800 masl and 900-1300 masl, respectively (Hammer and Haraldson,1975; Belay,1987; Asfaw *et al*., 2006). However, it can also be grown at altitudes as low 500masl, and as high as1900 masl with mean annual rainfall ranging between 550-700 mm, and uniform distribution throughout the growing period.

Based on maturity durations soybean is categorized as early, medium and late maturing (Amare, 1987). Generally, these three maturity groups have got their own sowing time. The early varieties late June, early June for inter mediate, and end of May is late maturing varieties. The adaptability of different maturity group soybeans was compared across Ethiopia based on mean yield of 15 years' trials, and early and inter mediate maturity groups were relatively better yielding; especially

in areas, where the rainfall is moderate (Asfaw *et al*., 2006). However, the late maturing varieties have better adapted to high rainfall areas, such as western Ethiopia (Asfaw *et al*., 2006).

In soybean, it was known that the influence of Genotype by environments interactions (Gurmu *et al*., 2009), similarly some previous studies in Ethiopia and elsewhere revealed significance presenAce of GEIs in soybean multi-environment yield trial data and the importance of GEI in soybean Ablett *et al*.,1994; Al-Assily *et al* (1996) and (2002); Amira *et al.*, 2013; Asfaw *et al*., 2009; Beaver and Johnson (1981); Bueno *et al*., 2013; Gurmu *et al*., 2009; Radi *et al*., (1993); Tukamuhabwa *et al*., 2012). The AMMI has been applied by several soybean researchers in GEI studies. Gurmu *et al*. (2009) grew twenty soybean genotypes at six locations and recorded for different character viz., grain yield, on different agronomic data, oil and proteins then employed the AMMI model and identified three high yielding and stable soybean cultivars. Cucolotto *et al*. (2007) produced similar observations. These results contrasted the findings of (Asfaw *et al*., 2009) who grew soybean for grain yield data of eleven genotypes evaluated at four sites for three cropping seasons across the soybean production ecology. AMMI analysis showed that grain yield variation due to environments. According to the AMMI and SREG GGE biplots models, no superior cultivars across four sites and three seasons. But in Ethiopia, no soybean there is no references have been found about that indicates inclusive for most stability procedures.

The magnitude of GEI and investigate the stability of the aimed genotypes using different stability statistics. Therefore, the present study is designed with the following objectives.

- To estimate the extent of GEI
- To identify stable soybean genotypes across soybean growing areas and location specific genotypes and
- To compare stability parameters.

2. LITERATURE REVIEW

2.1. The Biology of the Soybean Crop

It is assumed that the ancestor of the genus Glycine (x=10) has undergone tetraploidization approximately 59 and 13 million years ago, (Schmutz *et al*., 2010). However, all described species of the genus Glycine exhibit normal diploid meiosis and are primarily inbreeders (Cober *et al*., 2009). Therefore, soybean (2n=4x=40) can be considered as an ancient polyploid or paleopolyploid plant (Schmutz *et al*, 2010). The further evolution of soybean started from a common wild perennial progenitor (2n=4x=40) that evolved to a wild annual (2n=4x=40) and finally to the domesticated soybean (2n=4x=40) (Cober *et al*., 2009).

Typically for most legumes, flower petals of soybean enclose almost entirely the male and female organs. The soybean flower is papilionaceous, with a tubular calyx of five unequal sepal lobes and a five-parted corolla consisting of posterior standard petal, two lateral wing petals and two anterior keel petals in contact with each other but not fused (Carlson and Larsten, 1987).

Soybean inflorescence is a raceme bearing 5–35 flowers, and a single plant may produce up to 800 flowers during its lifetime, but each flower lasts only one day (Delaplane and Mayer, 2000). The zygomorphic flowers are white, pink or purple, hermaphrodite and self-fertile.

Stigma becomes receptive a day or two before opening of the flower and the pollen is released the night before or the morning of the day the flower opens, resulting in a high rate of self-pollination (Carlson *et al*., 2004).

The stigma is exposed to external influence only after having been nearly exclusively auto-

pollinated (Fehr, 1980; Delaplane and Mayer, 2000). The viability of soybean pollen is very limited and does not exceed two to four hours. Fertilization is completed within ten hours after the opening of the flower flowers during its lifetime, but each flower lasts only one day (Delaplane and Mayer, 2000). The zygomorphic flowers are white, pink or purple, hermaphrodite and self-fertile.

The pollen development of soybean during various phases of microsporogenesis is sensitive to increased temperature stress (Salem *et al*., 2007). Djanaguiraman *et al*. (2013) showed that decreases in pollen in vitro germination by high temperature stress are caused by anatomical changes in pollen, leading to decreased pod set percentage under these conditions.

The soybean pollen grains are spherical in shape10 with a mean size of 30.4-27.3µm (Yoshimura, 2011). Kaltchuk-Santos *et al*. (1993) reported dimorphism in soybean pollen with the normal microspores measured 26.23 µm in diameter and 23.09 µm in distance between two pores. While "P pollens" (pre-mitotic pollen, non-functional gametophyte) had a diameter of 23.87 µm and a distance of 18.49 µm between the pores. In general soybean pollen is among the smallest of all cultivated plants.

The size of the soybean plant and the structure of soybean flowers restrict significantly its transportation by wind over long distances (Fehr, 1987; Yoshimura, 2011). The study of Yoshimura (2011) showed little airborne pollen in and around the soybean field and that its dispersal is restricted to a small area. Therefore, wind-mediated pollination appears to be negligible.

2.2. Genotype x Environment Interaction

Genotype by environment interactions may be defined in the relative performance of a "character" of two or more genotypes measured in two or more environments (Kang *et al*.,2004). And it is said to be occur when two or more genotypes are compared across different environments and their relative performance are found to differ (Aquaah, 2004). That is, one cultivar may have the highest performance in one environment but perform poorly in others. Another way of stating this is that, over different environments, the relative performance of genotypes is inconsistent. GEI is a differential genotypic expression across multiple environments. The effect of this interaction is that the association between phenotype and genotype is reduced. This raises the important issue of adaptation because a breeder's selection in one environment of superior performers may not hold true in another environment. Genotype by environment interactions is major consequence to the breeders in the process of evaluation of improved varieties.

Genotype and environment may exhibit their interaction in several ways (MatherandJinks,1971). Environment may change genetic constitution of populations by pressure of selection it exercises on the populations. Genotype and environment may interact and produce differences among the individuals within a family. The interactions may appear in two ways, *viz* as non-heritable variation of characters. By measuring the GEI, the breeder will be better equipped to determine the best breeding strategy to use to develop the genotype that is most adapted to the target region (Acquaah, 2007).

2.3. The Analyses of Genotype X Environment Interaction and Stability

The reliability of cultivars performance across environments is an important consideration in plant breeding. Some cultivars are adapted to abroad range of environmental conditions, while others are more limited in their potential distributions. There are cultivars that perform uniformly regardless of the productivity level of the environment and others whose performance is directly related to the productivity potential of the environment (Fehr,1991).

The process of identification of stable genotypes is difficult because of genotype environment interaction. This has been largely due to the problems of defining and measuring the phenotypic stability. Lewis (1954) defined phenotypic stability as the ability of an individual or population to produce a certain narrow range of phenotypes in different environments. According to Allard and Bradshaw (1964) stability does not imply general constancy of phenotype in varying environments. It may depend on holding some aspects of morphology and physiology in steady state.

Wricke (1962) in Sharm (1998) proposed Ecovalence (W_i) as measure of genotypic stability across environments. Ecovalence is the contribution of each genotype to the GEI sum of squares. It is generally expressed in percentage. Low value of W_i means more stability of performance and vice-versa.

Finlay and Wilkinson (1963) used site mean and regression coefficient to measure adaptation in 227 barely varieties overall environments. Regression coefficients approximating to unity indicate average stability. When this is associated with high mean yield, varieties have general adaptability; when associated with low mean yield, varieties are poorly adapted to all the environments. Regression coefficient values increasing above one describe varieties with increasing sensitivity to environmental change, and greater specificity of adaptability to high-yielding environments.

Regression coefficients decreasing below one provide a measure of greater resistance to environmental change, and therefore, increasing specificity of adaptability to low yielding environments. The second index, the variety mean yield overall environments provides measure of performance of the individual varieties.

The regression analysis proposed by Finlay and Wilkinson (1963) to measure phenotypic stability was improved further by Eberhart and Russel (1966). They introduced (in addition to two parameters proposed by Finlay and Wilkinson, and b_i one more parameter, which accounts for unpredictable irregularities in the response of genotype to varying environments measured as the deviation from regression lines to characterize a stable genotype. In this model, the regression of each variety on an environmental index and a function of the squared deviations from this regression, would provide estimates of the desired stability parameters. Thus, the mode partitions the GEI of each variety in two parts:(1) the deviation due to the response of the variety to varying environmental indexes (sum of squares due to regression); and (2) the unexplainable deviation from the regression on the environmental index.

Thus, the adaptable variety in this model is the one with high mean yield, b=1.0 and S^2d_i=0and those significantly deviating from unity are either adapted to high yielding environments if b>1 or low yielding environments if b<1.Several authors regarded mean square for deviations from regressionasthemostappropriatecriteriaofstabilitywhile$b_i$asanindicationofthetypeof response of a cultivar to varying environments rather than a measure of stability (Chaudhary *et al*., 1994; Gupta *et al*.,1974; Odongo and Bockholf, 1997; Ombakho *et al*.,1997).

Two groups of multivariate techniques have been used to elucidate the internal structure of GEIs. These are ordination techniques such as principal components analysis and classification techniques such as cluster analysis (Crossa *et al.,* 1991). The principal component approach has been used to investigate interactions in various contexts.

However, it has not yet been much used in genotype x environment studies, though it may. Be

useful when regression on the environmental mean shows wide deviations from linearity (Freeman,1973). This analysis can effectively reduce the structure of at wo-way data matrix of G(genotypes) points in E(environments)dimensions in a subspace of fewer dimensions. The matrix can also be conceptualized as E points in G dimensions (Zobel *et al*., 1988; Crossa, 1990). Zobel *et al*. (1988) reported principal components analysis for seven soybean genotypes tested for yield in 35 environments. From the 35 possible axes, the analysis revealed that only the first three principal axes accounted for 76 % of the total variation and were found to be statistically efficient but cannot describe the additive main effects. As the first step in controlling GEIs, without requiring any knowledge of the environmental factors responsible, locations can be classified according to the similarity of their interactions with a set of entries (Abou-El-Fittouh *et al*.,1969). Ghadri and Crees (1980) classified environments and genotypes of wheat in to similar genotype x location effects using cluster analysis. According to Freeman (1973) in cluster analysis an attempt was made to find similarities between clusters (environments, here) on the basis of measurements taken on the individuals of a cluster, the measurements being the genotypes grown there. Kempton (1984), Gauch (1988), Zobel *et al*. (1988), and Gauch and Zobel (1989) described he additive main effects and multiplicative interaction (AMMI) as a model which incorporates both the additive and multiplicative components into an integrated, powerful, least square analysis with predictive assessment to give plant breeders and other plant scientists using two-way data sets, with a powerful statistical tool for the analysis of multi-location trials.

Furthermore, with the b_i plot facility that is from AMMI analysis, both genotypes and environments occur on the same scatter gram and a quick visual insight into the structure of the genotype x environment interaction is given(Kempton,1984). Zobel *et al*. (1988) stated that AMMI largely integrates and subsumes the several statistical models customarily applied to yield trial data, including the additive analysis of variance, multiplicative principal component axes(PCA), and Finlay and Wilkson linear regression model. It can also be used for model diagnosis to identify other sub cases as most appropriate for a given data set (Gauch, 1988; Gauch and Zobel, 1989).

AMMI analysis is more effective in explaining the percentage of GEI sum of square than joint

regression analysis does. In general, percentage of interaction sum of squares accounted for by interaction principal component axis one (IPCA1) was substantially higher than the heterogeneity of regression. This result gives further support to the claim of Gauch (1990, 1992) that AMMI analysis always does as well as, and frequently much better than JRA in recovery of sum of squares. Earlier empirical studies (Nachit *et al*.,1992; Riggs,1986; Zobel *et al*.,1988) on large regional or international yield trials showed that much more interaction sum of squares, can be accounted for by AMMI analysis over JRA in small and large data sets. AMMI analysis is less prone to the problem commonly encountered with JRA (i.e., the low amount of GEI explained).

Bi-plot is a powerful way of detecting important sources of GEI effect (Kempton,1984; Zobel *et al.*,1988). On a bi-plot, entries and sites having IPCA1 values close to zero have small interaction effects, while those having large positive or negativeIPCA1 values are largely responsible for the GEI. Entries yield relatively better in sites having IPCA1values of the same sign, but not in sites with IPCA1 value of opposite sign. Plant breeders can easily select from a bi-plot those entries that are high yielding and stable, and also those entries that yield well at specific sites (Yau,1994). Thus, AMMI analysis provides details about the GEI, which is an important feature not available in JRA.

From a multi-location soybean yield trial Mushoriwa, *et al.* (2007) reported that AMMI with the first IPCA axis explained 46.1% of the variation using about 10.6% of the total interaction degrees of freedom. Beside this, when IPCA2 was fitted, the two IPCAs explained 58.5% of the total interaction variation using approximately 20.8% of the total interaction degrees of freedom. Furtherly, when the model added IPCA3s and IPCA4s it explained 69.1% and 76.6% with 30.6% and 39.9% of the total interaction degrees of freedom respectively.

Similarly, Gurmu *et al*. (2009) on soybean grain yield trial reported that the first two interaction principal component axes (IPCA 1 and IPCA 2) have taken the largest portion (66.15%) of the

interaction sum of squares with 36.36% and 29.79% and 23 and 21 degrees of freedom respectively.

Generally, since GEI of cross-over type (an interaction that changes rank of genotypes across environments) pose major problems in breeding programs, the question of how frequently these interactions occur is important. In general, when different lines of cultivars of a given crop are evaluated in a sufficiently wide range of environments, GEI of cross over type seem to be very common (Basford and Cooper, 1998).

2.4. Insect impact on Cross Pollination

Soybean is exclusively a sexually reproducing, self-pollinating plant usually with a rate of self-pollination higher than 99% (Weber and Hanson, 1961; Caviness, 1966; Ray *et al*., 2003; Lu, 2005; Yoshimura *et al*., 2006; Abud *et al*., 2007; Anderson and Vicente, 2010).

Does not show obligate insect pollination (Rubis, 1970; McGregor, 1976; Ahrent and Caviness, 1994; Wolff, 2000). Some soybean cultivars are also visited by thrips and pollinivore predatory species of the order Hemiptera play a role as pollinator. This high rate of autogamy in soybeans is due to cleistogamy. However, entomophilous pollination occurs as a consequence of early opening flowers or visits of specialized foraging insect species, in search of pollen and nectar, which are mainly bees (Chiari *et al*., 2005).

These include species belonging to the genera Apis, Xylocopa and Megachile , as well as the family Halictidae (Halictus spp.). Soybean visited by Apis mellifera Africanized honeybees (Chiari *et al*., 2005). An increase of more than 61% in the number of pods, and more than 58% in yield, in comparison to plants protected against insect visitation, is reported.

Robacker *et al*. (1983) and Milfont *et al*. (2013) observed yield increases of about 10 to 40% in honeybee-pollinated compared to self-pollinated plants, whilst cage inclusion trials have shown up to 15% increase in production (Erickson *et al*., 1978). However, all studies do not provide clear evidence if the reported effects are caused by cross-pollination or by stimulation of self-pollinating, meaning stimulation of pollen transfer by visiting insects within the flowers.

Gumisiriza and Rubaihayo (1978) studied the impact of spacing reported 4.5% outcrossing in 30x30 cm spaced plots while 2.5 % and 2.0 % were recorded for 40cm x 40 cm and 50 cm x 50 cm spaced plots, respectively. According to Roumet and Magnier (1993), insects do not cause random dispersal of pollen since they prefer to move over short distances.

2.5. Implications of GEI for Crop Improvement and its Interpretation

If the interaction is so large as to cause rank changes among genotypes, then one can speak of rank interaction, which is also termed qualitative or crossover interaction. In this type of interaction, the true treatment differences vary not only in magnitude but also in direction. In contrast to quantitative or non-crossover interaction the treatment differences vary only in magnitude. A crop cultivar development program encompasses the breeding phase and performance evaluation phase.

2.6. Interpretations of GEI

According to Acquaah (2007), the general interpretations of GEI resulting from unpredictable causes areas follow:

1. If significant genotype × location effects are observed and the rankings fluctuate by wide

margins, the results indicate that the breeder should consider establishing separate breeding programs for the different locations. However, before making a decision, it is a good idea to examine the data to see what specific factors are responsible for the variation. If stable factors such as soil are the source of variation, separate breeding efforts may be warranted.

2. A significant genotype x year interactions are similar in effect to genotype × location. However, because the breeder cannot develop programs for different years, a good decision would be to conduct tests over several years and select the genotype with superior average performance over the years for release. Because conducting one trial per year for more years' will prolong the breeding program, the breeder may include more locations and decrease the number of years.

3. The breeding implications for complex interactions like genotype × years× location is for the breeder to select genotypes with superior average performance across locations and over years, for release as new cultivars for the production region. Farmers will benefit from growing more cultivar each cropping season. This strategy will reduce the effects of the fluctuations attributed to genotype × year interactions.

4. The magnitude of a GEI is influenced by the genetic structure of the genotype. Genotypes with less heterogeneity (e.g., pure lines, single-cross hybrids, clones) or heterozygosity interact more with the environment than open-pollinated genotypes or mixtures, because of lower amounts of adaptive genes.

5. Also, it is widely known that only GEI are useful for depicting adaptation patterns. This is because they are the only interaction that can be exploited by selecting for specific adaptation or by growing specifically adapted genotypes.

3. MATERIALS AND METHODS

3.1. Experimental Sites

The experiments were conducted at six different locations across Ethiopia viz., Dimtu, Jimma, Bako, Metu, Asosa and Pawe. These areas represent the highest potential and the main areas for soybean production in the country, with different edaphic and environmental conditions. The more detailed description biophysical description of the variation explored in the test environments is provided in Table 1.

3.2. Experimental Design and Trial Management

The experiments in all locations were designed in a randomized completely design (RCBD) with three replications per environment under rain feed conditions. Sowing was done manually in rows 60 cm and 5cm between plants. The plot size was 3m×2.4m and a spacing of 1mx1m was used. Fertilizer of 50 kg ha $^{-1}$ Urea, 100 kg ha $^{-1}$ DAP was applied. Hand weeding was done as and when necessary. At harvest data was collected from the inner two rows within a plot.

Table 1. Description of the testing sites

No.	Locations	Altitude (masl***)**	Geographic Coordinates (Latitude/ Longitude)	Agroecology zones (AEZs)	Annual Rain Fall(mm)	Temperature (0^c) Min to Max.	Soil Type	Zone
1.	Asosa (E1)	1580	10^o02'N 34^o34'E	Hot-warm moist lowland plain tepid to cool humid sub humid lowland plain tepid to cool sub humid mountain	1130	15.9-29	Dystric Nitosols	Asosa
2.	Bako (E2)	1590	9° 06 N,37° 09’ E	Mid altitude sub humid	1245	9-34.4	Nitosol	West Shewa
3.	Jimma (E4)	1753	7°40'9"N,36°47'6"E	Sub humid Tepid to cool mid highlands	1561	18.9-26.8	ChromicNitosol and Combisol	Jimma
4.	Pawe (E6)	1120	11019’N,036024'E	Hot-warm moist	1587	16.3-32.6	Nitosols, Vertisol and livesols	Metekel
5.	Metu (E5)	1550	8°18′N ,35°35′E	Tepid- cool humid mid highlands rainfall	1810	12.5-28.6	Dark red brown	Illuababa ora
6.	Dimtu (E3)	1640	7°55′0″N,37°20′0″E	Warm to cool sub-humid	1601	12.5-26.5	Nitosol	Jimma

Source: EIAR, *meter’s above sea levels

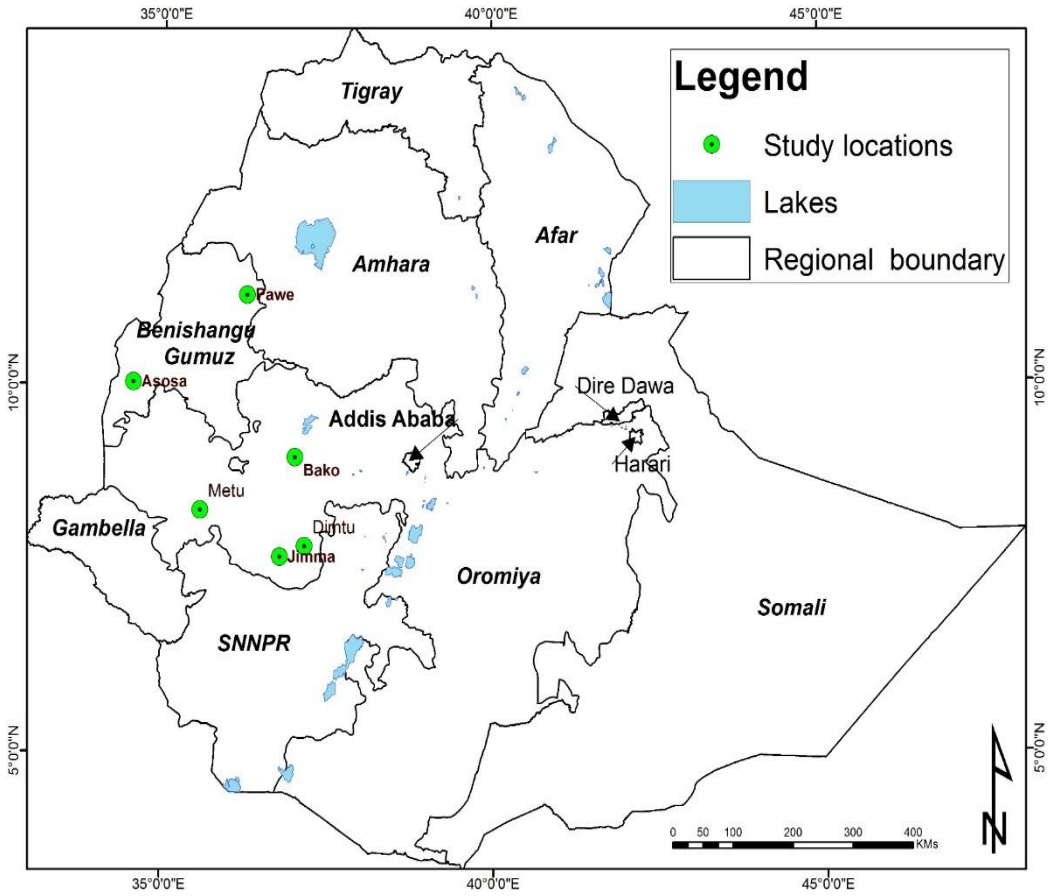


Figure 1.Geographic areas of the six study locations (Demeke Mekonnen,Unpublished)

Table 2. Description of the testing genotypes

Genotype				Genotype			
Code	Strain Sub-Designation	Cultivar Name	Seed Source*	Code	Strain Sub-Designation	Cultivar Name	Seed Source*
G1	Mod PI 634193	5002T	AON	G13	Mod PI 559932	Ks3496	AON
G2	Mod PI 570668	Ciaric	AON	G14	-	Clarck-63k	Released
G3	Mod PI 633970	Ozark	AON	G15	Mod PI 533050	Choska	AON
G4	Mod PI 603953	Motte	AON	G16	Mod PI 594669	Liu yue mang	AON
G5	Mod PI 595081	Ks4895	AON	G17	Mod PI 594675	Huang dou No-1	AON
G6	Mod PI	UA4805	AON	G18	Mod PI 594675	Hs93-4118	AON
G7	Mod PI 560207	Delsoy 4710	AON	G19	Mod PI 614153	Croton 3.9	AON
G8	Mod PI 553051	Spry	AON	G20	-	SCS-1	Released
G9	Mod 561702	Harbar	AON	G21	Mod PI 639740	LDOO-3309	AON
G10	TGX-1892-10F	AFGAT	Released	G22	Mod PI 612157	Prichard	AON
G11	Mod PI 594675	Graham	AON	G23	Mod PI 633610	Desha	AON
G12	Mod PI 559932	Manokin	AON	G24	Hawassa-04	AGS-7-1	Released

Source: EIAR/JARC ***** AON=Advanced Observation Nursery

3.3. Data Collection

According to the Soybean descriptors (1986) the following data were collected either on the plot basis or in in individual from ten randomly taken plants on:

1. **Date of emergence**- number of days from planting to 50% seedling emergence.

