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Agrosystems

Grain yield stability of soybean (*Glycine Max* (L.) Merrill) for different stability models across diverse environments of Ethiopia

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Abstract

For grain yield stability analysis, genotype by environment interactions are crucial in properly identifying and discriminating between varieties and locations. Hence, this experiment was conducted with the objectives to evaluate the stability of soybean using additive main effects and multiplicative interaction (AMMI), multi-trait stability index (MTSI), weighted average absolute scores biplot (WAASB), Eberhart and Russell regression model, and genotype plus genotype by environment interaction (GGE) biplot analysis for grain yield of soybean genotypes and identified stable genotypes in the different soybean agroecologies of Ethiopia. Twenty-four soybean genotypes were planted at six soybean environments with RCBD in three replications in the 2015/2016 cropping season. Stability measures, namely, AMMI, AMMI stability value, and GGE biplot analysis were used to identify the high-yielding and stable genotypes across the testing environments. AMMI-1 biplot showed Pawe as the ideal environment; Bako as a favorable environment; Asosa an average environment; and the rest namely, Dimtu, Jimma, and Metu as unfavorable environments. On the other hand, AMMI-2 biplot analysis certain genotypes like Prichard, Spry, Delsoy 4710, and Croton 3.9 were identified as stable genotypes. Bako and Metu were identified as the most discriminating environments. Mega environments and the best yielding soybean genotypes on each mega environment were revealed by the GGE biplot analysis model. For other multivariate statistics used for this study, MTSI, WAASB, and regression models, stable and superior varieties for grain yield were revealed. Through the MTSI, the four genotypes, namely, Liu yue mang, SCS-1, Clark-63k, and AFGAT, were found to be stable and superior over the rest tested genotypes. Overall, the genotypes SCS-1 and AGS-7-1 were stable across soybean growing environments and are recommended for mega environment production.

Abbreviations: AMMI, additive main effects and multiplicative interaction; ANOVA, analysis of variance; ASV, AMMI stability value; GEI, genotype by environment interaction; GGE, genotype plus genotype by environment interaction; IPCA, interaction principal component axis; MTSI, multitrait stability index; PDCAAS, protein digestibility-corrected amino acid score; WAASB, weighted average absolute scores biplot.

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1 | INTRODUCTION

Soybean (*Glycine max* (L) Merrill) is a self-pollinated diploid ($2n = 4x = 40$) species with a genome size approximately 1.115 Gb, the repeat sequences occupy more than 50% of the soybean genome (Chen et al., 2015). The crop is extraordinarily rich in protein (lysine rich) (~40%) and ~20% oil enriched with essential fatty acids. It is the world's foremost provider of high-quality, nutritionally excellent and inexpensive protein and dietary vegetable oil for use either as human food or animal feed (Qin et al., 2022; Sritongtae et al., 2021). According to Qin et al. (2022), soy-protein is a high-quality protein with a protein digestibility corrected amino acid score (PDCAAS) of 1.00, which is close to some of the proteins from animal sources, such as meat and dairy. Also, soy-proteins contain well-balanced essential amino acids except for sulfur-containing ones like methionine. In addition, it can improve soil fertility through its capability to fix atmospheric nitrogen; it is an ideal crop in improving and amending soil properties through nitrogen fixation and the ability to break lifecycles of pests and diseases in cereal rotation system (Hymowitz et al., 1981; Morsy et al., 2015).

Soybean is a crop of great promise for most developing countries faced with extensive malnutrition and food insecurity (Yirga et al., 2022) and is the most important legume crop because of its economic value and biological features for research (Chen et al., 2015). In the 2021/2022 crop year, soybeans were the leading type of oilseed in the world before rapeseed (70.62), sunflower seeds (57.26), peanuts (50.68), and cottonseeds (43.5). That year, almost 364 million metric tons of soybeans were produced worldwide with an average area of 129,523,964 hectares (<https://www.statista.com/statistics/267271/worldwide-oilseed-production-since-2008/>).

According to Tesfaye et al. (2018), with its diverse environmental and climatic conditions, Ethiopia is endowed with a very large area of land, where soybean can be suitably produced. The land suitability analysis shows that soybean is the second among legumes in terms of land area that is moderately and highly suitable for its production in the country, with an estimated 42,067,700 (37.2%) hectares of land (Nigussie, 2018). It can be grown in altitudes ranging from 1250 to 2200 m above sea level (m.a.s.l.). However, it performs well between 1300 and 1700 m.a.s.l. It can also be grown in an area receiving 450 to 1500 mm annual rainfall. However, to grow very well, and for optimum yields, soybean requires a minimum of 500 mm annual rainfall. Temperature ranging from 23°C to 25°C is reported to be optimum for soybean production. Similarly, it performs well at warm temperature and medium relative humidity. However, very high temperature adversely affects pod production and grain filling.

Core Ideas

- All the soybean agromorphological traits were significantly affected by genotype, environment and GEI.
- Analysis of soybean yield stability is critical for variety use and delineation of mega environments.
- The genotype plus genotype by environment interaction biplot revealed that the three winning genotypes across environments.
- For most traits, including the grain yield in the additive main effects and multiplicative interaction analysis, the first two interaction principal component axes were not only statistically different but accounted for the largest proportions of interaction sum squares.
- The six environments studied belonged to three mega-environments throughout all soybean-growing environments.

For strong breeding programs for crops like soybean, testing in different environments is very important to ensure that the selected genotypes perform well in different environments within the target area, which is one of the most reliable methods for detection. This trait is the most stable and well-tolerated cultivar (Qasemi et al., 2022). However, effective interpretation and utilization of data in making selection decisions remains a major challenge to researchers. The adaptability of cultivars to environmental changes is important for stable crop production across regions and years. Information on the GEI leads to a stable genotype assessment that can be used for general cultivation. Yield is a complex quantitative property and is strongly influenced by environmental variation. Hence, the selection for superior genotypes based on yield per se at a single location in a year may be very effective. The study of genotype by environment interaction (GEI) is crucial for indicating genotypes to each locality (Hamawaki et al., 2015). Qualifying a new soybean variety requires desirable traits such as pods per-plant, plant height at maturity, high protein and oil content, as well as high grain yield, production stability, and broad adaptability to a variety of environments.

Many researchers described importance of the GEI in stability analysis of soybean (Mwiinga et al. 2020; Whaley & Eskandari, 2019; Gurmu et al., 2009; Agoyi et al., 2017; Happ et al., 2021). The additive main effects and multiplicative interaction (AMMI), that considers genotypes and environments as fixed variables (Ranjesh & Talubaghi, 2023), and GGE biplot models can be powerful tools for effective analysis and interpretation of multi environment data

structure in breeding programs (Happ et al., 2021; Yan et al., 2000). In addition, a weighted average of absolute scores biplot (WAASB) as a linear mixed model-based quantitative stability index was proposed for analysis of GEI through biplots to select stable genotypes. That means the WAASB index integrates features of both AMMI and the best linear unbiased prediction model (BLUP) models into a unique stability index; BLUP was found to outperform AMMI in the analysis of four real MET trials (Olivoto et al., 2019). In Ethiopia, the application of AMMI and site regression model GGE models for explaining and analyzing the performance of genotypes and the tested environments have been very frequent among plant breeder in recent years. Various studies have been conducted in Ethiopia to analyze the effects of GEI on soybean genotypes (Gurmu et al., 2009; Asfaw et al., 2009; Adane et al., 2018), but only a few studies use the GGE biplot model. The studies on BLUP models and that of its graphics WAASB index has not been reported so far. Another research work by Lee et al. (2023) reported that the identification of recommended cultivars using the simultaneous selection of MTSI and WAASB would provide guidance to breeders to select ideal parents which fit the purpose of rice breeding. In addition, based on multiple traits, the MTSI index can provide a unique, robust, and powerful tool to develop better treatment and/or genotypes helping both breeders and agronomists as also reported previously (Abdelghany et al., 2021). In addition, Nataraj et al. (2021) recommend that breeder should apply MTSI to identify high-yielding, stable, drought-tolerant genotypes prior to testing them under multiple environments, which is ultimately required for approving variety in different environments.

Existence of genotype $\times$ environment interaction is one of the major problems in evaluating and introducing superior genotypes (Ranjesh & Talubaghi, 2023). Examination of GEI coverage and target genotype stability is aimed to use different stability statistics for genotypes stability and also the identification of recommended cultivars using the simultaneous selection of MTSI, that valuable to the plant breeders for the selection of genotypes based on many characters as being strong and simple selection process (Hussain et al., 2021) and WAASB (Nataraj et al., 2021), would provide guidance to breeders to select ideal parents which fit the purpose of soybean breeding. As a result, the current study aims to evaluate the GEI using AMMI, MTSI, WAASB, GGE-biplot analysis, and Eberhart and Russell (1966) regression model for grain yield of soybean genotypes and to identify stable soybean genotypes in the different agroecologies for breeding and variety testing purpose. Another intention was to explore the usefulness and unique features of the stability models, to examine the usefulness of a stability model comparing with the five classical model, widely and recently used models.

