GENOTYPE X ENVIRONMENT INTERACTION AND YIELD STABILITY OF SOYBEAN [*Glycine max (L.)* MERRILL] GENOTYPES IN WESTERN ETHIOPIA

MSc. THESIS

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GENOTYPE X ENVIRONMENT INTERACTION AND YEILD STABILITY OF SOYBEAN [*Glycine max (*L.*)* MERRILL] GENOTYPES IN WESTERN ETHIOPIA

A Thesis

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By

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Jimma, Ethiopia

DEDICATION

I dedicated this thesis to those individuals who miss their first, second and third choices in their academic life.

STATEMENT OF THE AUTHOR

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BIOGRAPHICAL SKETCH

The author, Tsegaye Mulualem, was born in April 1979 at Teppi district, Sheka zone of the Southern Nation, Nationality & Peoples' Regional Government (SNNPR), Ethiopia. He attended his primary education at Teppi Elementary School from 1986-1991 and his Secondary School at Teppi high school from 1992-1997. After successful completion of the Ethiopian Higher Education in the year 1997, he joined Sodo Agricultural Training Center in 1998 for one year with certificate in General Agricultural Courses. Since September 1999 he was employed by Southern Nation, Nationality & Peoples' Regional Government Bureau of Agriculture at Sheka Zone, Yeki woreda as Developmental Agent (DA) and again he joined Mizan Technical, Vocational, Education & Training (TVET) in 2002 and graduated in 2004 with Diploma in plant Science and again he joined Dilla University, College of Agriculture & Natural Resources in 2010 with Bachelor of Science Degree In Plant Science On November 14, 2014. Also since February 1, 2015 he was employed by Ethiopian Institute of Agricultural Research (EIAR) at Teppi Agricultural Research Center (TARC) as junior researcher and worked till he joined Jimma University College of Agriculture and Veterinary Medicine for MSc. study in Plant Breeding in the year 2019.

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LIST OF ABBREVIATIONS

AEC	Average Environment Coordinate
AMMI	Additive Main Effects and Multiplication Interaction
ANOVA	Analysis of Variance
ASV	AMMI Stability Value
Bi	Regression Coefficient
CV	Coefficient of Variation
CSA	Central Statistical Agency
GEI	Genotype by Environmental Interaction
GGE	Genotype by Genotype by Environment
GLM	General Linear Model
IPCA	Interaction Principal Component Analysis
IITA	International Institutes of Tropical Agriculture
JLRA	Joint Linear Regression Analysis
LSD	Least Significant Difference
MET	Multi Environment Trial
Pi	Lin and Binns cultivar superiority measure
S^2di	Deviation from regression
Wi	Wricke's ecovalence
t/ha	Tone per hectare
YSi	Kang's yield stability
σ^2i	Shukla's variance

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ABSTRACT

Soybean (Glycine max (L.) Merrill) is one of the most important oil crops globally. It is recently introduced crop in Ethiopia and currently getting important position among oil crops. However, production is affected by several factors. Lack of stable genotypes across the soybean production area is one of the problems. Thirty soybean genotypes were planted in alpha lattice design with three replications at six soybean major growing agro-ecologies of Western Ethiopia (Jimma, Mettu, Teppi, Bako, Assosa and Pawe) in 2020 cropping season. With the objectives of determining the effects of GEI, on yield of new soybean genetics and identifying better performing and well adapted soybean genotypes than the local varieties, and to prepare for registration and release of selected high yielding varieties in the different soybean agro-environment conditions of western Ethiopia. The eleven traits subjected to the combined analysis of variance showed a highly significant ($p<0.01$) effect of genotype, location, and genotype x location interactions (GLI). Similarly the combined AMMI ANOVA for grain yield revealed that there were highly significant differences among genotypes, locations and genotype by location interactions and accounted 11.3%, 41.8% and 25.2% of the total variations respectively. The highest percentages of environmental variations are an indication that environment is the major factor that influences the yield performance of soybean grain in Ethiopia. In addition, the first two IPCAs were significant and accounted for 69% of the total interactions sum squares. Eight stability measures viz; Wricke's Ecovalence (Wi), Shukla's stability variance($\sigma 2$), Lin and Binns Cultivar Superiority Measure(Pi), Eberhart and Russell analysis (bi and S2di), Additive Main Effect and Multiplicative Interaction (AMMI) model, AMMI Stability Value (ASV),Yield Stability Index (YSI),Genotype Main Effect and Genotype by Environment Interaction Effect (GGE) bi plot analysis Model were used to evaluate the stable genotypes across the testing locations. Genotypes TGX2014-16FM and TGX2002-3DM were more stable by Wricke's Ecovalence Analysis, and Shukla's Stability Variance. Genotypes S1150/5/22 and TGX2001-8DM were more stable by Eberhart and Russell analysis. Genotypes ScStatus and S1079/6/7 were more stable by Cultivar Superiority Measure. Genotypes S1150/5/22 and ScStatus were more stable by Yield Stability Index. Genotypes S1150/5/22 and TGX2014-16FM were more stable by AMMI Stability Value. Genotypes ScStatus and Pawe-3 were selected as better genotypes that appeared in the four locations by AMMI analysis. According to one year data, the six locations are grouped into three mega environments for soybean production with different winning genotypes and genotype ScStatus was an ideal genotype, while location Pawe was an ideal environment by GGE analysis. Genotypes ScStatus and S1079/6/7 are the two of the best performing genotypes than the other genotypes and control varieties (Pawe-2 and Pawe-3) in grain yield across locations. Therefore, those the two highest yielder genotypes have a potential to be registered in Ethiopia. However, this trail need to be repeated for one more season, and or two of the best performing genotypes will be verified along with the checks on farmers' fields for release.

Keywords: *Soybean, Stability, GGEbiplot, AMMI analysis*

INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important pulse crops and it belongs to the family (*Leguminosae*) and is a self-pollinated crop with a chromosome number of 2n=40. (Indu, 2014). It was originated in Asia (Hymowitz, 2004).

Soybean is cultivated all over the world, as a major source of oil (18%) and protein (40%). It used for cooking oil, soy milk, soy flour, and it is a good source of unsaturated fatty acids, minerals (Ca and P) and vitamins A, B, C and D (Mekonnen and Kaleb, 2014). Soybean is one of the fastest growing crop in the World and occupies an important position among grain legumes for its economic benefits (FAO,2019). Low and declining soil fertility has long been recognized as a major impediment to intensifying agriculture and biological nitrogen fixation in soybean economically and ecological beneficial in Africa, in addition, stimulating the local oil and food processing industries, the meal for livestock and poultry feed industries, and increased share of the international market (import substitution and export) (A.Raimi, *et al.,* 2017).

Ethiopia is endowed with favorable climatic and soil conditions for production in South and Western Ethiopia. Soybean grows in altitudes ranging from 1250 to 2200 masl, but performs well between 1300 to 1800 masl (Asfaw *et al.,*2006). The crop is grown over wider agro-ecologies with mean annual rainfall of 500 to 1500 mm. Nevertheless, critical moisture requirement stages are at germination and grain filling. Temperature ranging from 20 to 25°C, and prefers a soil pH of 5.5 (Zerihun *et al.,* 2015).

The global production of soybeans was 361.06 million tons, and productivity of the crops was 2.88 t/ha whereas in Africa, the production and productivity of the crops was 2.55 million tons, and 1.24 t/ha respectively. Currently, the area covered under soybean production in Ethiopia is 54,543 ha with a total annual production of 125,623 tons, and a productivity of 2.3 t/ha; which is low yield as compared to world average of yield (2.88 t/ha) and the potential of the country (FAO,2019). This showed that, there was a huge gap on the production and productivity of the soybean crop in Ethiopia.

The attainable yield of the crop through the best available technology and skill was 2.9 tons on research and actual yield of the crop is 2.3 tons at farmers managed field condition this reflect the current state of soils and climate, average skills of the farmers, and their average use of technology. Therefore, the yield gap is the difference between the two levels of yields which is 0.6 tons. The exploitable low productivity or yield gap accounts for both the unlikely alignment of all factors required for achievement of potential, the economic management and environmental constraints that preclude (Evans and Fischer 1999). Among which, limited varietal stability and narrow genetic bases of soybean cultivar (Asfaw *et al.*,2006); limited access to improved soybean seeds (Abush *et al.*,2018); lack of access to irrigation facilities; poor soil fertility; problem of insect pest and diseases; and poor agronomic practices (crop management); i.e., low fertilization, weeds and high or low plant populations are the major constraints for soybean production (Georgis *et al.*,1990).

Although soybean breeding and production have been going on in Ethiopia since the 1950's, 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), and searching for high yielding genotypes is a continuous process to replace the existing poorly performed genotypes with new and better adapted genotypes, hence evaluating more breeding lines will have paramount importance in enhancing the production and productivity of the crop.

Genotypes grown in different interactions mostly had inconsistent yield performance. Yield fluctuation of genotypes grown over locations and years is a result of the effect of different environmental conditions varying across locations and over years. Genotype by environment interaction (GEI) occurs when genotypes respond differently to diverse environments. Therefore, GEI is important in evaluation and identification of best performing genotypes, and to determine the yield stability of the genotypes under varying environmental conditions (Yan *et al.*,2000). GEI interaction should be exploited, either by selecting superior genotype for each specific target environment or to select a widely adapted and stable genotype across a wide range of environments. Knowledge of GEI is in valuable to soybean breeders in selecting in desirable genotype and to enabling breeders to design a proper genotype testing strategy.

Plant growth and development is the product of the interaction between the genotype and the environment in which the plant grown (Acquaah,2007). In soybean, it was known that the influence of genotype by environments interactions is significant (Gurmu *et al.*,2009). Similarly, some previous studies in Ethiopia and elsewhere revealed presence of significant GEIs effects in soybean multi environment yield trial data and the importance of GEI in soybean (Ablett *et al.*, 1994); (Al-Assily *et al.*, 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 additive main effects and multiplicative interaction (AMMI) has been applied by several soybean researchers in GEI studies. Gurmu *et al.*, (2009) tested twenty soybean genotypes at six locations and recorded different characters viz., grain yield, different agronomic data, oil and protein content then employed the AMMI model and identified three high yielding and stable soybean cultivars. Cucolotto *et al.*, (2007) also reported similar observations. Similarly, Deresse *et al.*, (2019) studied GEI and yield stability of soybean genotypes across five locations in Ethiopia and reported that the yield performance of soybean genotypes was highly influenced by GEI effects. However, information on the extent and pattern of GEI and performance stability on soybean for western Ethiopia specific agro-ecologies is scanty. More importantly GEI and stability analysis was not carried out on the materials considered in this study. The study was proposed with the following objectives:-

General Objective

- Identification of new soybean genetics performing better than the local varieties, and to prepare for registration and release of selected high yielding varieties.

Specific Objectives

- To identify better performing and well adapted soybean genotypes across six different locations.
- To determine the pattern and magnitude of GEI effect on yield of soybean genotypes across six different locations.
- To determine the stability of yield of soybean genotypes using different stability analysis.

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 fifty nine and thirteen million years ago (Schmutz *et al.*, 2010). However, all described species of the genus Glycine exhibit normal diploid meiosis and are primarily self-pollinated (Cober *et al.*,2009).Then 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).

2.2. Importance of the soybean crop

Soybean is a multipurpose crop, which can be used for a variety of purposes, including preparation of different kinds of soybean foods, animal feed, soy milk, and raw material for the processing factories, like tasty soya, fafa food factories. Currently, there are several factories producing oil from soybean showing increasing importance of soybean in the country. It also has counter effects on depletion of plant nutrients, especially nitrogen in the soil resulting from continuous mono-cropping of cereals, especially maize and sorghum, thereby contributing to increasing soil fertility (Mekonnen and Kaleb, 2014).

2.3. Genotype x Environment Interaction in soybean

The soybean production environments in western Ethiopia are characterized by differences in latitudes, altitudes, climatic conditions, soil moisture, soil type and or fertility levels from location to location coupled with seasonal variations. This raises concern over the performance of cultivars under different environmental conditions. In the same vein, when varieties are compared over several environments, the rankings change or differ and this presents challenges during selection as well as making cultivar recommendations (Cucolotto *et al.*, 2007). For this reason, genotype x environment interaction (GEI) is considered to be a hindrance to crop improvement. Variability in environmental conditions results in significant genotype x environment interactions in addition to the genotype main effects and the

environment main effects during the testing of soybean varieties. Rao et al. (2002) defined genotype x environment interaction as the failure of genotypes to achieve the same relative performance in different environments. Fox *et al.,* (1997) defined GEI as differential genotypic expression across environments. Crossa (1990) and Fox *et al.,* (1997) postulated that there are three types of GEI effects viz, cultivar x location interaction, cultivar x year interaction and cultivar x location x year interaction effects. The significance of these interactions is that they cause differences in the ranking order of genotypes under evaluation in the given multiple environment trials (METs). Therefore, it becomes prudent to test genotypes over several environments and seasons. This is especially important with quantitative traits such as yield because significant GEI is known to curtail the correlation between genotypic and phenotypic values which adversely affects response to selection (Comstock and Moll, 1963).

Brigid and Ric Coe (2012) defined Genotype and Environment separately, and the combination of the two plays a significant role in plant breeding. They defined Genotype as crop line, entry, or variety on which the breeder has or is collecting performance and trait information, whereas environment as the combinations of physical attributes and the climate and other attributes of a specific season (i.e. soil type, fertility, topography, temperature, rainfall, pest or disease) that affect the plant growth.

Environments were classified by Allard and Bradshaw (1964) into two predictable and unpredictable environments. The predictable environments includes the regular and permanent features of the environment, such as climate as determined by its longitude and latitude, soil type, rainfall, and day length. It also includes controllable variables (Perkins and Jinks, 1971) e.g. the level of fertilizer applied, sowing date and sowing density, amount of irrigation and others that can be artificially created. The unpredictable or uncontrollable environment, on the other hand, includes weather fluctuations such as differences between seasons in terms of amount and distribution of rainfall and the prevailing temperature during crop growth. In general, GEI occurs when two or more genotypes perform differently in different environments, and are thus described as differential genotypic sensitivities to environments.

2.4. Types of Genotype x Environment Interaction

There are generally two types of interactions that breeders encounter in GEI studies namely quantitative (non-crossover) and qualitative (crossover) (Gail and Simon, 1985). Quantitative interactions arise when there is variation in the response of genotypes to environments without rank changes while qualitative or cross over interactions occur when there are changes in rank order across the environments. In this case, qualitative interactions complicate selection and cultivar recommendations. Soybean breeders are concerned about the consistent expression of yield and all agronomic traits across a wide range of environments. Consistent performance is a key in crop improvement and acceleration of genetic gains. It is also critical to farmers because they are assured of salvaging something irrespective of environmental and seasonal changes. Since the presence of a crossover interaction has strong implications for breeding for specific adaptation, it is important to assess the frequency of crossover interactions (Singh *et al.,* 1999). According to Gregorius and Namkoong (1986), crossover interaction is not only non- additive in nature but also no separable. Therefore, the presence of crossover type interaction is important, because it implies that the choice of the best genotype is determined by the environment (Malosetti *et al.*, 2012), hence, the breeding environments may be classified into mega-environments and specifically adapted genotypes can be developed for each sub environment separately (Yan *et al.*, 2007).

2.5. Importance of GEI in Plant Breeding

Genotype x environment interactions poses a critical challenge to plant breeders because it can influence any stage of the breeding program, like identifying appropriate sources or parent material. But, it can also play a role in the expression of quantitative traits. Studying GEI is very important to plant breeders because it may limit the progress in the selection process and since it is a basic cause of differences between genotypes for yield stability. Understanding the cause of GEI is important in selecting varieties with the best adaptation that can produce stable yields.

Genotypes that show low GEI with high stable yields are desirable for crop breeders and farmers because the environment has less influence on such genotypes and their higher yields are largely due to their genetic composition. It is important to understand crop development in relation to biophysical conditions and seasons changes when selecting well-adapted genotypes and correct planting date (Linnemann *et al.,* 1995). The absence or low level of GEI effect will be useful for uncontrollable variables; whereas for the controllable variables a high level of interaction in the favorable direction is desirable to obtain maximal performance (Chahal and Gosal, 2002). Selection of stable cultivars that perform consistently across environments can reduce the magnitude of these interactions.

Significant GEI effects tend to be viewed as problematic in breeding because the lack of predictable response hinders progress from selection (Dudley and Moll, 1969). Seed yield is a quantitative character, largely influenced by the genotype, environment and their interaction and hence, has low heritability (Johnson,1989). Therefore, direct selection for seed yield may be unpredictable, unless there is good control of environmental variation (Ofori, 1996). Yield trials conducted in multiple locations are central to plant breeding efforts to evaluate and improve crops. The typical analysis of such trials assumes homogeneity of microenvironment error variances and GEI variances across environments and genotypes (Edwards and Jannink, 2006). Cultivars with lower GEI are more stable across environments. Prerequisites for GEI analysis are estimates of variance components relative to genotypes, G x E interactions, and the error term from trials conducted across locations (Gruneberg *et al.,* 2005).

The knowledge of phenotypic stability is important for the selection of crop varieties, as well as, for breeding programmes. Yield stability is an interesting feature of today's plant breeding programme due to the high annual variation in mean yield, especially in the arid and semiarid areas (Mohammad *et al.,* 2012). The varietal stability could be challenged due to the change in the test environment and change in growing season per environment (Dagnachew *et al.,* 2014). A genotype is stable if at a given location or plant population exhibits very little fluctuation in seed quantity from year to year.

2.6. Adaptation strategies in soybean

Studies involving genotype x environment interaction indicated that adaptability and stability assessments are crucial for identifying and recommending superior genotypes in specific environments and wide range of environments (Nascimento *et al.,* 2010). Miladinovic *et al.,* (2006) showed that the multi-locational trials are a reliable tool for variety adaptability. Generally, there are two types of adaptation strategies viz; specific and general or wide adaptation strategies.

2.6.1. Specific adaptation strategies and evidence of GEI

Annicchiarico (2002) classified genotypes with good performance over a limited number of environments as possessing narrow or specific adaptation. Suffice to say that specific adaptation exists when GEI is significant (Reddy *et al.,* 2011). Its merit in plant breeding is centered on raising genetic gains through the exploitation of positive interaction effects of genotypes with individual locations. Specific adaptation is extensively exploited by national programs and large seed companies which have research operations in several countries and as such having varied environmental conditions. In this case, it becomes logical to target each country as a sub region and tap on genotype x location (GL) interaction (GLI) effects through adaptive traits coupled with high heritability of yield derived from reduced GL interaction, thereby increasing crop yields (Annicchiarico *et al.*, 2005). In a comparative study of wide versus specific adaptation strategies in terms of observed and predicted yield gains for 24 cultivars of wheat over 3 years and 47 environments, specific adaptation gave 2 to 7 % yield gains above wide adaptation (Annicchiarico *et al.*, 2005).

2.6.2. Wide adaptation strategies and GEI studies

The development of varieties that are high yielding with stable yields across multiple environments and seasons is topical to commercial soybean production. This has the advantage of increasing both the production area and production volumes. Conducting field testing of genotypes under several heterogeneous environments, affords researchers a chance to identify genotypes with high mean yield and low GEI (Sreedhar *et al.,* 2011). A genotype is said to have wide adaptation when its average performance is greater than the mean over

multi-locations (Annicchiarico, 2002). Allard and Bradshow (1964) reiterated that the best genotype is the one that exhibits consistent performance across a multitude of production environments. Such cultivars that cope with broad range of environments are useful in breeding and are exploited in cropping systems. Gebeyehu and Assefa (2003) lamented that selection focused on high yielding genotypes appeared less stable than the average of all lines and selection for yield only results in throwing out stable genotypes. In view of the diversity of cultivar reactions to the characteristics of environments, it therefore becomes critical to have multi-environmental trials (MET) in order to obtain an accurate idea of their performance (Lecomte *et al.*, 2010), in addition, the merit of wide adaptation is that the data from several environments is pooled, which increases the precision of the genotypic means reported by Altin *et al.*, (2000).

Another key element is yield stability. A stable genotype is defined as a genotype's ability to perform consistently and produce mean performance that is above average in all the locations (Gurmu *et al.,* 2009). In summary, a high yielding stable genotype is characterized by reliable seed yield across environments. Many researchers reported on wide adaptation studies that focused on soybean. Al-Assily *et al.*, (2002) assessed the performance of five soybean genotypes and observed that three cultivars had mean yields that were above the trial mean with remarkable stability. In a similar regard, Cucolotto *et al.*, (2007) found four cultivars out of 30 that combined good adaptation and stability. The variation in wide range of ecologies and seasons has been found to significantly influence number of seeds per unit area (Egli, 1998). In order to advance genetic gains focus should be placed on physiological causes of GEI.

2.7. The Concept of Stability

The stability is defined as adaptation of varieties to unpredictable and transient environmental conditions and the technique has been used to select stable genotypes less affected by environmental changes (Allard and Bradshaw, 1964). Generally stability is consistency in performance that would mean minimum variation among environments for a particular genotype (Chahal, and Gosal, 2002).

Two different approaches commonly used to assessing stability are the static and the dynamic concepts (Becker and Léon,1988). The static (biological) concept refers to the constant performance of a genotype over a wide range of environments implying that its variance among environments is zero. This type is seldom a desired feature of crop cultivars since there is no response to improved growing conditions.

The dynamic (agronomical) concept of stability implies that a stable genotype should always give high yield expected at the level of productivity of the respective environments. The performance of a genotype that has a lower GEI, as small as possible, is stable. Usually, researchers (Becker and Léon, 1988) stated that all stability procedures based on quantifying GEI effects belong to the dynamic stability concept.

2.8. Mega-Environment Delineation

Mega environments is defined as a group of locations or environments that constantly share the same best genotypes (Yan *et al.,* 2000). Inconsistencies of genotype performance in different test environments make the job of a breeder difficult because no genotype is consistently superior in all test environments. In such situations, breeders may look for genotypes that perform relatively consistently across test environments, stable or broadly adapted genotypes, or choose different specifically adapted genotypes for production in different environments.