2. **Seedling vigor**-assessing when the first trifoliate leaf expanded.

3. Poor

5. Medium

7. Vigorous

3. **Days to flowering**-number of days from planting to 50% plants with at least one open flower.

4. **Plant height(cm)-** was recorded after harvesting. Height of the main stem from the ground level to the top of the main stem was measured.

5. **Days to maturity**- the number of days from sowing until approximately 95% pod turned into Brownish color.

6. **Hundred Seed Weight-** Absolute values in g normally measured at 13-15% moisture content.

7. **Number of pods per plant**- the total number of pods with seed in a plant in ten randomly taken plants.

8. **Number of seeds per pod**-the total number of seeds in ten randomly selected pods taken from randomly taken plants.

9. Harvest Index-grain yield (g) and total plant dry mass (g) were measured to calculate HI.

10. **Lodging score**-scored from leaning angle and lodging area.

It was Scored 1 (erect) to 5 (prostrate).

11. **Grain yield**-the total grain yield(Kg) harvested from the middle two rows and adjusted to 13% moisture.

12. **Shattering score**- estimated percent of pod splitting and seed shattering at a

- Early: Scored at harvest.
- Late: Scored on border rows, two weeks after maturity.
- Score based on percentage of open pods as follows:

1. = No shattering
2. =1 to 10 percent
3. =10 to 25 percent
4. =25 to 50 percent
5. = >50 percent

3.4. Statistical Analysis

Different statistical method are uses, i.e. SAS (2012), R-Software, GenStat version 15 &16, Microsoft Office Excel (2016), PBSTAT 1.2 and Plant Breeding Tools version 1.4 (2013). Analysis of variance was for each location. The Bartlett's test was made to test the homogeneity of error variance across all the locations. Combined analysis of variance was done for each trait to obtain estimates of environmental, genotype and GEI source of variation by using SAS 9.3 (2012) software.

3.5. Analysis of Variance

Statistical computation and estimation were carried out using Statistical Analysis System (SAS) software version 9.3(SAS, 2012). Each in a given season was considered as an individual environment. Data obtained from each location was initially analyzed separately by running a single ANOVA and thereafter data were pooled to perform the combined analysis of genotypes across locations. Analysis of variance was carried out to partition the variance due to genotype, environment and genotype by environment interaction. The mean comparison of the treatment was done by Duncan Multiple Range Test (DMRT) at 5% probability levels. Similarly, homogeneity of error variance was tested using Bartlett's test (1947) to determine the validity of the combined analysis of variance.

The ANOVA model for individual location is:

$$Y_{ij} = \mu + g_i + b_j + \varepsilon_{ij}$$

Where:

Y_{ij} =observed value of genotype i in block j,

μ = grand mean of the experiment,

g_i= effect of genotype i,

b_j= the effect of block j,

ε_{ij}= error effect of genotype i in block j

Table 3. Outline of analysis of variance for individual location

Source of Varation	Degree of Freedom	Sum Squares	Mean Sum Square	F_ratio
Block (b)	$b-1$	SSb	MSr	MSr / MSe
Genotypes (g)	$g-1$	SSg	MSg	MSg / MSe
Error (gxb)	$(b-1)$ (g-1)	SSe	MSe	MSe / SSe
Total	$(gb-1)$			

NB:r=replication, g=genotypes, e=error, SS=Sum Squares, SSr=sum squares due to replication, SSg=Sum squares due to genotypes, SSe=Sum squares due to error, MS=Mean Squares=mean squares due to replications, MSg= mean squares due to genotypes, MSe= mean squares due to error.

Where for combined analysis the following model:

$Y_{ijk} = \mu + g_i + e_j + (ge)_{ij} + bk(j) + \varepsilon_{ijk}$, Where:

Y_{ijk}= observed value of genotype i in block k of environment (location) j,

μ = grand mean,

g_i= effect of genotype i,

e_j = environment or location effect,

$(ge)_{ij}$= the interaction effect of genotype i with environment j,

$bk(j)$ = the effect of block k in location (environment) j,

ε_{ijk}= residual effect of genotype i in block k of environment j

Table 4. Outline of combined analysis of variance over locations

Source of Variation	Degree of freedom	Sum of squares	Mean Sum Squares	F_ratio	Expected Mean Squares
Block(Environments)	(e-1) (b-1)	SSb(e)	MSb(E)	MS/ MSe	$\sigma^2e + g\sigma^2B(E)$
Environment(E)	(e-1)	SSE	MSE	MS/MSe	$\sigma^2e+g\sigma^2B(E)+bg\sigma^2E$
Genotype(G)	(g-1)	SSG	MSG	MS/ MSe	$\sigma^2e +r\ \sigma\ ^2GE + eb\ \sigma^2G$
GEI	(g-1) (e-1)	SSGEI	MSGEI	MS/ MSe	$\sigma^2e+b\sigma^2GEI$
Pooled Error	e(g-1) (e-1)	SSe	MSe	MS/ MSe	σ^2e
Total	glr-1				

NB: r=replication, g=genotypes=environments=blocks, MSe=mean squares due to environments, MSb(e)=mean squares due to Block (Environments), MSg=Mean squares due to genotypes, MSGEI= Mean squares due to GEI and MSe=Mean squares due to residual.

3.6. Stability Analysis

3.6.1. The environmental variance (S^2_i)

To measure the static phenotypic stability of the genotype across a set of environments, the following could be used:

$$S^2{}_i = \frac{\sum_{j=1}^{e}(\mathrm{Y_{ij}} - \bar{Y})^2}{e}$$

i =1, 2…., g

Where y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, and $\bar{y}_i$ is the marginal mean of the genotype i. From the equation, a stable genotype has smaller variance.

3.6.2. Wricke's Ecovalence (W_i)

Ecovalence measures the contribution of a genotype to the GEI. The ecovalence (W_i) or stability of the genotype is its interaction with the environments, squared and summed across environments, and expressed mathematically as:

$$W_i = \sum_{j=1}^{e}[\, y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} - \bar{y}_{..}]^2$$

Where, y_{ij} is the mean performance of the genotype i in the j^{th} environment.

$\bar{y}_{i.}$=is the marginal mean of the i^{th}genotype.

$\bar{y}_{.j}$ =is the marginal mean of the j^{th} environment.

$\bar{y}_{..}$=is the overall mean

The interpretation of genotype with low value has smaller deviations from the overall mean across environments and are thus more stable. Since the ecovalence strongly depends on the environments included in the test and the breeder can manipulate the ecovalence by choosing specific location. A genotype with high ecovalence =0 is regarded as stable in all environments.

Becker and Léon (1988) illustrated ecovalence by using a numerical example of plot yields of genotypes in various environments against the respective mean of environments (Fig.2).

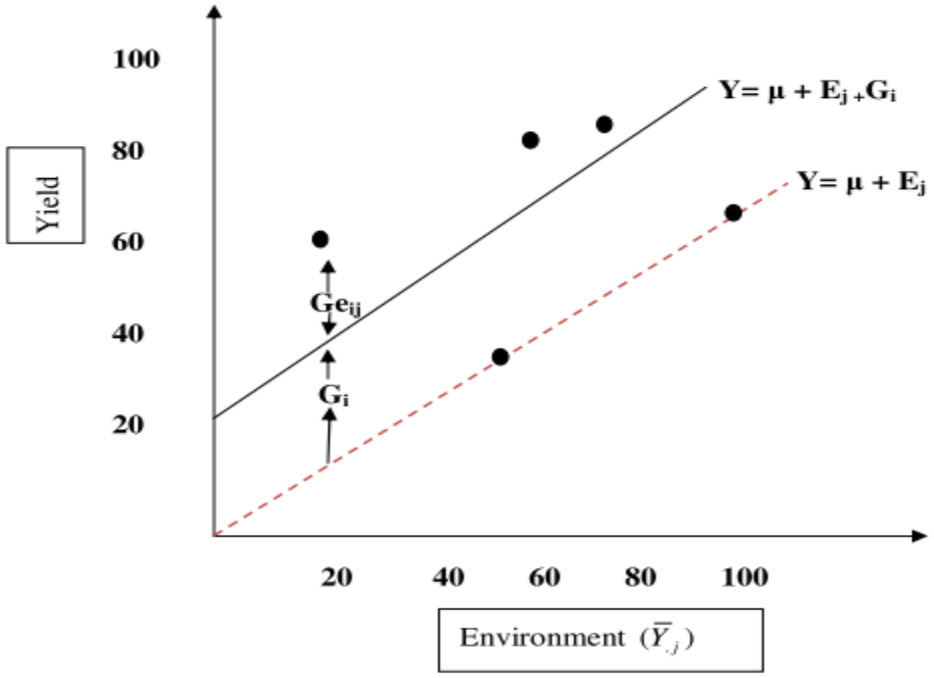


Figure 2. Graphical representation of GEI: the stability statistics ecovalence (W_i) is the sum of squares of deviations from the upper straight line (Adapted from Becker and Léon,1988).

The lower broken straight line estimates the average yield of all genotypes simply using information about the general mean (μ) and the environmental effects (E_j), while the upper unbroken line takes into account the genotype effect (G_i) and therefore estimates the yield of genotypes i. Deviations of yield from the upper straight line are the GEI effects of genotype i and are summed and squared across environments and constitutes ecovalence.

3.6.3. Shukla's stability variance(σ2)

Shukla's (1972) stability variance (σ^2) is based on the residuals in a two-way classification, the variance of a genotype across environments is the stability measure. Shukla's stability variance (σ^2_i) is the contribution of a genotype to the GEI sums of squares after adjusting for the average genotypic contribution to the GEI sums of squares.

$$\boldsymbol{\sigma_i^2} = \frac{\mathbf{1}}{\boldsymbol{(G-1)(G-2)(E-1)}}\left[\boldsymbol{(G(G-1)}\sum_{\boldsymbol{j}}\boldsymbol{(Y_{ij}-\overline{Y}_{i.}-\overline{Y}_{.j}+\overline{Y}_{..})^2}-\sum_{\boldsymbol{i}}\sum_{\boldsymbol{j}}\boldsymbol{(Y_{ij}-\overline{Y}_{i.}-\overline{Y}_{.j}+\overline{Y}_{..})^2}\right]$$

Where, Y_{ij} is the mean of the i^{th} genotype in the j^{th} environment,$Y_{.j}$ is the mean of all genotypes in the j^{th} environments and $\overline{Y}_{..}$ is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (σ^2) is equal to environmental variance $\sigma_e{}^2$.

3.6.4. Finlay and Wilkinson and Eberhart and Russell analysis

Finlay and Wilkinson's (1963) regression coefficient (b_i). The observed values are regressed on environmental indices defined as the difference between the marginal mean of the environments and the overall mean. The regression coefficient for each genotype is then taken as its stability parameter. They found that a genotype with high stability has a regression coefficient of larger than 1 and that a value of lower than 1 can be regarded as poor stability. A genotype that is well adapted must have a regression coefficient of exactly 1 (b=1). Eberhart & Russell (1966) defined a stable genotype as one with an average response to the environment. They further said that a large GEI interaction limits progress from selection and to reduce this, the environments have to be stratified to make them more similar. In their study, they found that GEI interaction is still large and they decided to select stable genotypes that interact less with the environments in which they are grown, and used only the more stable genotypes for the final stages of testing.

According to Finlay and Wilkinson (1963), a genotype with a b_i value less than 1.0 has above average stability and is especially adaptable to low-performing environments and if itis greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments. Whereas, a genotype with b_i value equals to 1.0 is adapted to the wide range of environments or an indication of its average stability. When this value is associated with high mean yield it indicates a genotype's good general adaptability; and when it is associated with low mean yield it shows the genotype's poor adaptability to all environments (Fig.3). Hence, in most cases the deviation from regression (S^2d_i) is taken as a parameter for stability rather than which is more about the responsiveness of genotypes.

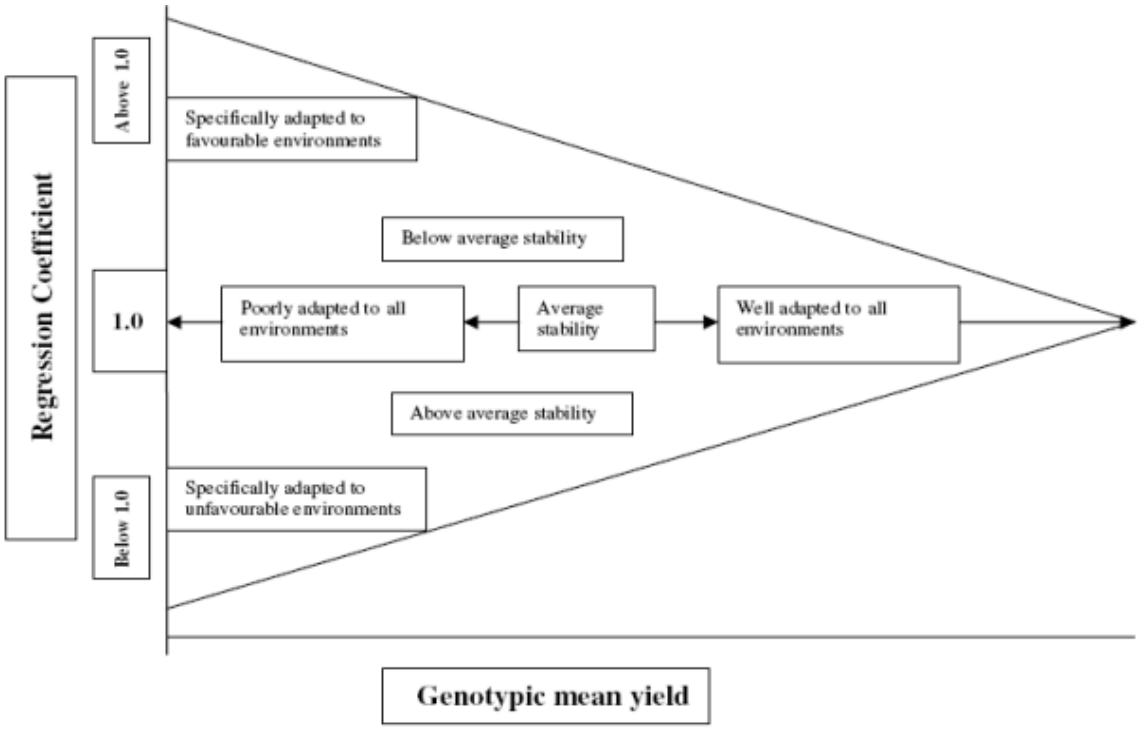


Figure 3. A generalized interpretation of the genotypic pattern obtained from genotypic regression coefficients plotted against genotypic mean yields, adapted from Finlay and Wilkinson (1963).

3.6.5. The AMMI Model and Principle Component Analysis (PCA)

The AMMI analysis uses analysis of variance (ANOVA) followed by a principal component analysis applied to the sums of squares allocated by the ANOVA to the genotype x environment interaction.

The AMMI Model Equation is: $\boldsymbol{Y_{ij}} = \mu + \boldsymbol{g_j} + \boldsymbol{e_j} + \sum_{\boldsymbol{k}}^{\boldsymbol{x}} \boldsymbol{\lambda_k}\, \boldsymbol{a_{jk}\gamma_{jk}} + \varepsilon_{\boldsymbol{ij}}$

Where, is the mean of the genotype in the environment, μ is the grand mean, is the genotype effect, is the environment effect, is the singular value for principal component, is the eigenvector score for genotype i and component k, is the eigenvector score for genotype i and component k and is the error for genotype i and environment j. From the equation of the AMMI model analysis were interpreted by a biplot between Principal Component (PC) Axis 1 versus PC Axis 2. A genotype or an environment with a PC score close to zero showed the small interaction effect and considered as stable.

3.6.6. AMMI Stability Value (ASV)

Since AMMI does not provide a quantitative measurement, it is necessary to quantify and rank genotypes and based on their yield (Purchase, 1997). AMMI Stability Value (ASV), length of genotype and environment markers of the origin in a two-dimensional plot of IPCA1 sores against IPCA2 scores was calculated according to Purchase *et al*. (1997) as:

$$\text{ASV} = \sqrt{[\frac{\text{IPCA1 Sum Squares}}{\text{IPCA2 Sum Squares}}(\text{IPCA1 Score})]^2 + [\text{IPCA2 Score}]^2}$$

Where: IPCA1 = interaction principal component axis 1; IPCA2 = interaction principal component, axis 2. According to Purchase (1997) genotypes with lower values of the ASV are considered to be more stable.

3.6.7. Lin and Binns Cultivar Superiority Measure

A general measure of cultivar superiority for GEI data is defined as the distance mean square between the cultivar's response and the maximum response averaged over all locations. Since the maximum response is the upper boundary in each location, a small mean square indicates general superiority of the test cultivar. This model has the following advantage:

(i) . the checks provide only a plausible maximum response for each location and are not required for assessing the test genotypes. (ii) The measure of general superiority consists of only one parameter, thus simplifying the screening process considerably. A subsidiary parameter for interaction can be used to indicate lack of general adaptability. (iii) The difference between the mean of the maximum response averaged over all locations and the mean of the best cultivar provides useful information as to how many cultivars are needed to achieve optimum productivity for the entire region. (iv) The specific adaptability of a cultivar can be identified by plotting the maximum and the test cultivar responses on the location means.

Lin and Binns (1988) defined the superiority measure (P_i) of the genotype as the mean square of the distance between the genotype and the genotype with maximum response as. According to Lin and Binns (1988) for cultivar superiority measure (P_i) analysis, the genotype with low or small (P_i) value is considered to be more stable.

Mathematically:

$$P_i = \frac{n(\bar{X}_i - \bar{M})^2 + \sum_j (X_{ij} - \bar{X}_i - M_j + \bar{M})^2}{2n}$$

Where, is the response of the genotype in the environment, the mean of the genotypes in overall environments, is the genotype with maximum response among all genotypes in the environment, is the mean of the genotypes with maximum response over all environments and n is the number of environments. Different authors (Magagane, 2012; Oliveira *et al*., 2012) used this stability

parameter to identify high yielding and stable soybean genotypes across different locations.

3.6.8. Francis and Kannenberg's coefficient of variability (CV_i)

Francis and Kannenberg (1978) proposed coefficient of variation (CV) as a stability parameter and defined as it is a variance of genotypes across environments, weighted by the cultivar mean and it reflects homeostasis or buffering ability of the cultivar. In addition, it represents a simple, descriptive method for grouping a large number of genotypes from yield data collected over several environments (Francis and Kannenberg, 1978). It is calculated as follows:

$$\mathrm{CV}(\%) = \frac{\left(\sqrt{\frac{\mathrm{evi}}{(\mathrm{E}-1)}}\mathrm{x}100\right)}{2\mathrm{a}}$$

Where, evi is the sum of squares of interaction effects and the remaining stands as specified in the equation in the above equation. Though CV is a simple method and frequently used by breeders and geneticists, but it has its own limitation's; while comparing genotypes across high and low yielding environments if the mean and standard deviation do not vary in a parallel way as performance increases, a bias would happen, whereby high means result in low CV and low means high CVs. On the basis of mean CV and grand mean, the fifteen number of maize hybrids were categorized into four groups. Out of which, group I was considered stable which had high mean and small variation. The other groups, *viz.,* II, III, and IV showed high yield with large, low yield with low and "low yield with high variation, respectively (Francis and Kannenberg, 1978).

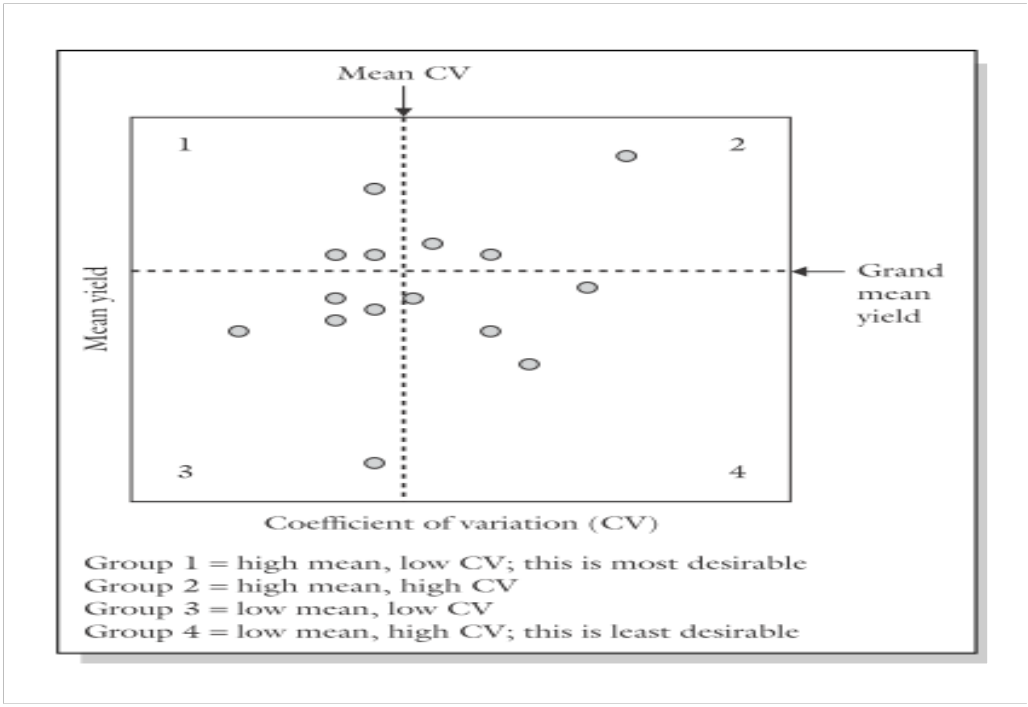


Figure 4. GEI based on the coefficient of variation (CV), adapted from Acquaah (2007).