2 | MATERIALS AND METHODS

2.1 | Plant materials, study locations, and experimental design

2.1.1 | Plant materials

In this study, 24 soybean genotypes, consisting of 12 cultivars introduced from the United States and five Ethiopian Soybean breeding released varieties (AFGAT, Hawassa 04, SCS-1 and Clark-63k), were used as control cultivars and various international cultivars. Twenty advanced lines representing a soybean breeding program and obtained from the Jimma Agricultural Research Center (JARC/EIAR) were used in this study (Table 1).

2.1.2 | Study locations

The experiments were conducted at six different locations across Ethiopia, namely, Dimtu ($7^{\circ}55'0''\text{N}$, $37^{\circ}20'0''\text{E}$), Jimma ($7^{\circ}40'9''\text{N}$, $36^{\circ}47'6''\text{E}$), Bako ($9^{\circ}06'\text{N}$, $37^{\circ}09'\text{E}$), Metu ($8^{\circ}18'\text{N}$, $35^{\circ}35'\text{E}$), Asosa ($10^{\circ}02'\text{N}$, $34^{\circ}34'\text{E}$), and Pawe ($11^{\circ}19'\text{N}$, $103^{\circ}60'24''\text{E}$). These areas represent the highest potential and the main areas for soybean production in the country, with different edaphic and environmental conditions. Table 2 shows the geographical specifications of the study areas.

2.1.3 | Field layout and experimental design

The experiments in all locations were designed in a randomized complete block design (RCBD) with three replications per environment under rain fed conditions. Sowing was done late May, 2015 to onset of June, 2015 manually in rows. The soil preparation was done by one plowing and two harrowing rights before grooving and fertilizing the soil. The experimental plot consisted of four row plots, 3 m long and 0.6 m apart. At maturity, the two middle rows of each plot were harvested to determine the seed yield in kilograms per plot (3.6 m^2). The experiments were harvested when plants reached the R8 stage, according to Fehr and Caviness (1977) scale, in both central lines of each plot, eliminating 0.5 m of each line row. Subsequently, the grain yield adjusted to the standard moisture contents of 12.5%. After drying, for determining the grain yield, the grains from each useful plot had their mass weighed and extrapolated to kg ha^{-1} . Fertilizer NPS (19% N, 38% P_2O_5 , and 7% S) and urea were applied at the recommended amount of 122 and 50 kg ha^{-1} during sowing and flowering in the test sites, respectively. Weeds were controlled three times and as necessary. The other agronomic management practices, namely, pest or diseases

TABLE 1 Description of the testing genotypes.

N ^o	Seed types	Genotype code	Genotypes	Seed types/status/origin	Seed sources	Remarks
1	PI 634193	G1	5002T	Advanced Observation Nursery	USA introduction	Promising line
2	PI 570668	G2	Ciaric	Advanced Observation Nursery	USA introduction	Promising line
3	PI 633970	G3	Ozark	Advanced Observation Nursery	USA introduction	Promising line
4	PI 603953	G4	Motte	Advanced Observation Nursery	USA introduction	Promising line
5	PI 595081	G5	Ks4895	Advanced Observation Nursery	USA introduction	Promising line
6	–	G6	UA4805	Advanced Observation Nursery	USA introduction	Promising line
7	PI 560207	G7	Delsoy 4710	Advanced Observation Nursery	USA introduction	Promising line
8.	PI 553051	G8	Spry	Advanced Observation Nursery	USA introduction	Promising line
9	PI561702	G9	Harbar	Advanced Observation Nursery	USA introduction	Promising line
10	TGX-1892-10F	G10	AFGAT	Variety (Check)	EIAR/JARC	Ethiopia–released
11	PI 594675	G11	Graham	Advanced Observation Nursery	USA introduction	Promising line
12	PI 559932	G12	Manokin	Advanced Observation Nursery	USA introduction	Promising line
13	PI 559932	G13	Ks3496	Advanced Observation Nursery	USA introduction	Promising line
14	–	G14	Clarck-63k	Variety (Check)	EIAR/JARC	Ethiopia–released
15	PI 533050	G15	Choska	Advanced Observation Nursery	USA introduction	Promising line
16	PI 594669	G16	Liu yue mang	Advanced Observation Nursery	USA introduction	Promising line
17	PI 594675	G17	Huang dou No-1	Advanced Observation Nursery	USA introduction	Promising line
18	PI 594675	G18	Hs93-4118	Advanced Observation Nursery	USA introduction	Promising line
19	PI 614153	G19	Croton 3.9	Advanced Observation Nursery	USA introduction	Promising line
20	–	G20	SCS-1	Advanced lines	CIMMYT-Zimbabwe	Promising line
21	PI 639740	G21	LDOO-3309	Advanced Observation Nursery	USA introduction	Promising line
22	PI 612157	G22	Prichard	Advanced Observation Nursery	USA introduction	Promising line
23	PI 633610	G23	Desha	Advanced Observation Nursery	USA introduction	Promising line
24	Hawassa-04	G24	AGS-7-1	Variety (Check)	EIAR/JARC	Ethiopia–released

Abbreviations: EIAR, Ethiopian Institute of Agricultural Research; JARC, Jimma Agricultural Research Centre.

control, were applied as recommended for each respective location.

2.1.4 | Phenotypic data collection

For this study, we considered nine quantitative traits (direct and positively contributing traits with yield) such as days to flower (DTF, days), days to maturity (DTM, days), plant height (PH, cm), hundred seed weight (HSW, gm), branches per plant (BPP), number of seeds per plant (NSPP), number of pods per plants (NPP), harvest index (HI%), and yield (Kg ha⁻¹). However, data were recorded according to soybean classification and descriptors by IBPGR (1984). Data were collected from 10 randomly selected plants from each plot.

2.2 | Statistical analysis

2.2.1 | Analysis of variance

Each environment underwent an individual analysis of variance (ANOVA), which was followed by a joint analysis of variance using the statistical model shown in equation (1):

$$Y_{ijk} = \mu + B/E_{jk} + G_{jk} + E_j + GE_{ij} + \varepsilon_{ijk} \quad (1)$$

where Y_{ijk} represents the i^{th} genotype in the j^{th} environment and the j^{th} block;

TABLE 2 Location specifications of the experiment performed areas.

Name	Altitude (masl)	Latitude	Longitude	Annual rain fall(mm)											
				Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Sep.	Oct.	Nov.	
Metu	1711	8°18'N	35°35'E	NA	NA	29.9	14	202.1	NA	NA	NA	190.6	NA	NA	
Dintu	1780	7°55'0"N,	37°20'0"E	NA	NA	NA	205.7	296.8	NA	NA	346.4	405.1	NA	NA	
Jimma	1718	7°40'9"N	36°47'6"E	6.1	16.9	77.5	176.3	NA	NA	NA	243.2	NA	NA	155.2	
Bako	1650	9° 06' N	37° 09'E	2.4	2.4	54	NA	99.7	119.7	208.5	193.1	145.5	66.5	NA	
Asosa	1600	10°02'N	34°34'E	0	0	11.2	1	153.9	174.9	225.7	249.7	NA	NA	NA	
Pawe	1119	11°01'N	03°02'4"E	33.8	37.4	38.4	37.7	34.4	30.8	29.8	29.2	29.8	30.7	31.4	

Source: National Meteorology Agency (<http://www.ethiomet.gov.et>). NA = data not available.

μ is the overall mean;

B/E_{jk} corresponds to the block within the j^{th} environment and in the k^{th} block;

G_i is the effect of the j^{th} genotype;

E_j is the effect of the j^{th} environment;

GE_{ij} is the effect of the interaction of the i^{th} genotype with the j^{th} environment; and ε_{ijk} is the effect of experimental error.

2.2.2 | Mean performance and stability indices based on multiple traits

Weighted average of absolute scores (WAASB)

The genotypic stability of each genotype was quantified by the WAASB from the singular value decomposition of the matrix of best linear unbiased predictions for the GEI effects generated by a linear mixed-effect model (Olivoto et al., 2019), estimated as indicated in eEquation (2):

$$WAASi = \sum_{k=1}^p |IPCA_{ik} \times EP_k| / \sum_{k=1}^p EP_k, \quad (2)$$

where is the weighted average of absolute scores of the i^{th} genotype;

is the score of the k^{th} genotype in the k^{th} Interaction Principal Component Axis (IPCA);

and is the explained variance of the k^{th} IPCA for $k = 1, 2, \dots, p$, considering $p = \min(g - 1; e - 1)$.

The genotype with the lowest WAASB value is considered the most stable, showing the least deviation from the average performance across environments (Olivoto et al., 2019).