Three obvious ways of dealing with GEI in a breeding program (Eisemann *et al.,* 1990) are: (1) ignore it, (2) avoid it, or (3) exploit it. Most breeders agree that GEI should not be ignored when it is significant and of crossover rank change type and indeed can be useful. Lack of consistency in genotype performance across environments provides additional information for the breeder (Busey, 1983). In addition to justifying the need for additional broad-based testing in different environments, the degree of inconsistency can help predict the variability expected among different farms (Busey,1983).

The second way of dealing with these interactions, i.e., avoiding them, involves minimizing the impact of significant interactions. This approach involves grouping similar environments or mega-environments via a cluster analysis. Within a cluster, environments would be more or

less homogeneous, and genotypes evaluated in them would not be expected to show crossover interactions. To identify genotypes with broad adaptation (i.e., stable performance) across many sites, clustering of test environments or genotypes, however, is not advisable.

The third approach encompasses one may determine stability of performance across diverse environments and analyze and interpret genotypic and environmental differences. This approach allows researchers to identify genotypes that exhibit stable performance across diverse test environments, ascertain the causes of GEI, and devise strategies to correct the problems, or exploit them. For a known cause of unstable performance, either the genotype could be improved by genetic means or the proper environment of inputs and management could be provided to maximize productivity. Thus, the third approach (exploiting GEI) is using specifically adapted varieties to maximize the productivity of each environment

Broad adaptation or stability of performance reliability across environments helps conserve limited resources. P. Annicchiarico (personal communication, June 2000) uses the term adaptation in relation to locations, areas, regions, farming systems, or other aspects whose effects can be known in advance, prior to planting. He advocates breeding for wide or specific adaptation to a given region but with emphasis always on high stability. To achieve greater success, crop environments must be characterized as fully as possible for developing cultivars with wide adaptability or judiciously targeting appropriate cultivars to production environments. The assessment of the potential for genotype by location interaction from multi location trials is important in crop improvement because these effects can be exploited for raising yields in a target region (Annicchiarico, 1999).

2.9. Stability Analyses Approach

2.9.1. AMMI Model

The Additive Main effect and Multiplicative Interaction (AMMI) method proposed by Gauch (1992) is a statistical tool that leads to the identification of stable genotypes with their adaptation behavior in an easy manner **(** Hongyu *et al.*, 2014**).** The AMMI method is used for three main purposes. The first is model diagnoses; it is more appropriate in the initial statistical analysis of yield trials because it provides an analytical tool for diagnosing other models as sub cases, when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the GEI.

AMMI summarizes patterns and relationships of genotypes and environments (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988; Crossa, 1990). Such gains may be used to reduce testing costs by reducing the number of replications, including more treatments in the experiments, or improving the efficiency in selecting the best genotypes. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype x environment interaction. It has proven helpful in understanding complex GEI. The results can be graphed in a useful bi plot that shows both main and interaction effects for both the genotypes and environments.

AMMI is popular for analyzing MET data with fixed effects. AMMI analysis considers the main and interaction effects as fixed. Sometimes, this feature is not suitable for analyzing field data. A factor is commonly taken as random, if the observed levels is the random sample from a population. Although the assumption of a truly random sample is often arguable for both environments and genotypes, it is frequently assumed that environments are random, because the environment included in MET is only the sample of large environment. This allows inferences that are not restricted to the observed environments (Piepho, 1998). When the environment effects are regarded as random and the genotype as fixed, the model is considered mixed model.

According to Liu *et al.,* (2017), the stability of seven agronomic traits was analyzed and the general stability of the soybean genotypes was determined based on the additive main effects and multiplicative interactions (AMMI) model using the founder parent. There were significant positive correlations between the phenotypic values and their own stability coefficient values for days to maturity, plant height, number of pods per plant, number of seeds per plant, and seed weight per plant. Thus, it appears difficult to breed cultivars that simultaneously have high yields and high stability (Liu *et al.*, 2017).

AMMI model is considered to be better at explaining the effects of G×E interactions; therefore, it has been widely used in the evaluation of the stability of yield-related traits (Adie *et al.,* 2014; Kahram *et al.,* 2013; Samonte *et al.,* 2005; Sousa *et al.,* 2015; Tang *et al.,* 2013; Wang *et al.,* 2016) and quality related traits (Guo *et al.,* 2004; Su *et al.,* 2010). In previous reports on soybean, Gurmu *et al.,* (2009) analyzed the stability of three traits, namely yield, protein content, and oil content, in 20 cultivars using three statistical methods, including the AMMI model.

Asfaw *et al.,* (2009) used the AMMI model to screen soybean cultivars with high and stable yields. In China, most studies have focused on yield stability in regional testing (Chen *et al.,* 2007; Liu *et al.,* 2015; Zheng, 2005; Zheng *et al.,* 2005). Liu *et al.,* (2011) conducted a stability analysis for three agronomic traits, such as plant height, 100-seed weight and yield. However, there have been no reports on the relationships among the stability coefficients of agronomic traits and the comprehensive evaluation of soybean cultivar stability.

2.9.2. GGE bi-plot analysis (Genotype + Genotype by Environment) Model

GGE bi plot is a multi-faceted tool developed by Gabriel (1971), and it has strongly captured the imagination of plant breeders and agronomists. GGE bi plot 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 (Asfaw *et al.,* 2009; Mulugeta *et al.,* 2013; Amira *et al.,* 2013; Adie *et al.,* 2014; Sousa *et al.,* 2015;). This method is important for mega-environment analysis (e.g. “Which- won- where” pattern), whereby specific genotypes can be

recommended to a specific mega-environments; genotype evaluation (mean vs stability), based on their mean performance and stability across mega-environments; and test environment evaluation, which provides discriminating power vs. representativeness of the test environment (Yan *et al.,* 2000; Yan *et al.,* 2007; Jalata, 2011; Atnaf *et al.,* 2013). In addition, Yan and Tinker (2006) reported the use of a bi plot is intriguing, as it graphically addresses important concepts, such as crossover GE, mega environment differentiation and specific adaptation.

As Krisnawati *et al.,* (2017) reported, the results of GGE analysis were presented by analysis of variance and bi plot graph. A bi plot was an enhanced scatter plot that summarizes two factors so that relationships among the factors and underlying interactions between them can be visualized. The GGE bi plot showed the first two principal components (PC1 and PC2, also referred as primary and secondary effects, respectively) derived from subjecting environment centered yield data (the yield variation due to GGE) to singular value decomposition. The first interaction principal component axes (IPCA1) represented genotype productivity, and the second interaction principal component axes (IPCA2) described the genotype stability (Rakshit *et al.,* 2012).

The best genotype in each environment and mega-environment differentiation was identified by a polygon that exposed the pattern of "which-won-where" (Gedif *et al.,* 2014). The "Which-won-where" graph was created by joining the most distance genotypes to form a polygon. Furthermore, perpendicular lines were drawn, starting from the origin of the bi plot to each side of the polygon and dividing the bi plot into several sectors with one genotype at the vertex of the polygon. Within a sector, genotype located at the vertex of the polygon is the best genotypes in each sector, and genotypes are well adapted in environments in that sector Yan, (2001). The yield performance and stability of the genotypes were evaluated using the method of average environment coordinate or AEC (Yan, 2001; Yan and Hunt, 2002; Yan, 2002).

Appropriate analysis of the yield response in the genotype by environment interaction studies allows environment characterization (Tukamuhabwa *et al.,* 2012 and Ashraf *et al.,* 2010). For instance, in the study conducted by Amira *et al.,* (2013) compared the discriminating powers

of GGE with AMMI analysis in characterizing the test environments based on soybean yield. The findings were that GGE is more effective and informative than AMMI in mega environment analysis and genotype by environment interaction evaluation. GGE bi plot in soybean has also been found to demonstrate an ability to provide information on genotypes and environments simultaneously in the evaluation of yield and other traits (Murphy *et al.*, 2009 and Zhe *et al.*, 2010).

2.9.3. Eberhart and Russel (1966) Stability Analysis

Eberhart & Russell (1966) defined a stable genotype as one with an average response to the environment. Three parameters are used to measure the adaptability i.e., the mean, the response (regression coefficient), and the stability of the performance (deviation from regression). The ideal genotype is one with a high mean yield, unit regression (b=1) and least deviation from regression ($S^2di=0$). 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. According to Eberhart and Russell's Joint Regression model, a genotype with a bi value less than1.0 has above average stability and is especially adaptable to low performing environments (specific adaptation to poor or unfavorable environments) and if it is greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments (specific adaptation to rich or favorable environments). Hence, in most cases the deviation from regression (S2di) is taken as a parameter for stability rather than which is more about the responsiveness of genotypes (Chaudhary *et al.*, 1994; Gupta *et al.*,1974; Odongo and Bockholf, 1997; Ombakho *et al.*,1997).

3. MATERIALS AND METHODS

3.1. Description of Experimental Area

The trials were conducted at six locations in Western Ethiopia viz., Teppi, Jimma, Bako, Mettu, Assosa and Pawe. These locations represent the major soybean growing agro ecologies of Western Ethiopia. A detailed description of the test locations is provided in (Table 1).

Table 1. Description of the testing area

Location	Region	Altitude(masl)	Latitude (N)	Longitude(E)	Soil type	RF (mm)	Temperature Min to Max (^{0}C)
Jimma	Oromia	1750	7°46’ N	36°0’ E	Reddish Brown	1572	18.9 to 26.8
Mettu	Oromia	1550	8°19'0" N	35°35'0"E	Dark red Brown	1829	12.5 to 28.6
Tepi	SNNP	1500	7º 3' N	35º18’E	Nitosols	1850	15.5 to 29.5
Bako	Oromia	1590	9°6’N	$37^0$9’E	Nitosols	1245	9 to 34.4
Pawe	Benishangul	1100	11°18’N	36°24'E	Nitosols	1587	16.3 to 32.6
Asosa	>>	1650	10°03’N	34°59’E	Reddish Brown	1130	15.9 to 29.0

Source: Ethiopian Institute of Agricultural Research (EIAR, 2019)

3.2. Soybean genotypes used for the study

The thirty entries in this study are obtained from eight different seed sources viz., twelve genotypes from Seed Co (Zimbabwe), six genotypes from IITA (Zambia), seven genotypes from EIAR (Ethiopia), one genotype from the Kenya Agricultural & Livestock Research Organization – KALRO (Kenya), one genotype from the Savanna Agricultural Research Institute – SARI/ CSIR (Ghana), one genotype from Semillas Panorama SAS (Colombia), one genotype from Sensako (South Africa), and one genotype from the Zambian Agricultural Research Institute (Zambia) (Table 2).

All these introduced or imported soybean materials released genotypes and contributed by the different breeding programs in Africa were evaluated for their yield performance. Among the

released varieties, recently released varieties used as a check varieties (Table 2). The check varieties PAWE-2 and PAWE-3 were released by Pawe Agricultural Research Center for the low land to mid-altitude agro-ecologies of testing areas (Western Ethiopia). Therefore, the check variety also gives a point of comparison when analyzing the performance of the test genotypes in the characteristics you are trying to measure.

Table 2. List of the tested soybean genotypes and their sources

Genotypes Name	Genotypes Code	Source	Remark
Favour	1	Ghana	Imported year (2019)
TGX2001-6FM	2	IITA (Zambia)	Imported year (2019)
TGX2014-5GM	3	IITA(Zambia)	Imported year (2019)
TGX2014-23FM	4	IITA(Zambia)	Imported year (2019)
TGX2001-8DM	5	IITA(Zambia)	Imported year (2019)
TGX2002-3DM	6	IITA(Zambia)	Imported year (2019)
TGX2014-16FM	7	IITA(Zambia)	Imported year (2019)
Panorama29-1	8	Colombia	Imported year (2019)
ScSaga	9	Zimbabwe	Imported year (2019)
ScSpike	10	Zimbabwe	Imported year (2019)
S1079/6/7	11	Zimbabwe	Imported year (2019)
Sc Signal	12	Zimbabwe	Imported year (2019)
Sc Saxon	13	Zimbabwe	Imported year (2019)
S1180/5/54	14	Zimbabwe	Imported year (2019)
S1140/5/4	15	Zimbabwe	Imported year (2019)
S1150/5/22	16	Zimbabwe	Imported year (2019)
ScSafari	17	Zimbabwe	Imported year (2019)
ScStatus	18	Zimbabwe	Imported year (2019)
SNK500	19	South Africa	Imported year (2019)
SCS-1	20	Kenya	Imported year (2019)
Clark-63k	21	Ethiopia (EIAR)	Released year (1981/82)
Gazelle	22	Ethiopia (EIAR)	Released year (2015)
Nyala	23	Ethiopia (EIAR)	Released year (2014)
ScSerenade	24	Zimbabwe	Imported year (2019)
ScSentinel	25	Zimbabwe	Imported year (2019)
Kafue	26	Zambia (ZARI)	Imported year (2019)
Afgat	27	Ethiopia(EIAR)	Released year (2007)
Pawe- 1	28	Ethiopia(EIAR)	Released year (2015)
Pawe- 2 (check-2)	29	Ethiopia(EIAR)	Released year (2015)
Pawe- 3 (check-1)	30	Ethiopia(EIAR)	Released year (2016)

IITA = International Institutes of Tropical Agriculture, ZARI =-Zambian Agricultural Research Institute, EIAR = Ethiopian Institute of Agricultural Research. Source; Jimma Agricultural Research Center (JARC,2019).

3.3. Experimental Design and Trial Management

The experiments in all the locations were designed in alpha design with three replications per environment under rain feed conditions. There were six blocks in each replication, and each block had five genotypes. Each plot consisted of four rows with inter-row spacing of 60cm, and intra-row spacing of 5cm, 4m length and 2.4m width. Therefore, the total area of each experimental plot was 9.6 m^2 (4m x 2.4m). The spacing between plots, blocks and replications were 0.6 m, 1m, and 1.5m, respectively. The sowing dates were at the onset of the main rainy season. Seed rate of 60 kg per ha and fertilizer rate of 121 kg/ha NPS per ha was applied at planting. Weeding and other agronomic practices were carried out as required. Harvest data were collected from the inner two rows within a plot.

3.4. Data collected

Data were collected both on plot and plant basis based on soybean descriptors (1984). Days to flowering, days to maturity, hundred seed weight, disease severity, lodging score, shattering score and yield were collected on a plot basis on the middle two rows. Five plants from the central row were randomly selected for data collection on plant basis, and the averages of the five plants in each experimental plot were used for statistical analysis for traits such as plant height, number of pods per plant and number of seeds per plant.

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

2. **Lodging score-** it was recorded using the method of Caldicott and Nuttall (1979). The angle of leaning was scored on a 0-5 scale where 0- stands for completely upright plants and 5 stands for completely lodged (flat on the ground) plants. The severity for each score was recorded as the percentage of the entire plot. Then; the lodging index was obtained as the average of the product sum of each degree of lodging and the corresponding severity percent.

4. Seed shattering Score- it is the estimation percent of pod splitting using the scale 0-5.

1=No shattering

2=1 to 10 percent shattering

3=10 to 25 percent shattering

4=25 to 50 percent shattering

5=> 50 percent shattering

5. Disease Score - many descriptors which are continuously variable are recorded on a 1-9 scale. The authors of this list have sometimes described only a selection of the states, e.g. 3,5 and 7 for such descriptors. Soybean descriptors (1984).

3= low susceptibility

5=medium susceptibility

7=high susceptibility

6. Plant height (cm)- height of the main stem from the ground level to the top of the main stem from five randomly taken plants were measured.

7. Number of pods per plant- the total number of pods with seeds from five randomly taken plants were counted and averaged.

8. Number of Seeds per Plant- number of seeds from five sample plants from each plot was counted and averaged.

9. Hundred Seed Weight (g)- hundred seeds counted indiscriminately from harvest of each plot were weighted with sensitive balance at 13-15% moisture content and adjusted to the standard moisture content of grain of pulse(10%) Adjusted 100-seed weight= (100-seed weight – actual moisture content)/ 100 – 10

10. Grain yield (t/ha)- the total grain yield t/ha was calculated for grain yield harvested from the middle two rows of each plot and adjusted to 13% grain moisture content. Adjusted grain yield/plot = (plot yield – actual moisture content)/100- 10, then convert it to t/ha

3.5. Analysis of Variance

The ANOVA was run for the six locations separately and combined over the six locations for all characters since all showed homogeneity of error variance. Analysis of variance was carried out to partition the variance due to genotype, environment and genotype by environment interaction, replication within environment and block within replication. The combined analysis of variance was carried out to estimate the additive effects of the environment, genotype and GEI. Significance levels of these components were determined using F-test. Prior to running combined analysis of variance the data were checked for the homogeneity of error variances across all locations using Bartlett's test. The mean comparison of the treatment means was performed using least significant difference (LSD) at 5% probability levels. The analyses were carried out using Statistical Analysis System (SAS) software version 9.3 (SAS Institute, 2014).

ANOVA model for a single location as: **Yijk= μ + Gi +Rj + Bkj + Eijk**
ANOVA model for the combined over locations as: **Yijkr = μ +Gi + Lj + Rk(Lj) + Br(LjRk) + GiLj + Eijkr.**

Where Y is the performance of genotype i in j^{th} location, k^{th} replication and r^{th} incomplete block, μ is the mean effect, Lj is the effect of j^{th} location, Rk(Lj) the effect of the k^{th} replication in location J, Br (LjRk) is the effect of r^{th} incomplete block in j^{th} location and k^{th} replication, GiLj is the interaction effect of genotype i and location j and ε_{ijkr} is the error associated with the i^{th} genotype, jth location, k^{th} replication, r^{th} incomplete block

Table 3. Skeleton of alpha lattice design at individual locations

Source	Df	SS	MS
Replications	(r-1)	SSR	
Blocks (adj.)	R (q-1)	SSB	MSB
Treatments	(t-1)	SST	MST
Intra block error	(q-1) (rq-q-1)	SSE	MSE
Total	rq-1	Total SS	

SSR = Sum Square of Replications, SSB = Sum Square of Blocks, SST = Sum Square of treatments, SSE = Sum Square of Error, Total SS= Total Sum Square, MSB = Mean Square of blocks, MSE = Mean Square of error, Df = Degree of freedom, SS=Sum of Square, MS= Mean Square.

Table 4. The general analysis of variance and mean square expectations for genotype by environment interaction over all locations

Source of variation	df	SS	Expected MS	F-value
E	e-1	MS1	σ2e +gσ2r (e) + rg + rg σ2e	MS1/MS2
R(E)	E (r-1)	MS2	σ2e +gσ2r (e)	MS2/MS5
G	g-1	MS3	σ2e +g σ2ge + erσ2g	MS3/MS4
GXE	(e-1) (g-1)	MS4	σ2g +σ2e+ σ2ge	MS4/MS5
Error	e(e-1) (g-1)	MS5		
Total	Erg-1			

E=Environment, R(E)=Replication within environment, G=genotype, GXE=Genotype by Environment,

3.6. Stability Analysis

Yield stability of the genotypes was evaluated using different models:Wricke's Ecovalence, Shukla's stability variance (σ2), Eberhart and Russell joint linear regression model (bi and S^2di), Cultivar superiority measure (Pi), Yield stability index (YSI),AMMI Stability Value (ASV), Additive Main Effect and Multiplicative Interaction (AMMI) model and Genotype Main Effect and Genotype x Environment Interaction Effect (GGE) biplot analysis were used to determine the effects of GEI on yields. These analyses were performed using Genstatversion2018 and GEA-R (genotype by environment analysis with R) software (Pachecoetal, 2015).

3.6.1. Wricke's Ecovalence (Wi)

Wricke (1962) defined the concept of eco-valence, to describe the stability of a genotype, as the contribution of genotype stability of the i^{th} genotype is its interaction with environments, squared and summed across environments to the GEI sum of squares. The ecovalence (Wi) or stability of the genotype is its interaction with the environments, squared and summed across environments, and expressed mathematically as:

Wi = Σ (Ȳij. - Ȳi.- Ȳ.j + Ȳ..)² Where: Ȳij. = Mean yield of the i^{th} genotype in the j^{th} environment, Ȳi. = Mean yield of the i^{th} genotype, Ȳ.j = Mean yield of the j^{th} environment, Ȳ.. = is the overall mean/ Grand 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 study, the breeder can manipulate the ecovalence by choosing specific location. A genotype with high ecovalence =0 is regarded as stable in all environments.

3.6.2. Shukla's stability variance (σ2)

Shukla's stability variance (σ^2i) 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^2i) 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 (Shukla, 1972).

$$\sigma^2 i = 1/(G-1)(G-2)(E-1)[(G(G-1)\Sigma(Yij - \bar{Y}i. - \bar{Y}.j + \bar{Y}..)2 - \Sigma\Sigma(Yij - \bar{Y}i. - \bar{Y}.j + \bar{Y}..)^2]$$

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
Ȳ is the mean of all the genotypes in all the environments.
A genotype is called stable, if its stability variance (σ^2) is equal to environmental variance

3.6.3. Eberhart and Russell joint linear regression model (bi and S2di)

The regression model proposed by Eberhart and Russell (1966) was used to estimate the stability of grain yield. Eberhart and Russell (1966) interprets the variance of regression deviations (S^2di) from predicted values as a measure of cultivar stability, and the linear regression coefficient (bi) as a measure of the environmental index were used to analyses stability.

The model is: **Yij=μi+biIj+ σij**

Where; yij is genotypic mean of i^{th} genotype in j^{th} environment;μi is the mean of i^{th} genotype over all environments, bi regression coefficient which measures the response of i^{th} genotypes to environments; Ij is the environmental index as means of all genotypes at j^{th} environment minus grand mean; σij is the deviation from regression coefficient of i^{th} genotype at j^{th} environment.The ideal genotype is one with a high mean yield, unit regression (b=1) and least deviation from regression ($S^2di=0$).

3.6.4. Cultivar superiority measure (Pi)

Lin and Binns (1988) defined the genotype's superiority measure (Pi) as the mean square of the distance between the genotype and the genotype with the maximum response. The genotype with low or small (pi) value is considered to be more stable. It consists of a non parametric analysis, which is simpler and addresses the limitations of a linear regression analysis (Oliveira *et al.*, 2013). The value of Pi is calculated as :

$Pi= \sum j\ (xij\text{-}Mj)^2/2n$, where n=number of locations, xij=the yield of genotype i in location j, Mj = the maximum yield response among all cultivars in the jth location

3.6.5. Yield stability index (YSI)

This measurement was developed by Farshadfar *et al.*, (2011). Stability by itself should not be the only measurement for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammad *et al.,* 2007). This method is vital to measure and rank genotypes based on grain yield stability. The summation of rank of ASV and rank of yield are used to calculate YSI. The genotype with least YSI is considered as the most stable with high grain yield (Dabessa *et al.,* 2016).