Plot of means versus coefficient of variation proposed by Francis and Kannenberg (1978), entails calculating for each variety, and the overall mean and the coefficient of variations (CVs) across the environments. A plot of means versus CVs yields a scatter gram that can be divided into four sections by transecting the average CV and the grand mean yield (Figure 4). The most desirable genotype will be found in group 1 (high yield, low CV) while the least desirable (low yield, high CV) will occur in group 4. In this method, mean and CV tolerance limits are flexible. For the plant breeder practicing mass hybrid screening, delimiting co-ordinates for mean and CV are conveniently set by check hybrids'(Francis and Kannenberg (1978).

3.6.9. GGE Model

The GGE biplot (Yan 2002) model formula:

$$\boldsymbol{Y_{ijr}} = \mu + \boldsymbol{e_j} \sum_{\boldsymbol{k=1}}^{\boldsymbol{x}} \boldsymbol{\lambda_k \alpha_{ik} \gamma_{ijk}} + \boldsymbol{\varepsilon_{ijr}},$$

With Y_{ijr} =observation of the replicate of the genotype in the environment, μ= the overall mean, =main effect of the environment, *x*=matrix rank$\{gge\}_{ij}$ when $gge_{ij}=g_i+ ge_{ij}$, the singular value for principal component *k*,= the eigenvector score for genotype i and component *k*, =the eigenvector scores for environment *j* and component *k*, and =the error for genotype and environment *j* and replicate *r*.

3.7. Combined Comparison of stability analysis procedures

To compare the nine stability analysis procedures, spearman's coefficient of rank correlation(rs) was employed (Steel and Torrie,1980). This is because spearman coefficient of rank correlation works to the data in the forms of ranks.

After computing the stability values according to the procedure and definition used, which were then ranked to determine Spearman's rank correlation coefficient between different procedures. Procedurally, by assuming n genotypes are arranged in the same following order according to two stability parameters, and indicates the ranking order of the genotype for the first parameter, while indicates the ranking number of the genotypes of the second parameter, then $d_i = x_i - Y_i$ (i=1, 2,……,n) and spearman's rank correlation coefficient (r_s) can be described as:

$$\mathrm{r_s} = 1 - \frac{6 \sum {d^2}_i}{\mathrm{n}(\mathrm{n}^2 - 1)}$$

The significance of r_s can be tested by means of student's *t* test, where $t=\frac{r_s\sqrt{n-2}}{\sqrt{1-{r^2}_s}}$, with n-2 degrees of freedom. If $t \geq t_{(0.01:\, n-2)}$, the null hypothesis is discarded and r_s is described as highly significant.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

Analysis of variance was performed for each environment, and the result revealed that highly significant difference ($p \leq 0.01$) was found for grain yield at locations Asosa, Jimma, Metu and Pawe, and significant difference ($p \leq 0.05$) at Bako and Dimtu.

Then after, the combined analysis was conducted for each trait with special focus on grain yield and other agronomic traits in order to examine the presence of environment, genotypes and genotype by environment interactions. Besides, the stability analysis was computed grain yield, which is normally polygenic trait.

Table 5. ANOVA of grain yield of soybean genotypes at individual environments.

Source of variation	DF	Environments					
		Asosa	Bako	Dimtu	Jimma	Metu	Pawe
Genotypes	23	977905.16***	55126728*	176368.34*	177564.36***	1029685.68**	177564.36***
Replication	2	417934.01ns	10153045.90**	224456.24ns	3834.55ns	174833.09ns	3834.55ns
Error	46	155,096.18	20357810	739777.70	43256.55	153297.13	43256.54
Mean		2972.51	14151.29	1556.83	1426.12	1268.43	1426.12
CV (%)		13.25	31.88	17.47	14.58	30.86	14.58
R^2		0.76	0.65	0.57	0.67	0.77	0.67

Significant at ** = 0.01 and *** = 0.001 probability level, ns = not significant

The combined ANOVA was done that illustrated in Table 6. The result shows that environmental, genotype and genotype by environment interaction variances were very highly significant ($p \leq 0.01$).

Table 6. Combined ANOVA of grain yield of soybean genotypes across six environments.

Source of Variations	Env	Gen	GEI	Rep(E)	Error	CV (%)
DF	5	23	115	12	276	
GYLD	39758606.5***	2890703.6***	520081.3***	1842049.6***	264193.7	24.98

Env=Environment;Gen=Genotypes;GEI=Genotype by environment interaction, Rep(E)=replication within environment, significant at**=0.01and***=0.001probability level, ns=not significant, GYLD=Grain yield.

The mean grain yield of the genotypes at individual environments was presented in Table 7. The mean grain yield ranged from 555.91 kg ha^{-1} (LD00-3309) at Metu to 4845.97 kg ha^{-1} (AFGAT) at Bako. Among the environments, Asosa (2972.51kg ha^{-1}) was the best environment in which most genotypes performed well in grain yield. On the contrary, Metu was the poorest environment with mean yield of only 1268.43 kg ha^{-1}. This is due to the yield of most of the genotypes declined by more than half due to very high rain fall and hail damage during the late time of the experiment that damaged most part of the leaf of the genotypes (Appendix 9). Beside this, environments Metu, Jimma and Dimtu considered as poor, but Asosa, Bako and Pawe are considered as better environments, this is due to the fact that these three environments show above grand mean grain yield.

The highest mean grain yield for each environment was 4117.27 kg ha^{-1} at Asosa (5002T), 4845.97 kg ha^{-1} at Bako (AFGAT), 2216.17 kg ha-^{1} at Dimtu (SCS-1), 1954.06 kg ha^{-1} at Jimma (SCS-1), 2726.15 kg ha^{-1} at Metu (AFGAT) and 3660.65 kg ha^{-1}at Pawe (AGS-7-1). Due to the high performance, these genotypes could be recommended for specific adaptation in these environments.

Genotypes AFGAT (G_{10}), SCS-1 (G_{20}) and Clarck-63k (G_{14}) were genotypes with the highest mean grain yield across the six environments with mean yield of 2903.39 kg ha^{-1}, 2852.63 kg $ha^{-1}$and 2769.52 kg ha^{-1} respectively. In contrary, genotype in the lowest mean yield Hang dou No-1 (G_{17}), Princhard (G_{22}), LD00-3309 (G_{21}), with the grain yield 1622.53 kg ha^{-1}, 1558.47 kg ha^{-1} and 1554.01 kg ha^{-1} respectively.

Table 7. Mean Grain Yield (GYLD) of Twenty-Four soybean genotypes across six environments

No.	Genotypes	Environments						
		Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean Yield
1	5002T	4117.27	3374.77	1171.38	1543.11	1101.08	2604.63	2318.71dce†
2	Ciaric	3882.82	3662.67	1215.39	1606.48	1544.02	2400.93	2385.38dc
3	Ozark	2320.00	2694.65	1610.96	1538.21	837.197	1891.67	1815.45hgf
4	Motte	3417.61	3378.27	1379.10	1018.36	2364.38	2465.28	2337.17cde
5	ks4895	3054.40	2541.77	1916.32	1578.23	1060.93	2572.69	2120.72def
6	UA4805	3010.00	2416.35	1440.01	1548.38	1304.79	2165.74	1980.88gfe
7	Delsoy 4710	2452.28	2464.38	1433.72	1602.70	1111.33	2164.35	1871.46hgf
8	Spry	2745.32	2654.78	1522.74	1473.74	1043.59	2013.43	1908.93hgf
9	Harbar	2899.67	2313.11	1721.98	1539.05	905.173	2175.47	1925.74gfe
10	AFGAT	3947.60	4845.97	1904.95	1443.33	2726.15	2552.31	2903.39a
11	Graham	3124.39	2748.12	1458.52	1394.90	1040.59	2392.59	2026.52dgfe
12	Manokin	2512.59	3418.74	1318.35	1491.16	1190.88	2070.37	2000.35dgef
13	ks3496	2755.79	2985.09	1517.54	1232.72	889.383	1898.15	1879.78hgf
14	Clarck-63k	3432.71	3893.78	1731.69	1527.92	2345.82	3685.18	2769.52ab
15	Choska	2870.28	1731.21	1692.25	1388.50	517.303	1646.76	1641.05hg
16	Liu yuemang	2621.78	1447.21	1478.59	1210.00	1211.23	1965.74	1655.76hg
17	Hang dou No-1	2200.02	1779.12	1167.57	924.229	1933.69	1730.56	1622.53hg
18	Hs93-4118	2591.08	2948.76	1716.36	1535.16	1001.00	2222.68	2002.51dgef
19	Croton 3.9	2398.07	1810.93	1482.98	1273.56	840.76	2132.41	1656.45hg
20	SCS-1	3884.58	4249.87	2216.17	1954.06	1900.48	2910.65	2852.63ab
21	LD00-3309	2195.66	2614.61	1520.10	854.419	555.91	1583.33	1554.01h
22	Princhard	2512.38	1708.58	1610.61	1369.83	659.61	1489.82	1558.47h
23	Desha	3175.53	2587.40	1563.00	1562.32	948.45	2596.76	2072.24def
24	AGS-7-1	3218.40	3656.05	1573.53	1616.54	1408.66	3660.65	2522.30bc
Env. Mean		2972.51	2830.26	1556.83	1426.12	1268.43	2291.34	2057.58
CV (%)		13.24	31.88	17.47	14.58	31.12	25.64	24.98

†Means followed by the same letter are not significantly different at 0.05 probability level

4.2. ANOVA of other traits

The ANOVA of data for individual environments showed a highly significant ($p \leq 0.01$) difference among genotypes for all traits at the six environments. The mean of each trait at each environment is given in Appendix 1-8.

The Combined ANOVA of nine different traits is presented in Table 8. For most of the traits studied, environment variance, genotype variance and GEI variance were highly significant ($p \leq 0.01$). This result is in line with the findings of Rao *et al* (2002) and Gurumu *et al*. (2006). The study also on nine traits revealed that environmental, genotypic and GEI variance for traits examined (data to flowering, date of maturity, plant height, hundred seed weight, branch per plant, number of seeds per plant, number of pods per plant, and harvest index) were significant.

Table 8. ANOVA of agronomic traits for soybean genotypes combined over six environments.

Source of Variations	Environment	Genotype	GEI	Rep(E)	Error
DF	5	23	115	12	276
DTF	382.28***	302.25 ***	47.41 ***	17.50ns	27.43
DTM	4298.33***	483.46***	50.11**	51.71ns	32.11
PH	5124.71***	1665.17***	155.77*	127.82ns	110.66
HSW	324.06***	48.57***	5.05**	20.83***	3.03
BPP	38.36***	10.45***	1.87***	1.81ns	1.01
NSPPL	4748.49***	1184.28**	855.36**	5507.49***	531.10
NPP	3257.24***	446.90***	202.76**	1266.60***	132.66
HI	4.18 ***	0.06***	0.05***	0.03ns	0.03

GEI=Genotype by Environment Interaction, Rep (E) = Replication within environments, significant at * = 0.05, ** =0.01 and *** = 0.001 probability level, ns = not significant; DTF= Days to flowering; DTM= Days to maturity; PH= Plant height; HSW= Hundred seed weight, BPP= Branch per plant; HI= Harvest index; NPP= Number of pods per plant.

4.3. Correlation among different traits

Correlation among different was conducted using Pearson correlation coefficient. Days to flower and days to maturity showed positive and significant correlations with most of the traits studied except HSW, NSPL and NPPP (Table 9). They showed negative correlation with HI (r=DF; P≤ 0.05) and r=DM; P≤ 0.05) where non-significant with the rest of the two traits viz., NSPL and NPPP. Grain yield showed significant positive correlation with DF, HSW, BPP, NSPL and NPPP with correlation coefficient (r=0.1; p≤ 0.05), r=0.58; p≤ 0.01), (r=0.17; p≤ 0.01), (r=0.20; p≤ 0.05), and (r=0.23; p≤ 0.05), respectively. But the grain yield is non-correlated with DM, PH and HI.

Plant height (PH) showed positive and significant correlation with BPP and NSPL with correlation coefficient of (r=0.25; p≤ 0.01) and r=0.15; p≤ 0.01) respectively. Plant height also showed significant negative correlation with HSW (r= -0.17; p≤ 0.01). But non-significant correlation with other traits like NPPP and HI.

Hundred seed weight (HSW) showed positive and significant correlation with grain yield (r= -0.58; p≤ 0.01) also negative and significant correlation with days to flower (DF) and plant height(PH) (r= -0.10; p≤ 0.05), r= -0.17; p≤ 0.01) respectively. But non-significant correlation with DM, BPP, NSPL, NPPP and HI.

Table 9. Correlation among different traits of soybean genotypes tested across six environments

	DTF	DM	PH	HSW	BPP	NSPL	NPPP	HI	GYLD
DTF									
DM	0.49**								
PH	0.36**	0.47**							
HSW	-0.10*	-0.09ns	-0.17**						
BPP	0.36**	0.35**	0.25**	0.00ns					
NSPL	-0.01ns	0.06ns	0.15*	0.08ns	0.12**				
NPPP	-0.05ns	0.02ns	0.07ns	0.09ns	0.17**	0.82**			
HI	-0.38ns	-0.19ns	-0.10ns	-0.10ns	-0.05ns	0.24**	0.31**		
GYLD	0.10ns	0.00ns	-0.04ns	0.58**	0.17**	0.20**	0.23**	-0.05ns	

NB: DTF= Days to flowering; DM= Days to maturity; PH= Plant height; HI= Harvest index; GYLD= Grain yield; HSW=Hundred seed weight; BPP= Number of branches per plant; NSPL= Number of seeds per plant; NPPP= Number of pods per plant. Significant at *=0.05, ** =0.01 probability level

4.3. Stability Analysis

4.3.1. The Environmental Variance (S^2_i)

The environmental variance (Roemer, 1917) is one of the major stability measures for static stability and it is calculated for each genotype across test environments. Having base on the Table 10. the genotypes G_{17} (1622.53), G_{16} (1655.76) and G_7 (1871.46) can be relatively more stable than other genotypes. But from the three stable genotypes none are exceeding the grand mean, which estimated 2057.58. From this stability parameter point of view, the grain yields for genotypes AFGAT (G_{10}), SCS-1 (G_{20}) and Clarck-63k (G_{14}) ranks one to three respectively. But on the contrary these aforementioned three genotypes rank 24th, 19th and 20th in stability respectively. Having the above stability method's results, the higher the stable genotypes the less grain yield. As a result, the method is in shortcoming in evaluating the stability across environments.

Table 10. Genotype means grain yield, environmental variance (S^2_i), and coefficient of variation (CV_i) for 24 soybean genotypes.

Genotype	Mean Yield(Kg/ha)	Rank	Environmental_ Variance(S^2_i)	Rank	CV_i
G_1	2318.71	7	1566471.92	23	53.98
G_{10}	2903.39	1	1629467.14	24	43.97
G_{11}	2026.52	10	710733.01	16	41.60
G_{12}	2000.35	12	731749.85	17	42.76
G_{13}	1879.78	16	704043.88	14	44.64
G_{14}	2769.52	3	1068081.19	20	37.32
G_{15}	1641.05	21	569674.35	12	45.99
G_{16}	1655.76	20	300094.47	2	33.09
G_{17}	1622.53	22	232223.34	1	29.70
G_{18}	2002.51	11	518715.71	10	35.97
G_{19}	1656.45	19	328488.78	4	34.60
G_2	2385.38	5	1311497.93	22	48.01
G_{20}	2852.64	2	1027933.21	19	35.54
G_{21}	1554.01	24	604848.02	13	50.05
G_{22}	1558.47	23	356690.17	5	38.32
G_{23}	2072.24	9	707998.69	15	40.60
G_{24}	2522.3	4	1205304.99	21	43.53
G_3	1815.45	18	421805.72	6	35.77
G_4	2337.17	6	985108.97	18	42.47
G_5	2120.72	8	542508.86	11	34.73
G_6	1980.88	13	443918.03	7	33.64
G_7	1871.46	17	323264.96	3	30.38
G_8	1908.93	15	470823.03	8	35.95
G_9	1925.74	14	478712.68	9	35.93

4.3.2. Francis and Kannenberg's Coefficient of Variability (CV_i)

According to Francis *et al.* (1978), stable genotype is the one that provides a high yield performance and consistent low CV. In these methods genotypes are investigated by plotting individual genotypes mean yields (Y axis) against the coefficient of variation (CV) percent for each genotype (X axis) (Fig.5). By drawing the horizontal lines through the genotype mean yields of 2200Kg ha^{-1} and a vertical line through the CV percent grand mean, four quadrants were formed. Genotypes with CV mean and mean yield of above grand mean were judged high yielding with

low stability. While genotypes with low CV percent and the mean yield below the grand mean were judged as low yielding with high stability. From the Fig.5, there is no genotypes that fell in quadrant I, which is considered as stable and high yielding. This suggests that there are no genotypes that well perform in all agro ecologies of the study. Whereas, in quadrant II is genotypes SCS-1 (G_{20}) and Clarck-63k (G_{14}) which considered as less stable but high yielding and therefore may be targeted to a specific agro ecology where it may perform well. In quadrant III, genotypes Choska (G_{15}), LD00-3309 (G_{21}) and ks3496 (G_{13}) had CV percent values higher than the grand means and their means were lower than the grand mean, thus they were considered unstable and low yielding, which is least desirable (Fig.5). Genotypes Delsoy 4710 (G_7), Hang douNo-1 (G_{17}), Liu yuemang (G_{16}), and UA4805 (G_6) fell within quadrant IV. They had CV percent values below the CV percent grand mean and a mean yield of below grand mean yield. Thus, they were judged as having high stability, but low yielding. A problem with this method is that, in general, genotypes with high phenotypic stability measured through the environmental variance show low yield. And according to Francis 1977 the mean-CV method was designed primarily to aid in studies on the physiological basis for yield stability. Beside this, Francis *et al.* (1978) this method was found more practical to characterize genotypes on a group basis rather than individually

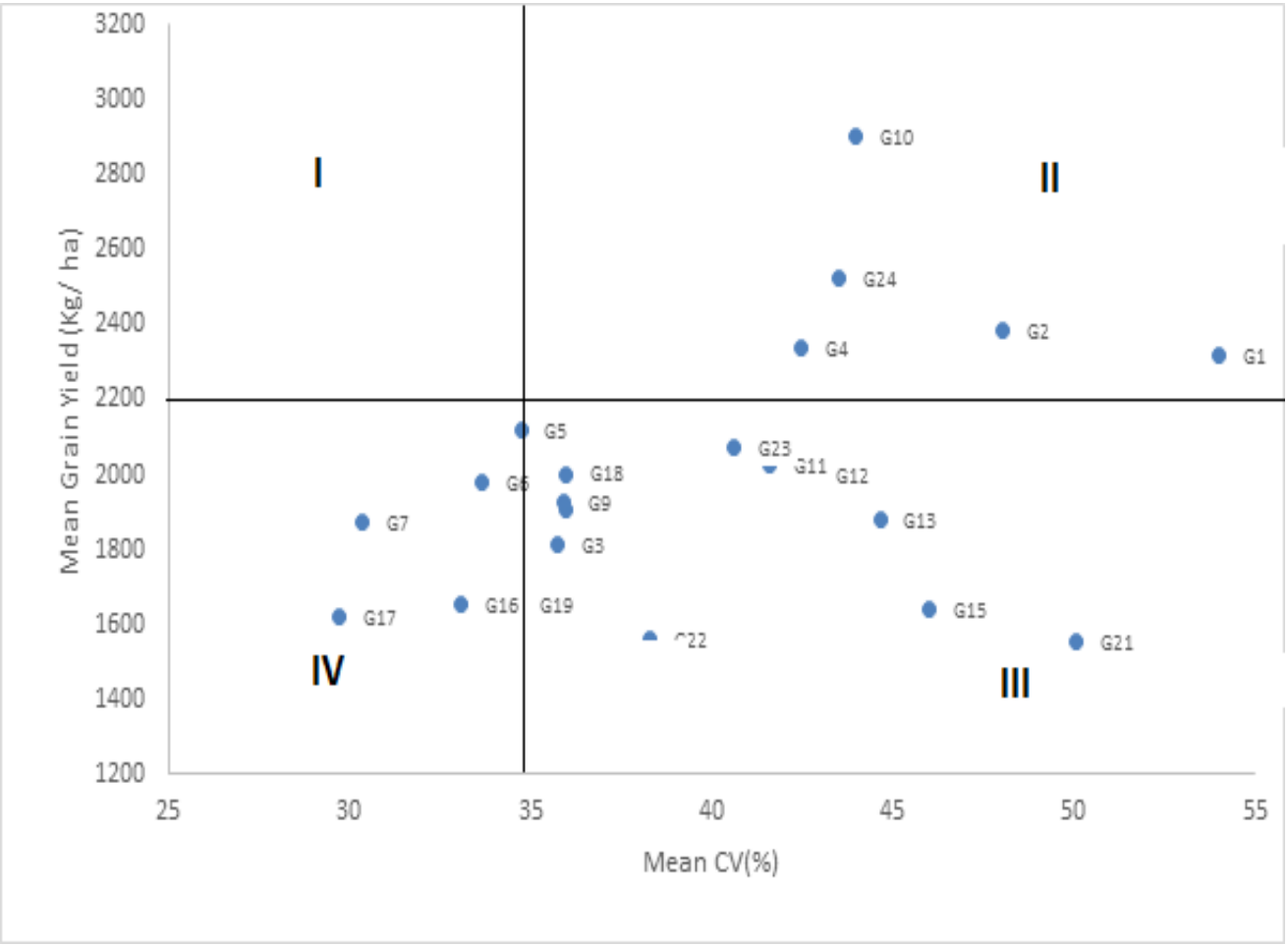


Figure 5. Coefficient of variability plotted against mean grain yield (Kg ha^{-1}) of tested genotypes.

NB:Gen.G1=5002T;G2=Ciaric;G3=Ozark;G4=Motte;G5=ks4895;G6=UA4805;G7=Delsoy4710;G8=Spry;G9=Harbar;G10=AFGAT;G11=Graham;G12=Manokin;G13=ks3496;G14=Clarck63k;G15=Choska;G16=Liuyuemang;G17=Hang dou No-1;G18=Hs93-4118;G19=Croton 3.9; G20=SCS-1;G21=LD00-3309;G22=Princhard;G23=Desha; G24=AGS-7-1.

4.3.3. Wricke's Ecovalence Analysis (W_i)

Wricke (1962) defined the concept of ecovalence, is the stability of the genotype in its interaction with environments, squared and summed across environments. The genotypes with the lowest ecovalence has fewer fluctuations across the environments and therefore it is considered to be more stable than others.