The multi-trait stability index

To estimate the multi-trait stability index (MTSI) (Olivoto et al., 2019), equation (3) below was used as follows:

$$MTSli = \left[\sum f_j = 1 (F_{ij} - F_j) 2 \right] 0.5, \quad (3)$$

where MTSI is the multi-trait stability index for the i^{th} genotype,

F_{ij} is j^{th} score of the i^{th} genotype,

and F_j is the j^{th} score of ideotype.

The genotype with the lowest MTSI is, therefore, closer to the ideotype and hence has a high mean performance and stability for all variables studied. The stability analyses of the multi-environment trial data using MTSI and WAASB

indexes were conducted using the metan package (Olivoto & Lúcio, 2020) of the R 4.2.2 software.

2.2.3 | The AMMI models

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^x \lambda_k \sigma_{ik} \gamma_{jk} + \varepsilon_{ijr}, \quad (4)$$

where Y_{ijr} = Observation of the r^{th} replicate of the i^{th} genotype in the environment,

μ = the overall mean,

g_i = main effect of the genotype,

e_j = main effect of the j^{th} environment,

x = matrix rank $\{ge\}_{ij}$,

λ_k = the singular value for principal component k ,

σ_{ik} = the eigen vector score for genotype i and component k , and

γ_{jk} = the eigen vector score for environment j and component k ,

AMMI stability value

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

$$ASV = \sqrt{\frac{IPCA1 \text{ Sum squares}}{IPCA2 \text{ Sum squares}} (IPCA1 \text{ score})^2 + [IPCA2 \text{ score}]^2}, \quad (5)$$

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

2.2.4 | The GGE model

The model from GGE biplot (Yan, 2002) based on the singular value decomposition of the first two principal components is in Equation 6:

$$Y_{ij} = \mu + e_j + \sum_{k=1}^x \lambda_k \sigma_{ik} \gamma_{jk} + \varepsilon_{ijr}, \quad (6)$$

Y_{ijr} = Observation of the r^{th} replicate of the i^{th} genotype in the environment, μ = the overall mean,
 λ_k = the singular value for principal component k ,
 e_j = The mean effect of the j^{th} environment,
 x = matrix rank $\{gge\}_{ij}$ when $\{gge\}_{ij}=g_i + ge_{ij}$
 σ_{ik} = the eigen vector score for genotype i and componenet k , γ_{jk} the eigenvector score for environment j and component k , and ε_{ijr} = the error for the genotype i and environment j and replicate r .

2.4.5. Eberhart and Russell regression model

$$Y_{ij} = \mu_i + biIj + S^2d_{ij}$$

where Y_{ij} is the mean performance of the i^{th} variety ($i = 1, 2, 3, \dots, n$) in the j^{th} environment;

μ_i is the mean of the i^{th} variety overall the environments;

b_i is the regression coefficient which measures the response of i^{th} variety to varying environments;

S^2d_{ij} is the deviation from regression of i^{th} variety in the j^{th} environment, and

I_j is the environmental index of the j^{th} environment.

3 | RESULTS AND DISCUSSION

3.1 | Combined analysis of variance

The combined analysis of variance (Table 3) for all traits under study showed a very highly significant interaction for environment ($p < 0.001$); a significant interaction ($p < 0.05$) for number of seeds per plant for other traits found a very highly significant interaction ($p < 0.001$). The results also indicated the GEI effects were very highly significant ($p < 0.001$) for days to flowering, number of seeds per plant, number of branches per plant, 100 seed weight (gm), and harvest index (%) and days to maturity, number of pods per plant are significantly different at $p < 0.001$ and plant height (cm) at $p < 0.05$. The results also showed that all the agromorphological traits were significantly affected ($p < 0.05$) to very highly significantly different ($p < 0.001$) by genotype, environment, and GEI (Table 3).

In the studies, Atnaf et al. (2013) and Mwiinga et al. (2020) reported a higher contribution of GEI to total variation with values of 60%, 41%, and 35%, respectively. The extent of the environment's influence in regulating grain yield expression was demonstrated. The conclusion was that settings had a greater influence on phenotypic value, which had an impact on selection effectiveness and breeding progress.

TABLE 3 Combined analysis of variance for agro-morphological traits of 24 genotypes across the six environments.

Mean square									
Sources of variations	df	Days to flowering	Days to maturity	Number of seeds per plant	Number of pods per plant	Number of branches per plant	Hundred seed weight(gm.)	Plant height(cm)	Harvest index (%)
ENV	5	382.3***	4298.3***	4748***	3257***	38.36***	324.07***	5125***	4.18***
REP(ENV)	12	17.5	51.7	5507	1267	1.81	20.84	128	0.04
GEN	23	302.3***	483.5***	1184**	447***	10.45***	48.57***	1665***	0.07***
GEN X ENV	115	47.4***	50.1**	855***	203**	1.87***	5.05***	156*	0.05***
Residuals	276	27.4	32.1	531	133	1.02	3.04	111	0.02
CV (%)		10.9	5.24	31.71sara	29.6	28.4	10.53	19.60	35.41
MSR+/MSR-		26.9	3.1	4.98	11.6	12.39	2.24	11.30	70.64
Grand mean		47.9	108.22	72.68	38.9	3.55	16.55	53.60	0.44

Abbreviations: ENV, environment; REP, replicate; GEN, genotypes; *df*, degree of freedom.

***: significant at $p < 0.01$ level of probability; ns: not significant.

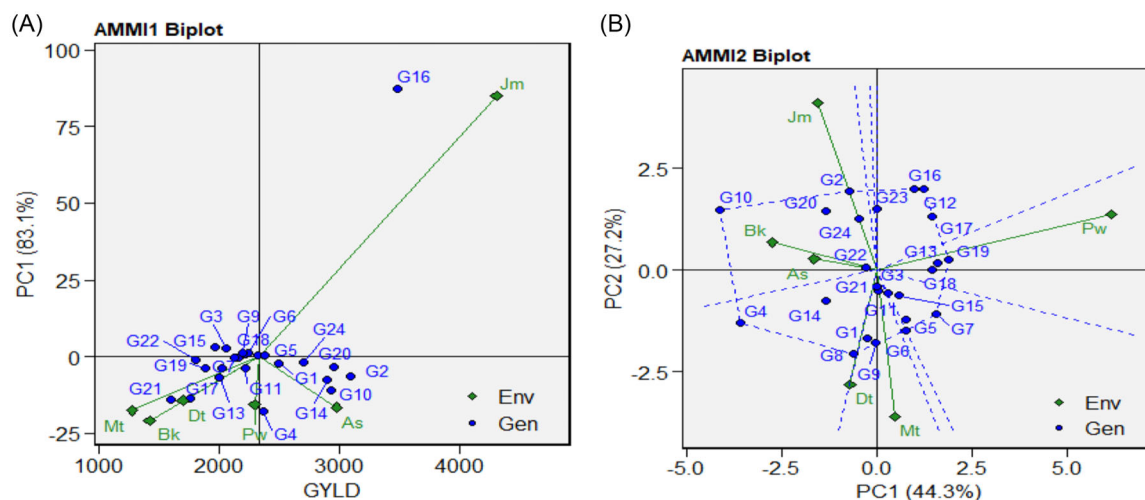


FIGURE 1 (A) Biplots principal component analysis (PCA) versus means yield (Kg ha^{-1}) for 24 soybean genotypes grown in six environments in 2015/2016 cropping season, and (b) biplots of PCA axis II versus axis I for yield.

3.2 | Additive main effects and multiplicative interactions

According to AMMI analysis for grain yield, the first two interaction principal components have taken the largest portions (70.34%) of the interaction sum squares with 50.3% and 20.04% respectively (Table 3). The AMMI model integrates the analysis of variance into a unified approach (Gauch & Zobel, 1996). IPCA scores of genotypes in the analysis are an indication of the stability of a genotype over the environments (Guach & Zobel, 1997).

The combined analysis of variance (ANOVA) of 24 genotypes at six locations according to AMMI model 2 is shown in Table 5. The ANOVA showed that a highly significant ($p \leq 0.01$) between environments, genotypes, and GEI for grain yield. The IPCAI axis was very highly significant ($p \leq 0.001$) for grain yield, while IPCAII axis was significant ($p \leq 0.05$). IPCAI and IPCAII axes explained 50.30% and 20.04% of the total GEI, while the remaining 29.66% were shared between the other IPCAs. This indicates that the AMMI model 2 is the most pertinent, which provides the intended information for this data set.

The AMMI model summarizes patterns and relationships of genotypes and environments. Figure 1A shows the AMMI model 2 biplot of grain yield for six locations. The IPCAI score plays a major role in GEI (Purchase, 1997), so they should be plotted against the IPCAII scores to further explore the adaptations. Genotypes closer to zero or center of the figure are more stable. Figure 1A indicates the IPCAI and IPCAII score for grain yield to further explore further adaptations. The further away from zero the IPCA score for the environments is the more interaction the environment has with

the genotypes, thus making difficult to choose genotypes for that environment.