YSI was calculated as: YSI = RASV + RY

Where: RASV is the rank of AMMI stability value, RY is the rank of mean yield of genotypes across environments.

3.6.6. AMMI Stability value (ASV)

The ASV is the distance from the coordinate point to the origin in a two dimensional scatter length of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase *et al.*,1997). AMMI Stability Value (ASV), length of genotype and environment markers of the origin in a two dimensional plot of IPCA1 scores against IPCA2 scores was calculated according to Purchase *et al.*, (1997) as follow:

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

Where: IPCA1= interaction principal component axis 1; IPCA2 = interaction principal component, axis 2. Genotypes with lower values of the ASV are considered to be more stable

3.6.7. Additive main effect and multiplicative interaction (AMMI) model

Additive Main Effect and Multiplicative Interaction (AMMI) is one of most widely used model to explain G×E interaction of multi-environment genotype trial and categorizing the genotypes into narrow or wider adaptation (Crossa *et al.*, 1990). 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 GEI (Kempton,1984).

The AMMI Model Equation is: $\bar{Y}_{ijk} = \mu + G_i + E_j + \Sigma_{mk=1} \lambda_k \alpha_{ik} \gamma_{jk} + P_{ij}$

Where: $\bar{Y}_{ijk}$.= the yield of the i^{th} genotype in the j^{th} environment,

Gi = the mean of the i^{th} genotype minus the grand mean,

Ej = the mean of the j^{th} environment minus the grand mean,

λk = the square root of the Eigen value of the kth IPCA axis,

αik and γjk = the principal component scores for IPCA axis k of the ith genotypes and the jth environment,

Pij = the deviation from the model

3.6.8. Genotype main effect and genotype by environment interaction (GGE) biplot analysis

The GGE biplot (Purchase, 1997) model is: $\mathbf{Y_{ij} - \mu - \beta j = \lambda 1 \varepsilon i 1 \eta j 1 + \lambda 2 \varepsilon i 2 \eta j 2 + \varepsilon_{ij}}$ where:

Y_{ij}= the performance of the i^{th} genotype in the j^{th} environment;

μ = the grand mean;

β_j = The main effect of the environment j:

λl and λ2 = Singular value for IPCA1 and IPCA2 respectively:

εi1 and εi2 = Eigen vectors of genotype i IPCA1 and IPCA2 respectively:

ηj1 and ηj2 = Eigen vectors of environment j for IPCA1 and IPCA2 respectively;

ε_{ij} = Residual associated with genotype i and environment j.

4. RESULTS AND DISCUSSION

4.1. Analysis of variance for grain yield and yield related traits at individual location

The ANOVA revealed highly significant differences ($p<0.01$) for grain yield at Jimma, Mettu, Bako, Pawe and Teppi and significant differences ($p <0.05$) at Assosa. The ANOVA on yield related-traits data for individual location showed significant ($p<0.05$) to highly significant differences ($p< 0.01$) among the tested soybean genotypes (Appendix. Table 1).

4.1.1. Grain yield

The mean grain yield of soybean genotypes at different location were presented in (Table 5 and Appendix. Table 2).

The mean yield of genotypes at different location was ranged from 0.39 to 1.97 t/ha, 0.47 to 2.32 t/ha, 1.04 to 2.94 t/ha, 1.35 to 4.05 t/ha, 1.15 to 3.42 t/ha, and 0.90 to 2.15 t/ha at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. Soybean genotypes S1079/6/7 (1.97 t/ha), ScSaga (1.94t/ha), ScSentinel (1.92t/ha), SNK500 (1.87t/ha), ScSerenade (1.84t/ha), Gazelle (1.84t/ha), SCS-1 (1.78t/ha), TGX2002-3DM (1.76t/ha), Nyala (1.75t/ha), ScSpike (1.74t/ha), S1150/5/22 (1.72t/ha), ScSafari (1.72t/ha), TGX2001-6FM (1.71t/ha), and ScStatus (1.69t/ha) were better in yield than the checks at Jima. Soybean genotypes ScSpike (2.32t/ha), ScSignal (1.89t/ha), and S1150/5/22 (1.74t/ha) were better in yield than the checks at Mettu.

No genotypes better in yield than the checks at Teppi. Soybean genotypes S1079/6/7 (4.05 t/ha), ScSignal (3.74 t/ha), Pawe-1 (3.65t/ha), ScStatus (3.55t/ha), Panorama29-1 (3.54t/ha), S1140/5/4 (3.43t/ha), TGX2001-6FM (3.28t/ha), S1150/5/22 (3.21t/ha), ScSaga (3.09t/ha), Clark-63k (3.07t/ha), and ScSpike (2.95t/ha) were better in yield than the checks at Bako. Soybean genotypes ScSpike (3.42t/ha), ScStatus (3.28t/ha), TGX2001-8DM (3.17t/ha), and ScSignal (3.02t/ha) were better in yield than the checks at Pawe. Soybean genotypes Panorama29-1 (2.15t/ha), and ScSafari (1.94t/ha) were better in yield than the checks at Assosa. This indicates, the genotypes showed inconsistent performance across the locations because of significant genotype x location interactions.

Generally, the soybean genotypes produced average grain yield of 1.54t/ha, 1.31t/ha, 1.75t/ha, 2.71t/ha, 2.22t/ha, and 1.45t/ha at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The highest yield was recorded at Bako, with mean value of 2.71t/ha while the lowest yield was recorded at Mettu with mean value of 1.31t/ha. Most of the genotypes at Bako and Pawe showed the best performance. This may due to the locations were characterized with suitable weather conditions and or agro-ecology, which favors vegetative growth and increased grain yield. While the others locations were exhibited low to medium performance, but at Mettu, the genotypes were found to have lower average grain yield as compared to other testing locations, although there were significant variations among genotypes performance. This may be due to erratic and un even distribution of rain fall occurred specially at the time of planting and grain filling and lead to decreased percentages of germination of the seed and the percentages of grain filling or seed setting. In addition, high temperature stress occurred at the time of pod setting and caused an anatomical changes in the pollen, thus leads to decrease the percentages of pod setting as well as seed setting. In general the poor soil fertility of the site, moisture stresses and drought stresses occurred at the end of the cropping season lead to the yield decrease.

Table 5. Mean grain yield of thirty tested soybean genotypes across six locations

		Grain yield							
		Locations						**Across**	
Genotypes Name	Code	**Jimma**	**Mettu**	**Teppi**	**Bako**	**Pawe**	**Assosa**	**Mean**	**Rank**
Favour	1	0.39	1.02	1.26	1.71	1.15	1.80	1.226	30
TGX2001-6FM	2	1.71	1.50	2.03	3.28	2.00	1.15	1.948	11
TGX2014-5GM	3	1.52	0.93	1.19	1.81	1.42	1.25	1.357	28
TGX2014-23FM	4	1.32	0.81	1.88	2.71	2.25	1.43	1.736	21
TGX2001-8DM	5	1.43	1.25	2.13	2.86	3.17	1.42	2.047	7
TGX2002-3DM	6	1.76	1.46	1.92	2.61	2.43	1.17	1.894	14
TGX2014-16FM	7	1.69	1.59	2.08	2.80	2.28	1.21	1.945	12
Panorama29-1	8	1.23	1.02	1.53	3.54	2.11	2.15	1.934	13
ScSaga	9	1.94	1.38	1.99	3.09	2.36	1.17	1.991	9
ScSpike	10	1.74	2.32	1.57	2.95	3.42	0.90	2.154	4
S1079/6/7	11	1.97	1.62	2.04	4.05	2.64	1.09	2.238	2
ScSignal	12	0.94	1.89	1.66	3.74	3.02	1.41	2.112	5
ScSaxon	13	1.37	1.71	1.23	2.77	2.49	1.41	1.832	18
S1180/5/54	14	1.31	1.60	1.98	1.89	2.29	1.63	1.786	20
S1140/5/4	15	1.39	1.27	1.67	3.43	2.05	1.48	1.884	16
S1150/5/22	16	1.72	1.74	2.08	3.21	2.16	1.50	2.072	6
ScSafari	17	1.72	1.22	2.04	1.99	2.43	1.94	1.893	15
ScStatus	18	1.69	1.64	2.74	3.55	3.28	1.67	2.430	1
SNK500	19	1.87	0.59	1.49	1.35	1.36	1.22	1.318	29
SCS-1	20	1.78	1.19	1.44	1.83	1.64	1.26	1.527	24
Clark-63k	21	1.51	1.34	1.29	3.07	2.08	1.92	1.873	17
Gazelle	22	1.84	1.26	1.56	2.44	2.22	1.54	1.812	19
Nyala	23	1.75	1.46	1.90	2.13	1.79	1.11	1.692	22
ScSerenade	24	1.84	0.85	1.46	2.52	1.383	1.76	1.640	23
ScSentinel	25	1.92	0.85	1.04	2.48	1.36	1.25	1.486	27
Kafue	26	1.38	0.71	1.97	1.73	1.92	1.22	1.488	26
Afgat	27	1.39	0.47	1.17	2.76	1.87	1.41	1.516	25
Pawe-1	28	1.28	1.44	1.38	3.65	2.68	1.25	1.950	10
Pawe-2(check-2)	29	1.08	1.35	2.03	2.92	2.90	1.92	2.037	8
Pawe-3 (check-1)	30	1.66	1.73	2.94	2.43	2.51	1.84	2.191	3
Mean		1.54	1.31	1.75	2.71	2.22	1.45	1.83	
CV (%)		11.94	21.44	25.88	4.29	16.66	29.45	20.18	
LSD(5%)		0.30	0.46	0.75	0.19	0.61	0.7	0.24	
F-test		**	**	**	**	**	*	**	

4.1.2. Yield related traits

The mean yield-related traits of soybean genotypes at different location were presented in (Appendix. Table 3).

4.1.2.1. Yield components traits (pods per plant, seeds per plant, and 100-seed weight)

The mean number of pods per plant at different location was ranged from 20.20 to 80.00, 37.20 to109.00, 20.80 to 64.10, 29.00 to 65.00, 33.26 to 70.13 and 15.66 to 36.00 at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The maximum number of pods per plant was recorded at Mettu; with mean value of 66.28, while the minimum number of pods per plant was recorded at Assosa; with mean value of 25.26.The mean number of seeds per plant at different location was ranged from 29.60 to 87.80, 24.20 to 57.60, 46.20 to 148.13, 46.00 to 103.00, 57.30 to 142.73, and 43.88 to 96.46 at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The maximum number of seeds per plant was scored at Pawe; with mean value of 94.29, while the minimum number of seeds per plant was scored at Mettu; with mean value of 35.29.

The mean seed weight at different location was ranged from 11.00 to 23.00 g,7.73 to 16.80 g , 11.66 to 17.66 g, 10.00 to 23.00 g, 7.50 to17.33 g , and 12.33 to 21.00 g at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The highest seed weight was recorded at Bako; with mean value of 17.67 g, while the lowest seed weight was recorded at Pawe with mean value of 12.70 g. Seed size (measured as 100-seed weight) is determined for each line and growers often prefer large seed varieties, as they are easier to thresh and clean compared to small seed varieties.

4.1.2.2. Plant growth trait (plant height)

The mean plant height at different location was ranged from 57.40 to126.00 cm, 57.30 to 133.10 cm, 33.00 to75.60 cm, 40.50 to107.00 cm, 41.90 to100.00 cm, and 35.60 to74.20 cm at Jimma, Mettu, Teppi, Bako, Pawe, and Assosa respectively. The highest plant height was recorded at Jimma; with mean value of 78.02 cm, while the shortest plant height was recorded at Assosa; with mean value of 49.17 cm.

4.1.2.3. Phenology traits (Days to flowering and maturity)

The mean of days to flowering at different location was ranged from 58 to 87, 56 to 82, 77 to 92, 61 to 84, 12 to 49, and 50 to 73 at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The highest days to flowering was recorded at Teppi; with a mean value of 81 days, while the least flowering days was recorded at Pawe; with mean value of 32. The mean of days to maturity at different location ranged was from 122 to178, 117 to174, 131to153, 119 to156, 91to121,and 116 to165 at Jimma, Mettu, Teppi, Bako, Pawe and Assosa respectively. The latest days to maturity was recorded at Teppi; with mean value of 143 days, while the earliest days to maturity was recorded at Pawe; with mean value of 100 days.

Maturity date is used to determine adaptation to diverse environments (Liu *et al.,* 2017) such as day length and temperature conditions. In general, this indicates, a wider range of variations were observed for all yield-related traits of the thirty genotypes of soybean evaluated at six locations. Hence, the genotypes were not situated as their rank position in other locations. Therefore, the presence of genotype by location interactions was clearly evident on tested genotypes across locations. This is due to moisture or drought stress and temperature stress occurred specially at the time of vegetative stage and at the end of the cropping season lead to decrease the mean performance of tested genotypes across locations.

4.2. Combined Analysis of Variance for yield and yield related traits

4.2.1. Combined Analysis of Variance for grain yield over locations

After testing the homogeneity of error variances of the test locations, the combined analysis of variance was conducted for each trait with special focus on grain yield and other agronomic traits in order to examine the presence of significant effect of locations, genotypes and genotype x location interactions. Besides, the stability analysis was computed on grain yield, which is normally polygenic trait. The Bartlett's test for homogeneity of yield variance (Appendix. Table 5).The combined analysis of variance revealed highly significant ($p<0.01$) of genotype x location interactions effect on grain yield and the result is presented in (Table 6). when significant G x E interactions is present, the effects of genotypes and environments are statistically non additive (the differences between genotypes depend on the environment). A

study conducted on GEI and yield stability of 12 food grade soybean genotypes indicated that variety x location interactions and location x year x variety interactions were significant (Rao *et al.,* 2002). Also this result is in line with the findings of (Deresse Hunde *et al.,* 2019), who grew 17 soybean genotypes for two consecutive years (2016-2017) at five environments (Pawe, Areka,Bako, sirinka and Assosa) and reported highly significant differences for grain yield.

4.2.2. Combined Analysis of Variance for grain yield- related traits over locations

The combined analysis of variance revealed highly significant ($p< 0.01$) genotype x location interactions effect on all studied yield related traits and the result is presented in (Table 6). Among the yield-related traits, for days to flowering, days to maturity, plant height, hundred seed weight, number of seeds per plant, number of pods per plant, lodging, seed shattering, blight and rust were highly significant ($p<0.01$) differences among the test locations and genotypes. Mesfen (2017) grew 24 soybean genotypes at six locations and reported highly significant differences for days to flowering, days to maturity, hundred seed weight, number of seeds per plant and number of pods per plant.

Table 6. Combined ANOVA of grain yield and grain yield-related traits of soybean genotype across six locations.

	Loc.	**Rep(Loc.)**	**Genotypes**	**GXL**	**Error**	**Mean**	**CV%**
Traits	**D.f=5**	**D.f=12**	**D.f=29**	**D.f=145**	**D.f=333**		
DF	23284.37**	8.39	352.94**	38.42**	15.86	63.09	6.31
DM	20925.30**	44.12	805.02**	123.97**	39.91	128.51	4.91
PH	13175.99**	77.83	1570.80**	170.86**	64.61	64.36	12.48
NPPP	19716.40**	169.30	783.16**	274.79**	71.28	40.86	20.65
NSPPL	79899.79**	703.50	1837.30**	695.35**	348.50	67.69	27.57
LODG	5.00**	0.13	0.16**	0.17**	0.024	1.09	14.38
SHATTER	0.04**	0.006	0.011**	0.012**	0.004	1.00	6.29
BLIGHT	81.66**	0.15	0.18**	0.22**	0.13	1.38	26.63
RUST	198.01**	0.13	0.43**	0.54**	0.26	1.60	32.08
HSW	458.45**	11.41	32.65**	10.65**	4.93	15.19	14.62
YIELD	25.79**	0.68	1.22**	0.53**	0.13	1.83	20.18

* Significant ($p <0.05$), ** highly significant ($p <0.01$), *** very highly significant ($p,< 0.001$); CV (%) = Coefficient of Variation, Loc. = Location, V X L = Variety by Location interaction, Rep=Replication, D.f = Degree of freedom, DF= Days to Flowering, DM= Days to Maturity, PH= Plant Height, NPPP= Number of Pod per Plant, NSPPL= Number of Seed per Plant, HSW= Hundred Seed Weight.

The total sum of squares was partitioned into components to estimate the magnitude of GEI for all traits (Table7). In this regard, the contribution of location to the total variation of was more than 50 % for the seven traits, rust (92.51%), days to flowering (83.7%), blight (81.94%), shattering (63.86%), days to maturity (63.8%), number of seeds per plant (58.1%) and number of pods per plant (51.5%) as well as 25 to 50% in four traits grain yield (41.8%), plant height (39.5%), lodging (37.94%) and hundred seed weight (32.9%).

Genotypes contributed to less than 20% to total treatment sum square in all the traits except plant height (27.35%). Genotype x Location Interactions contributed to 20% to 50 % of the total treatment sum square in four traits, i e., hundred seed weight (22.2%), grain yield (25.24%), lodging (38.45%) and shattering (46.4%) as well as less than 20% in seven traits blight (6.46%), rust (6.66%), days to flowering (4.0 %), days to maturity (10.97 %), plant height (14.9 %), number of pod per plant (19.3%), number seed per plant (14.7%) were contributed less than 20%.

Table 7. Percent contribution of each variance component to total sum of squares for all traits of soybean genotypes over six locations

TRAITS	GENOTYPE	LOCATION	GXL INTERACTION
Days to flowering	7.30%	83.70%	4.00%
Days to maturity	14.20%	63.80%	10.97%
Plant height	27.35%	39.55%	14.87%
Number of pods per plant	11.82%	51.55%	19.26%
Number of seeds per plant	7.75%	58.10%	14.68%
Hundred seed weight	13.60%	32.93%	22.18%
Blight	0.60%	81.94%	6.469%
Rust	1.10%	92.51%	6.664%
Lodging	7.30%	37.94%	38.45%
Shattering	8.60%	63.86%	46.36%
Grain yield	11.33%	41.81%	25.24%

In this study, the genotype showed small in variation among them, whereas location and genotype x location interaction explained most of the variations. Both genotype and genotype x location interaction had medium contribution to the determination of different traits, although the location contributed more than 25% to the total treatment sum square of these traits.

The finding of the current study are similar with the findings reported by different authors. Location and genotype x location interaction are both important in governing the expression of yield (Gedif *et al.,* 2014). Location effect was three times higher than the genotype and genotype x location interaction effects (Cravero *et al.,* 2010; Suwarto 2010).

When locations is large, the expression of the traits were mainly influenced by the location, hence the observed performance a set of genotypes in one location may not be very informative for the performance of the same genotypes in another location. Therefore, GEI with similar characteristics will induce corresponding responses in crops and lead to strong genetic correlations. GEI has wide ranging implications for trait development and for understanding how organisms will respond to environmental change. GEI was introduced in terms of the relative difference between genotypic means. GEI can also be regarded in terms of heterogeneity of genetic variance and covariance. As a consequences of GEI, the magnitude of genetic variance as observed within individual environments will change from one environment to the next. GEI has also consequences for the correlations between genotypic performances in different environments.

Often, the genetic variance tends to be larger in better environments than in poorer environments although the opposite can be observed as well (przystalski *et al.*,2008). In conclusion, given the complexity of the mechanisms and processes underlying the phenotypic response across diverse and changing environmental conditions frequently in an unpredictable way it is necessary to develop analytical tools to help breeders understand GEI (Acquaah 2007).

4.3. Mean comparisons of the genotypes over locations

The performance of genotypes based on mean yield-related traits evaluated across the six locations were presented in (Appendix. Table 3 and Appendix. Table 4). Across locations, days to flowering was ranged from 56 to 75 with an overall mean of 63 days and genotype SNK500 was the earliest flowering, while Favour is the latest flowering among the tested genotypes. Days to maturing was ranged from 119 to153 with an overall mean of 129 days and genotype Afgat was the earliest maturing, while Favour is the latest maturing among the

tested genotypes. Plant height was ranged from 46.84 to 97.79 with an overall mean of 64.36 cm and genotype Nyala was the shortest plant height, while Panorama29-1is the highest plant height among the tested genotypes.

Number of pods per plant was ranged from 31.54 to59.63 with an overall mean of 40.88 and genotype TGX2014-5GM was the minimum number of pods per plant, while Favour is the maximum number of pods per plant among the tested genotypes. Number of seeds per plant was ranged from 49.75 to 93.57 with an overall mean of 63.46 and genotype Nyala was the minimum number of seeds per plant, while Pawe-3 is the maximum number of seeds per plant among the tested genotypes. Hundred seed weight was ranged from11.26 to 17.82 with an overall mean of 15.19 g and genotype Pawe-3 was the lowest hundred seed weight, while ScSerenade is the highest hundred seed weight among the tested genotypes.

The performance of genotypes based on mean grain yield evaluated across the six locations were presented in (Table 5, Appendix.Table.2 and Appendix. Table 4). Grain yield was ranged from1.22 t/ha to 2.43 t/ha with an overall mean of 1.83 t/ha and genotype Favour was the lowest grain yield, while ScStatus is the highest grain yield among the tested genotypes. Soybean genotypes ScStatus (2.43 t/ha) and S1079/6/7 (2.23 t/ha) were best in grain yield than the other genotypes and the checks varieties.