Wricke's ecovalence was determined for grain yield of the twenty-four soybean genotypes at six locations during 2015/16 growing season (Table 11). Spry (G_8), AFGAT (G_{10}) and ks3496 (G_{13}) were the three most stable genotypes. The unstable genotypes are 5002T, Hang douNo-1(G_{17}) and AFGAT (G_{10}) had the highest stability ecovalence value and ranks 22^{th}, 23^{th} and 24^{th} respectively (Table 11). This result shows that the unstable genotypes contribute the highest amount of variation to the total GEI variance and this leads the genotype unstable. The genotypes AFGAT (G_{10}), SCS-1(G_{20}) and Clarck-63k (G_{14}) the highest grain yield performance, their highest ecovalence value made them unstable which not preferable for wider adaptations. The Wrick's Ecovalence stability parameter (Table 11) shows that higher yields have the highest ecovalence and vice versa that leads genotypes recommendation to the general wider adaptation is impossible.

Table 11. Wricke's Ecovalence value for 24 genotypes at six environments.

Genotype Code	Genotype	W_i	Rank	% SS_{GEI}	Mean Yield	Rank
G_1	5002T	1486259	22	7.45	2318.71	7
G_2	Ciaric	1113915	16	5.59	2385.38	5
G_3	Ozark	453581.1	10	2.28	1815.45	18
G_4	Motte	1458641	21	7.32	2337.17	6
G_5	Ks4895	340599.3	8	1.71	2120.72	8
G_6	UA4805	183111.6	3	0.92	1980.88	13
G_7	Delsoy 4710	283807.9	6	1.42	1871.46	17
G_8	Spry	81049.1	1	0.41	1908.93	15
G_9	Harbar	353870.8	9	1.77	1925.74	14
G_{10}	AFGAT	3036123	24	15.23	2903.39	1
G_{11}	Graham	96826.23	2	0.49	2026.52	10
G_{12}	Manokin	654123	14	3.28	2000.35	12
G_{13}	ks3496	218481.6	4	1.1	1879.78	16
G_{14}	Clarck-63k	1446254	20	7.25	2769.52	3
G_{15}	Choska	1176799	17	5.9	1641.05	21
G_{16}	Liu yuemang	1229190	18	6.17	1655.76	20
G_{17}	Hang douNo-1	1726479	23	8.66	1622.53	22
G_{18}	Hs93-4118	254908.8	5	1.28	2002.51	11
G_{19}	Croton 3.9	640470.4	13	3.21	1656.45	19
G_{20}	SCS-1	550994.4	12	2.76	2852.64	2
G_{21}	LD00-3309	465627.5	11	2.34	1554.01	24
G_{22}	Prichard	994376.3	15	4.99	1558.47	23
G_{23}	Desha	313168.6	7	1.57	2072.24	9
G_{24}	AGS-7-1	1377793	19	6.91	2522.3	4

4.3.4. Shukla's Stability Variance(σ^2_i)

Shukla (1972) proposed the stability variance (σ_i^2), the amount of genotype by environment variance associated with genotypes *i*. This stability variance is a linear function of with the wrick's ecovalence (Wricke and Weber 1980, Kang et al 1987, Piepho 1955). However, Shukla's model differs in the ranking of the genotypes from Wricke (1962) when covariates (locations means) were considered. A genotype is described as stable if the stability variance (σ_i^2) is the environmental variance (σ_e^2) which means that $\sigma_i^2 = 0$. The relatively large value of σ_i^2 indicates greater instability of genotype i. Similar to Wricke's (1962) ecovalence the Shukla (1972) identified similar genotypes as most stable regardless of their grain yield. Genotypes Spry (G_8), Graham (G_{11})and UA4805 (G_6) were stable, while the highest yielding genotypes were 24th, 12th and 20th in terms of Shukla's stability (Table 12).

Table 12 . Genotype mean grain yield and Shukla's stability variance (σ^2_i) for 24 soybean genotypes.

Genotype Code	Genotype	Stability variance (σ^2_i)	Rank	$\%SS_{GEI}$	Mean Yield	Rank
G_1	5002T	230838.98	22	7.59	2318.71	7
G_2	Ciaric	171736.75	16	5.64	2385.38	5
G_3	Ozark	66921.79	10	2.2	1815.45	18
G_4	Motte	226455.12	21	7.44	2337.17	6
G_5	Ks4895	48988.17	8	1.61	2120.72	8
G_6	UA4805	23990.11	3	0.79	1980.88	13
G_7	Delsoy 4710	39973.67	6	1.31	1871.46	17
G_8	Spry	7789.72	1	0.26	1908.93	15
G_9	Harbar	51094.76	9	1.68	1925.74	14
G_{10}	AFGAT	476849.08	24	15.67	2903.39	1
G_{11}	Graham	10294.03	2	0.34	2026.52	10
G_{12}	Manokin	98753.84	14	3.25	2000.35	12
G_{13}	ks3496	29604.41	4	0.97	1879.78	16
G_{14}	Clarck-63k	224488.93	20	7.38	2769.52	3
G_{15}	Choska	181718.24	17	5.97	1641.05	21
G_{16}	Liu yuemang	190034.38	18	6.25	1655.76	20
G_{17}	Hang douNo-1	268969.03	23	8.84	1622.53	22
G_{18}	Hs93-4118	35386.5	5	1.16	2002.51	11
G_{19}	Croton 3.9	96586.75	13	3.17	1656.45	19
G_{20}	SCS-1	82384.22	12	2.71	2852.64	2
G_{21}	LD00-3309	68833.92	11	2.26	1554.01	24
G_{22}	Prichard	152762.3	15	5.02	1558.47	23
G_{23}	Desha	44634.09	7	1.47	2072.24	9
G_{24}	AGS-7-1	213622.07	19	7.02	2522.3	4

4.3.5. Lin and Binns cultivar superiority measure (P_i)

The cultivar superiority measure varied from 139156 to 1851428 (Table 13). Genotypes with the lowest values are considered as the most stable. From the result of the cultivar superiority measure indicated that the most stable genotypes were genotype AFGAT (G_{10}) followed by SCS-1 (G_{20}) and genotype Clarck-63k (G_{14}). However, the most unstable genotypes according to this measure were Princhard (G_{22}), Choska (G_{15}) and Liu yuemang (G_{16}).

Table 12. Cultivar superiority index 24 genotypes across six environments.

Genotype	Cultivar Superiority(P_i)	P_i Rank	Grain Yield ($Kgha^{-1}$)	Rank	% Mean
5002T	602777	7	2318.71	7	112.69
Ciaric	490565	6	2385.38	5	115.93
Ozark	1265203	18	1815.45	18	88.23
Motte	486579	5	2337.17	6	113.59
ks4895	890071	10	2120.72	8	136.47
UA4805	1018758	13	1980.88	13	127.10
Delsoy 4710	1175039	17	1871.46	17	115.34
Spry	1085075	15	1908.93	15	116.32
Harbar	1159134	16	1925.74	14	116.31
AFGAT	139156	1	2903.39	1	175.28
Graham	898782	11	2026.52	10	111.63
Manokin	883085	9	2000.35	12	106.89
ks3496	1074345	14	1879.78	16	100.00
Clarck-63k	161355	3	2769.52	3	145.08
Choska	1740437	23	1641.05	21	85.22
Liu yuemang	1678100	22	1655.76	20	83.59
Hang dou No-1	1640843	21	1622.53	22	81.11
Hs93-4118	955753	12	2002.51	11	100.00
Croton 3.9	1594465	19	1656.45	19	81.74
SCS-1	140926	2	2852.64	2	137.66
LD00-3309	1624416	20	1554.01	24	73.28
Princhard	1851428	24	1558.47	23	67.21
Desha	866802	8	2072.24	10	88.66
AGS-7-1	373932	4	2522.3	4	105.74

4.3.6. Finlay and Wilkenson

Figure 6 graphically represents the regression coefficient (bi) plotted against the genotype mean yield as an indication of stability for six environments. However, the regression coefficient must also have associated and interpreted with the genotype mean yield to determine adaptability.

From the figure 6 Hang douNo-1 (G_{17}), Liu yuemang (G_{16}), Prichard (G_{22}), Croton 3.9 (G_{19}) and Delsoy 4710 (G_7) showed above average stability, but also specifically adapted to the unfavorable environment. The genotypes LD00-3309 (G_{21}), Choska (G_{15}), Ozark (G_3), ks3496 (G_{13}), Spry (G_8) and Harbar (G_9) all indicated average stability $0.8 < b_i < 1.1$, that shows with increasing adaptability in all environments in that order. The genotypes 5002T (G_1), Ciaric (G_2), AGS-7-1 (G_{24}), Clarck-63k, SCS-1 (G_{20}) and AFGAT (G_{10}) showed below average stability, with AFGAT (G_{10}), SCS-1 (G_{20}) and Clarck-63k (G_{14}) having good specific adaptability to high potential conditions, 5002T(G_1), Ciaric (G_2) and AGS-7-1 (G_{24}) showing that generally poor adaptability. Besides, these Hang douNo-1 (G_{17}), Liu yuemang (G_{16}), Prichard (G_{22}) and Croton 3.9 (G_{19}) showed above average stability, and also show very specific adaptation to low potential or unfavorable conditions.

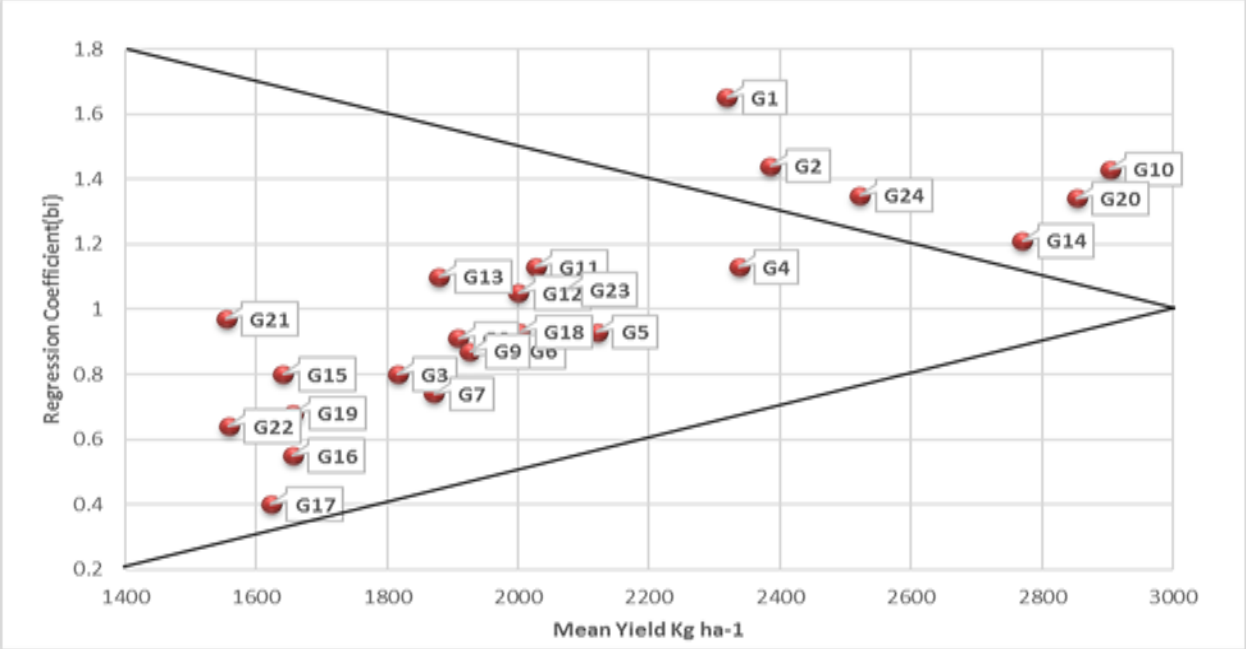


Figure 6. Regression coefficient plotted against genotype mean for six environments.

NB:Gen.G1=5002T;G2=Ciaric;G3=Ozark;G4=Motte;G5=ks4895;G6=UA4805;G7=Delsoy4710;G8=Spry;G9=Harbar;G10=AFGAT;G11=Graham;G12=Manokin;G13=ks3496;G14=Clarck63k;G15=Choska;G16=Liuyuemang;G17=Hang dou No-1;G18=Hs93-4118;G19=Croton 3.9; G20=SCS-1;G21=LD00-3309;G22=Princhard;G23=Desha; G24=AGS-7-1.

4.3.7. Eberhart and Russel's Model

Genotype by environment interaction ANOVA of the joint linear regression model is used for estimation and partitioning of GE interaction in two components. The ANOVA by Eberhart and Russel's Model of for soybean genotypes on mean grain (Kg ha^{-1}) tested across six locations is illustrated in Table 14. Eberhart and Russell (1966) procedure involves the use of joint linear regression where the yield of the genotype is regressed on the environmental mean yield. In this model, the SS due to the environments and GEI is partitioned into environments (linear), GEI (linear) and deviation from the regression (pooled deviations overall the genotypes).

The genotypes regressions term was tested for significance using an F-ratio by taking the deviation from regression mean square as the error term. The deviation from regressions mean square were tested for significance using the error term, for overall GEI in the ANOVA. The result of Eberhart and Russell's ANOVA revealed very highly significant ($P<0.001$) difference among the genotypes for grain yield indicating the yield performance of was different. GEI (linear) interaction was significant.

Eberhart and Russell's stability parameter coefficient of regression () and deviation from regression () were determined for the 24 soybean genotypes (Table 15). The result revealed that the slope (b_i) did not deviate from unity which indicates that all the tested genotypes had average responsiveness to changing environments. The result of an individual genotypes deviation from linear regression (Table14) showed that genotype 5002T (G_1), Ciaric(G_2), Ozark (G_3), Ks4895 (G_5), UA4805 (G_6), Delsoy 4710 (G_7), Spry (G_8), Harbar (G_9), Graham (G_{11}), Manokin (G_{12}), ks3496 (G_{13}), Liu yuemang (G_{16}), Hang douNo-1 (G_{17}), Hs93-4118 (G_{18}), Croton 3.9 (G_{19}), SCS-1(G_{20}), LD00-3309 (G_{21}), Prichard (G_{22}) and Desha (G_{23}) had non-significant deviation from regression.

However, the result of deviation from the regression varies and for most of the genotypes i.e. nineteen, it was significantly different from zero. The genotype that ranked first according to this stability model was Graham (G_{11}) which had a very small mean yield across environments. Genotypes Spry (G_8) and Delsoy 4710 (G_7) still ranked 2nd and 3rd and were stable. The top yielding genotypes; AFGAT (24), Clarck 63k (22) and AGS-7-1(20) were unstable. Genotype Motte (23) was also the most unstable genotype with Eberhart and Russell's stability model as well (Table 14). Hence, these five genotypes are not adaptable to the wider environment.

Table 13. Eberhart and Russel's Model of soybean genotypes on mean grain yield (kg ha^{-1}) across six locations.

Source of Variation	DF	Sum Sq.	Mean Sq.	Value	Pr (>F)
Total	143	107714226	753246		
Genotypes	23	22070243	959576	6.6108	<0.001***
Env+(GenxEnv)	120	85643983	713700		
Env(linear)	1	65880264	65880264		
GenxEnv(linear)	23	5829106	253439	1.746	0.032*
Pooled deviation	96	13934612	145152		
5002T	4	331003	82751	0.9769	0.420ns
Ciaric	4	435366	108842	1.285	0.276ns
Ozark	4	339733	84933	1.0027	0.406ns
Motte	4	1414540	353635	4.175	0.003**
Ks4895	4	328291	82073	0.9689	0.425ns
UA4805	4	139193	34798	0.4108	0.801ns
Delsoy 4710	4	97789	24447	0.2886	0.885ns
Spry	4	59562	14890	0.1758	0.951ns
Harbar	4	309523	77381	0.9135	0.456ns
AFGAT	4	2529547	632387	7.4659	<0.001***
Graham	4	54380	13595	0.1605	0.958ns
Manokin	4	640641	160160	1.8908	0.112ns
ks3496	4	189572	47393	0.5595	0.692ns
Clarck-63k	4	1320718	330179	3.8981	0.004**
Choska	4	1076346	269086	3.1768	0.014*
Liu yuemang	4	672404	168101	1.9846	0.097ns
Hang douNo-1	4	726104	181526	2.1431	0.076ns
Hs93-4118	4	234621	58655	0.6925	0.598ns
Croton 3.9	4	361736	90434	1.0677	0.373ns
SCS-1)	4	244256	61064	0.7209	0.578ns
LD00-3309	4	457887	114472	1.3514	0.251ns
Prichard	4	646436	161609	1.9079	0.109ns
Desha	4	282331	70583	0.8333	0.505ns
AGS-7-1	4	1042635	260659	3.0773	0.017*
Pooled error	288	24394652	84704		

***=very highly significant(P<0.001) **= highly significant (P<0.01), *= significant (P<0.05), ns=non-significant.

Table 14. Mean grain yield (Kg ha^{-1}), regression coefficient (b_i) and deviation from regression (S^2d_i) for the 24 genotypes tested across six environments.

Genotype Code	Genotype	GYLD (Kg ha^{-1})	Rank	Beta(b_i)	Deviation (S^2d_i)	Rank
G_1	5002T	2318.71	7	1.65	-5635.65ns	11
G_2	Ciaric	2385.38	5	1.44	20455.15ns	14
G_3	Ozark	1815.45	18	0.8	-3453.27ns	12
G_4	Motte	2337.17	6	1.13	265248.7**	23
G_5	Ks4895	2120.72	8	0.93	-6313.80ns	10
G_6	UA4805	1980.88	13	0.87	-53588.20ns	4
G_7	Delsoy 4710	1871.46	17	0.74	-63939.20ns	3
G_8	Spry	1908.93	15	0.91	-73496.00ns	2
G_9	Harbar	1925.74	14	0.87	-11005.80ns	9
G_{10}	AFGAT	2903.39	1	1.43	544000.2***	24
G_{11}	Graham	2026.52	10	1.13	-74791.5ns	1
G_{12}	Manokin	2000.35	12	1.05	71773.88ns	16
G_{13}	ks3496	1879.78	16	1.1	-40993.5ns	5
G_{14}	Clarck-63k	2769.52	3	1.21	241793.1ns	22
G_{15}	Choska	1641.05	21	0.8	180700.00**	21
G_{16}	Liu yuemang	1655.76	20	0.55	79714.67ns	18
G_{17}	Hang douNo-1	1622.53	22	0.4	93139.62ns	19
G_{18}	Hs93-4118	2002.51	11	0.93	-29731.3ns	6
G_{19}	Croton 3.9	1656.45	19	0.68	2047.567ns	13
G_{20}	SCS-1	2852.64	2	1.34	-27322.5ns	7
G_{21}	LD00-3309	1554.01	24	0.97	26085.35ns	15
G_{22}	Prichard	1558.47	23	0.64	73222.69ns	17
G_{23}	Desha	2072.24	10	1.06	-17803.6ns	8
G_{24}	AGS-7-1	2522.3	4	1.35	172272.3*	20

Significantly unstable at * = 0.05, **=0.01 and *** =0.001 probability level, GYLD=Grain yield

4.3.8. GGE biplot analysis

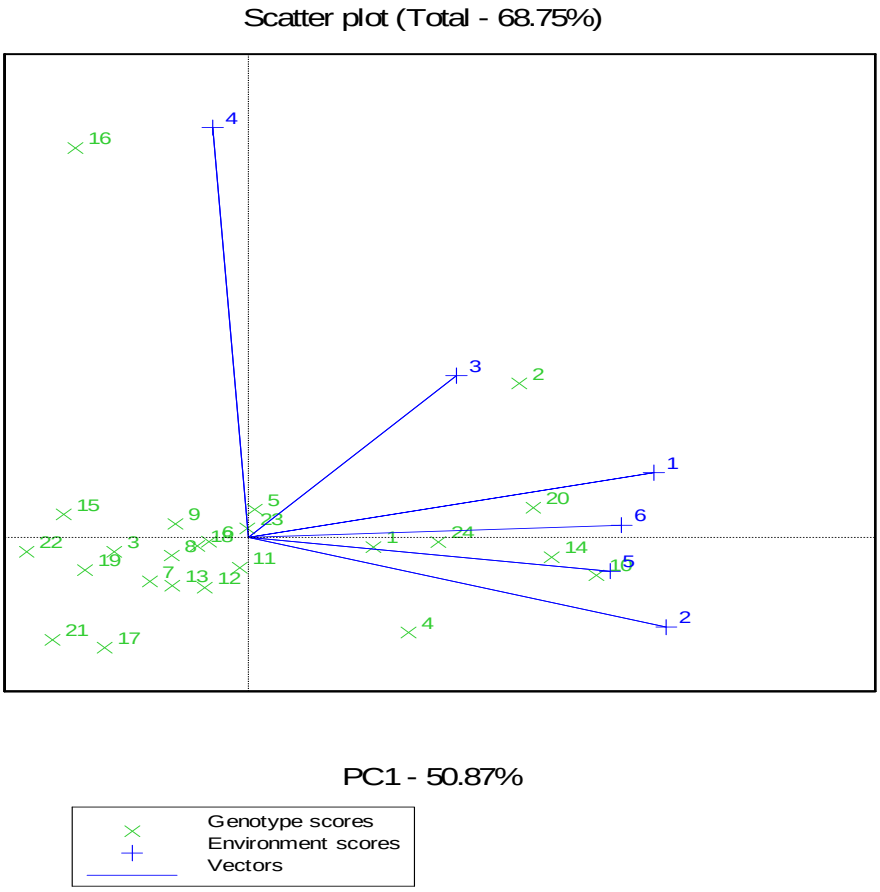
4.3.8.1. Performance of genotypes and environments

GGE biplots is a multi-faceted tool originated with Gabriel (1971), and it has strongly captured the imagination of plant breeder and production agronomist. GGE biplot analysis is increasingly being used in the GEI interaction data analysis in agriculture (Butrón *et al*., 2004; Crossa *et al*., 2002; Dehghani *et al.*, 2006; Kaya *et al*., 2006; Ma *et al*., 2004; Yan and Hunt 2001). GGE biplot analysis was also reported on soybean (Mulugeta *et al.*,2013; Sousa *et al*., 2015; Asfaw *et al*., 2009; M. Muchlish Adie *et al*., 2014). GGE biplots is one of the statistical tools with various uses, i.e., Mega-environment analysis (e.g. "Which- won- where" pattern), whereby specific genotypes can be recommended to specific mega-environments; genotype evaluation based on their mean performance and stability across mega environments, and test-environmental evaluation based on their discriminating ability and representativeness (Yan *et al*., 2000). GGE biplots of the first two interaction principal components (i.e. IPCA1 and IPCA2) accounted for 81.2% of the total variation with the value of 71.9% and 9.9% respectively. In this case GGE is greater efficient by retaining most of the variation in the first two IPCAs i.e. 81.2%, which is by far greater comparing with AMMI that is around 70.33%. This GGE result is lower than that observed by Amira *et al.* (2013) (86.6%), but higher than that found by Asfaw *et al*. (2009) (61.50%) and Atnaf *et al.* (2013)(63.4).