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

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

The environments having a small score had small interaction effects indicating all genotypes performed well in these locations. Pawe (E6) was relatively close to zero than other locations, it was more stable, but its mean yield is third compared with the rest locations; it might not be the best location with respect to yield. Generally, genotypes and environments with IPCAI scores of the same sign produce positive interaction effects, thus higher yield of the genotype at that particular location, whereas combination of the IPCAI scores of the opposite sign produces specific negative interactions. A

TABLE 4 The first and second interaction principal component axes (IPCA), grain mean yield, and various yield stability statistics investigated in soybean genotypes over rain fed conditions.

N ^o	Genotype		Grand mean		IPCAI	IPCAII	ASV	Rank	YSI
	Code	Genotypes	(Kg ha ⁻¹)	Rank					
1	G1	5002T	2319	7	-10.71	14.67	22.44	16	23
2	G2	Ciaric	2385	5	-14.42	6.57	23.78	17	22
3	G3	Ozark	1815	18	5.30	3.72	9.18	7	25
4	G4	Motte	2337	6	-15.66	-17.05	30.10	23	29
5	G5	ks4895	2121	8	8.63	3.88	14.22	11	19
6	G6	UA4805	1981	13	4.99	-3.08	8.49	6	19
7	G7	Delsoy 4710	1871	17	6.25	-1.72	10.05	8	25
8	G8	Spry	1909	15	3.24	1.62	5.39	3	18
9	G9	Harbar	1926	14	10.07	3.46	16.33	12	26
10	G10	AFGAT(Check)	2903	1	-28.11	-8.55	45.35	24	25
11	G11	Graham	2027	10	0.36	4.80	4.83	2	12
12	G12	Manokin	2000	12	-8.15	3.02	13.26	10	22
13	G13	ks3496	1880	16	-2.55	5.59	6.90	5	21
14	G14	Clarck-63k(Check)	2770	3	-14.54	-7.84	24.33	18	21
15	G15	Choska	1641	21	16.97	5.00	27.35	20	41
16	G16	Liu yuemang	1656	19	15.77	-12.34	27.87	21	40
17	G17	Hang dou No-1	1623	22	5.04	-28.54	29.63	22	44
18	G18	Hs93-4118	2003	11	2.17	4.44	5.61	4	15
19	G19	Croton 3.9	1656	20	13.20	-3.02	21.13	15	35
20	G20	SCS-1	2853	2	-11.07	6.55	18.72	14	16
21	G21	LD00-3309	1554	24	0.92	3.91	4.18	1	25
22	G22	Princhard	1558	23	16.52	-0.36	26.18	19	42
23	G23	Desha	2072	9	4.92	7.04	10.51	9	18
24	G24	AGS-7-1(Check)	2522	4	-9.16	8.20	16.67	13	17

Abbreviations: IPCAI, Interaction principal component one; IPCAII, Interaction principal component two; YSI, yield stability index.

TABLE 5 Ranking of four additive main effects and multiplicative interaction (AMMI) selections per environment for grain yield (Kg ha⁻¹).

N ^o	Environment	Mean (Kg ha ⁻¹)	IPCA score	Genotype ranking			
				1 st	2 nd	3 rd	4 th
1	Asosa	2973	-5.28	G20	G10	G14	G24
2	Bako	2830	-40.22	G10	G20	G14	G2
3	Dimtu	1557	28.09	G20	G5	G14	G24
4	Jimma	1426	25.46	G20	G5	G24	G14
5	Metu	1268	-9.13	G10	G14	G4	G17
6	Pawe	2291	1.07	G20	G10	G14	G24

Abbreviation: IPCA, interaction principal component axis.

genotype showing high positive interaction in an environment has the ability to exploit the agroecological and agro-management conditions of the specific environment and is therefore best suited to that environment. In this case, G15, G22, G16, and G19 are suited for Jimma, while G20 is suited for Asosa.

AMM 2 biplot presents the spatial pattern of the first two IPC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the GEI pattern and identifies genotypes or environments that exhibit low, medium, or high level of interaction effects. IPCAI and IPCAII of grain yield accounted for 50.30% and 20.04% of

TABLE 6 Combined analysis of variance for yield and yield related traits using the base model the additive main effect and multiplicative interaction (AMMI) for 24 soybean genotypes evaluated at six locations, during 2016/2017 cropping season in Ethiopia.

Phenology traits										
Source of variation	Days to flower				Days to maturity				Plant height(cm)	
	SS	MS	% TT	%GEI	SS	MS	% TT	%GEI	SS	MS
Total (546)	27551	50.46			53623.08	98.21			131829.09	241.45
Environments (5)	1911.41	382.28***	6.94		21491.69	4298.34***	40.08		25623.55	5124.71***
Rep (ENV) (12)	210.11	17.51	0.76		620.61	51.72	1.16		1533.90	127.82
Genotypes (23)	6951.96	302.26***	25.23		11119.66	483.46***	20.74		38299.05	1665.18***
GEI (115)	5452.48	47.41**	19.79		5763.54	50.12**	10.75		17914.05	155.77*
IPCAI (27)	2399.07	88.85**		44	2809.54	104.06***		48.7	7944.25	294.23***
IPCAII (25)	1575.95	63.04**		28.9	1079.39	43.18		18.7	4869.69	194.79*
Error (276)	7572.55556	27.44	27.49		8864.06	32.12	16.53		30544.49	110.67
Residuals (276)	7572.56	27.44			8864.06	32.12			30544.49	110.67
	CV (%) = 10.94				CV (%) = 5.24				CV (%) = 19.63	
Growth traits										
Source of variation	Hundred seed weight(gm)				Number of branches per plants				Number of pods per plant	
	SS	MS	% TT	%GEI	SS	MS	% TT	%GEI	SS	MS
Total (546)	4987.55	9.13			1166.00	2.14			125015.04	228.97
Environments (5)	1620.34	324.07***	32.49		191.81	38.36***	16.45		16286.23	3257.25 ns
Rep (ENV) (12)	250.02	20.84	5.01		21.75	1.81	1.87		15199.23	1266.60
Genotypes (23)	1117.20	48.57***	22.40		240.41	10.45**	20.62		10278.85	446.91***
GEI (115)	580.84	5.05***	11.65		215.33	1.87***	18.47		23318.49	202.77**
IPCAI (27)	222.30	8.23***		38.30	94.80	3.51***		44.00	11755.64	435.39***
IPCAII (25)	133.22	5.33*		22.90	49.12	1.96**		22.80	5478.70	219.15*
Error (276)	838.31	3.04	16.81		281.37	1.02	24.13		36613.77	132.66
Residuals (276)	838.31	3.04			281.37	1.02			36613.77	132.66
	CV (%) = 10.53				CV (%) = 28.41				CV (%) = 29.58	
(Continues)										

(Continues)

TABLE 6 (Continued)

Source of variation	Number of seeds per plant				Harvest index (%)				Yield (Kg ha ⁻¹)			
	SS	MS	% TT	% GEI	SS	MS	% TT	% GEI	SS	MS	% TT	% GEI
Total (546)	460389	843			41.8	0.1			420110521	974734		
Environments (5)	23742	4748 ns	5.16		20.9	4.2	50.00		198793045	39758609***	47.32	
Rep (ENV) (12)	66090	5507	14.36		0.4	0.0	1.06		22104567	1842047***	5.26	
Genotypes (23)	27239	1184**	5.92		0.1	2.8	0.16		66486177	2890703***	15.83	
GEI (115)	98367	855***	21.37		6.1	0.1	14.59		59809305	1114144***	14.24	
IPCAI (27)	47806	1771***		48.6	5.0	0.2		81.80	30081895	1114144***		50.30
IPCAII (25)	23919	957*		24.3	0.5	0.0		8.60	11984468	479379*		20.04
Error (276)	146583.87	531.10	31.84		6.7	0.0			72917426	264194		
Residuals (276)	146584	531			6.7	0.0			17742941	281634 ns		
	CV (%) = 31.71				CV (%) = 35.41				CV (%) = 24.98			

*, **Significant at $p < 0.05$ and $p < 0.01$, respectively.

Rep (Env), replication within environment; MS, mean square; %Total SS, percentage of total sum of square. The value in the bracket indicates the degree of freedom.