At Jimma, the highest yield was obtained from the soybean genotype S1079/6/7 (1.97 t/ha), while the lowest yield was obtained from the soybean genotype Favour (0.39 t/ha). At Mettu, the highest yield was recorded from the soybean genotype ScSpike (2.32 t/ha), while the lowest yield was recorded from the soybean genotype SNK500 (0.59 t/ha). At Teppi, the highest yield was recorded from the soybean genotype Pawe-3 (2.94 t/ha), while the lowest yield was obtained from the soybean genotype ScSentinel (1.04 t/ha). At Bako, the highest yield was exhibited from the soybean genotype S1079/6/7 (4.05 t/ha), while the lowest yield was recorded from the soybean genotype SNK500 (1.35t/ha). At Pawe, the highest yield was obtained from the soybean genotype ScSpike (3.42 t/ha), while the lowest yield was recorded from the soybean genotype Favour (1.15t/ha). At Assosa, the highest yield was exhibited from

the soybean genotype Panorama29-1 (2.15t/ha), while the lowest yield was recorded from the soybean genotype ScSpike (0.90 t/ha).

However, there was a rank change in grain yield performance of genotypes across the locations. This may be due to the environmental factors (non-genetic factors) such as uneven rainfall distribution, low or high temperatures, prevalence of plant disease and insect pests, soil factors varying across locations and over years may have positive or negative impacts on genotypes. Radiation, water, and nutrients availability are among the environmental factors strongly influence crop growth and yield (Mather and Jinks 1982), (Mukai 1988, and Wu and OíMalley 1998).

These inconsistence yield ranking of genotypes from location to location revealed that the GEI effect was cross over type as described by Matus-Cadiz *et al.,* (2003). The findings in this study are in line with cross over results of Farshadfar *et al.,* (2012) in wheat; Dagnachew *et al.,* (2014) in finger millet and Shitaye (2015) in durum wheat.

Crossover interaction is not only non-additive in nature but also non-separable. Therefore, the presence of crossover type interaction is important, because it implies that the choice of the best genotype is determined by the location, hence, the breeding location may be classified into mega-environments and specifically adapted genotypes can be developed for each sub environment separately (Rea *et al.,* 2016). Since the presence of a crossover interaction has strong implications for breeding for specific adaptation, it is important to assess the frequency of crossover interactions. 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 (Acquaah,2007).

It is important to understand crop development in relation to biophysical conditions and seasons changes when selecting well-adapted genotypes. A high level of interaction in the favorable direction is desirable to obtain maximal performance. Selection of stable cultivars that perform consistently across environments can reduce the magnitude of these interactions. Genotypes that show low GEI with high stable yields are desirable for crop breeders and farmers because the environment has less influence on such genotypes and their higher yields

are largely due to their genetic composition. Hence, consistent performance is key in crop improvement and acceleration of genetic gains. It is also critical to farmers because they are assured of salvaging something irrespective of environmental and seasonal changes.

Significant GEI effects tend to be viewed as problematic in breeding because the lack of predictable response hinders progress from selection (Dudley and Moll,1969). The significance of these interactions is that they cause differences in the ranking order of genotypes under evaluation in the given multiple environment trials (METs). Therefore, it becomes prudent to test genotypes over several environments and seasons. This is especially important with quantitative traits such as yield because significant GEI is known to curtail the correlation between genotypic and phenotypic values which adversely affects response to selection (Comstock and Moll, 1963).

In such situation, breeders may look for genotypes that perform relatively consistently (broadly adapted) across test environments or choice for specifically adapted genotypes for production in different environments. Therefore, stability analysis helps to identify such types of genotypes to recommend them for specific or wider environmental conditions.

4.4. Stability Analysis for grain yield

In this study, the stability parameters of Wricke's ecovalence, Shukla's Stability Variance, Cultivar Superiority Measure, Eberhart and Russel joint regressions analysis, AMMI Stability Value, Yield Stability Index, AMMI Model and GGE bi plot Model were used to evaluate the yield stability of the studied genotypes across location.

4.4.1 Wricke's Ecovalence Analysis (Wi)

According to the Wricke (1962) method, the genotypes with the lowest ecovalence value were considered to be more stable than others. Wricke's ecovalence was determined for grain yield of the thirty soybean genotypes at six locations during 2020 main cropping season. Genotypes TGX2014-16FM (G7),TGX2002-3DM (G6) and Gazelle (G22) were the three more stable genotypes identified based on Wricke's ecovalence criteria. However, those genotypes were not the highest in rank for mean yield. Unstable genotypes identified by this criterion were Sc

Spike (G10) and Sc Signal (G12). In line with this result, Gurmu *et al.,* (2009) reported a significant difference in stability among twenty soybean genotypes in Southern Ethiopia based on Wricke's ecovalence analysis. Similar results about the ability of Wricke's Ecovalence Analysis (Wi) to classify stable genotypes were reported by Gadissa (2018) in bread wheat (Table.8).

4.4.2. Shukla's Stability Variance (σi2)

Shukla (1972) proposed the stability variance (σi2), 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 (σi2) is the environmental variance (σe2) which means that σi2=0. The relatively large value of σi2 indicates greater instability of genotype i. Similar to Wricke's ecovalence (1962) the Shukla (1972) identified similar genotypes as most stable regardless of their grain yield.

Genotypes TGX2014-16FM (G7), TGX2002-3DM (G6) and Gazelle (G22) showed low Shukla's stability variance value this indicates that these genotypes are less responsive to favorable environments, but should perform well in a more predictable and stable manner. On the other hand, unstable genotypes were ScSpike (G10) and ScSignal (G12) exhibited highest Shukla's stability variance value which implies that these genotypes should perform better in increasingly favorable environments (Table.9).

Table 8. Mean soybean grain yield and Wricke's Ecovalence value for thirty soybean genotypes over six locations.

Genotype code	Genotype name	Grain yield	Rank	Wi	Rank
1	Favour	1.226	30	1.690	27
2	TGX2001-6FM	1.948	11	0.535	7
3	TGX2014-5GM	1.357	28	0.592	12
4	TGX2014-23FM	1.736	21	0.252	5
5	TGX2001-8DM	2.047	7	0.807	16
6	TGX2002-3DM	1.894	14	0.211	2
7	TGX2014-16FM	1.945	12	0.204	1
8	Panorama29-1	1.934	13	1.372	25
9	ScSaga	1.991	9	0.315	6
10	ScSpike	2.154	4	2.284	30
11	S1079/6/7	2.238	2	1.485	26
12	ScSignal	2.112	5	1.937	29
13	ScSaxon	1.832	18	0.551	8
14	S1180/5/54	1.786	20	0.884	19
15	S1140/5/4	1.884	16	0.566	9
16	S1150/5/22	2.072	6	0.246	4
17	ScSafari	1.893	15	0.907	20
18	ScStatus	2.430	1	0.839	18
19	SNK500	1.318	29	1.732	28
20	SCS-1	1.527	24	0.757	14
21	Clark-63k	1.873	17	0.584	11
22	Gazelle	1.812	19	0.213	3
23	Nyala	1.692	22	0.607	13
24	ScSerenade	1.640	23	1.001	22
25	ScSentinel	1.486	27	0.988	21
26	Kafue	1.488	26	0.829	17
27	Afgat	1.516	25	0.580	10
28	Pawe-1	1.950	10	1.267	24
29	Pawe-2	2.037	8	0.760	15
30	Pawe-3	2.191	3	1.159	23

Table 9. Mean soybean grain yield and Shukla's Stability Variance for thirty soybean genotypes over six locations.

Genotype code	Genotype name	Grain yield	Rank	σi^2	Rank
1	Favour	1.226	30	0.355	26
2	TGX2001-6FM	1.948	11	0.108	7
3	TGX2014-5GM	1.357	28	0.120	12
4	TGX2014-23FM	1.736	21	0.047	5
5	TGX2001-8DM	2.047	7	0.166	16
6	TGX2002-3DM	1.894	14	0.038	2
7	TGX2014-16FM	1.945	12	0.037	1
8	Panorama29-1	1.934	13	1.287	30
9	ScSaga	1.991	9	0.061	6
10	ScSpike	2.154	4	0.483	29
11	S1079/6/7	2.238	2	0.311	25
12	ScSignal	2.112	5	0.409	28
13	ScSaxon	1.832	18	0.111	8
14	S1180/5/54	1.786	20	0.183	19
15	S1140/5/4	1.884	16	0.114	9
16	S1150/5/22	2.072	6	0.045	4
17	ScSafari	1.893	15	0.188	20
18	ScStatus	2.430	1	0.172	18
19	SNK500	1.318	29	0.364	27
20	SCS-1	1.527	24	0.155	14
21	Clark-63k	1.873	17	0.118	11
22	Gazelle	1.812	19	0.039	3
23	Nyala	1.692	22	0.123	13
24	ScSerenade	1.640	23	0.208	22
25	ScSentinel	1.486	27	0.205	21
26	Kafue	1.488	26	0.171	17
27	Afgat	1.516	25	0.117	10
28	Pawe-1	1.950	10	0.265	24
29	Pawe-2	2.037	8	0.156	15
30	Pawe-3	2.191	3	0.241	23

4.4.3. Lin and Binns Cultivar Superiority Measure (Pi)

According to cultivar superiority measure (Pi) analysis, the genotype with low or small Pi value is considered to be the more stable (Lin and Binns,1988). Therefore, the highest yielding genotypes, ScStatus (G18) and S1079/6/7 (G11) showed the low cultivar superiority value and highest yield performance indicating stability of those genotypes. On the other

hand, genotypes Favour (G1) and SNK500 (G19) showed the high Pi values and lowest mean yield were considered to be unstable (Table 10).

Mesfin (2017) employed the Lin and Binns Cultivar Superiority Measure (Pi) and identified three high yielding and stable soybean cultivars from 24 soybean genotypes tested at six locations in Ethiopia. Similar results about the ability of cultivar superiority measure to classify high yielder and stable genotypes were reported by several authors including Afework (2017) in coffee; Yirga (2016) in sesame and Gadissa (2018) in bread wheat.

4.4.4. Eberhart and Russell's Joint Regression Analysis

According to Eberhart and Russell's Joint Regression model, an ideal genotype is one with a high mean yield, regression slop (b) =1.0 and least deviation from regression (S^2di)=0. 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 locations. Therefore, the genotypes S1150/5/22 (G16), TGx2001-8DM (G5), and pawe-2 (G29) showed high mean yield (>2.0 t/ha) and close to one bi value and close to zero S^2 di values found to be more stable genotypes based on Eberhart and Russell's Joint Regression analysis whereas genotypesTGX2014-23FM (G4), Afgat (G27), and Kafue (G26) showed low mean yield (≤ 1.7 t/ha) and were unstable. Based on regression slop; genotypes S1079/6/7 (G11), ScSignal Sc (G12), ScStatus (G18) and Pawe-1 (G28) showed high mean yield (≥2.0 t/ha) with a bi value greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments whereas genotypes SNK500 (G19), SCS-1 (G20), Favour (G1) and S1180/5/54 (G14) showed low mean yield (≤ 1.7 t/ha) with a bi value less than 1.0 has above average stability and is especially adaptable to low performing environments (Table.11).

Table 10. Mean soybean grain yield and Cultivar Superiority Measure (Pi) for thirty soybean genotypes over six locations.

Genotype code	Genotype name	Grain yield	Rank	Pi	Rank
1	Favour	1.226	30	1.481	30
2	TGX2001-6FM	1.948	11	0.433	11
3	TGX2014-5GM	1.357	28	1.255	28
4	TGX2014-23FM	1.736	21	0.628	20
5	TGX2001-8DM	2.047	7	0.343	6
6	TGX2002-3DM	1.894	14	0.490	14
7	TGx2014-16FM	1.945	12	0.427	10
8	Panorama29-1	1.934	13	0.519	15
9	ScSaga	1.991	9	0.402	9
10	ScSpike	2.154	4	0.393	8
11	S1079/6/7	2.238	2	0.254	2
12	ScSignal	2.112	5	0.309	3
13	ScSaxon	1.832	18	0.563	17
14	S1180/5/54	1.786	20	0.678	21
15	S1140/5/4	1.884	16	0.483	13
16	S1150/5/22	2.072	6	0.323	4
17	ScSafari	1.893	15	0.615	18
18	ScStatus	2.430	1	0.091	1
19	SNK500	1.318	29	1.460	29
20	SCS-1	1.527	24	1.041	26
21	Clark-63k	1.873	17	0.559	16
22	Gazelle	1.812	19	0.625	19
23	Nyala	1.692	22	0.778	22
24	ScSerenade	1.640	23	0.919	23
25	ScSentinel	1.486	27	1.112	27
26	Kafue	1.488	26	1.039	25
27	Afgat	1.516	25	0.960	24
28	Pawe-1	1.950	10	0.434	12
29	Pawe-2	2.037	8	0.347	7
30	Pawe-3	2.191	3	0.333	5

Table 11. Mean soybean grain yield and Eberhart and Russell's Joint Regression Analysis (bi and S2di) for thirty soybean genotypes over six locations.

Genotype code	Genotype name	Grain yield	Rank	Beta(bi)	Rank	Deviation (S^2di)	Rank
1	Favour	1.226	30	0.368	3	0.243	29
2	TGX2001-6FM	1.948	11	1.250	21	0.074	15
3	TGX2014-5GM	1.357	28	0.450	5	0.003	2
4	TGX2014-23FM	1.736	21	1.229	20	0.008	4
5	TGX2001-8DM	2.047	7	1.381	24	0.113	20
6	TGX2002-3DM	1.894	14	0.960	13	0.016	6
7	TGx2014-16FM	1.945	12	0.980	14	0.014	5
8	Panorama29-1	1.934	13	1.472	26	0.226	27
9	ScSaga	1.991	9	1.226	19	0.024	8
10	ScSpike	2.154	4	1.216	18	0.518	30
11	S1079/6/7	2.238	2	1.815	30	0.096	17
12	ScSignal	2.112	5	1.776	29	0.232	28
13	ScSaxon	1.832	18	1.035	15	0.101	18
14	S1180/5/54	1.786	20	0.394	4	0.053	11
15	S1140/5/4	1.884	16	1.434	25	0.037	10
16	S1150/5/22	2.072	6	1.063	16	0.023	7
17	ScSafari	1.893	15	0.462	6	0.086	16
18	ScStatus	2.430	1	1.504	27	0.067	13
19	SNK500	1.318	29	0. 201	1	0.167	23
20	SCS-1	1.527	24	0.363	2	0.007	3
21	Clark-63k	1.873	17	1.074	17	0.107	19
22	Gazelle	1.812	19	0.772	11	-0.001	1
23	Nyala	1.692	22	0.512	7	0.030	9
24	ScSerenade	1.640	23	0.693	10	0.180	24
25	ScSentinel	1.486	27	0.806	12	0.197	26
26	Kafue	1.488	26	0.617	9	0.118	21
27	Afgat	1.516	25	1.311	23	0.073	14
28	Pawe-1	1.950	10	1.773	28	0.066	12
29	Pawe-2	2.037	8	1.253	22	0.130	22
30	Pawe-3	2.191	3	0.560	8	0.184	25

4.4.5. Additive Main Effects and Multiplicative Interaction (AMMI) Model

The AMMI model integrates the analysis of variance into a unified approach (Gauch,1988; Gauch and Zobel, 1996). The IPCA1scores of genotypes in AMMI analysis are an indication of the stability or adaptation over locations (Guach and Zobel, 1997). The AMMI analysis of variance of the sum of squares due to GEI was further partitioned into principal component analysis. The percentage contributions to the interaction sum of squares captured by the different principal components (IPCAs) were IPCA1 (44.3%), IPCA2 (24.6%), IPCA3

(12.5%,), IPCA4 (11.6%) and IPCA5 (6.9%), and cumulatively the first two principal components explained 69.0%. All the interaction principal components of mean square were highly significant (P< 0.01) (Table12).

The result of the current study is in agreement with Farshadfar and Mojgan (2014) who reported that the first two interaction principal component can explain the genotype X location interaction in multi-location trails, the remaining interaction principal components did not help in the accurate prediction and are not interpretable. The most accurate model for AMMI can be predicted using the first two IPCAs. Agyeman *et al.,* (2015) illustrated that most of the interaction occurs in the first few axes.

In the present study the total sum of squares of the model attributed to genotypes and genotype by environment interaction were 11.33 % and 25.24 %, respectively. Only a small portion of the total sum of squares was attributed to genotypic effects. Therefore, according to AMMI analysis for grain yield, the first two interaction principle components have contributed to the largest portions (69.0 %) of the interaction sum squares with respective IPCA1 and IPCA2 contributions of 44.3 % and 24.6 % (Table 12).

Table 12. Analysis of variance of AMMI for grain yield of thirty soybean genotypes grown in six locations in 2020 main cropping season.

				Sum Square Explained (%)		
Source of Variation	**D.F**	**SS**	**MS**	**Total variation explained**	**Gen*Loc. explained**	**Gen*Loc. commutative**
Locations	5	129.21	25.84**	41.81	-	-
genotypes	29	35.40	1.22**	11.33	-	-
Reps (loc)	12	8.18	0.68**	-	-	-
Blocks (Rep)	15	12.61	0.84**	-	-	-
Gen * Loc.	145	78.48	0.53**	25.24	-	-
IPCA-1	33	35.21	1.06**	-	44.35	44.35
IPCA-2	31	19.57	0.63**	-	24.65	69.00
IPCA-3	29	9.91	0.342**	-	12.49	81.4
IPCA-4	27	9.19	0.340**	-	11.58	93.0
IPCA-5	25	5.49	0.21*	-	6.91	100
Residuals	360	57.715	0.16	-	-	-

**indicates significance at P< 0.01 probability level, *indicates significance at P< 0. 05 probability level, Loc.= locations; DF = Degree Freedom; SS= Sum Square, MS= Mean Square, Gen * Loc = Genotype by Location Interaction, IPCA= Interaction Principal Component Analysis.

Eigen values of the first two axes were greater than the mean of all Eigen values. Hence, much of the variability was accounted by the first two IPCA components. This means that, Amare and Tamado (2014) indicated the most accurate model for AMMI can be forecasted by using the first two IPCA (Table12). The environment revealed a high variability for both the main and interaction effects (Table12). This means that, it was necessary to group the environments to identify and recommend target genotypes according to their adaptations. Eberhart and Russell (1966) in maize, Tiruneh (2000) in tef, and Asfaw *et al.*, (2009) on soybean in Ethiopia have reported grouping of environment and genotypes based on the G x E patterns.

4.4.5.1 AMMI 1 bi plot Analysis for grain yield

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.

According to Alberts, (2004), AMMI-I considers genotype and locations main effects plus the 1^{st}PC (PC1) to interpret the residual matrix and represented genotype productivity. It is further stated that any genotype with PCA1 value close to zero shows general adaptation to the tested locations whereas a large genotypic PCA1 score reflects more specific adaptation to location with PCA1 scores of the same size. Genotypes and locations with IPCA1 scores of the same sign produce positive interaction suggesting adaptation of genotypes in those locations whereas the reverse sign of PCA value of genotypes and locations depicts negative interaction i.e., poor performance of genotypes in such locations. In summary, a stable genotype might not be the highest yielding.

Genotypes having a zero IPCA1 score are less influenced by the locations and adapted to all locations. The closer the IPCA score to zero, the more stable the genotypes over the tested locations. Since IPCA1 scores of soybean genotypes TGX2002-3DM (G6), Clark-63k (G21),

ScSaga (G9), S1150/5/22T (G16), Pawe-2 (G29), TGX2014-16FM (G7), Gazelle (G22) TGX2014-23FM (G4), and Afgat (G27) were close to zero, they were more stable genotypes that across these locations. However, the mean yield of genotypes TGX2014-23FM (G4) and Afgat (G27) had a mean yield below average, therefore, they are least preferable. Whereas the remaining genotypes TGX2002-3DM (G6), Clark-63k (G21), ScSaga (G9), S1150/5/22T (G16), Pawe-2 (G29), TGX2014-16FM (G7), and Gazelle (G22) had a mean yield above average, therefore, they are more preferable (Figure1).

A genotype showing high positive interaction in an location has the ability to exploit the agro-ecological and agro-management conditions of the specific location and is therefore best suited to that location. In this case, soybean genotypes ScSignal (12), ScSpike (G10), S1079/6/7 (G11), and Pawe-1 (G28) are suited for Bako. Soybean genotypes ScStatus (G18), TGX2001-8DM (G5), Panorama29-1(G8), TGX2001-6FM (G2), ScSaxon (G13), and S1140/5/4 (G15) are suited for Pawe. Soybean genotype Afgat (G27) is suited for Mettu. Soybean genotypes ScSentinel (G25), Pawe-3 (G30), ScSerenade (G24), S1180/5/54 (G14), Nyala (G23) and ScSafari (G17) are suited for Teppi. Soybean genotype TGX2014-5GM(G3) is suited for Jimma. Soybean genotypes SCS-1 (G20), Kafue (G26) Favour (G1) and SNK500 (G19) are suited for Asosa (Figure1). Adane *et.al.,* (2018) reported in six locations by using seven soybean genotypes for two consecutive year during 2016 and 2017 main cropping season in Western Ethiopia. Similar results were also reported by Temesgen *et al.,* (2014) on linseed and Niger seed in Western Ethiopia. On a bi-plot, genotypes and locations having IPCA1 values close to zero have small interaction effects, while those having large positive or negative IPCA1 values are largely responsible for the GEI.

The graph space (Figure1) are divided into IV from lower yielding in quadrants I and IV to the higher yielding in quadrants II and III. In Addition, quadrant II considered as ideal environment. So, from the graph in (Figure1), Bako (E4) and Pawe (E5), which is in quadrant II, are ideal locations, while quadrant III characterizes in high yielding location with unstable genotypes, in this quadrant Teppi (E3) is found. Similarly, in quadrant I characterized, stable genotypes and low yielding and in contrast quadrant IV unstable genotypes with the low yielding locations. These results similar with (Mesfen and Abush, 2019).