4.3.8.2.Performance of genotypes in a specific environment

The distance between two environments, measures their dissimilarity and discriminate the genotypes which helps in the identification of mega-environments. Lines connecting the environments to the biplot origin are called environmental vectors. Length of the environmental vectors is proportional to their standard deviation which is a measure of the discriminating ability of the environments. The interpretation rule as stated by Yan *et al*. (2006) that the performance of a genotype in an environment is better than average, if the angle between its vector and the

environment's vector is <90°; it is lower than average, if the angle is >90°; and it is near average, if the angle is about 90°. In this case, Choska was below average in nearly all environments except E3 and E4 whereas Choska was above average in all environments except in E5 (Fig.9).



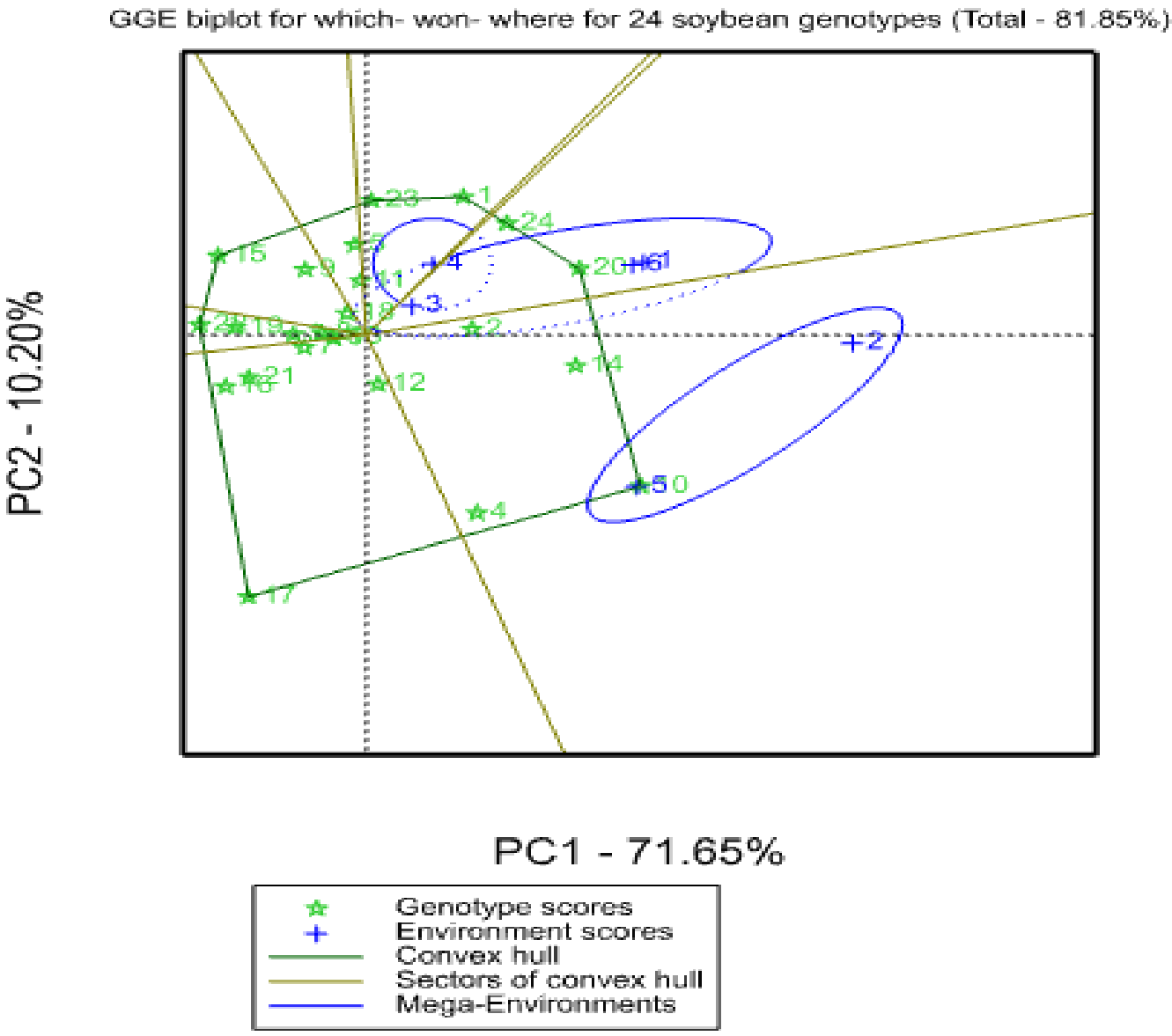
Performance of each genotype in each environment

Figure 8**.** The GGE biplot showing the performance of each genotype in each environment.

NB:Env.1=Asosa;2=Bako;3=Dimtu;4=Jimma;5=Metu;E6=Pawe;Gen.;1=5002T;2=Ciaric;3=Ozark;4=Motte;5=ks4895;6=UA4805;7=Delsoy4710;8=Spry;9=Harbar;10=AFGAT;11=Graham;12=Manokin;13=ks3496;14=Clarck63k;15=Choska;16=Liuyuemang;17=HangdouNo-1;18=Hs93-4118;19=Croton3.9;20=SCS-1;21=LD00-3309;22=Princhard;23=Desha;24=AGS-7-1.

4.3.8.3.The Which-won-where pattern

According to Yan *et al*., 2002 the polygon view of GGE biplot indicates the best genotypes in each environment and group of environments. In this situation, the polygon is formed by connecting the signs of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. In this case, the polygon connects all the farthest genotypes and perpendicular lines divide the polygon into sectors. Sectors help to visualize the mega-environments. This means that winning genotypes for each sector are placed at the vertex. The pattern on the environment in the above biplot suggests that the existence of three different mega-environments(Fig.9). But, this pattern may not be repeatable across years (Yan *et al*. 2000). To confirm the repeatability of the mega-environment result, there need to be multiyear data (Yan *et al*. 2005).



Which genotype won where?

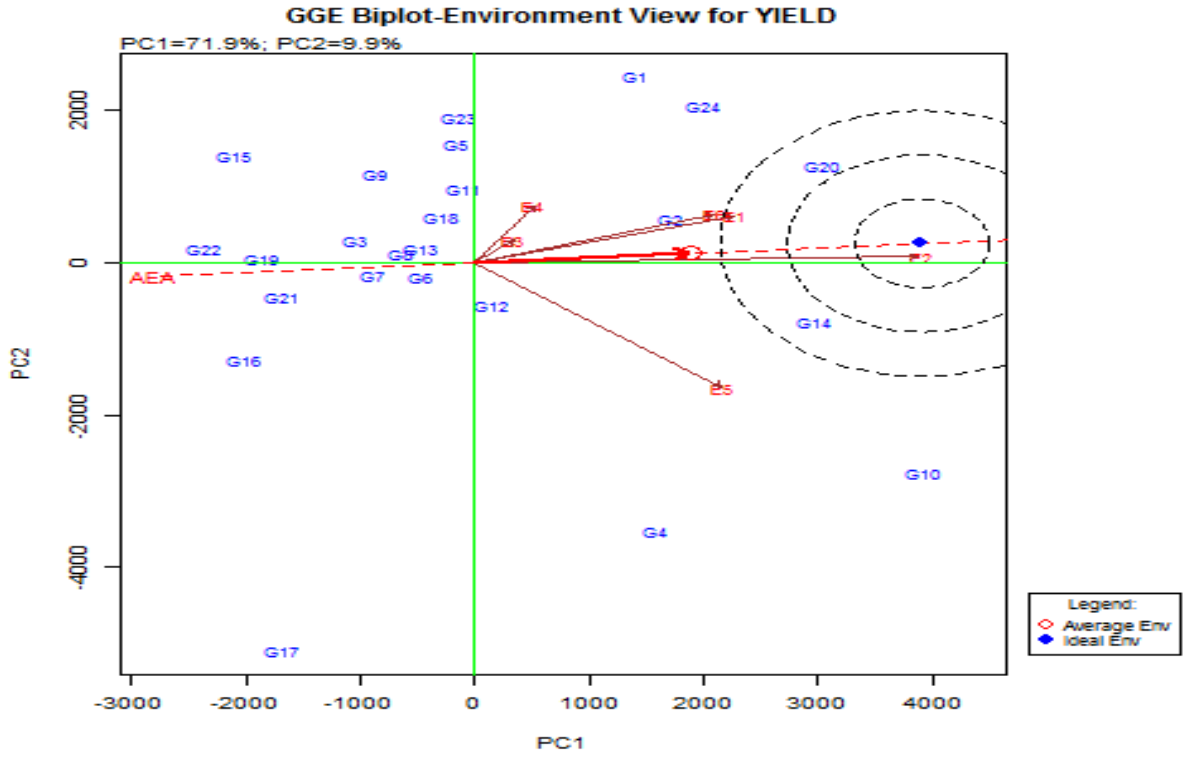
Figure 5. "Which-won-where" or "Which is best for what'' pattern of GGE biplot based on 24 soybean genotypes evaluated in six soybean agro-ecologies of Ethiopia.

NB:Env.1=Asosa;2=Bako;3=Dimtu;4=Jimma;5=Metu;6=Pawe;Gen.;1=5002T;2=Ciaric;3=Ozark;4=Motte;5=ks4895;6=UA4805;7=Delsoy4710;8=Spry;9=Harbar;10=AFGAT;11=Graham;12=Manokin;13=ks3496;14=Clarck63k;15=Choska;16=Liuyuemang;17=Hang dou No-1;18=Hs93-4118;19=Croton 3.9; 20=SCS-1;21=LD00-3309;22=Princhard;23=Desha; 24=AGS-7-1.

For studying the possible existence of different mega-environments in a region, visualization of "which -won-where" Pattern of the Meta environment trial is important as described by Yan *et al*, 2000,2001). The vertex genotypes in this investigation were Hang dou No-1 (G_{17}), AFGAT (G_{10}), SCS-1 (G_{20}), 5002T (G_1), Choska (G_{15}) and Princhard (G_{22}). This means that the vertex genotypes for each sector are the one that gave the highest yield for the environments that fall within that sector. Besides, it is evident from the GGE biplot in fig.9 that environmental groupings, which suggests the possible existence of different mega environments. Thus, based on the biplot analysis of six environments of the data. The highest yielding in the environment in five and two are AFGAT (G_{10}). And in environment six and one AGS-7-1 (G_{24}). The other vertex genotypes are Choska (G_{15}), Prichard (G_{22}) and Hang douNo-1 (G_{17}) are poor performing in all the six environments.

4.3.8.4. Ideal test environments for selecting generally adapted genotypes

Within a single mega-environment, the ideal test environment should be most discriminating (informative) and also most representative of the target environment. Figure 10 defines an "ideal test environment", which is the center of the concentric circles. It is a point on the Average Environment Coordinate in the positive direction ("most representative") with a distance to the biplot origin equal to the longest vector of all environments ("most informative"). E2 (Bako) is closest to this point and is, therefore, best, whereas E5 and E4 were poorest for selecting cultivars adapted to the whole region. Note that additional years are required to confirm that a specific test location is "ideal".



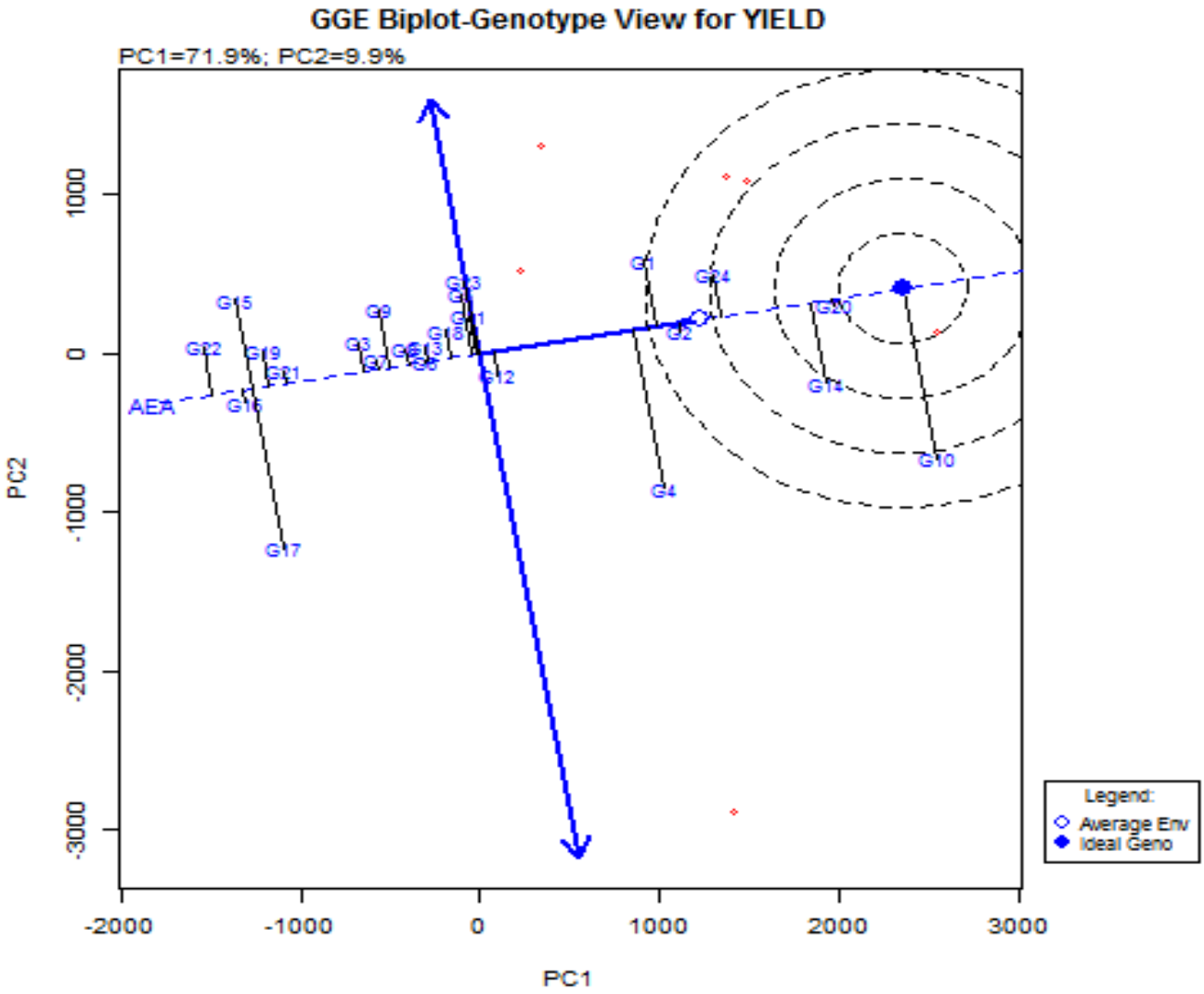
Ranking environments based on both discriminating ability and representativeness

Figure 6.The discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

NB:Env.E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe;Gen.Code=Genotype;G1=5002T;G2=Ciaric;G3=Ozark;G4=Motte;G5=ks4895;G6=UA4805;G7=Delsoy4710;G8=Spry;G9=Harbar;G10=AFGAT;G11=Graham;G12=Manokin;G13=ks3496;G14=Clarck63k;G15=Choska;G16=Liuyuemang;G17=Hang dou No-1;G18=Hs93-4118;G19=Croton 3.9;G20=SCS-1;G21=LD00-3309;G22=Princhard;G23=Desha;G24=AGS-7-1

4.3.8.5.Ranking of genotypes based on relative to the ideal genotypes

The ideal genotypes (the center of concentric circles) to be a point on AEA in the positive direction and has a vector length equals to the longest vector of the genotypes on the positive side of the AEA (“highest mean performance’’). As a result, genotypes located closer to the “ideal genotypes” are more desirable than the others. Hence, the GGE biplots (Fig.11) shows that G_{10} is an ideal genotype, with other genotypes like G_{20} and G_{14} are desirable genotypes as they are closer to the ideal genotype on the bi-plot.



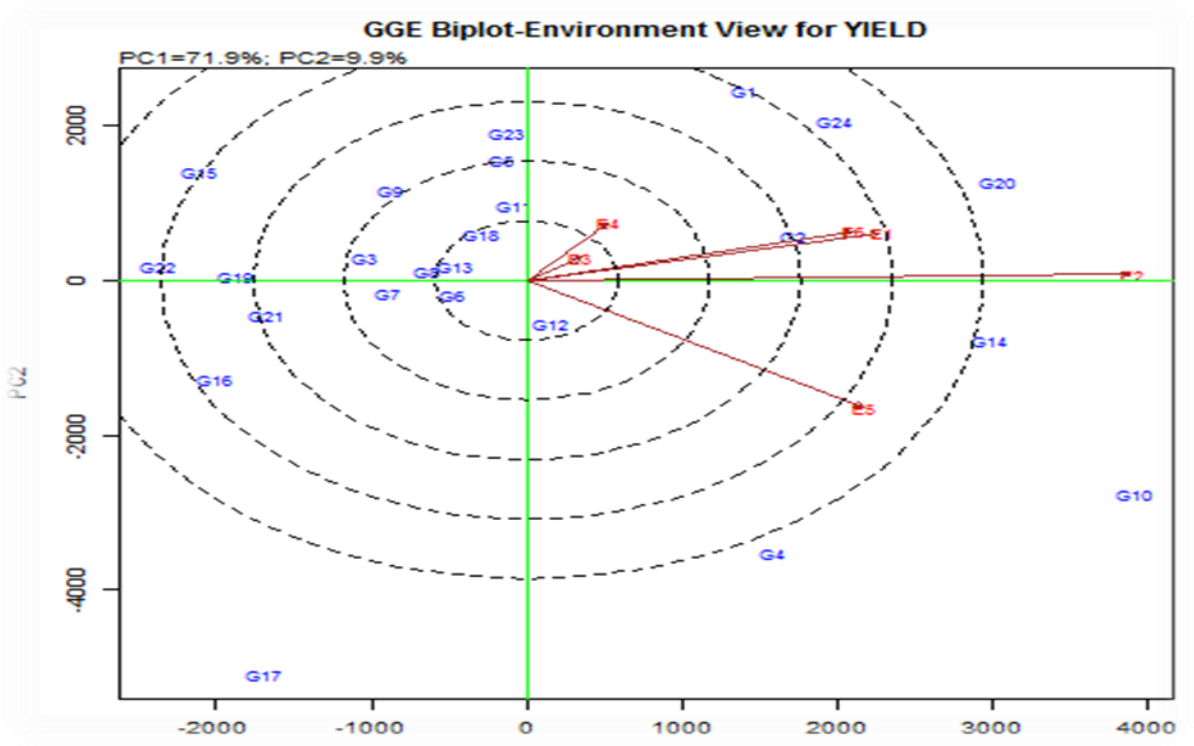
Ranking genotypes based on both mean and stability

Figure 7. The average-environment coordination (AEC) view to rank genotypes relative to an ideal genotype.

NB:Env.E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe;Gen.Code=Genotype;G1=5002T;G2=Ciaric;G3=Ozark;G4=Motte;G5=ks4895;G6=UA4805;G7=Delsoy4710;G8=Spry;G9=Harbar;G10=AFGAT;G11=Graham;G12=Manokin;G13=ks3496;G14=Clarck63k;G15=Choska;G16=Liuyuemang;G17=Hang dou No-1;G18=Hs93-4118;G19=Croton 3.9;G20=SCS-1;G21=LD00-3309;G22=Princhard;G23=Desha;G24=AGS-7-1

4.3.8.6. Relationships among test environments

As displayed in Fig.12 the lines that connect the environments to the biplot origin are called environment vectors, and the length of environmental vectors is proportional to their standard devation, which measures the discriminating ability of the environments. At the same time the angle between the vectors of two environments is related to the correlation coefficient between them. According to Kroonenberg (1995) and Yan (2002) the cosine angle between the vectors of two environments approximates the correlation coefficient between them. Based on the angles of environment vectors, the six sites are grouped into three groups. Accordingly, group one includes Jimma and Dimtu; group two Asosa and Pawe, and group three Bako and Metu.



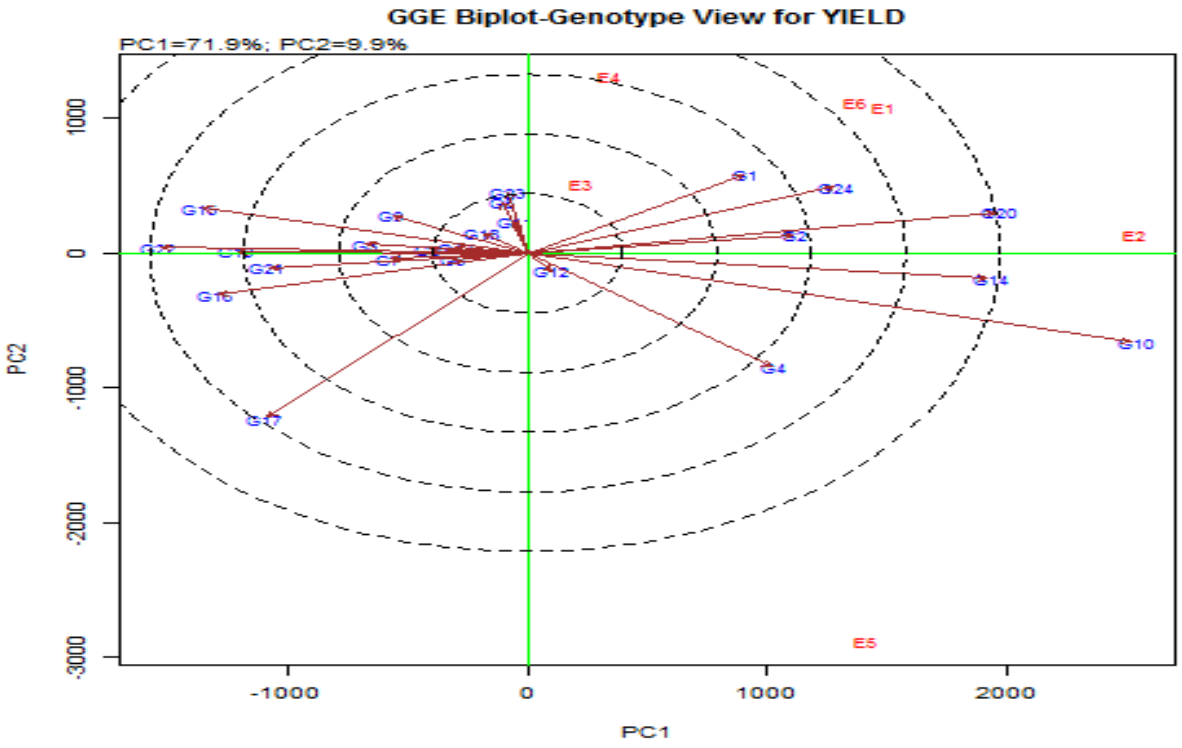
Discrimitiveness vs. reperesentativeness of test environments

Figure 12.GGE biplots based on environment focused scaling for environments to show relationship among test environments in discriminating genotypes.