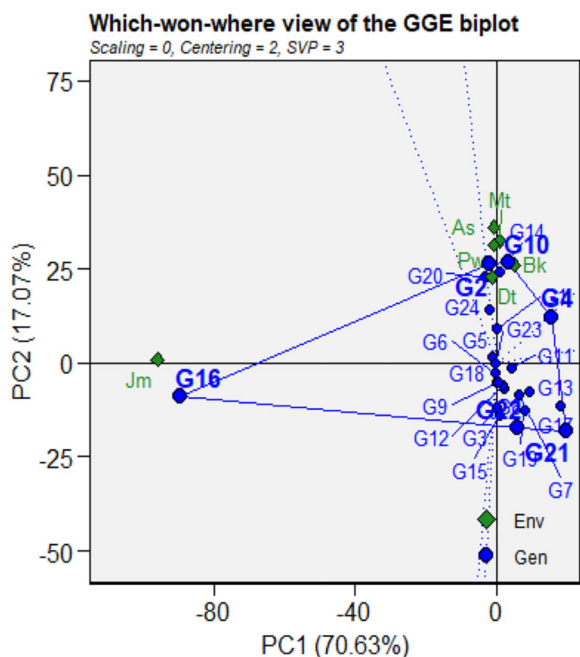


FIGURE 2 “Which-won-where” or “Which is best for what” pattern of genotype plus genotype by environment interaction (GGE) biplot based on 24 soybean genotypes evaluated in six soybean agro-ecologies of Ethiopia.

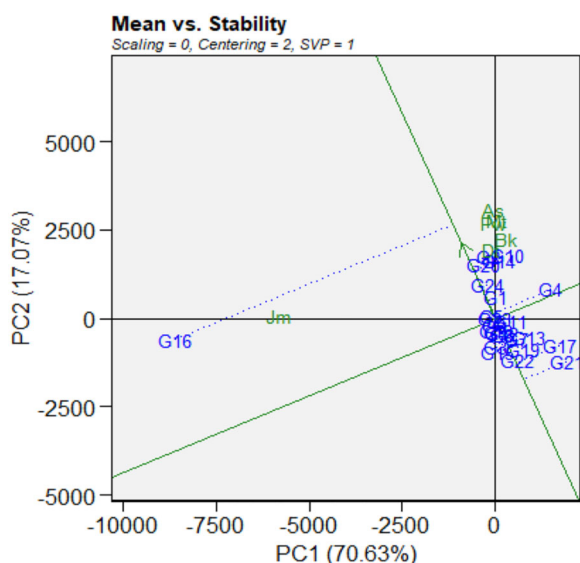


FIGURE 3 Genotype plus genotype by environment interaction (GGE) biplot showing the ranking of 24 genotypes (G1–G24) for both mean yield and stability based on the “average environment coordinate” (AEC).

the interaction, respectively. The stability of a genotype or an environment is determined by the end point of its vector from the origin (0,0). Genotypes near the origin are non-sensitive to environmental interactive forces, hence may be considered stable ones and those distant from origin are sensitive and have large interactions. Genotypes G22, G8, G7, G19, and

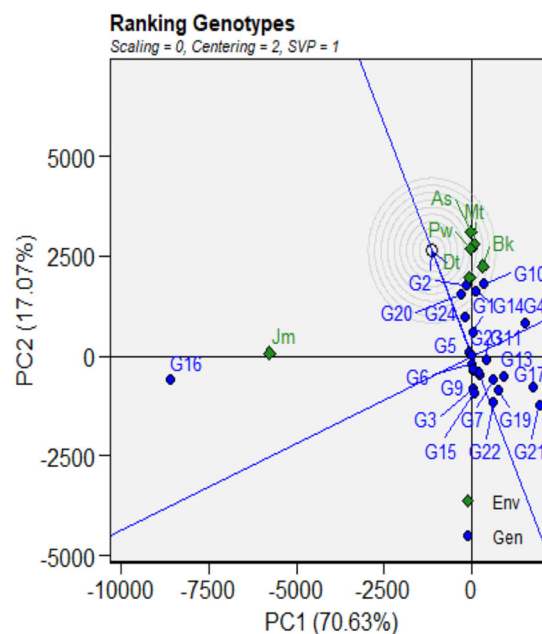


FIGURE 4 The genotype vector views to show similarity among genotypes in their performances in them individual environments.

G12 were closer to the origin than any of the other genotypes; hence, they are most stable (Figure 1B). In AMMI-2 biplot, the environment scores are joined to the origin by the side lines. Environments with short spokes (length of arrow lines) do not exert strong interactive forces. Those with long spokes (length of arrow lines) exert strong interaction. Metu (Mt) and Bako (Bk) having longer spokes exert high interaction while Asosa (As), Pawe (Pw), Dimtu (Dt), and Jimma (Jm) having shorter spokes produce a relative weak interaction.

The graph space (Figure 1B) are divided into IV quadrants from lower yielding environments in quadrant I and IV to high yielding in quadrants II and III. In addition, quadrant II is considered as the ideal environment. So, from the graph in Figure 1B, Asosa (As), Bako (Bk) and Pawe (Pw), which is in quadrant II, are ideal environments, while quadrant III characterizes in high yielding environment with unstable genotypes, in this quadrant Metu (Mt) is found. Similarly, quadrant I characterized stable genotypes and low yielding and in contrast quadrant IV unstable genotypes with the low yielding environment.

3.2.1 | AMMI stability value

The ASV measure was proposed by Purchase et al. (2000) to cope up to the fact that the AMMI model does not make a provision for a quantitative stability measure. In this method, as described by Purchase (1997) was calculated for each genotype in order to identify the stable one. Depending on this method, genotype with least ASV score is the stable;

TABLE 7 Estimation of selection differential, heritability, and indicators based on multi-trait stability index (MTSI) for agronomic traits.

Traits	Factor	Xo	Xs	SD	SD (%)	h ²	SG	SG (%)	Indicators	Goal
Number of seeds per plant	FA 1	72.7	72.9	0.242	0.333	0.278	0.0672	0.0924	Increase	100
Number of pods per plant	FA 1	38.9	38.3	-0.604	-1.55	0.546	-0.330	-0.847	Increase	0
Days to maturity	FA 2	108	108	-0.495	-0.458	0.896	-0.444	-0.410	Increase	0
100 Seed Weight (gm.)	FA 2	16.6	18.2	1.69	10.2	0.896	1.510	9.140	Increase	100
Number of branches per plant	FA 2	3.55	3.75	0.195	5.49	0.821	0.160	4.510	Increase	100
Days to flower	FA 3	47.9	46.7	-1.19	-2.48	0.483	-0.999	-2.090	Increase	0
Plant height (cm)	FA 3	53.6	50.6	-3.01	-5.62	0.906	-2.730	-5.090	Increase	0
Harvest index (%)	FA 3	0.440	0.434	-0.00657	-1.49	0.217	-0.00143	-0.324	Increase	0

Note: Xo, mean of genotype; Xs, mean of selected genotypes; SD, selection differential; G, selection gain; h², broad sense heritability.

Selected genotypes: G5, G15, G1 and G11.

TABLE 8 Combined analysis of variance and Eberhart and Russel's (1966) analysis for soybean genotypes on mean grain yield (kg ha⁻¹) tested in six across locations in Ethiopia.

Sources of variations	Degree of freedom	Sum squares	Mean square
Genotype (GEN.)	23	90884568.52	3951502.98***
ENV. + (GEN x ENV)	120	752777625.22	6273146.88
ENV. (linear)	1	481000078.87	481000078.87
GEN x ENV (linear)	23	165313381.97	7187538.35***
Pooled deviation	96	106464164.39	1109001.71
Total	143	843662193.75	5899735.62
G1	4	4395915.93	1098978.98 ns
G2	4	14229243.43	3557310.86 ns
G3	4	973341.62	243335.40 ns
G4	4	4653410.06	1163352.51 ns
G5	4	493249.91	123312.48 ns
G6	4	191603.33	47900.83 ns
G7	4	137813.95	34453.49 ns
G8	4	56360.73	14090.18 ns
G9	4	222549.79	55637.45 ns
G10(Check)	4	3392776.59	848194.15 ns
G11	4	694503.47	173625.87 ns
G12	4	924851.47	231212.87 ns
G13	4	617671.96	154417.99 ns
G14(Check)	4	3869870.17	967467.54 ns
G15	4	1113418.32	278354.58 ns
G16	4	59998913.80	14999728.45***
G17	4	2260632.73	565158.18 ns
G18	4	454019.69	113504.92 ns
G19	4	480681.76	120170.44 ns
G20	4	462677.98	115669.50 ns
G21	4	1399273.25	349818.31 ns
G22	4	847566.18	211891.55 ns
G23	4	598141.72	149535.43 ns
G24(Check)	4	3995676.53	998919.13 ns
Pooled error	276	633045756.28	2293644.04 ns

*, ** and *** = significance at 0.05, 0.01, and 0.001 level.

TABLE 9 Average performance of 24 soybean genotypes tested across six environments for grain yield.