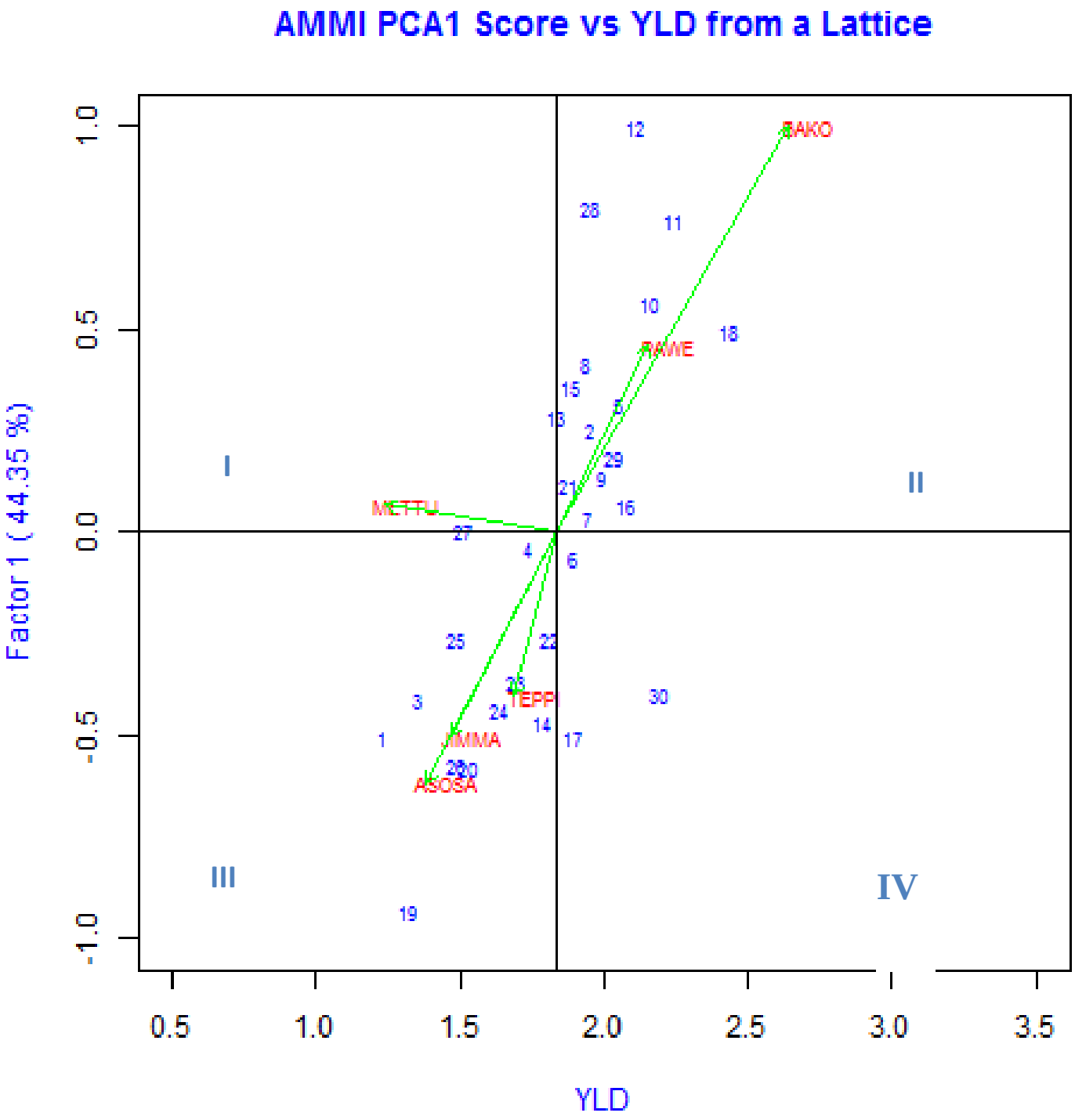

Figure V. AMMI bi plot of IPCA 1 against grain yield of thirty soybean genotypes across six locations

4.4.5.2 AMMI 2 bi plot for grain yield

AMMI-2 considers main effects plus the first two PCs (PC1 and PC2) for non-additive effects and described the genotype stability (Rakshit *et al.,* 2012). IPCA1 and IPCA2 of grain yield accounted for 44.3 % and 24.6 % of interaction respectively (Table13). The results of AMMI analysis can be presented graphically in the form of bi plots (Ebdon and Gauch,2002). AMM 2 bi plot 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 locations that exhibit low, medium, or high level of interaction effect (Sharma *et al.,* 1998).

In conclusion, genotypes that falls near the center of the biplot (small IPCA1 and IPCA2 values) is expected to be more stable and widely adapted (Broader adaptation) whereas genotypes that occur close to particular locations on the IPCA2 vs IPCA1 biplot shows specific adaptation to those locations.

The stability of a genotype or location is determined by the end point of its vector from the origin (0,0). Hence, soybean genotypes S1150/5/22 (G16), ScSaga (G9) and TGX 2014-23FM (G4), were stable but except TGX2014-23FM (G4) the others were exhibited grain yield higher than grand mean. Genotypes that show low GEI with high stable yields are desirable for crop breeders and farmers because the environment has less influence on such genotypes and their higher yields are largely due to their genetic composition. Therefore, these genotypes were considered as a high yielding and widely adapted genotypes indicating their minimum contribution to the total GEI variance.

In AMMI 2 bi plot, the location scores are joined to the origin by the site lines. Locations with short spokes (length of arrow lines) do not exert strong interactive forces. This indicates that they are stable location and the least discriminating location. Based on the length of the arrows of the locations, Bako and Assosa had strong discriminating power followed by Jimma, Teppi and Pawe, whereas location Metu which had short distance from the origin showed similar performance of genotypes in it (Figure 2). The most discriminating location means that, the locations provided very high information about genotypic differences. vise versa.

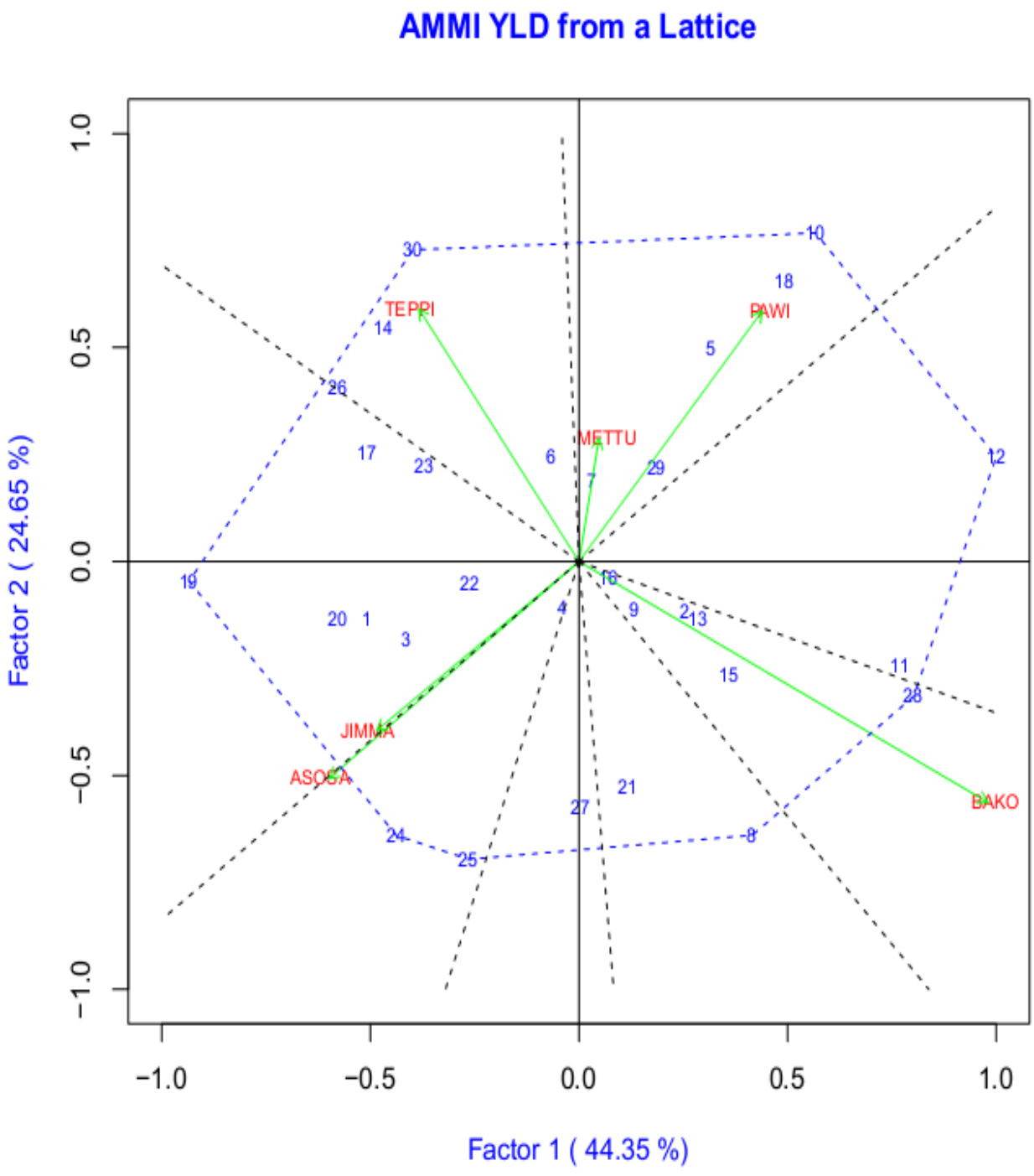

Figure VI. AMMI2 bi plot for grain yield of thirty soybean genotypes showing the plot of IPCA1 and IPCA2.

4.4.5.1.1 AMMI Selections for the highest four yielding genotypes across six locations

The AMMI model selected four best genotypes for in each locations and illustrated in (Table13). According to this information, genotypes ScStatus (G18) and Pawe-3 (G30) were the best adapted at four locations among six tested locations. The genotype ScStatus (G18) was ranked first at Mettu (E2), second at Teppi (E3), and Pawe (E5), and fourth at Jimma (E1) whereas genotype Pawe-3 (G30) was ranked first at Jimma (E1) and Teppi (E3), second at Assosa (E6), and third at Mettu (E2).

In addition to these genotypes; genotype ScSpike (G10) were the best adapted at three locations. Moreover, genotypes ScSafari (G17), ScSerenade (G24), ScSignal (G12), Panorama29-1 (G8), and TGX2001-8DM (G5) were best adapted at two locations. Nevertheless, genotypes S1150/5/22 (G16), Pawe-1(G28), and S1079/6/7 (G11) appeared only once at locations among six tested locations.

Generally, genotypes ScStatus (G18) and Pawe-3 (G30) were the only two genotypes that were best adapted with the highest mean yield across four locations. Therefore, these genotypes were recommended for each testing locations and other areas which have similar agro-ecology with this testing locations.

Table 13. Ranking of four AMMI selections per location for grain yield

Location	**Number**	**mean**	**IPCA1-score**	**Score**			
				1	2	3	4
Jimma	1	1.541	-0.7677	G30	G17	G24	G18
Mettu	2	1.311	0.0592	G18	G10	G30	G5
Teppi	3	1.760	-0.5090	G30	G18	G10	G17
Bako	4	2.713	1.3013	G11	G12	G28	G8
Pawe	5	2.224	0.6031	G10	G18	G12	G5
Assosa	6	1.452	-0.6870	G24	G30	G8	G16

G5= TGX2001-8DM, G8= Panorama29-1, G10= ScSpike, G11= S1079/6/7, G12= ScSignal, G16= S1150/5/22, G17= ScSafari, G18= ScStatus, G24= ScSerenade, G28= Pawe-1, and G30= Pawe-3. E1= Jimma, E2= Mettu, E3= Teppi, E4= Bako, E5= Pawe, and E6= Assosa

4.4.6 The 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. This value is finally used to measure the grain yield stability of the genotypes and cluster the genotypes and environments into different groups Purchase *et al.,* (2000). Even if both IPCA1 and IPCA2 are useful for stability indication, variation was observed in measuring the stable genotypes between the two IPCAs. That means, a genotype which is considered to be stable in IPCA1 may not show itself stable in IPCA2 as the first case (Letta, 2009).

In this method, as described by Purchase (1997) ASV was calculated for each variety. Genotype with least ASV values are the most stable (Purchase *et al.,* 2000). Accordingly, genotypes S1150/5/22 (G16), TGX2014-16FM (G7) and TGX2002-3DM (G6) relatively exhibited higher grain yield than grand mean and were more stable. While, the genotypes SNK500 (G19) and SCS-1 (G20) were the most unstable genotypes (Table 14).

4.4.7. Yield Stability Index (YSI)

This method is vital to measure and rank genotypes based on grain yield stability. The summation of rank of ASV and rank of yield are used to calculate YSI. The genotype with least YSI is considered as the most stable with high grain yield (Dabessa *et al.,* 2016). According to YSI, the most stable genotypes with high seed yield and general adaptation were S1150/5/22 (G16), ScStatus (G18) and Pawe-2 (G29). Conversely, the genotypes SNK500 (G19) and SCS-1 (G20) were the most unstable genotypes (Table14).

Table 14. Mean soybean grain yield, AMMI Stability Value (ASV), and interaction principal component axis (IPCA1, IPCA2) and yield stability index (YSI) scores of the thirty soybean genotypes tested across six locations.

Genotypes Code	Genotypes Name	Yield Mean	Rank	IPCA1	IPCA2	ASV	Rank	YSI	**Rank**
G1	Favour	1.226	30	-0.31437	0.12198	0.81933	21	51	19
G2	TGX2001-6FM	1.948	11	0.165630	0.12734	0.25025	5	16	6
G3	TGX2014-5GM	1.357	28	-0.36774	0.12917	1.05487	24	52	20
G4	TGX2014-23FM	1.736	21	0.03043	0.00099	0.93534	23	44	17
G5	TGX2001-8DM	2.047	7	0.19979	-0.39761	0.41009	10	17	7
G6	TGX2002-3DM	1.894	14	-0.01547	-0.20877	0.20877	3	17	7
G7	TGX2014-16FM	1.945	12	0.01241	-0.14564	0.14564	2	14	4
G8	Panorama29-1	1.934	13	0.25742	0.54044	0.55417	15	28	10
G9	Sc Saga	1.991	9	0.10330	0.00806	1.32396	25	34	13
G10	Sc Spike	2.154	4	0.41573	-0.59775	0.66401	18	22	8
G11	S1079/6/7	2.238	2	0.52869	0.15420	1.81921	26	28	10
G12	Sc Signal	2.112	5	0.70881	-0.13987	3.59471	28	33	12
G13	Sc Saxon	1.832	18	0.20480	-0.07241	0.58375	16	34	13
G14	S1180/5/54	1.786	20	-0.31829	-0.38129	0.46473	11	31	11
G15	S1140/5/4	1.884	16	0.28628	0.30828	0.40708	8	24	9
G16	S1150/5/22	2.072	6	0.08782	0.08805	0.12420	1	7	1
G17	Sc Safari	1.893	15	-0.42570	-0.20328	0.91436	22	37	14
G18	Sc Status	2.430	1	0.28890	-0.30229	0.40940	9	10	2
G19	SNK500	1.318	29	-0.67718	0.04653	9.85553	29	58	22
G20	SCS-1	1.527	24	-0.41330	0.00538	31.75035	30	54	21
G21	Clark-63k	1.873	17	0.09370	0.38484	0.38552	7	24	9
G22	Gazelle	1.812	19	-0.16364	0.03647	0.73515	20	39	15
G23	Nyala	1.692	22	-0.29705	-0.13970	0.64689	17	39	15
G24	Sc Serenade	1.640	23	-0.31811	0.51830	0.55385	14	37	14
G25	Sc sentinel	1.486	27	-0.18794	0.48722	0.49258	13	40	16
G26	Kafue	1.488	26	-0.39101	-0.24241	0.67568	19	45	18
G27	Afgat	1.516	25	0.07328	0.37409	0.37437	6	31	11
G28	Pawe-1	1.950	10	0.59947	0.10300	3.49049	27	37	14
G29	Pawe-2	2.037	8	0.16928	-0.19962	0.24588	4	12	3
G30	Pawe-3	2.191	3	-0.33593	-0.40369	0.49103	12	15	5

IPCA1=Interaction principal component analysis one, IPCA2= Interaction principal component analysis two, ASV=AMMI stability value, YSI=Yield stability index

4.4.8. Genotype Main Effect and Genotype by Environment Bi-plot Analysis for Grain Yield

GGE bi plot is important to visualize the genotype by environment interaction. GGE bi plots of the first two interaction principal components (i.e. IPCA1 and IPCA2) that contributed 41.49 % and 23.52% of the interaction sum of squares, respectively, explained 65.01% of the total variation for yield. This contribution of the two IPCAs in this study are lower than (86.6%) reported by Amira *et al*., (2013), but higher than (61.50% and 63.4%). reported by Asfaw *et al.,* (2009) and Atnaf *et al.,* (2013). The GGE bi plot graphic analyses of the thirty soybean genotypes tested across the six locations are presented in the figures below.

4.4.8.1 The Which-Won-Where/What pattern

According to Yan *et al.,* (2002), the polygon view of GGE bi plot indicates the best genotypes in each environment and group of environments. In this situation, the polygon is formed by connecting the genotypes that are farthest away from the bi plot origin, such that all the 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. Polygon view of the soybean genotypes tested at six locations presented in (figure 3). Genotypes at the vertex of the polygon are either the best or poorest in one or more environments (Alake *et al.,* 2012). The genotypes found at the vertex of the polygon perform best in the environments within the sector (Yan and Tinker, 2006). Six rays divide the bi plot in to six sector and the locations fall in to three different mega-environments (Figure.3).

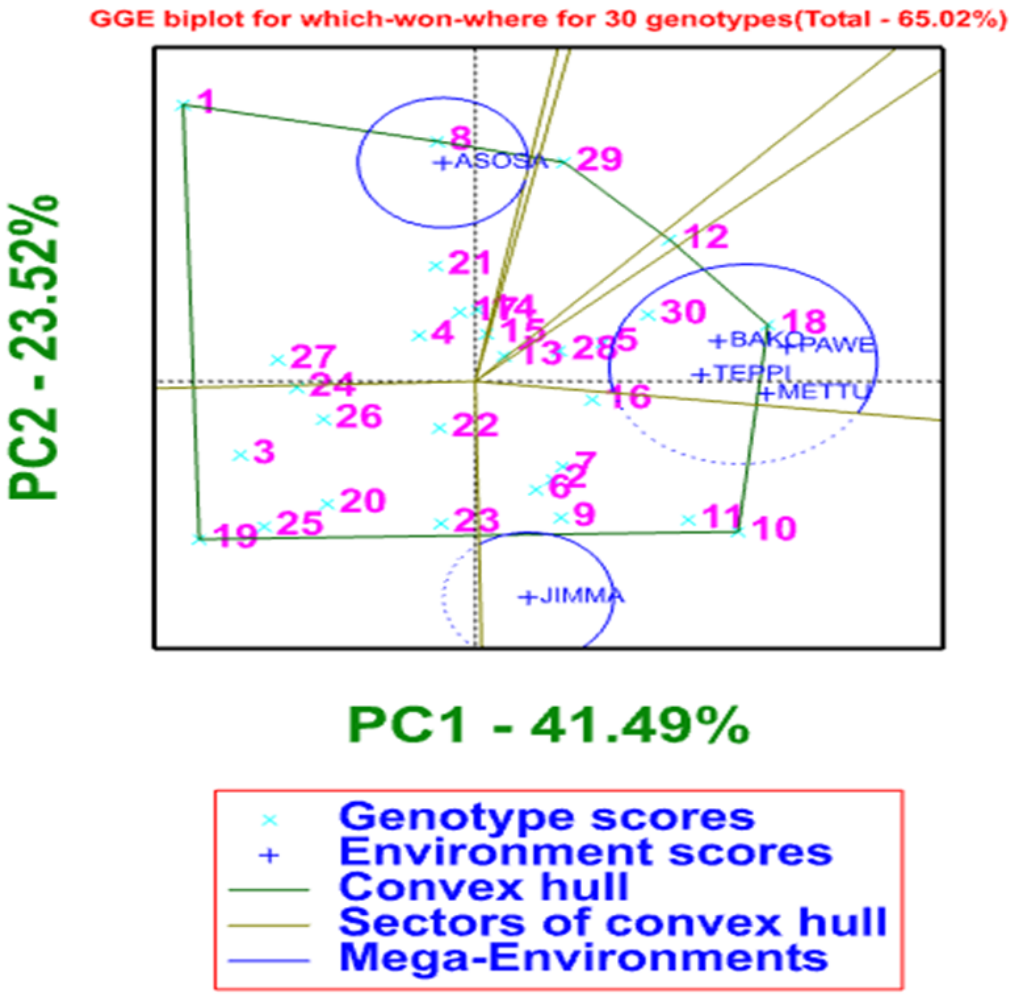

Figure VII. Polygon views of the GGE-biplot based on symmetrical scaling for ‘‘which-won-where’’ and mega- environment delineation.

Genotypes, Favour (G1), Pawe-2 (G29), ScStatus (G18), ScSpike (G10) and SNK500 (G19) were the vertex genotypes. From this figure, ScStatus (G18) best performer at Bako, Pawe, Mettu and Teppi in the first mega environment. The second environment containing the higher yielding environment Jimma, with a winner genotypes ScSpike (G10). The third environment include Assosa with a winner genotype Favour (G1). From the figure, SNK 500 (G19) and Pawe-2 (G29) had no environment on the vertex. This indicates that genotypes in the vertex without environment performed poorly in all the locations (Alake *et al.,* 2012). However, genotypes within the polygon, particularly those located near the bi plot origin were less responsive than the genotypes on the vertices, and the ideal genotype would be the one closest to the origin (Nwangburuka *et al* ., 2011). Therefore, genotypes Pawe-1 (G28), Sc Saxon (G13),S1140/5/4 (G15), TGX2014-23FM (G4) and Gazelle (G22) were more stable (Figure.3).

4.4.8.2. Mean yield and stability performance

The ranking of the genotypes based on their mean performance and stability presented in (Figure 4). It has been established that if the PC1 of a GGE bi plot approximates the genotype main effects (mean performance), PC2 must approximate the GE effects associated with each genotype, which is a measure of instability (Yan *et al.*, 2000; 2001). The line passing through the bi plot origin and the average environment indicated by a circle is called the average environment, coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all the environments (Yan and Kang, 2003). The axis of the AEC abscissa, or "average environment axis," is the single-arrowed line that passes through the bi plot origin and at the center of the small circle. By using the average principal components in all the environments, the average environment coordinate (AEC) method was employed to evaluate the yield stability of genotypes.