NB:Env.E1=Asosa;E2=Bako;E3=Dimtu;E4=Jima;E5=Metu;E6=Pawe;Gen.Code=Genotype;G1=5002T;G2=Ciaric; G3=Ozark;G4=Motte;G5=ks4895;G6=UA4805;G7=Delsoy4710;G8=Spry;G9=Harbar;G10=AFGAT;G11=Graham; G12=Manokin;G13=ks3496;G14=Clarck63k;G15=Choska;G16=Liuyuemang;G17=Hang dou No-1;G18=Hs93-4118;G19=Croton 3.9;G20=SCS-1;G21=LD00-3309;G22=Princhard;G23=Desha;G24=AGS-7-1

4.3.8.7. Comparison among all genotypes

The is the distance between two genotypes approximates the Euclidean distance between them, which is a measure of the overall dissimilarity between them (Yan *et al*., 2006). In this case, Ciaric (G_2) and SCS-1 (G_{20}) are quite similar, whereas Hang douNo-1 (G_{17}) and AFGAT (G_{10}) are very different.This implies that the dissimilarity is because of the variation in mean yield and or interaction with the environments (GEI). In addition, the biplot origin represents a "virtual" genotype that assumes an average value in each of the environment. This "average" genotype has zero contributions to both G and GE (Yan *et al*.,2006) and inversly genotypes with larger vectors have large contributions to either G or GE or both. In this case Manokin (G_{12}) and other genotypes in the smaller concentric circle are the average genotypes.



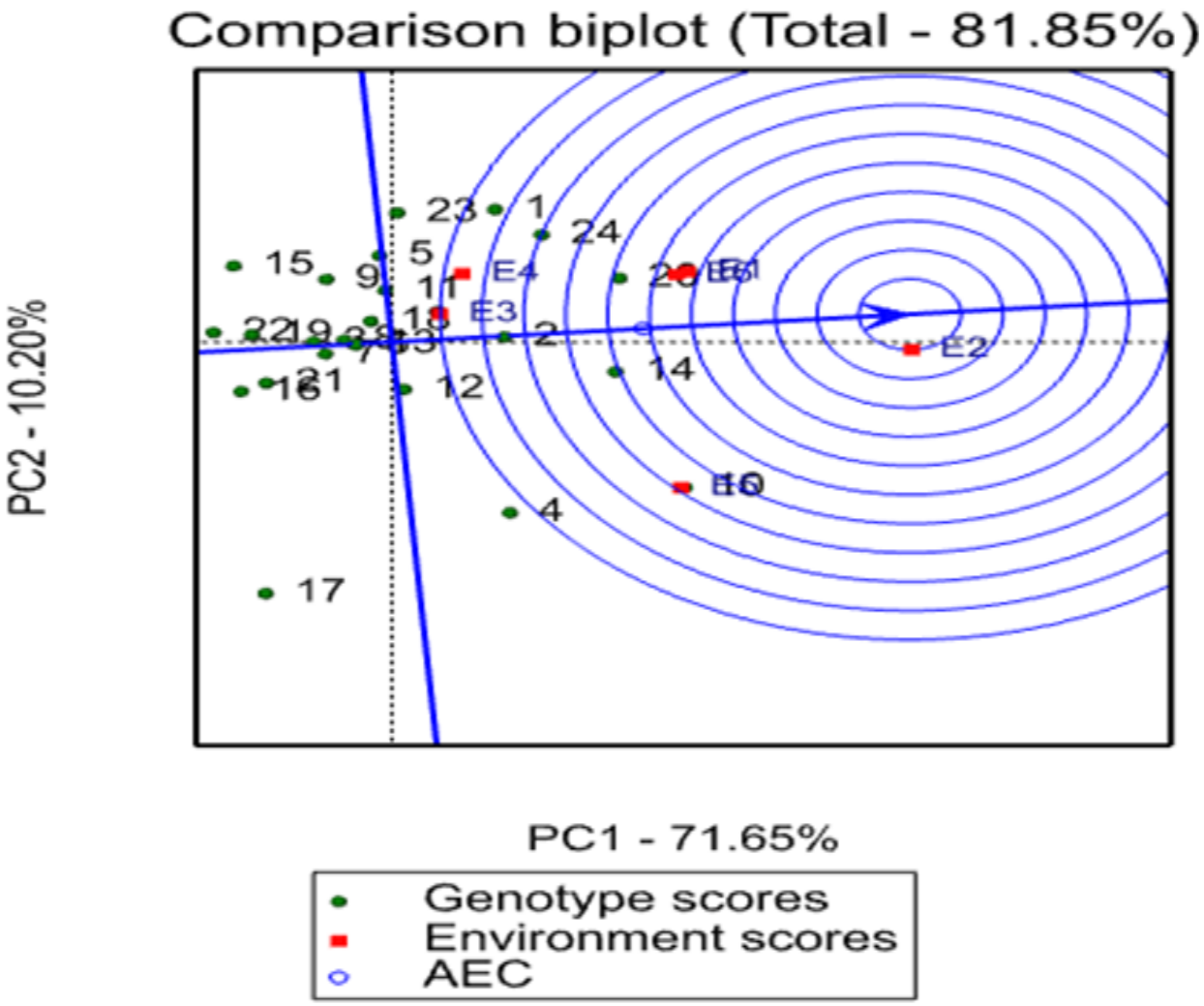
Similarity among genotypes

Figure 8. The genotype vector views to show similarity among genotypes in their performances in their individual environments.

NB:Env.E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe;Gen.Code=Genotype;G_1=5002T;G_2=Ciaric;G_3=Ozark;G_4=Motte;G_5=ks4895;G_6=UA4805;G_7=Delsoy4710;G8=Spry;G9=Harbar;G_{10}=AFGAT;G_{11}=Graham;G_{12}=Manokin;G_{13}=ks3496;G_{14}=Clarck63k;G_{15}=Choska;G_{16}=Liuyuemang;G_{17}=Hang dou No-1;G_{18}=Hs93-4118;G_{19}=Croton 3.9;G_{20}=SCS-1;G_{21}=LD00-3309;G_{22}=Princhard;G_{23}=Desha;G_{24}=AGS-7-1

4.3.8.8.Mean Yield and Stability Performance of Genotypes

Stability can be identified based on concentric circles and also ideal genotypes are on the center of concentric circles i.e., high mean and stable. Beside this, good genotypes are close to ideal genotypes. A genotype is more desirable if it is closer to 'ideal' genotype (Kaya *et al*., 2006 and Mitrovic *et al*., 2012). Figure 14. illustrates an important concept regarding "stability". The term "high stability" is meaningful only when associated with mean performance. According to Fig.14, Clarck-63k > SCS-1> AFGAT > AGS-7-1> Ciaric >5002T is stable in their order and more desirable than other genotypes, where those ranked last, i.e. Hang douNo-1, Liu yuemang and LD00-3309on their rank, were unfavorable since there are too far from the ideal genotypes.



Ranking genotypes based on both mean and stability

Figure 14.GGE biplot showing the ranking of 24 genotypes (G_1–G_{24}) for both mean yield and stability based on the "average environment coordinate" (AEC).

NB:Env.E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe;Gen.;1=5002T;2=Ciaric;3=Ozark;4=Motte;5=ks4895;6=UA4805;7=Delsoy4710;8=Spry;9=Harbar;10=AFGAT;11=Graham;12=Manokin;13=ks3496;14=Clarck63k;15=Choska;16=Liuyuemang;17=Hang dou No-1;18=Hs93-4118;19=Croton 3.9; 20=SCS-1;21=LD00-3309;22=Princhard;23=Desha; 24=AGS-7-1.

4.3.9. Additive Main Effects and Multiplicative Interactions (AMMI)

According to AMMI analysis for grain yield, the first two interaction principle components have taken the largest portions (70.34%) of the interaction sum squares with 50.3% and 20.04 and 27 and 25 degree of freedom respectively (Table 16). The AMMI model integrates the analysis of variance into a unified approach (Gauch, 1988; Gauch and Zobel, 1996). IPCA scores of genotype in the analysis are an indication of the stability of a genotype over the environments (Guach and Zobel, 1997).

The combined analysis of variance (ANOVA) of twenty-four genotypes at six locations according to AMMI model 2 is shown in Table 16. The ANOVA showed that a highly significant ($P \leq 0.01$) between environments, genotypes and genotype by environment interaction (GEI) for grain yield. The IPCA 1 axis was very highly significant ($P \leq 0.001$) for grain yield, while IPCA 2 axis was significant ($P \leq .0.05$). IPCA 1 and IPCA 2 axes explained 50.30% and 20.04% of the total GEI, while the remaining 29.66% were shared between other IPCA's. This showed that AMMI model 2 was best suited because gave for this data set.

Table 15. Analysis of Variance of AMMI model for grain yield (Kg ha^{-1}) of 24 soybean genotypes grown six environments in 2015/2016.

Source of variation	DF	SS	MS	Sum Square Explained		GEI Cumulative (%)
				% TT	%GEI	
Treatments	143	325088528	2273346***	77.38		
Genotypes	23	66486177	2890703***	15.83		
Environments	5	198793045	39758609***	47.32		
Reps within E	12	22104567	1842047***	5.26		
GEI	115	59809305	520081***	14.24		
IPCA1	27	30081895	1114144***		50.30	
IPCA2	25	11984468	479379*		20.04	70.33
Residuals	63	17742941	281634ns		29.67	
Error	276	72917426	264194			
Total	431	420110521	974734			
CV (%)=24.98		R^2=0.83				

***P<0.001; *P<0.05; IPCA=Interaction Principle components axis term 1 to 2; DF=Degree of freedom; SS=Sum of Squares; MS=Mean Square, =Coefficient of variation; R=Coefficient determination.

The AMMI analysis permits the estimation of interaction effects of genotype in each and it helps identify the genotypes best suited for specific environments. Selection of genotypes can be obtained with the aid of biplot analysis.

The AMMI model summarizes patterns and relationships of genotypes and environments. Fig 7(a). Shows the AMMI model 2 biplot of grain yield for six locations. The IPCA2 score plays a major role in GEI (Purchase, 1997), so they should be plotted against the IPCA1 scores to further explore the adaptations. Genotypes closer to zero or center of the figure are more stable Fig 7(a) indicates the IPCA1 and IPCA2 score for grain yield to further explore further adaptations. The further away from zero the IPCA score for the environments is the more interaction the environment has with the genotypes, thus making difficult to choose genotypes for that environment.

In AMMI biplot 1 showing main effects means on the abscissa and principal component (IPCA) values as the ordinates, genotypes (environments) that appear almost on a perpendicular line have similar means and those that fall on the almost horizontal line have similar interaction patterns. Genotypes that group together have similar adaptation while environments which group together influences the genotypes in the same way. Genotypes (environments) with large IPCA1 scores (either positive or negative) have high interactions whereas genotypes (environments) with IPCA1 score near zero have small interactions.

Genotypes having a zero IPCA 1 score are less influenced by the environments and adapted to all environments. Since IPCA 1 scores of varieties Graham (G_{11}), LD00-3309 (G_{21}), Hs93-4118 (G_{18}) ks3496 (G_{13}) and Spry(G_8) were close to zero, they were most stable genotypes that across these environments (Figure 7(a)). However, the mean yield of genotype Spry (G_8) was higher than genotype the remaining genotypes, hence it is more preferable since it had a mean yield above average, but the rest four genotypes have mean below average. In summary, a stable variety might not be the highest yielding. These results are in line with Asfaw *et al*. (2009).

The environments having a small score had small interaction effects indicating all genotypes performed well in these locations. Pawe (E6) was relatively close to zero than other locations, it was more stable. But its mean yield is third compared with the rest locations; it might not be the best location with respect to yield. Generally, genotypes and environments with IPCA1 scores of the same sign produce positive interaction effects, thus higher yield of the genotype at that particular location, whereas combination of the IPCA 1 scores of the opposite sign produce specific negative interactions. A genotype showing high positive interaction in an environment has the ability to exploit the agro-ecological and agro-management conditions of the specific environment and is therefore best suited to that environment. In this case, Choska (G_{15}), Prichard (G_{22}), Liu yuemang (G_{16}), and Croton 3.9 (G_{19}) are suited for E4 (Jimma). While SCS-1(G_{20}) is suited for E1 (Asosa).

AMM 2 biplot presents the spatial pattern of the first two IPC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the GEI pattern and identify genotypes or environments that exhibit low, medium, or high level of interaction effects (Sharma *et al*., 1998). IPCA1 and IPCA2 of grain yield accounted for 50.30% and 20.04% of interaction respectively. The stability of a genotype or an environment is determined by the end point of its vector from the origin (0,0). Genotypes near the origin are non-sensitive to environmental interactive forces, hence may be considered stable ones and those distant from origin are sensitive and have large interactions. Genotypes Prichard, Spry, Delsoy 4710, Croton 3.9, and Manokinwere closer to the origin than any of other genotypes, hence they are most stable (Fig.7b). In AMMI 2 biplot, the environment scores are joined to the origin by the site lines. Environments with short spokes (length of arrow lines) do not exert strong interactive forces. Those with long spokes (length of arrow lines) exert strong interaction. Metu (E5) and Bako (E2) having longer spokes exert high interaction while Asosa (E1), Pawe (E6), Dimtu (E3) and Jimma (E4) having shorter spokes produce a relative weak interaction.

The graph space Fig.7 (b) are divided into IV quadrant from lower yielding environments in quadrant I and IV to high yielding in quadrants II and III. In Addition, quadrant II considered as ideal environment. So, from the graph in Fig.7b, Asosa (E1), Bako (E2) and Pawe (E6), which is in quadrant II, are ideal environments, while quadrant II characterizes in high yielding environment with unstable genotypes, in this quadrant Metu (E5) is found. Similarly, in quadrant I characterized, stable genotypes and low yielding and in contrast quadrant IV unstable genotypes with the low yielding environment.

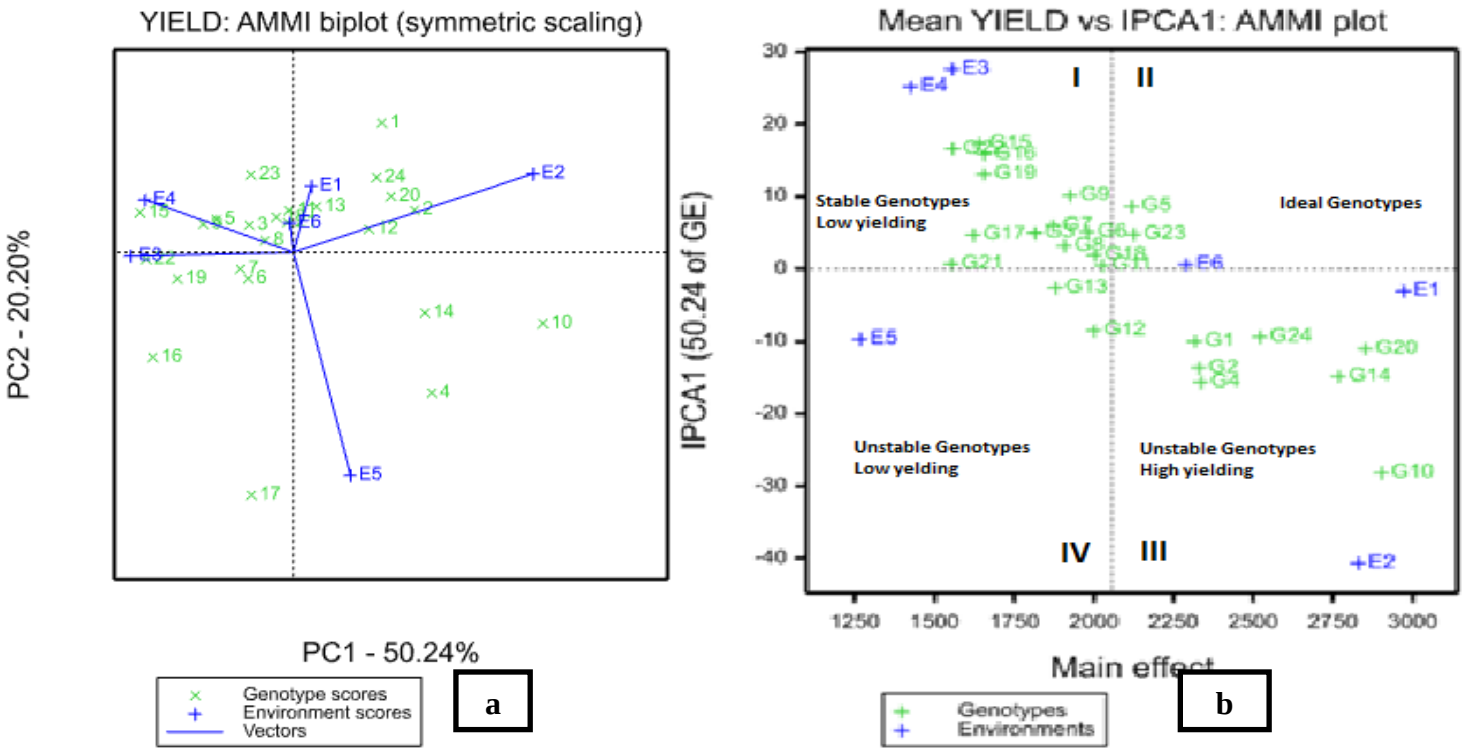


Figure 7**(**a**).** Biplots principle component analysis(PCA) vs mean yield (Kg ha^{-1}) for twenty-four soybean genotypes grown in six environments in 2015/2016 cropping season and (b)Biplots of principle components analysis(PCA) axis 2 vs axis 1 for yield.

NB:E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe;Gen.;1=5002T;2=Ciaric;3=Ozark;4=Motte;5=ks4895;6=UA4805;7=Delsoy4710;8=Spry;9=Harbar;10=AFGAT;11=Graham;12=Manokin;13=ks3496;14=Clarck63k;15=Choska;16=Liuyuemang;17=Hang dou No-1;18=Hs93-4118;19=Croton 3.9; 20=SCS-1;21=LD00-3309;22=Princhard;23=Desha; 24=AGS-7-1 and G1-G24 is equivalent with 1-24 genotype designation in Fig.6(b).

4.3.9.1.AMMI stability value (ASV)

The ASV measure was proposed by Purchase *et al.* (2000) to cope up the fact that the AMMI model does not make a provision for a quantitative stability measure. In this method, as described by Purchase (1997) was calculated for each genotype. Depending on this method, genotype with least ASV score is the stable, accordingly, genotype LD00-3309 (G_{21}) followed by Graham (G_{11}) and Spry (G_8) in third place were the most stable respectively. While genotypes AFGAT (G_{10}), Motte (G_4), Hang dou No-1(G_{17}), Liu yuemang (G_{16}) and Choska (G_{15}) were undesirable. This result also similar to the three genotypes grain mean yield rank. This method illustrated in Table 17. Shows the ASV for 24 genotypes compared with mean grain yield.

The greater the IPCA scores (Negative or Positive), the more specifically adapted a genotype is to certain environment. The closer the IPCA scores to zero, the more stable the genotype over the tested locations. The further away from zero the IPCA score for the environments is the more interaction the environment has with the genotypes, thus making difficult to choose genotypes for that environment.

4.2.6.2. Yield Stability Index (YSI)

Yield stability index incorporates both mean yield and stability in a single criterion. The minimum values of YSI desirable genotypes with high mean yield and stability.

Table 16. The first and second IPCA, Grain Mean yield and various yield _stability statistics investigated in soybean genotypes over rain feed conditions.

Genot. ID	Genotypes	GM (Kg ha^{-1})	Rank	IPCA1	IPCA2	ASV	Rank	YSI
G_1	5002T	2319	7	-10.71	14.67	22.44	16	23
G_2	Ciaric	2385	5	-14.42	6.57	23.78	17	22
G_3	Ozark	1815	18	5.30	3.72	9.18	7	25
G_4	Motte	2337	6	-15.66	-17.05	30.10	23	29
G_5	ks4895	2121	8	8.63	3.88	14.22	11	19
G_6	UA4805	1981	13	4.99	-3.08	8.49	6	19
G_7	Delsoy 4710	1871	17	6.25	-1.72	10.05	8	25
G_8	Spry	1909	15	3.24	1.62	5.39	3	18
G_9	Harbar	1926	14	10.07	3.46	16.33	12	26
G_{10}	AFGAT	2903	1	-28.11	-8.55	45.35	24	25
G_{11}	Graham	2027	10	0.36	4.80	4.83	2	12
G_{12}	Manokin	2000	12	-8.15	3.02	13.26	10	22
G_{13}	ks3496	1880	16	-2.55	5.59	6.90	5	21
G_{14}	Clarck-63k	2770	3	-14.54	-7.84	24.33	18	21
G_{15}	Choska	1641	21	16.97	5.00	27.35	20	41
G_{16}	Liu yuemang	1656	19	15.77	-12.34	27.87	21	40
G_{17}	Hang dou No-1	1623	22	5.04	-28.54	29.63	22	44
G_{18}	Hs93-4118	2003	11	2.17	4.44	5.61	4	15
G_{19}	Croton 3.9	1656	20	13.20	-3.02	21.13	15	35
G_{20}	SCS-1	2853	2	-11.07	6.55	18.72	14	16
G_{21}	LD00-3309	1554	24	0.92	3.91	4.18	1	25
G_{22}	Princhard	1558	23	16.52	-0.36	26.18	19	42
G_{23}	Desha	2072	9	4.92	7.04	10.51	9	18
G_{24}	AGS-7-1	2522	4	-9.16	8.20	16.67	13	17

NB:GM=Grain Mean; IPCA1= interaction principle component one; IPCA1= interaction principle component two; YSI=Yield Stability Index.

4.3.9.2. AMMI Selections for the highest four yielding cultivars across six environments

The AMMI model selected four best genotypes for in each environment and illustrated in Table 18. The genotype that appeared in the top four environments in at least six environments was Clarck-63k, which is followed by; SCS-1(five env.), AFGAT (four), AGS-7-1(four), Ks4895(two). The other cultivar, Hang douNo-1, Ciaric and Motte appeared only once.

Table 17. Ranking of four AMMI selections per environment for grain yield (Kg ha^{-1}).

		Mean	IPCA	Genotype Ranking			
Number	Environment	(Kg ha^{-1})	Score	1st	2nd	3rd	4th
3	Dimtu	1557	28.09	G_{20}	G_5	G_{14}	G_{24}
4	Jima	1426	25.46	G_{20}	G_5	G_{24}	G_{14}
6	Pawe	2291	1.07	G_{20}	G_{10}	G_{14}	G_{24}
1	Asosa	2973	-5.28	G_{20}	G_{10}	G_{14}	G_{24}
5	Metu	1268	-9.13	G_{10}	G_{14}	G_4	G_{17}
2	Bako	2830	-40.22	G_{10}	G_{20}	G_{14}	G_2

NB:Env.1=Asosa;2=Bako;3=Dimtu;4=Jimma;5=Metu;6=Pawe;Gen.;G2=Ciaric;G4=Motte;G5=ks4895;7=Delsoy4710;8=Spry;9=Harbar;G10=AFGAT;11=Graham;12=Manokin;13=ks3496;G14=Clarck63k;15=Choska;G17=Hang dou No-1; G20=SCS-1; G24=AGS-7-1.