Nº.	Genotype	Mean yield	Regression coefficient (b_i)	s^2d_i	RMS	R^2
1	G1	2319	1.144131	−398221.7 ns	494.18372	0.86
2	G2	2385	0.773540	421222.3 ns	889.10827	0.46
3	G3	1815	1.016154	−683436.2 ns	232.53932	0.96
4	G4	2337	0.427036	−376763.8 ns	508.45136	0.44
5	G5	2121	1.062433	−723443.9 ns	165.53783	0.98
6	G6	1981	1.051614	−748581.1 ns	103.17281	0.99
7	G7	1871	0.840815	−753063.5 ns	87.50046	0.99
8	G8	1909	0.981464	−759851.3 ns	55.95669	1.00
9	G9	1926	1.071796	−746002.2 ns	111.19297	0.99
10	G10(Check)	2903	0.622689	−481816.6 ns	434.15157	0.70
11	G11	2027	0.951228	−706672.7 ns	196.42690	0.96
12	G12	2000	0.919208	−687477.1 ns	226.67297	0.95
13	G13	1880	0.785696	−713075.4 ns	185.24338	0.95
14	G14(Check)	2770	0.769722	−442058.8 ns	463.67315	0.75
15	G15	1641	1.154644	−671763.2 ns	248.70982	0.96
16	G16	1656	3.632344***	4235361.5***	1825.72533	0.82
17	G17	1623	0.429924	−576162.0 ns	354.38779	0.62
18	G18	2003	0.984805	−726713.0 ns	158.81850	0.98
19	G19	1656	0.868595	−724491.2 ns	163.41524	0.97
20	G20	2853	0.942714	−725991.5 ns	160.32571	0.97
21	G21	1554	0.500942	−647941.9 ns	278.81428	0.78
22	G22	1558	0.956203	−693917.5 ns	216.99541	0.96
23	G23	2072	1.101154	−714702.9 ns	182.29124	0.98
24	G24(Check)	2522	1.011148	−431575.0 ns	471.14969	0.84

Note: Variance of b_0 : 127424.7; variance of b_i : 0.1144438. b_i = regression coefficient; S^2d_i = deviation from regression.

accordingly, genotype G21 followed by G11 and G8 in the third place were the most stable, respectively, while genotypes G10, G4, G17, G16, and G15 were undesirable. This result was also similar to the three genotypes' grain mean yield rank. This method illustrated in Table 4 shows the ASV for 24 genotypes compared with mean grain yield.

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

3.2.2 | Yield stability index

Yield stability index (YSI) incorporates both mean yield and stability in a single criterion. The low values of YSI selected as the desirable genotypes with high mean yield and stability.

3.2.3 | AMMI selections for the highest four yielding cultivars across six environments

The AMMI model selected four best genotypes in each environment and is illustrated in Table 5. The genotype that appeared in the top four environments in at least six environments was G14, which is followed by G20 (five env.), G10 (four), G24 (four), and G5 (two). The other cultivars G17, G2, and G4 appeared only once (Table 4).

3.3 | Analysis of variance for grain yield from ER's and AMMI models

The Bartlett's test revealed homogeneity of error variances of the individual locations, which indicated the possibility to perform combined analysis of variance for grain yield across the six environments. Results of the analysis of variance based on the AMMI model revealed highly significant ($p < 0.01$) differences among genotypes, environments, and

GEI for grain yield (Table 6). The GEI explained the highest proportion (30.36%) of the total sum of squares for grain yield, followed by genotypes (15.8%) and environments (9.9%). The mean squares for the first two interaction principal components (IPCAI and IPCAII) were highly significant ($p < 0.001$), explaining 55.1% and 28.4%, of the GEI, respectively, for grain yield with cumulative contributions of 83.5%.

The genotype explained the highest proportion (25.23%) of the total sum of squares for days to 50% flowering, followed by GEI (19.79%) and environments (6.94%), whereas the environments explained the highest proportion (40.08%) of the total sum of squares for days to maturity, followed by genotypes (20.74%) and GEI (10.75%), respectively (Table 5). The mean squares for IPCAI and IPCAII were highly significant and explaining 44% and 29.8%, and 48.7% and 18.7% of the GEI for days to flowering and maturity with cumulative contributions of 73.8% and 67.4%, respectively.

For the traits like hundred seed weight (gm) and harvest index (%), the environment explained the highest portion (50% and 32.49%), respectively; then, genotypes and GEIs which indicated those traits influenced more by environments than genotypes. On the contrary, traits like plant height (cm) and number of branches per plant exhibited a large proportion of genotype effect (29.05% and 20.62%) than that of the environments and/ or the GEIs, respectively. In addition, for the traits like number of seeds per plants and the number of pods per plants, the GEIs take the largest proportions (21.37% and 18.65%), respectively. The mean squares for both IPCAI and IPCAII were highly significant and explaining 44% and 28.9% for days to flower, 48.7% and 18.7% for days to maturity, 44.3% and 27.2% for plant height, 38.30 and 22.90% for hundred seed weight (gm), 44% and 22.80% for number of branches per plants, 50.4% and 23.5% for number of pods per plant, 48.6% and 24.3% for number of seeds per plant, 81.80% and 8.60% for harvest index (%) with cumulative contributions of respectively (Table 6).

3.4 | GGE biplot

3.4.1 | The which-won-where pattern

According to Yan et al. (2001), the polygon view of GGE biplot indicates the best genotypes in each environment and group of environments. In this situation, the polygon is formed by connecting the signs of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. In this case, the polygon connects all the farthest genotypes and perpendicular lines divide the polygon into sectors. Sectors help to visualize the mega-

environments. This means that winning genotypes for each sector are placed at the vertex. The pattern on the environment in the above biplot suggests the existence of three different mega-environments (Figure 2), but this pattern may not be repeatable across years (Yan et al., 2000). To confirm the repeatability of the mega-environment result, there need to be multiyear data (Yan, 2015).

For studying the possible existence of different mega-environments in a region, visualization of “which-won-where” pattern of the Meta environment trial is important as described by Yan et al. (2000, 2001). The vertex genotypes in this investigation were G17, G10, G20, G1, G15, and G22. This means that the vertex genotypes for each sector are the one that gave the highest yield for the environments that fall within that sector. Besides, it is evident from the GGE biplot in Figure 2 that environmental groupings, which suggests the existence of different mega environments. Thus, based on the biplot analysis of six environments of the data, the highest yielding in the environment in five and two are G10, and in environment Pawe and Asosa, G24. The other vertex genotypes, G15, G22, and G17, are poor performing in all the six environments.

3.4.2 | Mean yield and stability performance of genotypes

Stability can be identified based on concentric circles and also ideal genotypes are on the center of concentric circles, that is, high mean and stable. Besides this, good genotypes are close to ideal genotypes. A genotype is more desirable if it is closer to the “ideal” genotype (Mitrović et al., 2012). As illustrated in Figure 3, an important concept regarding “stability” only makes sense when accompanied by moderate performance. According to Figure 3, $G14 > G20 > G10 > G24 > G2 > G1$ is stable in their order and more desirable than other genotypes, where those ranked last, that is, G17, G16, and G21 on their rank, were unfavorable since there are too far from the ideal genotypes.

3.4.3 | Comparison among all genotypes

The distance between two genotypes approximates the Euclidean distance between them, which is a measure of the overall dissimilarity between them (Yan et al., 2006). In this case, Figure 4 illustrated G2 and G20 are quite similar, whereas G17 and G10 are very different. This implies that the dissimilarity is because of the variation in mean yield and or interaction with the environments. In addition, the biplot origin represents a “virtual” genotype that assumes an average value in each of the environment. This “average” genotype

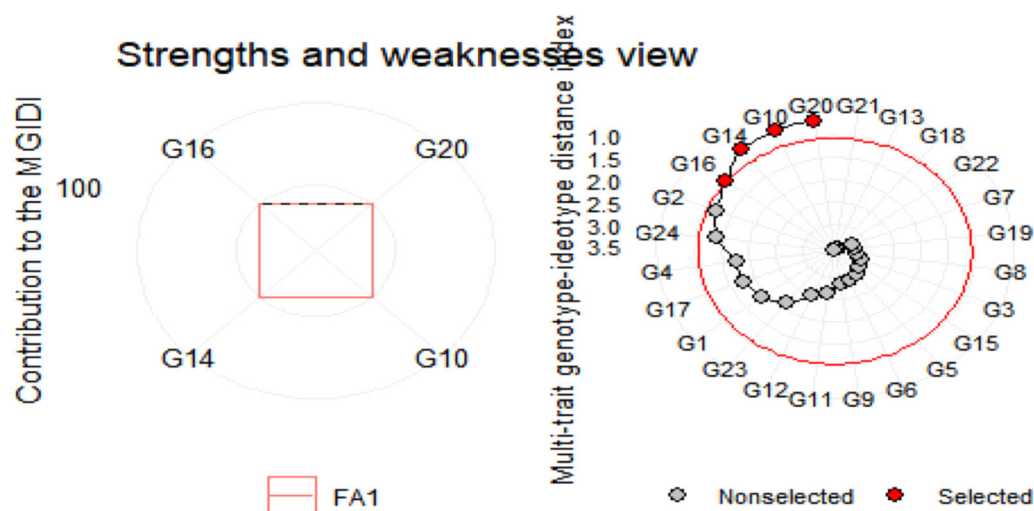


FIGURE 5 (A) Ranking of genotypes based on MGIDI index/MTSI analysis of genotypes for grain yield. (B) The selected genotypes are shown in the red and the spiral depicts the cut points according to the selection pressure. MTSI, multi-trait stability index.

has zero contributions to both G and GE (Yan et al., 2006) and inversely genotypes with larger vectors have large contributions to either G or GE or both. In this case, G12 and other genotypes in the smaller concentric circle are the average genotypes.