A line drawn through the average environment and the bi plot origin, having one direction pointed to a greater genotype main effect. Moving in either direction away from AEC ordinate and from the bi plot origin indicates the greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from those with above average means. Hence, in this study genotypes ScStatus (G18), ScSpike (G10), ScSignal (G12),

S1079/6/7 (G11), Pawe-3 (G30), TGX2001-8DM (G5), S1150/5/22 (G16), Pawe-2 (G29), Pawe-1 (G28), TGX2014-16FM (G7), ScSaga (G9), TGX2001-6FM (G2), TGX2002-3DM (G6), S1140/5/4 (G15) and ScSaxon (G13) had yield performances greater than the mean yield. While genotype on the right side of the ordinate line produced yield less than the average mean yield, accordingly, Gazelle (G22), TGX2014-23FM (G4), Nyala (G23), SNK500 (G19), Favour (G1), TGX2014-5GM (G3), ScSentinel (G25), Afgat (G27), ScSerenade (G24), SCS-1 (G20) and Kafue (G26) had yield performance lower than the mean.

Fentaw *et al*., (2015) reported that a genotype which has shorter absolute length of projection in either of the two directions of AEC ordinate (located closer to AEC abscissa), represents a smaller tendency of GEI, which means it is the most stable genotype across different environments or vice versa. Therefore, TGX2001-8DM (G5), S1150/5/22 (G16), Pawe-1 (G28), ScSaxon (G13), S1140/5/4 (G15), TGX2014-23FM (G4) and Gazelle (G22) were identified as the more stable genotypes across the test locations. On the other hand, genotypes having a position in either direction away from AEC ordinate and from the bi plot origin indicates the greater GEI effect and reduced stability (Yan, 2002). Then, Favour (G1), Panorama29-1 (G8), Pawe-2 (G29), ScSpike (G10), and S1079/6/7 (G11) were identified as the least stable than other genotypes. Atnaf *et al.,* (2013) found three ideal soybean genotypes as it exhibits both high mean yield and high stability performances across the test environments in Ethiopia. (Figure 4).

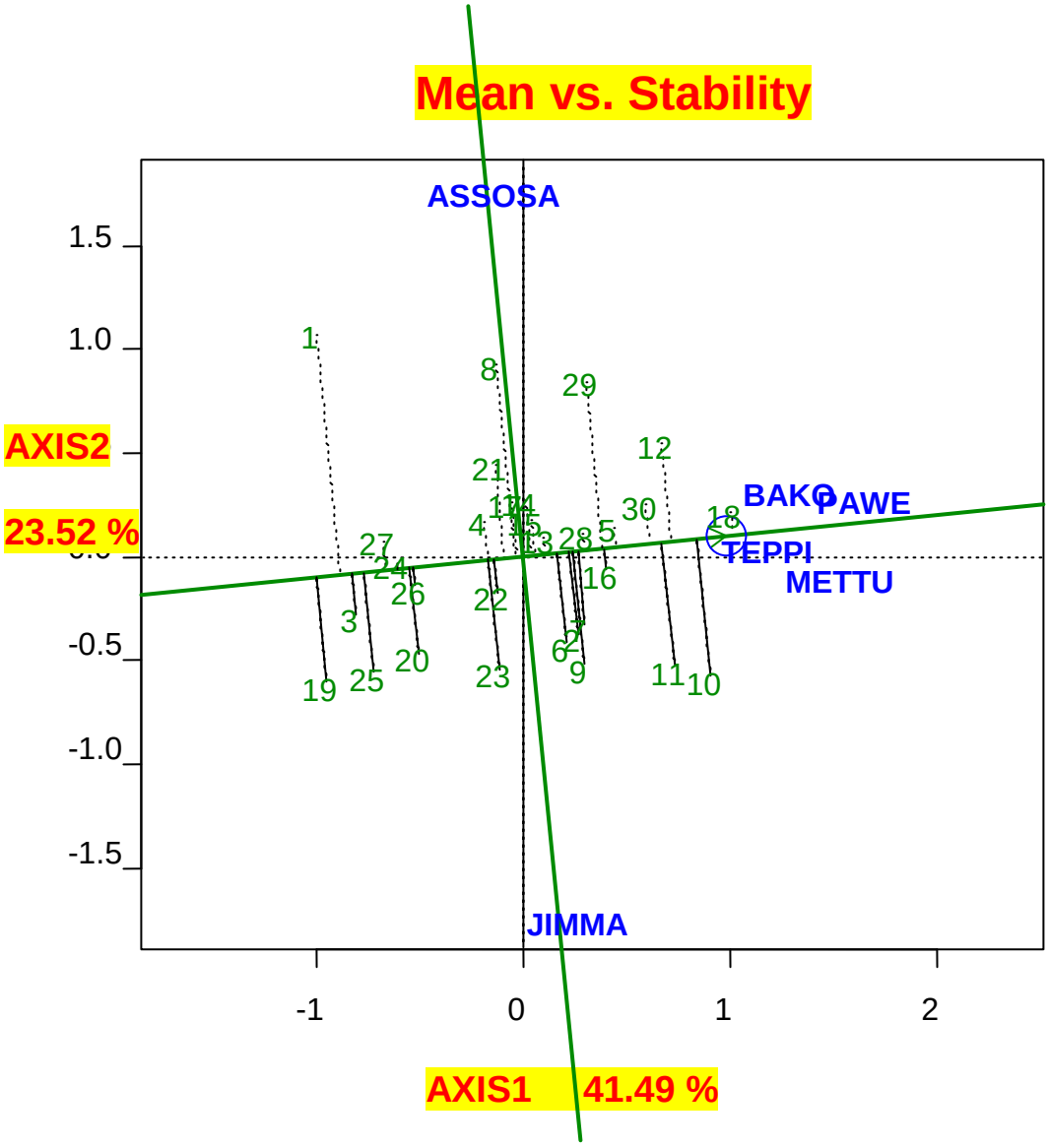

Figure VIII. GGE-bi plot showing the best soybean genotypes based on mean grain yield performance and stability across locations.

4.4.8.3. Ranking of Genotypes

Stability can be identified using concentric circles and also ideal genotypes are at the center of the concentric circle i.e., high mean and stable genotype. The ideal genotype is the one that with the highest mean performance and absolutely stable (Yan and Kang, 2003). The genotypes that are closer to the ideal genotypes are the best performing genotypes. Hence, the GGE bi plots shows that ScStatus (G18) is an ideal genotype, with other genotypes, like

Pawe-3 (G30), TGX2001-8DM (G5), ScSignal (G12), S1150/5/22 (G16), S1079/6/7 (G11) and ScSpike (G10) are desirable genotypes as they are closer to the ideal genotype on the bi plot. The genotypes SNK500 (G19) and Favour (G1) are the most undesirable genotypes as they are too far to the ideal genotype on the bi plot. Similar result was reported by (Mitrovic *et al.*,(2012); Farshadfar *et al.*, (2012); Yirga (2016); Afework (2017) (Figure 5).

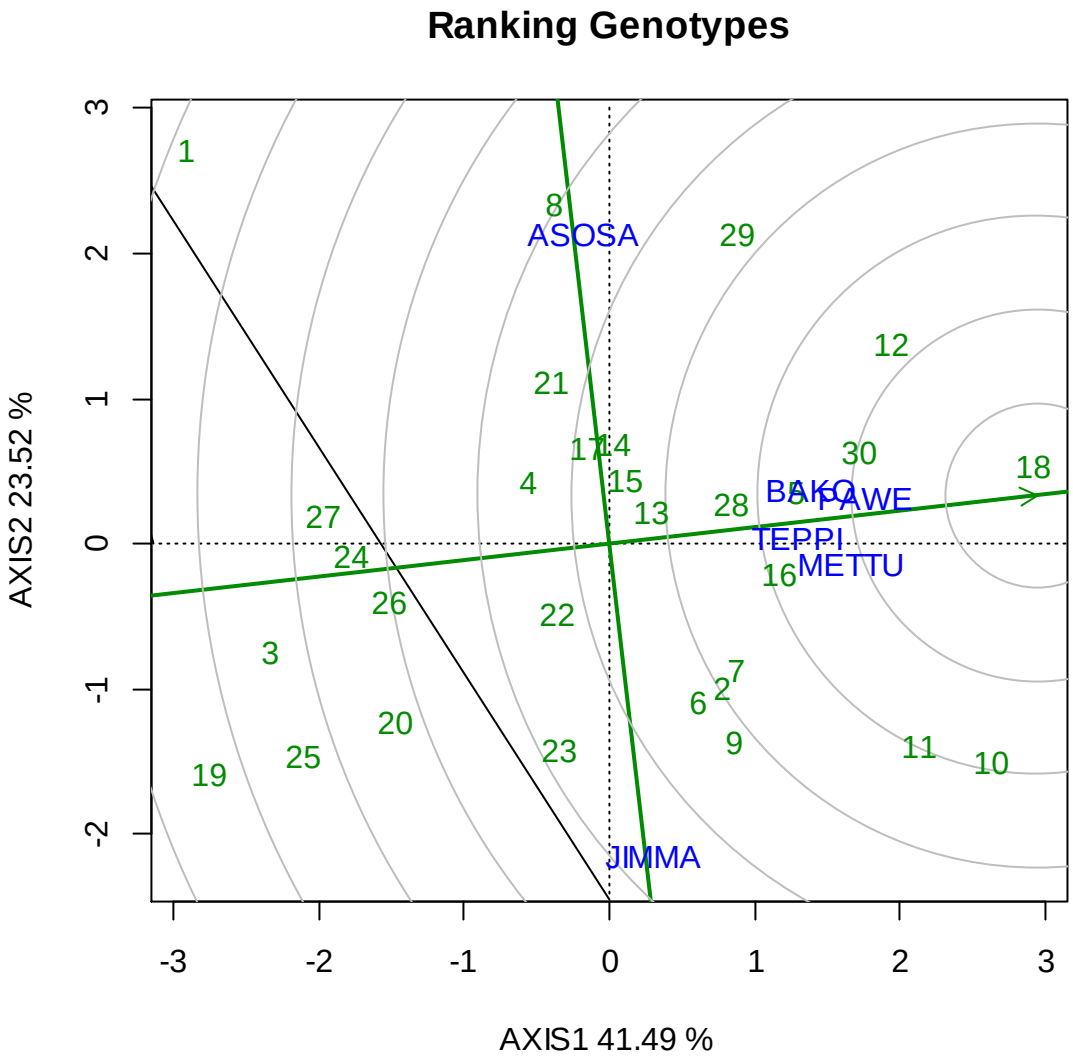

Figure IX. Ranking of the genotypes based on the ideal genotype

4.4.8.4. Ranking of Locations

The ideal test location the most representative of the locations (ability to represent the mega-environment) and the most powerful to discriminate genotypes (ability to delineate the tested genotypes). Naroui *et al.,* (2013) reported that the ideal environment is the one located at the center of the concentric circles, and it is possible to identify desirable environments based on their closeness to the ideal environment. Mahdieh *et al.,* (2016) reported that a testing location has less power to discriminate genotypes when located far away from the center of the concentric circle or to an ideal location.

Therefore, Among the test locations, location Pawe which fell into the center of concentric circles was an ideal test location in terms of being the most representative of the overall locations and the most powerful to discriminate the performance of the tested genotypes Next to the first concentric circle location, locations Mettu, Bako and Teppi were close to the ideal location with relative to the rest tested locations in terms of being the most representative of the locations and powerful to discriminate genotypes. While, Jimma and Assosa were detected as the weakest locations to discriminate genotypes (able to prove biased information about the performance of the tested genotypes) due to the great distance from the ideal location (center of concentric circles) (Figure 6). This result in line with Yirga (2016) and Habte *et al*., (2019).

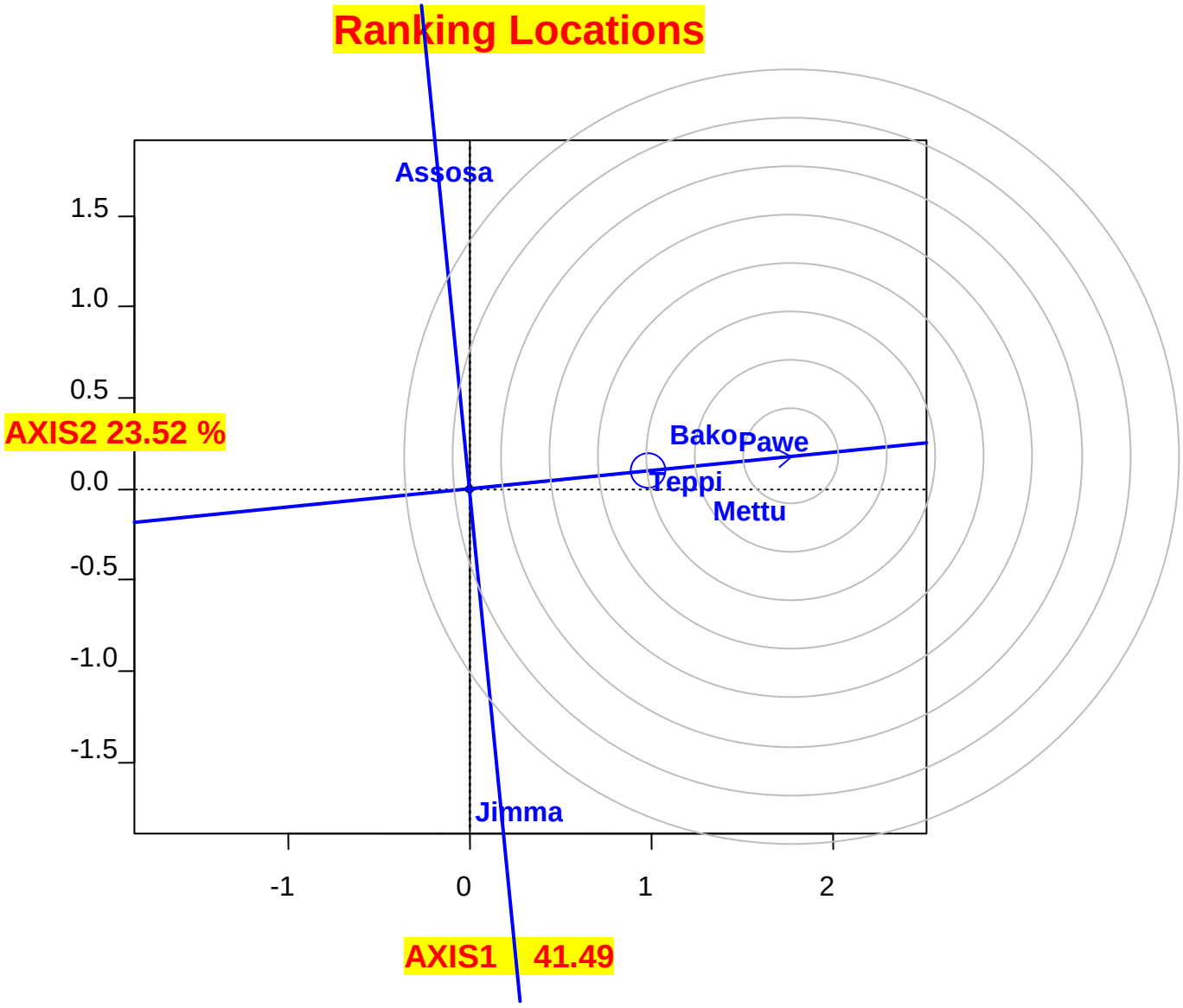

Figure X. Ranking of the locations based on the ideal locations

5. SUMMARY AND CONCLUSION

Soybean (*Glycine max* L.) is often called the miracle crop due to the high quality protein and edible oil it provides for both human food and animal feed. Additionally, it can increase soil fertility through its capacity to fix atmospheric nitrogen. Soybean belongs to the family *leguminosae*, subfamily *papilionideae,* and the genus *Glycine*. Crop performance is a function of genotype, location, and genotype x location interaction. Understanding of the crop management and growing locations are the major attributes to increase crop production and productivity.

The experiment was carried out to evaluate GEI for grain yield of different soybean genotypes and to identify stable and/or high yielding genotypes and assess their performance across locations. Thirty soybean genotypes were tested at six locations in Western Ethiopia during the 2020 main cropping season. The experiment was laid out in alpha lattice designs with three replications across all the locations.

Analysis of variance showed significant to highly significant difference for yield and other parameters at Jimma, Mettu, Bako, Pawe, Teppi, and Assosa in 2020 cropping season. Similarly, the combined ANOVA for soybean grain yield and yield related traits showed highly significant differences among the genotypes, locations and genotype x location interaction. Variation explained was 11.33 % for genotype, 41.81 % for location, and 25.24 % for genotype by location interaction.

The total sum of squares was partitioned into components to estimate the magnitude of GEI for all traits. In this regard, the genotype showed small in variation among them, whereas location and genotype x location interaction explained most of the variations. Genotype by location interaction was more important in the determination of agronomic traits; and its contribution was always higher than the contribution of the genotypes, whereas location and genotype by location interaction are both important in governing the expression of yield. Hence, the breeding environments may be classified into mega-environments and specifically adapted genotypes can be developed for each sub environment separately.

Across location, number of pods per plant was ranged from 31.54 to 59.63 with an overall mean of 40.88 and genotype TGX2014-5GM was the minimum number of pods per plant, while Favour is the maximum number of pods per plant among the tested genotypes, number of seeds per plant was ranged from 49.75 to 93.57 with an overall mean of 63.46 and genotype Nyala was the minimum number of seeds per plant, while Pawe-3 is the maximum number of seeds per plant among the tested genotypes and hundred seed weight was ranged from11.26 to 17.82 with an overall mean of 15.19 g and genotype Pawe-3 was the lowest hundred seed weight, while ScSerenade is the highest hundred seed weight among the tested genotypes.

The grain yield of the thirty soybean genotypes at different locations was ranged from 0.39 to1.97, 0.47 to 2.30, 1.04 to 2.94,1.35 to 4.05, 1.15 to 3.42, and 0.90 to2.15 t/ha at Jimma , at Mettu, at Teppi, at Bako, at Pawe, and at Assosa respectively. Most of the genotypes at Bako exhibited the best performance with average grain yield of 2.71 t/ha, while at Mettu exhibited the lowest average yield of 1.31 t/ha. The mean grain yield value of the thirty soybean genotypes across the six locations was ranged from 1.22 to 2.43 t/ha with an overall yield mean of 1.83 t/ha and coefficient of variation (CV %) of 20.18 %.The highest mean performance was observed from the genotype ScStatus (2.43 t/ha), while the lowest yield mean performance was observed from the genotype Favour (1.22 t/ha). Soybean genotypes ScStatus (2.43 t/ha) and S1079/6/7 (2.23 t/ha) were best in yield than the other genotypes and the checks varieties.

However, there was a rank change in grain yield performance of genotypes across locations because of significant genotype x location interactions. Radiation, water, and nutrients availability are among the environmental factors (non-genetic factors) strongly influence crop growth and yield.Using different stability analysis approach the following more stable genotypes were identified. Genotypes TGX2014-16FM and TGX2002-3DM were more stable by Wricke's Ecovalence Analysis, and Shukla's Stability Variance. Genotypes S1150/5/22 and TGX2001-8DM were more stable by Eberhart and Russell analysis. Genotypes ScStatus and S1079/6/7 were more stable by Cultivar Superiority Measure. Genotypes S1150/5/22 and ScStatus were more stable by Yield Stability Index. Genotypes S1150/5/22 and TGX2014-16FM were more stable by AMMI Stability Value. Genotypes ScStatus and Pawe-3 were

selected as better genotypes that appeared in the four locations by AMMI analysis. According to one year data, the six locations are grouped into three mega environments for soybean production with different winning genotypes and genotype ScStatus was an ideal genotype, while location Pawe was an ideal environment by GGE analysis.

Based on the results of this study the following recommendations were made;

Plant growth and development is the product of the interaction between the genotype and the location in which the plant grown. The genotype x location interaction study is especially important in countries with various agro-ecologies like Ethiopia. Despite its potential and market demand, production of soybean is not yet popularized among farmers in western Ethiopia. These could be attributed to the lack of information on the effect of genotype, predictable and unpredictable environmental variations and their interaction on yield. The environment contributed most to the variability in grain yield.

Knowledge of GEI is in valuable to soybean breeders in selecting in desirable genotype and enabling breeders to design a proper genotype testing strategy. Multiple year and multiple location testing is a key approach for identifying and selecting high yielding and stable soybean genotypes adapted to diverse or specific agro-environment conditions in Ethiopia.

Therefore, based on one year data, soybean genotypes ScStatus (G18) and S1079/6/7 (G11) are the two of the best performing genotypes than the other genotypes and control varieties (Pawe-2 (G29) and Pawe-3 (G30) in grain yield across locations and those the two highest yielder genotypes have a potential to be registered in Ethiopia. However, this trail need to be repeated for one more season, and or two of the best performing genotypes will be verified along with the checks on farmers' fields for release.