4.4. Comparison of stability procedures

From the Table 19 various stability procedures have been compared for stability ranking genotypes. The trends of the table indicate that, though there was a quite different result by different stability parameters in ranking the genotypes UA4805, Delsoy 4710 and Spry had been the most stable genotypes by most of the stability parameters: namely AMMI stability value (ASV), coefficient of variation (Francis and Kannenberg,1978), ecovalence (Wricke, 1962), stability variance (Shukla, 1972), Eberhart and Russell (1966). But these three genotypes have less grain yield than the average and doesn't satisfy the assumption of stability. The grain yield of the combined ANOVA is similar with Linn and Binn's (1988) the stability model in identifying the three most stable genotypes. This is similar a result with study in Bambara groundnut by Masindeni (2006). At the same time Wricke (1962) and Shukla (1972) is similar in all genotype ranking.

Table 18. Values and Ranking order for stability according to six different GEI stability procedures on 24 soybean genotypes evaluated over six environments 2015/2016.

	GEI Stability Analysis Procedures																	
Gen. Code	GYLD (Kg ha^{-1})	R	ASV	R	CV_i	R	S^2_i	R	W_i	R	σ^2_i	R	b_i	R	S^2d_i	R	P_i	R
G_1	2319	7	22.44	16	53.98	24	1566471.9	23	1486259	22	230839	22	1.65	24	-5635.652	11	602777	7
G_2	2385	5	23.78	17	48.01	22	1311497.9	22	1113915	16	171736.8	16	1.44	23	20455.15	14	490565	6
G_3	1815	18	9.18	7	35.77	8	421805.72	6	453581	10	66921.79	10	0.8	6	-3453.271	12	1265203	18
G_4	2337	6	30.1	23	42.47	16	985108.97	18	1458641	21	226455.1	21	1.13	18	265248.7	23	486579	5
G_5	2121	8	14.22	11	34.73	6	542508.86	11	340599	8	48988.17	8	0.93	12	-6313.796	10	890071	10
G_6	1981	13	8.49	6	33.64	4	443918.03	7	183112	3	23990.11	3	0.87	8	-53588.24	4	1018758	13
G_7	1871	17	10.05	8	30.38	2	323264.96	3	283808	6	39973.67	6	0.74	5	-63939.24	3	1175039	17
G_8	1909	15	5.39	3	35.95	10	470823.03	8	81049.1	1	7789.72	1	0.91	10	-73495.97	2	1085075	15
G_9	1926	14	16.33	12	35.93	9	478712.68	9	353871	9	51094.76	9	0.87	9	-11005.77	9	1159134	16
G_{10}	2903	1	45.35	24	43.97	19	1629467.1	24	3036123	24	476849.1	24	1.43	22	544000.2	24	139156	1
G_{11}	2027	10	4.83	2	41.6	15	710733.01	16	96826.2	2	10294.03	2	1.13	17	-74791.45	1	898782	11
G_{12}	2000	12	13.26	10	42.76	17	731749.85	17	654123	14	98753.84	14	1.05	14	71773.88	16	883085	9
G_{13}	1880	16	6.9	5	44.64	20	704043.88	14	218482	4	29604.41	4	1.1	16	-40993.52	5	1074345	14
G_{14}	2770	3	24.33	18	37.32	12	1068081.2	20	1446254	20	224488.9	20	1.21	19	241793.1	22	161355	3
G_{15}	1641	21	27.35	20	45.99	21	569674.35	12	1176799	17	181718.2	17	0.8	7	180700	21	1740437	23
G_{16}	1656	19	27.87	21	33.09	3	300094.47	2	1229190	18	190034.4	18	0.55	2	79714.67	18	1678100	22
G_{17}	1623	22	29.63	22	29.7	1	232223.34	1	1726479	23	268969	23	0.4	1	93139.62	19	1640843	21
G_{18}	2003	11	5.61	4	35.97	11	518715.71	10	254909	5	35386.5	5	0.93	11	-29731.26	6	955753	12
G_{19}	1656	20	21.13	15	34.6	5	328488.78	4	640470	13	96586.75	13	0.68	4	2047.567	13	1594465	19
G_{20}	2853	2	18.72	14	35.54	7	1027933.2	19	550994	12	82384.22	12	1.34	20	-27322.52	7	140926	2
G_{21}	1554	24	4.18	1	50.05	23	604848.02	13	465628	11	68833.92	11	0.97	13	26085.35	15	1624416	20
G_{22}	1558	23	26.18	19	38.32	13	356690.17	5	994376	15	152762.3	15	0.64	3	73222.69	17	1851428	24
G_{23}	2072	9	10.51	9	40.6	14	707998.69	15	313169	7	44634.09	7	1.06	15	-17803.59	8	866802	8
G_{24}	2522	4	16.67	13	43.53	18	1205305	21	1377793	19	213622.1	19	1.35	21	172272.3	20	373932	4

Gen.Code=Genotype;G_1=5002T;G_2=Ciaric;G_3=Ozark;G_4=Motte;G_5=ks4895;G_6=UA4805;G_7=Delsoy4710;G8=Spry;G9=Harbar;G_{10}=AFGAT;G_{11}=Graham;G_{12}=Manokin;G_{13}=ks 3496;G_{14}=Clarck63k;G_{15}=Choska;G_{16}=Liuyuemang;G_{17}=Hang dou No-1;G_{18}=Hs93-4118;G_{19}=Croton 3.9;G_{20}=SCS-1;G_{21}=LD00-3309;G_{22}=Princhard;G_{23}=Desha;G_{24}=AGS-7-1;CV=Francis and Kannenberg's (1978) coefficient of variability; environmental Variance(S^2i); Pi=Lin and Binns's (1988) cultivar performance measure; σ^2_i= Shukla's (1972) stability variance; W_i=Wricke's (1962) ecovalence; bi= Finlay and Wilkinson's (1963) regression coefficient; S^2d_i= Eberhart and Russell's' (1966) deviation from regression.

4.5. Association among stability measures

Spearman rank correlation was computed for the various parametric and non-parametric measure for grain yield are presented in (Table 20). The mean grain yield had a positive and highly significant correlation with P_i, but negative and significant correlation with bi and S^2i, but non-significant correlation with the rest procedures viz., ASV, CV_i, W_i, σ^2_i, and S^2d_i

The ASV had significant ($P \leq 0.01$) positive rank correlation with W_i, σ^2_i, and S^2d_i indicating that there is similarity in the ranking of genotypes made based on these three stability indices. Though there seems a difference in the value of Wricke (1962) and Shukla (1972) stability parameters, the rankings made based on each of these two parameters were exactly the same.

Correlation between coefficient of variation CV_i, S^2_i and b_i was significant at one percent probability level. Besides this, S^2_i has positive and significant correlation with b_i (r=0.97**) and negative significant correlation with that of P_i (r=-0.87**). The higher rank between CV_i and environmental variance(S^2_i) was in accord with the report of other researcher like Akram *et al.*, 2012 soybean and Akcura *et al* (2006) in Durum Wheat On the other hand, Wricke's ecovalence showed highly significant positive rank correlation with ASVs and that of S^2d_i and σ^2_i. At the same time, it has a negative correlation with the grain yield. This implies that there is little chance that the high yielding genotypes picked as stable genotypes by these stability parameters

Shukla's stability variance had a highly significant correspondence with ASVs, W_i,and S^2d_i, this means that one of these four parameters could be used as a substitute for others in GEI stability analysis. In addition, it is noted that perfect positive correlation between σ^2_i and W_i (r=1**) and ranked the genotypes in exactly the same way indicates that these two stability measures are similar in genotype ranking purpose. This was in conformation to the findings of Akram *et al*., (2012), Lin *et al*., (1986), Kang *et al*., (1987) and Pham and Kang (1988). Beside the fact that Shukla and Wricke, either can be good effect in describing stability respective genotypes, but lacks

information supplied is limited in that the response pattern and adaptation of bread wheat genotypes cannot be gleaned from these procedures (Purchase *et al*, 2000). From the above facts, these two stability procedures need to synchronized with other regression approach and or preferably with AMMI model in identifying and recommending superior genotypes for soybean production areas.

The Eberhart and Rusesll's deviation from regression showed a highly significant and positive correspondence with Shukla's stability variance, Wricke's ecovalence, ASV, environmental Variance (S^2i); and negative correlation with grain yield.

The Lin and Binn's cultivar superiority measure (P_i) showed negative and a highly significant rank correlation with the environmental variances (r=-0.85) and b_i (r=-0.88), but positive and significant correlation with the parameters like grain yield (r= 0.97). As grain yield is one of the most important cultivar performance trait, stability parameters that positively associated with grain yield seems the appropriate stability parameter that helps identify both high yielding and relatively stable genotypes. However, it is only P_i that has significant and positive association with grain yield. Therefore, P_i seems the only stability parameter that can provide genotypes that are both high yielding and relatively stable.

Table 19. Spearman's rank correlation coefficients for different GEI stability statistical methods for mean grain yield of 24 genotypes grown in six environments of Ethiopia.

	GYLD	ASV	CV_i	$S^2{}_i$	W_i	$\sigma^2{}_i$	b_i	S^2d_i	P_i
GYLD									
ASV	-0.18								
CV_i	-0.25	0.00							
$S^2{}_i$	-0.81**	0.14	0.75**						
W_i	-0.21	0.87**	0.24	0.33					
$\sigma^2{}_i$	-0.21	0.87**	0.24	0.33	1.00**				
b_i	-0.84**	0.03	0.68*	0.97**	0.21	0.21			
S^2d_i	-0.08	0.79**	0.27	0.25	0.90**	0.90**	0.09		
P_i	0.97**	-0.11	-0.32	-0.85**	-0.20	-0.20	-0.88**	-0.09	

NB: * $P \leq 0.05$, ** $P \leq 0.01$, GYLD=Grain yield, CV_i=Francis and Kannenberg's (1978) Coefficient of variability; environmental Variance(S^2i); $\sigma^2{}_i$ = Shukla's (1972) stability variance; W_i=Wricke's (1962) ecovalence; b_i=Finlay and Wilkinson's (1963) regression coefficient; S^2d_i=Eberhart and Russell's (1966) deviation from regression, ASV=AMMI stability value, P_i=Lin and Binns's (1988) cultivar superiority measure.

5. SUMMERY AND CONCLUSION

The study was undertaken to compare different methods of analysis to determine the most suitable procedure to evaluate performance of soybean genotypes under diverse soybean agro-ecologies and assess the suitability of these statistical procedures for characterizing grain yield stability. The principal objectives of the present study were (i) to estimate the genotype by environment interaction through stability parameters and (ii) to identify genotypes that are widely and specifically adapted for grain yield.

Twenty-four soybean genotypes along with three standard checks were planted at six locations during 2015/2016 season. Grain yield and other parameters, were determined and genotypes were evaluated for performance and yield stability in all six soybean production areas using nine different statistical procedures i.e.(i) Shukla (1972), (ii). Lin and Binns Cultivar Superiority Measure (P_i) (iii). Francis and Kannenberg's (1978) Coefficient of Variability (CVi) (iv). the environmental variance (S^2i), (V). Wricke Ecovalence (1962), (Vi). Finlay and Wilkenson (1963), (Vii). Eberhart and Russel (1966), (Viii), the AMMI model and (ix) the GGE biplot model. Finally, these different stability procedures were compared using Spearman's rank correlation coefficient and the significance of the correlation coefficient was determined by means of Student's t test.

The relatively large value of σi2 indicates greater instability of genotype i. Similar to Wricke's (1962) ecovalence the Shukla (1972) identified similar genotypes as most stable regardless of their grain yield. Genotypes Spry, Graham and UA4805 were stable, while the highest yielding genotypes ranked 24^{th}, 12^{th} and 20^{th} in terms of Shukla's stability index.

Lin and Binns' cultivar performance measure indicated good yield stability, and was the only stability parameter that identified the high yielding genotypes as stable. The result of cultivar superiority measure indicated that the most stable genotypes were AFGAT followed by SCS-1 and

Clarck-63k. On the other hand, genotypes Prichard, Choska and Liu yuemang were the most unstable.

According to Finlay and Wilkinson (1963), genotypes Hang douNo-1, Liu yuemang, Prichard, Croton 3.9 and Delsoy 4710 showed above average stability ($b_i \leq 0.9$), but also specifically adapted to unfavorable environments. Genotypes LD00-3309, Choska, Ozark, ks3496, Spry and Harbar indicated average stability $0.8 < b_i < 1.1$ that shows increasing adaptability in all the environments in that order. Genotypes 5002T, Ciaric, AGS-7-1, Clarck-63k, SCS-1 and AFGAT showed below average stability, with AFGAT, SCS-1 and Clarck-63k having good specific adaptability to high potential conditions, 5002T, Ciaric and AGS-7-1 showing that generally poor adaptability. Besides, these Hang douNo-1, Liu yuemang, Prichard and Croton 3.9 showed above average stability, and also show very specific adaptation to low potential or unfavorable conditions.

Eberhart and Russell's stability parameters i.e., regression coefficient (b_i) and deviation from regression (S^2d_i) were determined for the 24 soybean genotypes. The result revealed that the slope (b_i) did not deviate from unity which indicates that all the tested genotypes had average responsiveness to changing environments. The result of an individual genotypes deviation from linear regression showed that genotype 5002T, Ciaric, Ozark, Ks4895, UA4805, Delsoy 4710, Spry, Harbar, Graham, Manokin, ks3496, Liu yuemang, Hang douNo-1, Hs93-4118, Croton 3.9, SCS-1, LD00-3309, Prichard and Desha had non-significant deviation from regression.

Wrick's ecovalance procedures showed the genotypes Spry, Graham and UA4805 were the three most stable genotypes. The unstable genotypes are 5002T, Hang douNo-1 and AFGAT had the highest stability ecovalence value and ranked 22^{th}, 23^{th} and 24^{th} respectively. AFGAT, SCS-1 and Clarck-63k which were the highest yielding genotypes produced the highest ecovalence value which shows that these genotypes are unstable for performance across wider environments.

Francis and Kannenberg's Coefficient of Variability (CV_i) analysis procedures according to Francis et al. (1978), a stable genotype is the one that provides high yield performance and consistent low CV. Therefore, genotypes SCS-1 and Clarck-63k which produced higher mean grain yield and relatively lower coefficient of variation can be considered as the second group of choices.

Based on AMMI analysis varieties Graham, LD00-3309, Hs93-4118 and ks3496 was close to zero, and hence the most stable genotypes across the study environments. However, the mean yield of genotype Spry was higher than genotype the remaining genotypes, hence it is more preferable since it had mean yield above average, but the rest four genotypes have mean below average.

Environments are having small score had small interaction effects indicating all genotypes performed well in these locations. E6 (Pawe) was relatively closer to zero than other locations, and hence, less interactive with the genotypes and most genotypes performs well in this environment. But, it is the third highest performance environment for grain yield. Genotypes, Choska, Prichard, Liu yuemang, and Croton 3.9 are appropriate for E4 (Jimma); while SCS-1 is suited for E1 (Asosa).

Based on GGE Biplot method, genotypes Clarck-63k > SCS-1> AFGAT > AGS-7-1> Ciaric >5002T were the most stable genotypes in that order and are more desirable than the other genotypes. On the other hand, genotypes Hang douNo-1, Liu yuemang and LD00-3309, ranked last and were too far from the ideal genotypes.

Spearman's rank correlation coefficient was used to compare the association among the different parametric and non-parametric stability procedures for grain yield. Mean grain yield had positive and highly significant correlation with Pi, but significant and negative correlation with b_i and S^2_i. The ASV had a positive and significant correlation ($P<0.01$) between W_i, $\sigma^2 i$, and $S^2 d_i$ suggests that these three stability indices were similar in the ranking of genotypes for stability. Correlation

between Coefficient of variation CV_i, S^2_i and b_i were significant at $P< 0.01$ level of probability. S^2_i has positive and significant correlation with b_i and negative significant correlation with Pi. Wricke's ecovalence shows highly significant positive rank correlation with ASVs, S^2d_i and σ_i^2. At the same time, it has negative correlation with grain yield. Shukla's stability variance had highly significant correlation with ASVs, W_i, and S^2d_i. In addition, the perfect positive rank correlation between σ_i^2 and W_i ($r =1$) and ranked the genotypes in exactly the same way indicates that these two stability measures are similar in genotype ranking. The Eberhart and Rusesll's deviation from regression showed a highly significant and positive correspondence with Shukla's stability variance, Wricke's ecovalence, ASV, Environmental Variance (S^2_i); and negative correlation with grain yield. The Lin and Binn's cultivar superiority measure (P_i) showed highly significant and negative rank correlation with the environmental variances and b_i, but it was the only stability procedure that showed positive and significant correlation with grain yield. The comparison between GGE biplot and AMMI model indicated that the GGE model was effective and informative in delineation of mega-environments.

Genotypes SCS-1 and AGS-7-1 were recommended for soybean mega environment production. To fully utilize the GEI data, plant breeders and agronomists should use the combination of stability parameters, and according to the best models for easiness and user friendly features of stability parameters. The genotypes SCS-1 and AGS-7-1 were the most stable across soybean growing environments.

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7. APPENDICES

Appendix 1: Mean DTF of twenty-four soybean genotypes across six environments

		Environments						
No	Genotypes	Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean
1	5002T	48.00	52.67	52.33	47.00	55.00	45.00	50.00 edc†
2	Ciaric	50.33	55.33	55.00	54.33	57.67	46.33	53.17bac
3	Ozark	47.67	50.33	45.67	42.00	49.00	42.67	46.22 iefhg
4	Motte	50.33	44.67	45.33	46.33	51.67	42.00	46.72 iefhg
5	ks4895	48.00	42.33	45.33	42.33	48.00	42.67	44.78 ijhk
6	UA4805	47.67	47.00	48.67	47.33	51.00	42.00	47.28 ijhk
7	Delsoy 4710	48.33	47.33	40.00	40.67	42.00	40.33	43.11ijk
8	Spry	47.00	48.67	42.67	49.33	45.33	40.33	45.56 ijhg
9	Harbar	49.00	47.33	43.67	44.67	47.00	43.33	45.83 ijfhg
10	AFGAT	44.33	51.00	55.33	58.00	62.67	57.67	54.83ba
11	Graham	48.00	48.67	45.00	44.00	48.67	42.00	46.06iefhg
12	Manokin	50.33	52.00	43.33	46.33	49.00	41.67	47.11iefhg
13	ks3496	47.33	44.33	41.00	36.67	42.00	40.33	41.94jk
14	Clarck-63k	48.67	53.67	64.00	59.33	60.67	45.67	55.33a
15	Choska	48.00	47.33	45.33	44.00	47.33	43.00	45.83ijfhg
16	Liu yuemang	50.33	50.33	48.33	55.00	59.00	45.00	51.33bdc
17	Hang douNo-1	55.67	42.67	64.67	57.33	59.33	45.00	54.11ba
18	Hs93-4118	46.00	43.00	41.33	37.33	42.33	38.33	41.39k
19	Croton 3.9	50.00	47.00	41.33	46.33	43.00	40.67	44.72 ijhk
20	SCS-1	52.33	56.33	66.00	59.33	42.00	46.67	53.78ba
21	LD00-3309	48.00	47.33	39.67	46.67	42.33	40.67	44.11 ijhk
22	Princhard	47.00	45.67	47.67	45.67	48.67	42.67	46.22 Iefhg
23	Desha	48.00	47.33	50.00	48.00	56.67	44.67	49.11efdg
24	AGS-7-1	48.33	47.00	49.67	52.00	57.67	44.67	49.89efdc
Env.Mean		48.69	48.31	48.39	47.92	50.33	43.47	47.85
CV (%)		8.90	14.81	7.89	17.97	3.57	3.81	

†Means followed by the same letter are not significantly different at 0.05 probability level

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Appendix 2:Mean DTM of twenty- four soybean genotypes across six environments

No	Genotypes	Environments						Mean
		Asosa	Bako	Dimtu	Jimma	Metu	Pawe	
1	5002T	104.67	111.67	110.33	115.33	112.67	97.67	108.72fegh†
2	Ciaric	107.67	112.33	114.33	120.33	121.00	99.00	112.44b-e
3	Ozark	100.33	100.67	111.67	111.67	107.00	96.67	104.67ljikh
4	Motte	116.33	102.67	117.00	116.33	111.00	101.67	110.83fecd
5	ks4895	103.67	101.67	109.33	110.00	113.67	90.67	104.83jikh
6	UA4805	100.33	102.67	111.33	112.67	111.00	88.67	104.44ljikh
7	Delsoy 4710	103.33	99.00	105.00	107.33	106.67	88.00	101.56lk
8	Spry	96.67	103.00	108.67	115.33	111.00	88.00	103.78ljik
9	Harbar	104.33	116.00	116.00	114.00	111.33	96.33	109.67fegd
10	AFGAT	107.33	119.00	119.33	119.67	113.33	107.00	114.28bc
11	Graham	110.67	105.00	118.33	115.33	115.67	101.00	111.00fecd
12	Manokin	103.67	109.33	112.33	117.33	109.33	92.67	107.44figh
13	ks3496	101.00	100.33	104.33	103.33	105.33	91.67	101.00lk
14	Clarck-63k	107.67	115.33	129.33	125.00	126.67	94.67	116.44ba
15	Choska	103.67	103.33	111.00	114.33	109.33	96.33	106.33jigh
16	Liu yuemang	96.00	115.67	112.67	114.00	125.00	92.67	109.33fegd
17	Hang dou No-1	106.67	118.00	124.67	117.00	124.00	90.67	113.50bcd
18	Hs93-4118	103.33	99.33	106.00	103.33	102.67	88.00	100.44l
19	Croton 3.9	94.67	102.00	105.00	113.00	112.67	90.33	102.94ljk
20	SCS-1	116.00	116.67	128.00	124.33	127.33	104.67	119.50a
21	LD00-3309	104.67	104.67	106.67	117.00	105.33	91.67	105.00jikh
22	Princhard	108.00	104.00	104.00	113.33	105.00	86.67	103.50ljik
23	Desha	106.33	110.33	125.00	116.00	116.33	98.33	112.06dce
24	AGS-7-1	106.33	119.00	118.67	118.67	120.67	97.67	113.50bcd
Env.Mean		104.72	107.99	113.71	114.78	113.50	94.61	108.22
CV (%)		6.63	5.91	4.64	5.91	3.84	4.17	

†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 3:Mean plant height (PH) of twenty-four soybean genotypes across six environments