3.5 | Multi-trait stability index and genotype selection

The ranking of the 24 soybean genotypes based on MTSI values is presented in Table 6. The nine seed related traits, that is, number of seeds per plant, number of seeds per plant, number of pods per plant, days to maturity, hundred seed weight (gm), number of branches per plant, days to flower, plant height (cm), and harvest index (%) were used to estimate the MTSI (Figure 5). Figure 5B shows the ranking of genotypes for the MTSI presuming 15% selection intensity; four genotypes were selected, namely, G20, G20, G14, and G16 as the most stable and out performers out of 24 genotypes in present research work. The MTSI of 9.90 serve as the cut point (Figure 5, red circle) considering the selection intensity. The G2 and G16 genotypes were in close proximity to this red circle and may possibly possess remarkable characters. Therefore, in further research, it would be attractive to explore the performance of the genotypes near and close to the base cut point (Olivoto et al., 2019; Hussain et al., 2021). Besides, FA1 indicated the highest contribution for genotypes G16, G20, G10, and G14 (Figure 5A).

MTSI is an advanced tool used by the breeder to calculate the distance between an ideotype and genotype which identifies desirable genotypes for multiple traits (Munda et al., 2023). More interestingly, the MTSI has been recently used to help in selecting elite genotypes based on the stability and

mean performance of multiple traits (Olivoto et al., 2019). With respect to the criteria of MTSI, the genotypes with lower values of MTSI indicate higher stability based on multiple traits measured. In terms of feasibility of such index, the selection of these genotypes would greatly help in improving the overall mean performance as indicated by the high percentage of selection differentials. In a recent study on 46 soybean, stable soybean cultivars were identified under drought and salinity conditions based on the criterion of MTSI (Zuffo et al., 2020).

3.6 | Principal component analysis, factor analysis, and phenotypic breeding values

The mean of all the genotypes (X_o) as well as the mean of all the selected genotypes (X_s) were computed. The results demonstrated that the X_s was higher than X_o for the traits like number of seeds per plant, 100 seed weight (gm), plant height (cm), and harvest index (%). The selection differential was negative for traits like number of pods per plant (−0.604), days to maturity (−0.495), days to flower (−1.19), plant height (cm) (−3.01), and harvest index (%) (−0.00657) and positive values for number of seeds per plant (0.242), 100 seed weight (gm) (1.69), and number of branches per plant (0.195) (Table 7). According to the Robinson et al. (1949) heritability classification, the heritability of the traits for number of seeds per plant (27.8%) and harvest index (%) (21.7%) was found low, medium heritability for traits like number of pods per plant (54.6%), and high heritability for days to flower (48.3%), days to maturity (89.6%), 100 seed weight (gm) (89.6%), and number of branches per plant (82.1%), respectively. Similar result was obtained by Zuffo et al. (2020) where the heritability values were higher than 78%, indicating success with

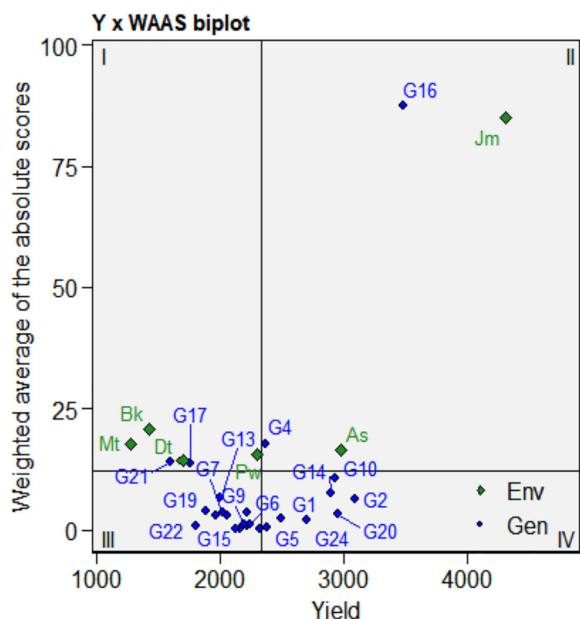


FIGURE 6 Seed yield per plant $\times$ WAASB biplot based on combined interpretation of Yield and stability (WAASB) for 24 soybean genotypes evaluated across six environments during main 2015/16 cropping season.

superior genotype selection for most evaluated traits, except for SDM in drought. Traits were rescaled by assigning all traits a value between 0 and 100 based on the MTSI/MGIDI index, which is an ideotype concept, 0 defines the least valued trait and 100 the most valuable/desirable trait, reflecting the facilitated definition of ideotypes (Donald, 1968)

3.7 | Weighted average absolute scores (Y $\times$ WAAS) biplot

A Y $\times$ WAAS biplot was created with seed yield on the X-axis and WAAS values on the Y-axis (Figure 6). The figure divides the genotypes into four quadrants, allowing simultaneous genotype selection with high seed yield and stability of the variables involved. According to the biplots (Figure 6), three genotypes, including “Mt” (Metu), “Bk” (Bako), “Dt” (Dimtu), and “Pw” (Pawe), were the first quadrant’s genotypes with low productivity and strong discriminative ability shows greater genotypic instability. Two genotypes, including “Jm” (Jimma) and “As” (Asosa), are in the second quadrant with low stability and high grain yield, advising special attention to the environment to increase grain yield (Huang et al., 2021). The third quadrant included 13 genotypes having more stability (due to the low WAAS value) but lesser productivity, while the remaining 7 genotypes found in the fourth quadrant had greater stability and fantastic performance for grain yield production. In the future, research using the genotypic stability index WAASB, which was developed in this study, may be able to provide accurate estimates of stability, enabling

collaborative interpretation of performance and stability in a bidimensional plot involving two or more IPCA (Olivoto et al., 2019) and WAASB statistic was used to better characterize ideal genotypes based on both yield performance and stability (Pour-Aboughadareh et al., 2021).

3.8 | Eberhart and Russel’s model

Cultivars with high mean ($\bar{X}$), unit regression coefficient ($b_i = 1.0$) has deviations from regression as small as possible ($S_{dij} = 0$). Hence, the definition of a stable variety in this paper will be one with $b = 1.0$ and $s \sim a = 0$.

The genotype–environment interaction component (GEI) was elaborated by using the joint regression model of stability analysis (Eberhart & Russell, 1966). The mean grain yield per plot among the genotypes ranged from 1554 to 2903 Kg ha⁻¹, with an overall genotype mean of 2057.58 Kg ha⁻¹. The check variety AFGAT gave the maximum grain yield per plant (2903 Kg ha⁻¹), whereas minimum grain yield per plot was observed in LDOO-3309 (1554 Kg ha⁻¹) (Table 8). The Eberhart and Russell (1966) regression model has been widely used in the past few decades mainly because variability in performance of any genotype could be subdivided into predictable (regression) and unpredictable (var-dev) components and provided useful information on stable genotypes; a broader picture in conjunction with high yield could not be wholly predicted (Alwala et al., 2010). From Table 9, the genotype G16 is significantly deviated from the regression.

4 | CONCLUSIONS

The main objective and need of breeders, researchers, and growers who can thrive in various settings is high crop productivity. Using different multivariate analyses, such AMMI, WAASB, GGE biplot, Eberhart and Russell’s model, and MTSI evaluation, a multi-location study for a season was carried out on 24 germplasm of soybean. Four genotypes (G20, G20, G14, and G16) were determined to be the best and most stable for the grain yield attributes by a multi-trait stability index analysis. The chosen genotypes could be suggested for commercial production and used in a program to develop new soybean varieties. Dimtu and Jimma were the two environments that made up the first mega environment. Asosa and Pawe were the two environments that made up the second mega environment. Additionally, the GGE biplot’s discriminating power versus representativeness view has proven to be a useful tool for assessing test environments. Of the evaluated soybean genotypes, environment Bako was the most discriminating for grain yield, while Metu and Jimma were the worst at choosing cultivars suited to the entire region. While, MTSI is a new technique for evaluating stability based on many variables for larger adaptations, the multivariate

techniques utilized in the current study are shown to be extremely effective in identifying superior and stable genotypes.