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APPENDICE

Appendix Table 1. ANOVA of grain yield and yield related traits of soybean genotypes at individual locations (The Lattice Procedure)

Source of Variation	DF	Grain yield					
		Locations					
		Jimma	Mettu	Teppi	Bako	Pawe	Asosa
Replications	2	0.17	0.62	2.49	0.01	0.85	0.04
Blocks(R)	15	0.15	0.05	0.36	0.13	0.21	0.51
Treatments	29	0.35**	0.51**	0.37**	0.47**	1.03**	0.28*
Error	43	0.06	0.07	0.14	0.14	0.13	0.18
Total	89	0.16	0.22	0.3	0.25	0.46	0.27
Mean		1.54	1.31	1.75	2.71	2.22	1.45
CV (%)		11.94	21.44	25.88	4.29	16.66	29.45
LSD (5%)		0.30	0.46	0.75	0.19	0.61	0.70
R-Square		0.89	0.83	0.78	0.70	0.85	0.67
Efficiency Relative to RCBD		162.81	90.88	120.64	96.7	104.43	123.01

Source of Variation	DF	Hundred Seed Weight					
		Locations					
		Jimma	Mettu	Teppi	Bako	Pawe	Asosa
Replications	2	0.699	9.387	0.52	8.54	36.25	8.54
Blocks(R)	15	11.87	1.76	2.49	5.19	1.57	4.08
Treatments	29	25.16**	10.06**	4.95**	24.49**	14.20**	4.56*
Error	43	2.69	2.13	2.17	2.28	1.34	1.85
Total	89	13.56	4.81	3.09	10.15	6.35	3.26
Mean		15.90	12.79	13.59	17.67	12.7	17.65
CV (%)		16.96	11.40	10.77	8.66	9.14	7.63
LSD (5%)		4.57	2.39	2.40	2.67	1.89	2.39
R-Square		0.74	0.78	0.66	0.88	0.89	0.73
Efficiency Relative to RCBD		106.70	95.45	100.47	115.55	100.60	114.47

		Number of Seeds per Plant					
		Locations					
		Jimma	Mettu	Teppi	Bako	Pawe	Asosa
Replications	2	40.85	67.42	621.81	2951.03	225.51	193.59 ns
Blocks(R)	15	91.04	50.82	574.47	943.89	568.48	194.87 ns
Treatments	29	424.78**	43.80*	438.88**	867.27**	1479.05**	368.13**
Error	43	80.12	20.20	122.68	378.38	310.92	119.17
Total	89	193.39	34.13	313.07	690.80	733.03	214.72
Mean		48.52	35.29	70.94	110.93	94.29	58.59
CV (%)		18.73	12.87	15.87	17.00	18.87	18.60
LSD (5%)		14.63	7.97	20.08	34.50	30.73	18.88
R-Square		0.79	0.70	0.80	0.75	0.79	0.73
Efficiency Relative to RCBD		100.39	119.84	160.93	119.49	108.40	105.59

APPENDIX Table 1. (Continued)

Source of Variation	DF	Number of Pods per Plant					
		Locations					
		Jimma	**Mettu**	**Teppi**	**Bako**	**Pawe**	**Asosa**
Replications	2	6.28ns	527.45ns	214.57ns	192.90ns	9.70ns	115.66ns
Blocks(R)	15	19.88ns	193.19ns	97.30ns	91.70ns	66.50ns	61.34ns
Treatments	29	361.27**	331.67*	71.99**	79.00*	263.41**	38.61*
Error	43	31.38	85.80	25.67	51.12	44.78	24.73
Total	89	136.37	193.96	44.20	70.23	118.90	37.47
Mean		31.16	66.28	33.45	42.16	46.86	25.26
CV (%)		18.01	13.96	15.09	16.36	14.30	20.18
LSD (5%)		9.15	16.35	9.13	12.44	10.90	8.80
R-Square		0.88	0.78	0.78	0.669	0.81	0.66
Efficiency Relativeto RCBD		90.51	115.24	143.63	107.86	103.64	119.22
		Plant Height					
		Locations					
		Jimma	**Mettu**	**Teppi**	**Bako**	**Pawe**	**Asosa**
Replications	2	77.99	18.12	55.38	150.34	117.79	47.4ns
Blocks(R)	15	66.77	61.48	156.07	62.97	36.25	61.68ns
Treatments	29	585.15**	634.68**	298.79**	495.40**	417.37**	125.20*
Error	43	45.15	67.76	62.54	39.97	42.96	51.93
Total	89	225.49	250.31	155.13	194.73	165.51	77.35
Mean		78.02	77.94	55.65	57.75	67.63	49.17
CV (%)		8.76	10.60	14.27	11.07	9.74	14.87
LSD (5%)		10.98	13.45	14.02	10.33	10.71	11.77
R-Square		0.89	0.87	0.80	0.89	0.87	0.66
Efficiency Relative to RCBD		103.56	97.60	119.50	104.78	95.96	100.71
Source of Variation	**DF**	**Days to Maturity**					
		Locations					
		Jimma	**Mettu**	**Teppi**	**Bako**	**Pawe**	**Asosa**
Replications	2	22.30	30.48	41.14	24.70	42.48	120.68ns
Blocks(R)	15	21.08	18.90	67.86	18.11	57.35	80.44ns
Treatments	29	334.11**	345.58**	123.94**	134.18**	99.74*	221.20**
Error	43	14.74	15.29	31.73	14.66	45.69	43.10
Total	89	120.04	123.87	68.07	54.17	65.19	109.17
Mean		138.67	133.77	142.98	129.33	99.92	126.55
CV (%)		2.81	2.95	4.00	2.96	6.79	5.23
LSD (5%)		6.27	6.39	9.90	6.15	11.04	11.46
R-Square		0.93	0.90	0.76	0.87	0.65	0.80
Efficiency Relativeto RCBD		102.98	101.07	113.36	101.42	101.22	108.98

*=significant (p<0.05),**=highly significant (p<0.01),***= very highly significant (p<0.001) probability level, ns = not significant, CV= Coefficient of Variation

Appendix Table 2. Rank and Mean grain yield of thirty tested soybean genotypes at different locations.

Genotypes Name	Code	Locations												Across	
		Jimma	R	Mettu	R	Teppi	R	Bako	R	Pawe	R	Asosa	R	Mean	R
Favour	1	0.39 ^{j}	26	1.02 ^{fi}	21	1.26 ^{fi}	23	1.71 ^{p}	29	1.15 ^{n}	29	1.80 ^{af}	5	1.226 ^{0}	30
TGX2001-6FM	2	1.71 ^{ad}	11	1.50 ^{be}	10	2.03 ^{be}	6	3.28 ^{ef}	7	2.00 ^{hl}	21	1.15 ^{eh}	19	1.948 ^{ci}	11
TGX2014-5GM	3	1.52 ^{cg}	14	0.93 ^{gj}	22	1.19 ^{hi}	25	1.81 ^{op}	27	1.42 ^{ln}	26	1.25 ^{bh}	15	1.357 ^{no}	28
TGX2014-23FM	4	1.32 ^{gh}	20	0.81 ^{hj}	24	1.88 ^{ch}	12	2.71 ^{jl}	17	2.25 ^{gk}	14	1.43 ^{bh}	12	1.736 ^{jl}	21
TGX2001-8DM	5	1.43 ^{dg}	16	1.25 ^{dh}	18	2.13 ^{bc}	3	2.86 ^{ij}	13	3.17 ^{ac}	3	1.42 ^{bh}	13	2.047 ^{bg}	7
TGX2002-3DM	6	1.76 ^{ac}	7	1.46 ^{cf}	11	1.92 ^{cg}	10	2.61 ^{km}	18	2.43 ^{di}	10	1.17 ^{eh}	18	1.894 ^{eg}	14
TGX2014-16FM	7	1.69 ^{ad}	12	1.59 ^{be}	9	2.08 ^{bd}	4	2.80 ^{ik}	14	2.28 ^{gj}	13	1.21 ^{eh}	17	1.945 ^{di}	12
Panorama29-1	8	1.23 ^{gh}	23	1.02 ^{fi}	21	1.53 ^{ch}	17	3.54 ^{cd}	5	2.11 ^{gk}	18	2.15 ^{a}	1	1.934 ^{dj}	13
ScSaga	9	1.94 ^{ab}	2	1.38 ^{cg}	13	1.99 ^{cf}	7	3.09 ^{fh}	9	2.36 ^{ej}	11	1.17 ^{eh}	18	1.991 ^{ch}	9
ScSpike	10	1.74 ^{ac}	9	2.32 ^{a}	1	1.57 ^{ci}	15	2.95 ^{hi}	11	3.42 ^{a}	1	0.90 ^{h}	22	2.154 ^{bd}	4
S1079/6/7	11	1.97 ^{a}	1	1.62 ^{be}	7	2.04 ^{be}	5	4.05 ^{a}	1	2.64 ^{cg}	7	1.09 ^{gh}	21	2.238 ^{ab}	2
ScSignal	12	0.94 ^{i}	25	1.89 ^{ab}	2	1.66 ^{ci}	14	3.74 ^{b}	2	3.02 ^{ad}	4	1.41 ^{bh}	14	2.112 ^{be}	5
ScSaxon	13	1.37 ^{fh}	19	1.71 ^{bd}	5	1.23 ^{hg}	24	2.77 ^{ik}	15	2.49 ^{dh}	9	1.41 ^{bh}	14	1.832 ^{fk}	18
S1180/5/54	14	1.31 ^{gh}	21	1.60 ^{ce}	8	1.98 ^{cf}	8	1.89 ^{op}	25	2.29 ^{ej}	12	1.63 ^{ag}	8	1.786 ^{jk}	20
S1140/5/4	15	1.39 ^{eg}	17	1.27 ^{eg}	16	1.67 ^{ci}	13	3.43 ^{de}	6	2.05 ^{gk}	20	1.48 ^{ah}	11	1.884 ^{ej}	16
S1150/5/22	16	1.72 ^{ad}	10	1.74 ^{bc}	3	2.08 ^{bd}	4	3.21 ^{fg}	8	2.16 ^{gk}	17	1.50 ^{ah}	10	2.072 ^{bf}	6
ScSafari	17	1.72 ^{ad}	10	1.22 ^{eh}	19	2.04 ^{be}	5	1.99 ^{no}	24	2.43 ^{ei}	10	1.94 ^{ab}	2	1.893 ^{ej}	15
ScStatus	18	1.69 ^{ae}	12	1.64 ^{ce}	6	2.74 ^{ab}	2	3.55 ^{cd}	4	3.28 ^{ab}	2	1.67 ^{ag}	7	2.430 ^{a}	1
SNK500	19	1.87 ^{ab}	4	0.59 ^{ij}	26	1.49 ^{ci}	18	1.35 ^{q}	30	1.36 ^{mn}	28	1.22 ^{ch}	16	1.318 ^{no}	29
SCS-1	20	1.78 ^{ac}	6	1.19 ^{eh}	20	1.44 ^{ci}	20	1.83 ^{op}	26	1.64 ^{jn}	25	1.26 ^{bh}	14	1.527 ^{ln}	24
Clark-63k	21	1.51 ^{cg}	15	1.34 ^{cg}	15	1.29 ^{ei}	22	3.07 ^{gh}	10	2.08 ^{fk}	19	1.92 ^{ac}	3	1.873 ^{ek}	17
Gazelle	22	1.84 ^{ab}	5	1.26 ^{eh}	17	1.56 ^{ci}	16	2.44 ^{m}	21	2.22 ^{fk}	16	1.54 ^{ah}	9	1.812 ^{gk}	19
Nyala	23	1.75 ^{ac}	8	1.46 ^{ce}	11	1.90 ^{ch}	11	2.13 ^{n}	23	1.79 ^{m}	24	1.11 ^{fh}	20	1.692 ^{jm}	22
ScSerenade	24	1.84 ^{ab}	5	0.85 ^{hj}	23	1.46 ^{ci}	19	2.52 ^{lm}	19	1.38 ^{mn}	27	1.76 ^{ag}	6	1.640 ^{km}	23
ScSentinel	25	1.92 ^{ab}	3	0.85 ^{hj}	23	1.04 ^{i}	27	2.48 ^{m}	20	1.36 ^{mn}	28	1.25 ^{bh}	15	1.486 ^{mn}	27
Kafue	26	1.38 ^{fh}	18	0.71 ^{ji}	25	1.97 ^{cf}	9	1.73 ^{p}	28	1.92 ^{hm}	22	1.22 ^{dh}	16	1.488 ^{mn}	26
Afgat	27	1.39 ^{fg}	17	0.47j	27	1.17 ^{hi}	26	2.76 ^{ik}	16	1.87 ^{im}	23	1.41 ^{bh}	13	1.515 ^{ln}	25
Pawe-1	28	1.28 ^{gh}	22	1.44 ^{ce}	12	1.38 ^{di}	21	3.65 ^{bc}	3	2.68 ^{cf}	6	1.25 ^{bh}	15	1.950 ^{ci}	10
Pawe-2(check)	29	1.08 ^{hi}	24	1.35 ^{cg}	14	2.03 ^{ce}	6	2.92 ^{hi}	12	2.90 ^{ce}	5	1.92 ^{ad}	3	2.037 ^{bg}	8
Pawe -3 (check)	30	1.66 ^{ce}	13	1.73 ^{bc}	4	2.94 ^{a}	1	2.43 ^{m}	22	2.51 ^{dh}	8	1.84 ^{ae}	4	2.191 ^{ac}	3
Mean		1.54		1.31		1.75		2.71		2.22		1.450		1.83	
CV(%)		11.94		21.44		25.88		4.29		16.66		29.45		20.18	
LSD(5%)		0.30		0.46		0.75		0.19		0.61		0.7		0.24	
Ftest		**		**		**		**		**		*		**	

R= Rank . Means followed by a common letter with in a column are not significantly different from each other at $P \leq 0.05$, LSD (5%)= Least Significant Difference, CV =Coefficient of Variation *=significant ($p<0.05$),**=highly significant ($p<0.01$),***= very highly significant ($p<0.001$) probability level, CV(%)= Coefficient of Variation.

Appendix Table 3. Mean of yield related traits for soybean genotypes at different locations

Genotypes Name	Code	Hundered seed weight							
		Locations						Across	
		Jimma	Mettu	Teppi	Bako	Pawe	Assosa	Mean	Rank
Favour	1	13.00	11.63	13.00	11.66	8.83	18.66	12.85	29
TGX2001-6FM	2	14.82	12.03	17.00	22.00	11.00	12.33	13.58	20
TGX2014-5GM	3	17.70	15.10	15.33	15.33	14.50	19.33	17.32	8
TGX2014-23FM	4	18.13	12.20	17.66	19.33	13.16	21.00	16.91	3
TGX2001-8DM	5	13.79	13.13	14.66	18.00	15.00	19.66	15.71	12
TGX2002-3DM	6	14.51	13.56	13.66	15.66	13.16	18.66	14.87	19
TGX2014-16FM	7	19.68	13.46	13.33	18.00	12.66	21.00	16.35	6
Panorama29-1	8	12.44	10.40	13.00	16.33	9.83	19.00	13.50	27
ScSaga	9	18.73	14.50	14.00	20.00	14.50	14.66	16.06	10
ScSpike	10	18.94	16.83	13.00	18.66	14.83	16.33	16.49	5
S1079/6/7	11	16.07	15.03	14.66	19.66	12.00	16.33	15.62	13
ScSignal	12	12.33	12.96	13.33	17.66	11.50	13.66	13.57	26
ScSaxon	13	14.74	12.13	15.33	17.66	12.83	17.66	15.06	16
S1180/5/54	14	11.05	12.20	14.33	16.66	14.33	19.66	14.70	22
S1140/5/4	15	15.88	13.50	14.00	19.00	11.50	17.66	15.25	15
S1150/5/22	16	13.83	12.20	17.60	19.33	17.33	15.00	15.89	11
ScSafari	17	14.82	11.26	13.66	13.66	11.66	20.66	14.29	24
ScStatus	18	14.95	10.93	12.66	15.00	13.00	18.33	14.14	25
SNK500	19	15.93	10.46	14.00	18.66	12.00	18.33	14.90	18
SCS-1	20	16.41	11.73	13.66	17.66	11.00	18.33	14.80	21
Clark-63k	21	16.96	15.36	15.66	19.66	12.83	21.00	16.91	4
Gazelle	22	18.33	13.43	14.66	18.00	12.66	19.33	16.07	9
Nyala	23	21.79	12.90	13.66	23.00	16.00	17.33	17.44	2
ScSerenade	24	23.03	14.90	15.66	21.33	15.33	16.66	17.82	1
ScSentinel	25	18.91	14.83	16.66	19.00	13.00	15.33	16.29	7
Kafue	26	12.79	11.46	14.33	14.33	9.66	15.66	13.04	28
Afgat	27	16.33	11.70	11.66	16.00	12.50	19.33	14.58	23
Pawe-1	28	14.61	13.33	13.33	20.00	13.50	15.33	15.01	17
Pawe-2(check)	29	15.24	12.70	14.00	19.00	14.50	17.00	15.40	14
Pawe -3 (check)	30	11.70	7.73	13.66	10.00	7.50	17.00	11.26	30
Mean		15.90	12.79	13.59	17.67	12.7	17.65	15.19	
CV (%)		16.96	11.40	10.77	8.66	9.14	7.63	14.60	

APPENDIX Table 3. (continued)

Genotypes Name	Code	Number of Seeds per Plant							
		Locations						Across	
		Jimma	Mettu	Teppi	Bako	Pawe	Assosa	Mean	Rank
Favour	1	70.00	36.33	103.70	83.33	101.67	73.83	78.14	3
TGX2001-6FM	2	53.93	36.33	85.63	88.00	101.00	64.26	71.52	5
TGX2014-5GM	3	35.20	27.36	59.83	55.33	80.93	45.93	50.76	28
TGX2014-23FM	4	40.93	29.00	69.20	79.33	93.27	63.81	62.59	13
TGX2001-8DM	5	39.93	40.20	47.13	90.33	140.87	50.73	68.19	6
TGX2002-3DM	6	69.00	44.20	64.07	70.33	79.60	43.88	61.84	19
TGX2014-16FM	7	45.73	30.96	75.30	85.00	76.00	70.85	63.97	10
Panorama29-1	8	46.66	48.16	71.60	84.66	86.27	71.38	68.12	8
ScSaga	9	49.66	27.13	56.83	62.33	87.60	55.07	56.43	26
ScSpike	10	46.80	39.13	65.57	74.00	85.13	53.66	60.71	20
S1079/6/7	11	50.33	32.46	57.83	60.00	102.40	51.97	59.16	23
ScSignal	12	37.46	49.43	99.33	103.00	142.40	68.93	83.42	2
ScSaxon	13	40.46	33.86	63.80	66.00	105.47	56.59	61.03	18
S1180/5/54	14	51.46	35.86	59.83	77.00	108.87	59.05	65.34	15
S1140/5/4	15	43.86	37.43	67.83	72.33	90.20	52.61	60.71	16
S1150/5/22	16	52.60	37.80	58.47	63.33	57.33	49.94	53.24	27
ScSafari	17	52.06	30.70	65.50	62.33	97.93	60.27	61.46	14
ScStatus	18	54.00	35.83	62.20	74.00	78.40	48.57	58.83	17
SNK500	19	63.73	26.76	71.20	57.00	83.47	57.16	59.88	22
SCS-1	20	43.40	33.73	60.27	56.66	88.60	55.96	56.43	25
Clark-63k	21	33.33	29.26	46.20	85.00	77.33	45.46	52.76	21
Gazelle	22	42.00	24.23	58.83	46.00	82.00	51.41	50.74	29
Nyala	23	45.46	34.31	49.73	58.00	61.33	49.67	49.75	30
ScSerenade	24	43.46	25.53	59.33	59.00	141.20	49.97	63.08	12
ScSentinel	25	52.20	31.43	148.13	82.00	84.07	96.46	82.38	4
Kafue	26	47.33	26.86	72.73	74.33	98.47	58.56	63.04	9
Afgat	27	48.86	34.13	81.00	88.00	86.87	62.58	66.90	7
Pawe-1	28	38.26	39.93	86.60	72.00	91.27	63.13	65.19	11
Pawe-2(check)	29	29.60	46.43	50.00	81.33	76.07	44.79	54.70	24
Pawe -3 (check)	30	87.86	57.63	107.5	84.66	142.73	81.08	93.57	1
Mean		48.51	35.41	70.83	73.15	94.29	58.58	63.46	
CV (%)		18.73	12.87	15.87	17.00	18.87	18.60	27.57	

APPENDIX Table 3. (continued)

Genotypes Name	Code	Number of Pods per Plant							
		Locations						Across	
		Jimma	Mettu	Teppi	Bako	Pawe	Asosa	Mean	Rank
Favour	1	80.00	81.00	45.66	65.00	50.13	36.00	59.63	1
TGX2001-6FM	2	30.86	68.77	43.66	51.66	58.20	31.53	47.44	5
TGX2014-5GM	3	22.40	46.47	27.36	36.00	33.40	23.66	31.54	30
TGX2014-23FM	4	24.40	60.20	34.46	47.66	48.13	28.40	40.54	11
TGX2001-8DM	5	28.00	67.87	20.80	52.00	70.13	26.06	44.14	7
TGX2002-3DM	6	44.93	88.33	33.03	40.66	40.46	16.93	44.05	8
TGX2014-16FM	7	26.66	59.73	35.56	46.33	42.66	27.80	39.79	12
Panorama29-1	8	30.60	101.33	36.76	40.33	49.73	31.93	48.44	4
ScSaga	9	32.00	49.27	26.10	42.00	48.40	17.40	35.86	25
ScSpike	10	29.93	73.33	28.36	36.33	35.66	19.26	37.14	24
S1079/6/7	11	31.93	66.73	27.56	33.33	47.86	16.33	37.29	23
ScSignal	12	24.33	94.13	48.93	52.00	65.53	28.80	52.28	3
ScSaxon	13	29.66	69.20	28.40	37.33	48.13	23.40	39.35	16
S1180/5/54	14	36.40	63.90	27.90	39.33	49.80	15.66	38.83	17
S1140/5/4	15	27.26	65.81	31.90	40.33	41.06	30.66	39.50	13
S1150/5/22	16	32.93	64.47	28.83	34.00	34.86	30.26	37.55	22
ScSafari	17	32.93	56.53	29.80	34.66	47.00	30.06	38.49	19
ScStatus	18	30.80	75.23	27.80	37.33	45.60	20.06	39.47	15
SNK500	19	35.40	37.20	34.23	29.00	41.53	23.13	33.41	27
SCS-1	20	29.73	63.20	29.66	34.66	46.40	26.73	38.39	20
Clark-63k	21	21.93	45.13	22.53	52.66	39.66	21.13	33.84	26
Gazelle	22	28.20	43.20	29.83	34.00	41.26	22.60	33.18	28
Nyala	23	27.20	57.73	22.76	34.33	33.26	17.86	32.19	29
ScSerenade	24	29.00	52.20	29.23	34.66	64.73	27.13	39.49	14
ScSentinel	25	29.73	61.73	64.10	51.00	47.53	22.46	46.09	6
Kafue	26	26.66	37.80	33.93	50.33	47.46	31.06	37.87	21
Afgat	27	24.26	57.73	31.66	51.66	47.53	18.33	38.52	18
Pawe-1	28	20.20	79.00	39.93	34.66	42.40	35.40	41.93	9
Pawe-2(check)	29	20.33	99.20	25.83	44.00	36.26	18.00	40.60	10
Pawe -3 (check)	30	46.06	109.03	57.46	47.66	64.73	32.66	59.60	2
Mean		31.15	66.51	33.46	42.16	46.98	25.02	40.88	
CV (%)		18.01	13.96	15.09	16.36	14.30	20.18	20.65	