		Environments						
No	Genotypes	Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean
1	5002T	63.73	48.60	61.92	66.40	76.03	44.80	60.25edc†
2	Ciaric	57.33	61.07	38.08	74.07	64.93	44.77	56.71efdg
3	Ozark	44.53	35.20	44.17	59.60	59.73	33.33	46.09ij
4	Motte	76.93	77.93	76.58	80.47	80.47	38.47	71.81a
5	ks4895	50.27	37.27	45.75	53.07	63.41	40.47	48.37ihj
6	UA4805	45.73	33.33	45.58	51.00	62.03	36.87	45.76ij
7	Delsoy 4710	49.53	43.47	52.33	61.93	72.43	51.93	55.27efhg
8	Spry	44.97	48.67	43.00	41.67	59.70	29.73	44.62ikj
9	Harbar	47.80	34.47	42.33	44.40	58.01	29.60	42.77kj
10	AFGAT	82.33	80.40	67.67	89.20	67.20	38.60	70.90ba
11	Graham	48.40	37.27	45.08	54.33	56.77	36.80	46.44ij
12	Manokin	49.07	46.80	48.83	75.00	57.27	54.47	55.24efhg
13	ks3496	42.87	38.67	45.92	54.20	51.40	47.13	46.70ij
14	Clarck-63k	56.47	61.67	69.17	78.53	75.41	43.47	64.12bdc
15	Choska	43.40	43.93	44.12	53.07	58.77	40.00	47.21ij
16	Liu yuemang	67.73	62.27	51.50	78.07	66.82	64.60	65.16bac
17	Hang douNo-1	62.20	53.60	49.58	68.93	62.02	61.07	59.57efdc
18	Hs93-4118	45.07	41.73	46.42	51.93	51.05	47.47	47.28ij
19	Croton 3.9	49.93	43.13	50.08	57.33	55.07	54.40	51.66ihg
20	SCS-1	66.07	54.67	59.92	88.60	69.23	44.87	63.89bdc
21	LD00-3309	38.00	36.10	39.08	51.33	53.81	30.17	41.42kj
22	Princhard	43.27	22.93	33.67	54.00	49.97	23.33	37.86k
23	Desha	53.43	40.70	49.92	72.13	53.30	42.27	51.96ifhg
24	AGS-7-1	65.33	57.70	55.25	85.20	74.10	51.47	64.84bac
Env.Mean		53.93	47.57	50.25	64.35	62.46	42.92	53.58
CV (%)		8.73	33.25	18.84	20.74	12.14	18.99	

†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 4:Mean Hundred Seed Weight (HSW) of twenty-four soybean genotypes across six environments

No	Genotypes	Environments						Mean
		Asosa	Bako	Dimtu	Jimma	Metu	Pawe	
1	5002T	20.33	20.33	17.50	19.40	16.46	16.33	18.39bc†
2	Ciaric	21.00	21.00	14.57	19.30	14.86	14.67	17.57dfce
3	Ozark	16.33	16.33	15.57	18.80	12.76	15.83	15.94hdfge
4	Motte	18.00	18.00	13.90	19.60	13.66	15.17	16.39hdfg e
5	ks4895	17.33	17.33	15.17	18.30	12.94	17.00	16.35h dfge
6	UA4805	16.00	16.00	13.23	16.80	10.77	14.00	14.47lkj
7	Delsoy 4710	16.33	16.33	14.87	18.37	15.78	15.33	16.17hdfge
8	Spry	21.33	21.33	17.53	21.67	14.93	18.33	19.19ba
9	Harbar	17.00	17.00	14.10	18.20	12.07	18.33	16.12hifg
10	AFGAT	15.67	15.67	10.90	16.13	12.07	12.67	13.85lm
11	Graham	18.33	18.33	15.03	18.93	13.51	17.00	16.86dfge
12	Manokin	16.67	16.67	15.37	18.00	13.19	12.83	15.45hij
13	ks3496	17.33	17.33	15.53	18.27	14.41	14.67	16.26hdfge
14	Clarck-63k	17.00	17.00	11.20	15.40	14.91	14.83	15.06hij
15	Choska	21.67	21.67	19.47	21.27	15.78	19.33	19.86a
16	Liu yuemang	13.33	13.33	12.30	14.33	13.70	11.67	13.11m
17	Hang dou No-1	15.67	15.67	13.73	14.00	13.34	14.00	14.40lkm
18	Hs93-4118	17.00	17.00	15.57	21.07	14.49	14.67	16.63dfge
19	Croton 3.9	18.67	18.67	16.07	18.03	15.86	16.83	17.36dce
20	SCS-1	18.33	18.33	13.03	16.80	14.13	15.50	16.02higj
21	LD00-3309	15.67	15.67	14.93	17.07	12.93	11.83	14.68ikJ
22	Princhard	18.33	18.33	16.13	18.37	12.99	17.33	16.91dfce
23	Desha	18.67	18.67	13.43	19.77	13.03	19.33	17.15dc
24	AGS-7-1	17.00	17.00	13.83	17.60	16.18	16.00	16.27hfge
Env.Mean		17.63	17.63	14.71	18.14	13.95	15.56	16.27
CV (%)		10.95	10.95	11.91	8.08	11.99	9.10	

†Means followed by the same letter are not significantly different at 0.05 probability level

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Appendix 5:Mean Branch per plant (BPP) of twenty-four soybean genotypes across six environments

		Environments						
No	Genotypes	Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean
1	5002T	3.53	5.07	3.33	4.33	4.00	3.40	3.94ebdfc†
2	Ciaric	3.00	5.33	4.33	4.27	5.67	3.27	4.31bac
3	Ozark	3.07	5.47	2.70	3.47	4.00	2.67	3.56egdfc
4	Motte	2.27	7.27	2.53	3.80	6.33	3.20	4.23bdac
5	ks4895	2.47	4.53	3.47	3.53	3.67	2.73	3.40egf
6	UA4805	3.80	4.87	2.67	2.80	4.67	3.47	3.71egdfc
7	Delsoy 4710	1.40	3.93	1.80	2.53	2.33	1.73	2.29 ih
8	Spry	3.00	3.93	3.40	3.67	4.33	3.80	3.69egdfc
9	Harbar	2.20	4.67	3.00	4.13	3.67	3.87	3.59egdfc
10	AFGAT	2.87	4.33	6.20	4.27	5.00	2.60	4.21 a-d
11	Graham	2.27	5.07	2.93	3.67	4.00	3.60	3.59egdfc
12	Manokin	2.00	3.33	2.77	3.20	4.00	2.67	2.99gh
13	ks3496	2.53	3.80	1.93	1.60	3.00	0.93	2.30ih
14	Clarck-63k	3.20	4.27	5.40	5.00	5.00	2.00	4.14ebdac
15	Choska	3.40	4.53	3.73	4.07	4.67	4.00	4.07ebdfc
16	Liu yuemang	6.07	4.40	5.00	4.27	5.33	4.20	4.88a
17	Hang dou No-1	1.30	3.47	4.67	3.33	4.67	2.40	3.31gf
18	Hs93-4118	1.87	4.07	2.33	2.20	2.67	1.93	2.51egf
19	Croton 3.9	2.33	4.07	2.80	2.00	2.67	0.80	2.44 ih
20	SCS-1	3.60	4.93	6.20	4.13	6.00	2.20	4.51ba
21	LD00-3309	1.73	3.00	1.47	2.40	3.67	0.73	2.17i
22	Princhard	2.73	4.80	3.47	3.80	3.67	2.20	3.44egdf
23	Desha	2.73	5.60	4.00	3.73	3.67	6.07	4.30 bac
24	AGS-7-1	2.80	4.47	4.13	3.80	4.67	2.47	3.72egdfc
Env.Mean		2.76	4.55	3.51	3.50	4.22	2.79	3.55
CV (%)		29.69	25.393	20.15	13.127	20.99	58.00	

†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 6:Mean Number of Seed per plant (NSPP) of twenty-four soybean genotypes across six environments

		Environments						
No	Genotypes	Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean
1	5002T	79.40	98.67	66.33	101.07	77.67	82.80	84.32ba†
2	Ciaric	53.53	91.20	76.00	105.80	58.33	88.20	78.84bac
3	Ozark	67.40	64.80	56.67	86.20	44.33	70.33	64.96bdec
4	Motte	64.93	146.27	82.07	60.67	94.67	90.40	89.83a
5	ks4895	56.53	58.33	77.40	92.13	73.00	63.73	70.19bdec
6	UA4805	87.00	65.40	51.27	84.40	50.33	70.53	68.16bdec
7	Delsoy 4710	50.47	56.00	113.13	81.40	45.33	87.00	72.22bdec
8	Spry	63.53	62.80	132.27	74.40	66.00	70.87	78.31bdac
9	Harbar	88.40	54.80	58.80	80.20	40.67	82.60	67.58bdec
10	AFGAT	72.00	84.53	72.40	102.40	98.67	71.27	83.54ba
11	Graham	67.03	60.20	71.80	84.93	48.67	73.47	67.68bdec
12	Manokin	55.07	63.93	69.27	97.47	88.00	88.27	77.00bdec
13	ks3496	52.53	69.27	56.47	74.60	46.00	72.80	61.94dec
14	Clarck-63k	68.33	75.93	76.73	84.00	81.67	79.67	77.72bdac
15	Choska	64.93	70.67	82.67	91.80	56.67	64.47	71.87bdec
16	Liu yuemang	86.07	83.33	65.93	87.07	57.00	110.87	81.71bac
17	Hang dou No-1	51.33	54.13	74.93	68.07	72.67	91.87	68.83bdec
18	Hs93-4118	57.33	60.20	102.40	69.00	42.67	74.87	67.74bdec
19	Croton 3.9	65.47	68.67	61.93	67.40	44.33	90.40	66.37bdec
20	SCS-1	68.67	129.73	43.13	67.27	91.67	72.40	78.81bdac
21	LD00-3309	46.87	58.00	46.53	62.87	45.00	86.53	57.63e
22	Princhard	50.33	52.27	84.87	75.60	47.00	66.13	62.70de
23	Desha	61.00	71.20	102.47	92.93	53.00	58.07	73.11bdec
24	AGS-7-1	52.93	81.93	56.80	92.47	71.00	83.73	73.14bdec
Env.Mean		63.80	74.26	74.26	82.67	62.26	78.80	72.68
CV (%)		26.60	41.63	44.27	20.87	29.90	18.69	

†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 7:: Mean number of pod per plant (NPPP) of twenty-four soybean genotypes across six environments

		Environments						
No	Genotypes	Asosa	Bako	Dimtu	Jimma	Metu	Pawe	Mean
1	5002T	37.20	57.73	38.13	47.60	35.00	39.00	42.44bdec†
2	Ciaric	25.53	43.33	45.60	53.73	26.67	47.60	40.41bdec
3	Ozark	31.07	42.20	31.40	43.93	20.33	42.60	35.26fdec
4	Motte	33.33	78.67	56.13	32.80	40.67	60.00	50.27a
5	ks4895	25.93	34.67	49.07	43.07	27.33	38.27	36.39fdec
6	UA4805	39.67	49.20	33.40	38.80	24.00	44.60	38.28fdec
7	Delsoy 4710	29.20	34.53	63.80	37.73	21.67	42.27	38.20fdec
8	Spry	31.87	34.27	65.87	36.80	30.67	45.40	40.81bdec
9	Harbar	24.80	27.93	35.20	40.00	20.33	51.67	33.32fe
10	AFGAT	33.93	51.93	36.13	49.67	48.33	46.33	44.39 bac
11	Graham	39.27	35.47	37.07	44.67	23.33	40.97	36.79fdec
12	Manokin	30.80	38.87	43.07	56.73	39.00	58.00	44.41bdac
13	ks3496	28.80	38.60	34.07	35.73	21.67	41.33	33.37fe
14	Clarck-63k	31.80	42.47	39.33	44.33	40.33	46.20	40.74bdec
15	Choska	32.27	36.13	43.47	45.07	27.00	46.60	38.42fdec
16	Liu yuemang	52.13	46.27	47.60	49.27	31.33	59.87	47.74ba
17	Hang dou No-1	25.87	30.73	39.80	38.40	35.33	52.47	37.10fdec
18	Hs93-4118	31.80	32.07	49.27	32.87	22.00	41.47	34.91fde
19	Croton 3.9	32.53	35.80	38.87	31.33	20.33	43.93	33.80fe
20	SCS-1	38.20	68.80	28.27	40.20	48.33	41.53	44.22bac
21	LD00-3309	29.00	32.20	28.13	32.93	21.67	42.47	31.07f
22	Princhard	22.47	31.93	45.20	37.20	22.67	40.27	33.29fe
23	Desha	29.00	42.47	61.60	40.80	24.00	42.87	40.12fbdec
24	AGS-7-1	23.00	53.73	29.53	48.07	32.67	45.20	38.70fdec
Env.Mean		31.64	42.50	42.50	41.74	29.36	45.87	38.94
CV (%)		15.91	36.437	40.337	19.46	25.661	23.29	

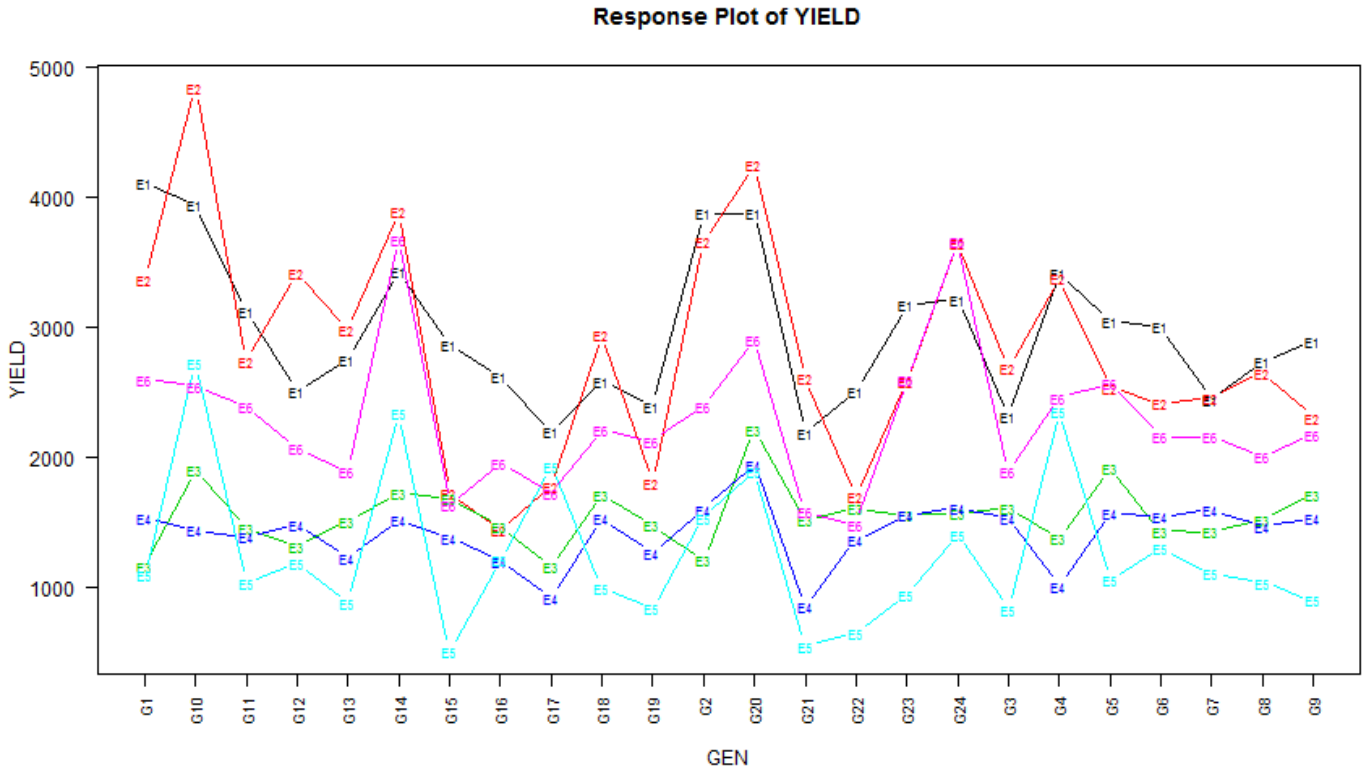
†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 8:A Mean Harvest index (HI) of twenty-four soybean genotypes across six environments

No	Genotypes	Environments						Mean
		Asosa	Bako	Dimtu	Jimma	Metu	Pawe	
1	5002T	0.14	0.39	0.32	0.58	0.31	0.99	0.45bdc†
2	Ciaric	0.15	0.33	0.31	0.47	0.39	1.16	0.47bdc
3	Ozark	0.16	0.37	0.37	0.54	0.36	0.75	0.42edc
4	Motte	0.20	0.30	0.35	0.46	0.38	1.05	0.46bdc
5	ks4895	0.10	0.34	0.38	0.54	0.35	0.76	0.41edc
6	UA4805	0.15	0.42	0.37	0.57	0.40	0.59	0.42edc
7	Delsoy 4710	0.11	0.40	0.57	0.52	0.40	0.79	0.46bdc
8	Spry	0.18	0.33	0.49	0.39	0.38	0.64	0.40ed
9	Harbar	0.13	0.25	0.40	0.52	0.38	0.93	0.43edc
10	AFGAT	0.19	0.44	0.34	0.42	0.43	1.57	0.56ba
11	Graham	0.14	0.37	0.35	0.40	0.36	0.87	0.41edc
12	Manokin	0.12	0.34	0.31	0.62	0.38	0.60	0.39ed
13	ks3496	0.22	0.34	0.44	0.55	0.41	0.64	0.43edc
14	Clarck-63k	0.17	0.47	0.36	0.38	0.45	0.94	0.46bdc
15	Choska	0.19	0.40	0.33	0.55	0.33	0.94	0.45bedc
16	Liu yuemang	0.10	0.25	0.21	0.51	0.39	0.90	0.39ed
17	Hang dou No-1	0.15	0.20	0.31	0.28	0.44	0.88	0.38ed
18	Hs93-4118	0.11	0.53	0.56	0.74	0.41	0.83	0.53bac
19	Croton 3.9	0.12	0.47	0.48	0.57	0.41	0.68	0.46bdc
20	SCS-1	0.18	0.41	0.40	0.46	0.51	1.69	0.61a
21	LD00-3309	0.09	0.30	0.47	0.40	0.43	0.72	0.40ed
22	Princhard	0.13	0.22	0.28	0.41	0.33	0.57	0.32e
23	Desha	0.19	0.41	0.39	0.43	0.39	0.50	0.39ed
24	AGS-7-1	0.12	0.35	0.26	0.41	0.42	1.04	0.44edc
Env.Mean		0.15	0.36	0.38	0.49	0.39	0.88	0.44
CV (%)		24.30	27.44	19.24	39.84	9.55	34.29	

†Means followed by the same letter are not significantly different at 0.05 probability level

Appendix 9:Mean performance of 24 genotypes across six environments in Ethiopia



NB:ENV=E1=Asosa;E2=Bako;E3=Dimtu;E4=Jimma;E5=Metu;E6=Pawe.Gen.Code=Genotype;G_1=5002T; G_2=Ciaric;G_3=Ozark;G_4=Motte;G_5=ks4895;G_6=UA4805;G_7=Delsoy4710;G8=Spry;G9=Harbar;G_{10}=AFGAT;G_{11}=Graham;G_{12}=Manokin;G_{13}=ks3496;G_{14}=Clarck63k;G_{15}=Choska;G_{16}=Liuyuemang;G_{17}=Hang dou No-1;G_{18}=Hs93-4118;G_{19}=Croton 3.9;G_{20}=SCS-1;G_{21}=LD00-G_{22}=Princhard;G_{23}=Desha;G_{24}=AGS-7-1.

Appendix 10:Monthly rainfall (mm), altitude, durations of rainfall and minimum and maximum temperature during the growing seasons (2015/16) at Asosa, Pawe, Metu, Dimtu, Bako and Jimma

Name	**Location**	**Elevation**	**Geogr1**	**Geogr2**	**Year**	**Jan**	**Feb**	**Mar**	**Apr**	**May**	**Jun**	**Jul**	**Aug**	**Sep**	**Oct**	**Nov**
Pawe	Metekel	1119	36.41	11.31	2015	0.0	0.0	0.0	0.0	190.6	149.6	176.1	247.8	232.1	94.6	50.1
Metu Hospital	Illuababora	1711	35.57	8.28	2015	NA	NA	29.9	14.0	202.1	NA	NA	NA	190.6	NA	NA
Dimtu	Jimma	1780	37.23	7.85	2015	NA	NA		205.7	296.8	NA	NA	346.4	405.1	NA	NA
Jimma	Jimma	1718	36.82	7.67	2015	6.1	16.9	77.5	176.3	NA	NA	NA	243.2	NA	NA	155.2
Bako	West Shewa	1650	37.08	9.12	2015	2.4	2.4	54.0	NA	99.7	119.7	208.5	193.1	145.5	66.5	NA
Bako	West Shewa	1650	37.08	9.12	2016	2.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Asosa	Asosa	1600	34.52	10.00	2015	0.0	0.0	11.2	1.0	153.9	174.9	225.7	249.7	NA	NA	NA
Name	**Location**	**Elevation**	**Geogr1**	**Geogr2**	**Year**	**Jan**	**Feb**	**Mar**	**Apr**	**May**	**Jun**	**Jul**	**Aug**	**Sep**	**Oct**	**Nov**
Pawe	Metekel	1119	36.41	11.31	2015	33.8	37.4	38.4	37.7	34.4	30.8	29.8	29.2	29.8	30.7	31.4
Pawe	Metekel	1119	36.41	11.31	2015	12.4	15.7	19.8	20.4		18.4	18.5	18.0	17.6	17.9	16.4
Metu Hospital	Illuababora+	1711	35.57	8.28	2015	NA	NA	32.3	32.2	28.6	NA	NA	NA	26.4	NA	NA
Metu Hospital	Illuababora	1711	35.57	8.28	2015	NA	NA	9.3	9.3	9.8	NA	NA	NA	9.8	NA	NA
Jimma	Jimma	1718	36.82	7.67	2015	29.8	31.6	31.7	29.9	NA	NA	NA	26.6	27.6	NA	27.7
Jimma	Jimma	1718	36.82	7.67	2015	6.3	8.4	10.8	13.5	NA	NA	NA	14.1	14.1	NA	12.7
Bako	West Shewa	1650	37.08	9.12	2015	31.4	NA	33.7	NA	29.0	26.7	26.9	25.8	27.1	29.5	NA
Bako	West Shewa	1650	37.08	9.12	2016	31.0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bako	West Shewa	1650	37.08	9.12	2015	10.1	NA	13.8	NA	14.3	14.4	14.1	14.3	13.5	12.9	NA
Bako	West Shewa	1650	37.08	9.12	2016	11.6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Asosa	Asosa	1600	34.52	10.00	2015	29.8	32.2	31.8	30.7	27.1	25.7	24.9	25.2	NA	NA	NA
Asosa	Asosa	1600	34.52	10.00	2015	11.9	12.5	15.8	15.1	16.5	16.4	15.8	16.3	NA	NA	NA