APPENDIX Table 3. (continued)

Genotypes Name	Code	Plant Height							
		Locations						Across	
		Jimma	Mettu	Teppi	Bako	Pawi	Asosa	Mean	Rank
Favour	1	100.00	79.33	75.63	68.66	75.53	48.80	74.65	4
TGX2001-6FM	2	74.66	74.60	52.63	58.53	66.26	44.13	61.80	17
TGX2014-5GM	3	83.50	75.93	44.60	47.53	53.06	40.06	57.44	24
TGX2014-23FM	4	88.00	82.36	70.50	64.46	68.26	53.93	71.25	7
TGX2001-8DM	5	93.33	96.33	67.60	68.33	71.66	51.66	74.81	3
TGX2002-3DM	6	95.06	87.06	66.50	68.60	76.20	36.66	71.68	6
TGX2014-16FM	7	75.23	71.06	59.20	57.00	61.53	55.73	63.29	16
Panorama29-1	8	125.66	133.13	46.20	107.26	100.33	74.20	97.79	1
ScSaga	9	73.03	77.26	64.53	55.26	69.80	45.06	64.15	13
ScSpike	10	81.53	86.33	64.76	59.53	85.00	42.53	69.94	9
S1079/6/7	11	76.01	69.06	62.06	55.13	76.53	44.60	63.89	15
ScSignal	12	81.93	89.80	58.13	72.73	80.03	56.46	73.18	5
ScSaxon	13	83.36	81.03	58.70	54.46	70.40	57.93	67.64	10
S1180/5/54	14	73.06	76.73	48.96	40.53	59.33	35.60	55.70	28
S1140/5/4	15	85.93	103.33	67.60	72.60	81.20	62.66	78.88	2
S1150/5/22	16	67.93	69.60	47.73	49.06	49.06	60.93	57.38	25
ScSafari	17	69.04	71.53	51.23	49.20	64.40	50.86	59.37	18
ScStatus	18	71.34	68.60	62.50	50.00	55.33	46.00	58.96	20
SNK500	19	57.41	64.13	39.13	41.40	49.20	41.06	48.72	29
SCS-1	20	63.86	73.13	52.03	47.26	60.06	45.00	56.89	27
Clark-63k	21	60.76	74.73	48.16	57.60	64.46	45.13	58.47	21
Gazelle	22	67.44	71.13	49.63	48.60	64.60	44.80	57.70	23
Nyala	23	60.10	61.66	33.00	42.53	41.93	41.86	46.84	30
ScSerenade	24	65.60	67.20	59.43	52.73	59.60	49.53	59.01	19
ScSentinel	25	81.80	82.46	48.66	53.06	69.40	48.20	63.93	14
Kafue	26	70.90	57.33	53.70	52.66	71.33	41.40	57.88	22
Afgat	27	65.76	61.13	47.90	52.40	67.60	49.46	57.37	26
Pawe-1	28	77.80	77.46	55.60	63.40	68.33	51.06	65.60	11
Pawe-2(check)	29	85.03	71.90	46.10	63.60	71.66	53.53	65.30	12
Pawe -3 (check)	30	85.50	82.90	67.06	58.20	76.60	56.33	71.09	3
Mean		78.01	77.94	55.64	57.74	67.62	49.17	64.36	
CV (%)		8.76	10.60	14.27	11.07	9.74	14.87	12.48	

APPENDIX Table 3. (continued)

Genotypes Name	Code	Days of Maturity							
		Locations						Across	
		Jimma	Mettu	Teppi	Bako	Pawe	Asosa	Mean	Rank
Favour	1	178.00	174.33	147.66	156.33	121.66	138.33	152.72	1
TGX2001-6FM	2	135.00	130.00	143.66	126.33	97.66	119.66	125.39	19
TGX2014-5GM	3	128.66	123.66	137.66	127.33	91.66	121.33	121.72	26
TGX2014-23FM	4	144.33	139.33	140.33	133.33	92.33	123.00	128.78	15
TGX2001-8DM	5	147.33	142.33	137.00	130.00	102.00	122.33	130.17	11
TGX2002-3DM	6	143.66	140.00	147.33	128.66	96.33	119.66	129.27	13
TGX2014-16FM	7	129.66	124.66	138.66	126.66	100.66	123.00	123.88	22
Panorama29-1	8	152.00	147.00	142.66	135.00	97.66	164.33	139.78	2
ScSaga	9	135.66	130.66	149.00	127.66	99.66	119.66	127.05	17
ScSpike	10	143.00	138.00	147.00	132.00	105.66	136.33	133.67	6
S1079/6/7	11	135.33	130.33	135.33	134.00	101.66	119.66	126.05	18
ScSignal	12	144.00	139.00	153.00	128.66	105.00	123.00	132.11	7
ScSaxon	13	138.33	133.33	149.33	131.00	101.33	123.00	129.39	12
S1180/5/54	14	145.00	140.00	150.00	132.66	103.66	119.66	131.83	9
S1140/5/4	15	147.00	142.00	146.66	132.66	100.33	123.00	131.94	8
S1150/5/22	16	135.00	130.00	135.33	123.00	92.33	119.66	122.55	25
ScSafari	17	132.33	127.33	136.66	123.00	105.00	117.00	123.55	23
ScStatus	18	140.66	135.66	147.00	129.33	98.66	122.33	128.94	14
SNK500	19	122.00	117.00	139.00	120.00	100.33	121.33	119.94	29
SCS-1	20	132.33	126.66	135.33	125.66	104.66	120.33	124.16	20
Clark-63k	21	128.66	123.66	136.00	136.33	93.33	120.33	123.05	24
Gazelle	22	128.33	123.33	136.66	124.00	95.33	122.33	121.66	27
Nyala	23	128.66	123.66	131.00	124.33	94.33	123.00	120.83	28
ScSerenade	24	135.00	130.00	148.33	128.66	100.33	122.33	127.44	16
ScSentinel	25	142.00	137.00	152.00	130.00	100.66	123.00	130.78	10
Kafue	26	135.33	130.33	135.66	121.66	101.00	120.33	124.05	21
Afgat	27	123.66	119.33	144.33	119.66	92.66	116.00	119.27	30
Pawe-1	28	142.00	137.00	143.00	130.33	100.00	150.33	133.78	5
Pawe-2(check)	29	143.00	138.00	150.66	131.00	101.00	165.00	138.11	3
Pawe -3 (check)	30	144.00	139.00	153.33	130.66	100.66	137.00	134.11	4
Mean		138.67	133.77	142.98	129.33	99.92	126.55	128.50	
CV (%)		2.81	2.95	4.00	2.96	6.79	5.23	4.91	

APPENDIX Table 3. (continued)

Genotypes Name	Code	Days of Flowering							
		Locations						Across	
		Jimma Assosa	Mettu	Teppi	Bako	Pawe		Mean	Rank
Favour	1	86.66	81.66	92.33	84.00	45.66	60.33	75.10	1
TGX2001-6FM	2	72.66	67.66	81.33	67.00	38.66	57.00	64.05	14
TGX2014-5GM	3	68.66	63.66	78.66	63.66	11.66	54.00	56.71	28
TGX2014-23FM	4	72.33	67.33	79.33	66.00	32.33	54.00	61.88	19
TGX2001-8DM	5	80.33	75.33	80.66	68.00	39.00	59.00	67.05	5
TGX2002-3DM	6	75.66	70.66	81.66	67.33	38.00	56.00	64.88	8
TGX2014-16FM	7	61.00	56.00	79.66	67.00	33.00	58.00	59.11	24
Panorama29-1	8	82.66	77.66	81.66	67.00	41.33	61.00	68.55	4
ScSaga	9	67.33	63.00	77.33	62.66	22.66	52.66	57.60	26
ScSpike	10	71.00	66.00	79.66	65.66	34.66	55.33	62.05	18
S1079/6/7	11	73.66	68.66	82.00	65.66	38.00	60.00	64.66	11
ScSignal	12	72.00	67.00	84.33	65.66	38.66	58.00	64.27	13
ScSaxon	13	81.00	76.00	85.66	66.33	41.00	72.66	70.44	3
S1180/5/54	14	75.00	70.00	80.00	66.66	40.33	57.00	64.83	9
S1140/5/4	15	78.00	73.00	84.66	67.00	39.66	57.33	66.60	6
S1150/5/22	16	70.33	65.33	79.00	62.33	29.00	53.33	59.88	22
ScSafari	17	74.00	69.66	79.33	64.66	38.00	55.33	63.49	15
ScStatus	18	71.33	66.33	78.66	66.33	29.00	56.33	61.33	20
SNK500	19	63.33	58.33	81.00	63.33	20.00	50.33	56.05	30
SCS-1	20	73.66	68.66	80.33	62.66	30.33	58.00	62.27	17
Clark-63k	21	68.00	63.00	79.00	64.33	29.00	55.33	59.77	23
Gazelle	22	66.66	61.66	79.33	64.33	29.00	53.33	59.05	25
Nyala	23	61.00	56.00	77.66	61.33	28.33	53.66	56.33	29
ScSerenade	24	67.66	62.66	81.00	67.00	37.33	59.00	62.44	16
ScSentinel	25	73.33	68.33	83.33	65.66	39.33	56.00	64.33	12
Kafue	26	64.00	59.00	80.00	64.66	34.66	58.33	60.10	21
Afgat	27	58.00	55.33	80.00	62.66	28.66	59.33	57.33	27
Pawe-1	28	73.00	68.00	84.66	67.00	38.66	59.00	65.05	7
Pawe-2(check)	29	73.33	68.33	83.00	66.66	38.66	59.00	64.83	10
Pawe -3 (check)	30	81.33	76.33	86.33	80.33	49.00	62.66	72.66	2
Mean		71.90	67.02	81.38	66.43	34.42	57.37	63.09	
CV(%)		5.09	5.61	3.98	2.02	17.05	7.25	6.3	
LSD(5%)		6.02	6.1	5.3	2.3	9.54	6.8	2.6	
Ftest		**	**	*	**	**	**	**	

CV= coefficient of variation, LSD=least significant difference

Appendix Table 4. Mean performance for morpho-phenologic, grain yield and agronomic traits of thirty soybean genotypes evaluated across six locations

Genotypes Name	Code	Yield		Days of Flowering		Days of Maturity		Plant Height	
		mean	rank	mean	rank	mean	rank	mean	rank
Favour	1	1.226 o	30	75.11 [a]	1	152.72 [a]	1	74.66 [b-c]	4
TGX2001-6FM	2	1.948c-i	11	64.05 [f-j]	14	125.38 [h-l]	19	61.80 [g-j]	17
TGX2014-5GM	3	1.357 n-o	28	56.72 [qr]	28	121.72 [l-o]	26	57.45 [jk]	24
TGX2014-23FM	4	1.736 j-l	21	61.88 [j-m]	19	128.77 [f-i]	15	71.25 [c-d]	7
TGX2001-8DM	5	2.047 b-g	7	67.05 [de]	5	130.11 [d-g]	11	74.82 [b-c]	3
TGX2002-3DM	6	1.894e-j	14	64.72 [e-h]	8	129.16 [e-i]	13	71.68 [c-d]	6
TGX2014-16FM	7	1.945 d-i	12	59.11 [n-q]	24	123.88 [j-n]	22	63.29 [f-i]	16
Panorama29-1	8	1.934 d-j	13	68.55 [cd]	4	139.77 [b]	2	97.80 [a]	1
ScSaga	9	1.991 c-h	9	57.611 [o-r]	26	127.05 [g-k]	17	64.16 [f-h]	13
ScSpike	10	2.154 bcd	4	62.056 [i-m]	18	133.66 [d]	6	69.95 [c-e]	9
S1079/6/7	11	2.238 ab	2	64.66 [e-i]	11	125.16 [i-l]	18	63.90 [f-h]	15
ScSignal	12	2.112 b-e	5	64.27 [f-j]	13	133.00 [de]	7	73.18 [c]	5
ScSaxon	13	1.832f-k	18	70.444 [bc]	3	129.38 [e-h]	12	67.65 [e-f]	10
S1180/5/54	14	1.786 j-k	20	64.833 [e-h]	9	131.72 [def]	9	55.706 [k]	28
S1140/5/4	15	1.884 e-j	16	66.611 [d-f]	6	131.94 [def]	8	78.88 [b]	2
S1150/5/22	16	2.072 b-f	6	59.88 [l-p]	22	122.55 [l-o]	25	57.38 [jk]	25
ScSafari	17	1.893 e-j	15	63.50 [g-k]	15	123.55 [j-n]	23	59.38 [h-k]	18
ScStatus	18	2.430a	1	61.33 [k-n]	20	128.94 [e-i]	14	58.96 [h-k]	20
SNK500	19	1.318 n-o	29	56.056 [r]	30	119.88 [no]	29	48.72 [l]	29
SCS-1	20	1.527 l-n	24	62.27 [h-m]	17	124.16 [j-m]	20	56.89 [jk]	27
Clark-63k	21	1.873 e-k	17	59.77 [m-p]	23	123.00 [k-o]	24	58.47 [i-k]	21
Gazelle	22	1.812g-k	19	59.05 [n-q]	25	121.66 [l-o]	27	57.70 [jk]	23
Nyala	23	1.692 j-m	22	56.33 [r]	29	120.83 [m-o]	28	46.85 [l]	30
ScSerenade	24	1.640 k-m	23	62.44 [g-l]	16	127.38 [g-i]	16	59.01 [h-k]	19
ScSentinel	25	1.486 m-n	27	64.33 [f-j]	12	130.77 [d-g]	10	63.93 [f-h]	14
Kafue	26	1.488 m-n	26	60.11 [l-o]	21	124.00 [j-n]	21	57.88 [jk]	22
Afgat	27	1.516 l-n	25	57.33 [p-r]	27	119.27 [o]	30	57.37 [jk]	26
Pawe-1	28	1.950 c-i	10	65.05 [e-g]	7	133.77 [d]	5	65.61 [e-g]	11
Pawe-2 (check)	29	2.037 b-g	8	64.83 [e-h]	10	138.11 [b-c]	3	65.30 [e-g]	12
Pawe -3 (check)	30	2.191 ac	3	72.66 [ab]	2	134.11 [c-d]	4	71.10 [c-d]	3
Mean		1.83		63.09		128.5		64.36	
Cv (%)		20.18		6.3		4.91		12.48	
Lsd (5%)		0.24		2.6		4.14		5.27	
Ftest		**		**		**		**	

APPENDIX Table 4. (Continued)

Genotypes Name	Code	Number of pod per plant		Number of seed plant		Hundred Seed Weight	
		Mean	Rank	Mean	Rank	Mean	Rank
Favour	1	59.63 [a]	1	78 [bc]	4	12.85 [n]	29
TGX2001-6FM	2	47.45 [b-d]	5	71.53 [cde]	5	13.58 [l-n]	25
TGX2014-5GM	3	31.55 [n]	30	50.77 [j-l]	28	17.32 [abc]	3
TGX2014-23FM	4	40.54 [f-i]	11	62.59 [e-i]	14	16.91 [a-d]	4
TGX2001-8DM	5	44.14 [c-f]	7	68.2 [c-f]	6	15.71 [d-j]	12
TGX2002-3DM	6	44.06 [c-g]	8	61.85 [f-k]	15	14.87 [g-m]	19
TGX2014-16FM	7	39.79 [f-i]	12	63.97 [c-h]	11	16.35 [a-e]	7
Panorama29-1	8	48.45 [b-c]	4	68.12 [c-g]	7	13.50 [mn]	27
ScSaga	9	35.86 [h-n]	25	56.44 [h-l]	23	16.06 [b-h]	10
ScSpike	10	37.15 [h-m]	24	60.72 [g-l]	18	16.491 [a-e]	6
S1079/6/7	11	37.29 [h-m]	23	59.17 [g-l]	21	15.62 [d-j]	13
ScSignal	12	52.28 [b]	3	83.43 [ab]	2	13.57 [l-n]	26
ScSaxon	13	39.35 [f-j]	16	61.03 [f-k]	17	15.06 [e-k]	16
S1180/5/54	14	38.83 [f-k]	17	65.35 [e-j]	9	14.70 [h-m]	21
S1140/5/4	15	39.50 [f-i]	13	60.71 [e-j]	19	15.25 [e-k]	15
S1150/5/22	16	37.56 [h-m]	22	53.25 [l]	26	15.89 [c-i]	11
ScSafari	17	38.50 [h-k]	19	61.17 [j]	16	14.29 [j-n]	23
ScStatus	18	39.47 [f-i]	15	58.83 [e-j]	22	14.14 [k-n]	24
SNK500	19	35.86 [k-n]	27	59.89 [g-l]	20	14.90 [g-m]	18
SCS-1	20	38.40 [h-l]	20	56.44 [h-l]	24	14.80 [h-m]	20
Clark-63k	21	33.84 [j-n]	26	52.76 [g-l]	27	16.91 [a-d]	5
Gazelle	22	33.18 [l-n]	28	50.75 [k-l]	29	16.07 [b-h]	9
Nyala	23	32.19 [m-n]	29	49.75 [l]	30	17.44 [ab]	2
ScSerenade	24	39.49 [f-i]	14	63.08 [e-i]	12	17.82 [a]	1
ScSentinel	25	46.09 [c-e]	6	82.38 [bcd]	3	16.29 [b-g]	8
Kafue	26	37.87 [h-l]	21	63.05 [c-h]	13	13.04 [n]	28
Afgat	27	38.53 [g-k]	18	66.91 [c-g]	8	14.58 [i-m]	22
Pawe-1	28	41.93 [d-g]	9	65.2 [-h]	10	15.01 [f-l]	17
Pawe-2(check)	29	40.60 [e-i]	10	54.7 [h-l]	25	15.40 [e-k]	14
Pawe -3 (check)	30	58.98 [a]	2	93.58 [a]	1	11.26 [o]	30
Mean		40.86		67.69		15.19	
Cv (%)		20.65		27.57		14.6	
Lsd (5%)		5.53		12.24		1.45	
Ftest		**		**		**	

Appendix. Table 4. (continued)

Genotypes Name	Code	Lodging		Shattering		Blight		Rust	
		mean	rank	mean	rank	mean	rank	mean	rank
Favour	1	1.33 [a]	1	1.00 [b]	4	1.33 [bc]	4	1.66 [abc]	3
TGX2001-6FM	2	1.08 [e-h]	8	1.00 [b]	4	1.33 [bc]	4	1.66 [abc]	3
TGX2014-5GM	3	1.13 [c-f]	6	1.00 [b]	4	1.33 [bc]	4	1.77 [ab]	2
TGX2014-23FM	4	1.08 [e-h]	8	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
TGX2001-8DM	5	1.08 [e-h]	8	1.00 [b]	4	1.55 [ab]	2	1.77 [ab]	2
TGX2002-3DM	6	1.11 [d-g]	7	1.00 [b]	4	1.44 [abc]	3	1.66 [abc]	3
TGX2014-16FM	7	1.08 [e-h]	8	1.00 [b]	4	1.33 [bc]	4	1.33 [c]	5
Panorama29-1	8	1.05 [f-h]	9	1.00 [b]	4	1.22 [c]	5	1.66 [abc]	3
ScSaga	9	1.02 [g-h]	10	1.027 [b]	3	1.33 [bc]	4	1.33 [c]	5
ScSpike	10	1.00 [h]	11	1.00 [b]	4	1.33 [bc]	4	1.33 [c]	5
S1079/6/7	11	1.00 [h]	11	1.00 [b]	4	1.33 [bc]	4	1.66 [abc]	3
ScSignal	12	1.02 [g-h]	10	1.00 [b]	4	1.44 [abc]	3	1.61 [bc]	4
ScSaxon	13	1.02 [g-h]	10	1.00 [b]	4	1.44 [abc]	3	1.61 [bc]	4
S1180/5/54	14	1.05 [f-h]	9	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
S1140/5/4	15	1.00 [h]	11	1.00 [b]	4	1.22 [c]	5	1.77 [ab]	2
S1150/5/22	16	1.00 [h]	11	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
ScSafari	17	1.00 [h]	11	1.00 [b]	4	1.44 [abc]	3	1.61 [bc]	4
ScStatus	18	1.02 [g-h]	10	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
SNK500	19	1.22 [bc]	3	1.11 [a]	1	1.33 [bc]	4	1.61 [bc]	4
SCS-1	20	1.02 [g-h]	10	1.00 [b]	4	1.33 [bc]	4	1.66 [abc]	3
Clark-63k	21	1.16 [cde]	5	1.00 [b]	4	1.33 [bc]	4	2.00 [a]	1
Gazelle	22	1.19 [bcd]	4	1.00 [b]	4	1.33 [bc]	4	1.66 [abc]	3
Nyala	23	1.11 [d-g]	7	1.00 [b]	4	1.55 [ab]	2	1.77 [ab]	2
ScSerenade	24	1.05 [f-h]	9	1.00 [b]	4	1.44 [abc]	3	1.61 [bc]	4
ScSentinel	25	1.00 [h]	11	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
Kafue	26	1.27 [ab]	2	1.08 [a]	2	1.33 [bc]	4	1.33 [c]	5
Afgat	27	1.19 [bcd]	4	1.00 [b]	4	1.33 [bc]	4	1.61 [bc]	4
Pawe-1	28	1.13 [c-f]	6	1.02 [b]	3	1.66 [a]	1	1.66 [abc]	3
Pawe-2(check)	29	1.08 [e-h]	8	1.00 [b]	4	1.66 [a]	1	2.00 [a]	1
Pawe-3 (check)	30	1.33 [a]	1	1.00 [b]	4	1.55 [ab]	2	1.33 [c]	5
Mean		1.09		1.00		1.38		1.60	
Cv (%)		14.3		6.29		26.6		32.0	
Lsd (5%)		0.10		0.04		0.24		0.33	
Ftest		**		**		*		*	

Means followed by a common letter with in a column are not significantly different from each other at P≤0.05, CV= coefficient of variation, LSD=least significant difference

Appendix Table 5. Bartlett's test for Homogeneity of yield variance

Source	DF	Chi-Square	Pr > ChiSq
locations	5	2.41E-13	1.0000