AUTHOR CONTRIBUTIONS

Mesfin Hailemariam Habtegebriel: conceptualization; data curation; formal analysis; funding acquisition; investigation; methodology; resources; software; validation; visualization; writing—original draft; writing—review and editing. **Abush Tesfaye Abebe:** conceptualization; data curation; formal analysis; funding acquisition; project administration; resources; software; supervision.

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DATA AVAILABILITY STATEMENT

Available in the supplementary materials.

CONFLICT OF INTEREST STATEMENT

The authors declare no competing interests.

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REFERENCES

- Abdelghany, A. M., Zhang, S., Azam, M., Shaibu, A. S., Feng, Y., Qi, J., Li, J., Li, Y., Tian, Y., Hong, H., Lamlo, S. F., Li, B., & Sun, J. (2021). Exploring the phenotypic stability of soybean seed compositions using multi-trait stability index approach. *Agronomy*, 11(11), 2200. <https://doi.org/10.3390/agronomy11112200>
- Adane, A., Alemayehu, D., Meseret, T., & Chala, D. (2018). Genotype and genotype by environment interaction and grain yield stability of medium maturity groups of soybeans [*Glycine max* (L.) Merrill] varieties in Western Oromia, Ethiopia. *African Journal of Plant Science*, 12(9), 227–237. <https://doi.org/10.5897/AJPS2018.1674>
- Agoyi, E.E., Odong, T.L., Tumuhairwe, J.B., Chigeza, G., Diers, B. W., & Tukamuhabwa, P. (2017). Genotype by environment effects on promiscuous nodulation in soybean (*Glycine max* L. Merrill). *Agriculture & Food Security*, 6. <https://doi.org/10.1186/s40066-017-0107-7>
- Alwala, S., Kwolek, T., Mcpherson, M., Pellow, J., & Meyer, D. (2010). A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. *Field Crops Research*, 119(2-3), 225–230. <https://doi.org/10.1016/j.fcr.2010.07.010>
- Asfaw, A., Alemayehu, F., Gurum, F., & Atnaf, M. (2009). AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. *Scientific Research and Essays*, 4(11), 1322–1330. <https://doi.org/10.5897/sre.9000148>
- Atnaf, M. (2013). GGE biplots to analyze soybean multi-environment yield trial data in north Western Ethiopia. *Journal of Plant Breeding and Crop Science*, 5(12), 245–254. <https://doi.org/10.5897/JPCBS13.0403>
- Chen, H., Chung, M.-C., Tsai, Y.-C., Wei, F.-J., Hsieh, J.-S., & Hsing, Y.-I. C. (2015). Distribution of new satellites and simple sequence repeats in annual and perennial *Glycine* species. *Botanical Studies*, 56, 22. <https://doi.org/10.1186/s40529-015-0103-9>
- Donald, C. M. (1968). The breeding of crop ideotypes. *Euphytica*, 17, 385–403. <https://doi.org/10.1007/BF00056241>
- Eberhart, S. A., & Russell, W. A. (1966). Stability parameters for comparing Varieties. *Crop Science*, 6(1), 36–40. <https://doi.org/10.2135/cropsci1966.0011183x000600010011x>
- Fehr, W. R., & Caviness, C. E. (1977). *Stages of soybean development. Special report-80*. Iowa State University of Science and Technology. <https://dr.lib.iastate.edu/handle/20.500.12876/90239>
- Gauch, H. G., & Zobel, R. W. (1996). Optimal replication in selection experiments. *Crop Science*, 36(4), 838–843. <https://doi.org/10.2135/cropsci1996.0011183X003600040002x>
- Gauch, H. G., & Zobel, R. W. (1997). Identifying mega-environments and targeting genotypes. *Crop Science*, 37, 311–326. <https://doi.org/10.2135/cropsci1997.0011183x003700020002x>
- Gurmu, F., Mohammed, H., & Alawa, G. (2009). Genotype x environment interactions and stability of soybean for grain yield and nutrition quality. *African Crop Science Journal*, 17(2), 87–99. <https://doi.org/10.4314/acsj.v17i2.54202>
- Hamawaki, R. L., Hamawaki, O. T., Nogueira, A. P. O., Lemes Hamawaki, C., Sousa, L., Lightfoot, D., & Kantartzi, S. (2015). Adaptability and stability analysis of soybean genotypes using toler and centroid methods. *American Journal of Plant Sciences*, 6, 1509–1518. <https://doi.org/10.4236/ajps.2015.69150>
- Happ, M. M., Graef, G. L., Wang, H., Howard, R., Posadas, L., & Hyten, D. L. (2021). Comparing a mixed model approach to traditional stability estimators for mapping genotype by environment interactions and yield stability in soybean [*Glycine max* (L.) Merr.]. *Frontiers in Plant Science*, 12, 630175. <https://doi.org/10.3389/fpls.2021.630175>
- Huang, X., Jang, S., Kim, B., Piao, Z., Redona, E., & Koh, H.-J. (2021). Evaluating genotype x environment interactions of yield traits and adaptability in rice cultivars grown under temperate, subtropical and tropical environments. *Agriculture*, 11(6), 558. <https://doi.org/10.3390/agriculture11060558>
- Hussain, T., Akram, Z., Shabbir, G., Manaf, A., & Ahmed, M. (2021). Identification of drought tolerant chickpea genotypes through multi trait stability index. *Saudi Journal of Biological Sciences*, 28(12), 6818–6828. <https://doi.org/10.1016/j.sjbs.2021.07.056>
- Hymowitz, T., & Newell, C. A. (1981). Taxonomy of the genus *Glycine*, domestication and uses of soybeans. *Economic Botany*, 35, 272–288. <https://doi.org/10.1007/BF02859119>
- International Board for Plant Genetic Resources (IBPGR). (1984). *Descriptors for soyabean*. International Board for Plant Genetic Resources.
- Lee, S. Y., Lee, H. S., Lee, C. M., Ha, S. K., Park, H. M., Lee, S. M., Kwon, Y., Jeung, J.-U., & Mo, Y. (2023). Multi-environment trials and stability analysis for yield-related traits of commercial rice cCultivars. *Agriculture*, 13(2), 256. <https://doi.org/10.3390/agriculture13020256>
- Mitrović, B., Treski, S., Stojaković, M., Ivanović, M., & Bekavac, G. (2012). Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analyses. *Turkish Journal of Field Crops*, 17(1), 35–40.
- Morsy, A., Fares, W., Ragheb, S., & Ibrahim, M. (2015). Stability analysis of some soybean genotypes using a simplified statistical model.

- J. Plant Prod. Mansoura Univ*, 6(12), 1975–1990. <https://doi.org/10.21608/jpp.2015.52124>
- Munda, S., Paw, M., Saikia, S., Begum, T., Baruah, J., & Lal, M. (2023). Stability and selection of trait specific genotypes of *Curcuma caesia* Roxb. using AMMI, BLUP, GGE, WAAS and MTSI model over three years evaluation. *Journal of Applied Research on Medicinal and Aromatic Plants*, 32, 100446. <https://doi.org/10.1016/j.jarmap.2022.100446>
- Mwiinga, B., Sibiyi, J., Kondwakwenda, A., Musvosvi, C., & Chigeza, G. (2020). Genotype x environment interaction analysis of soybean (*Glycine max* (L.) Merrill) grain yield across production environments in Southern Africa. *Field Crops Research*, 256, 107922. <https://doi.org/10.1016/j.fcr.2020.107922>
- Nataraj, V., Bhartiya, A., Singh, C. P., Devi, H. N., Deshmukh, M. P., Verghese, P., ... Gupta, S. (2021). WAASB-based stability analysis and simultaneous selection for grain yield and early maturity in soybean. *Agronomy Journal*, 113(4), 3089–3099. <https://doi.org/10.1002/agj2.20750>
- Nigussie, D. (2018). GIS-based land suitability mapping for legume crops technology targeting and scaling-up. *Ethiopian Journal of Crop Science*, 6(3), 179–198.
- Olivoto, T., Lúcio, A. D., da Silva, J. A., Marchioro, V. S., de Souza, V. Q., & Jost, E. (2019). Mean performance and stability in multi-environment trials I: Combining features of AMMI and BLUP techniques. *Agronomy Journal*, 111(6), 2949–2960. <https://doi.org/10.2134/agronj2019.03.0220>
- Olivoto, T., & Lúcio, A. D. (2020). metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, 11(6), 783–789. <https://publons.com/publon/10.1111/2041-210X.13384>
- Pour-Aboughadareh, A., Sanjani, S., Nikkhah-Chamanabad, H., Mehrvar, M. R., Asadi, A., & Amini, A. (2021). Identification of salt-tolerant barley genotypes using multiple-traits index and yield performance at the early growth and maturity stages. *Bulletin of the National Research Centre*, 45, 117. <https://doi.org/10.1186/s42269-021-00576-0>
- Purchase, J. L. (1997). *Parametric analysis to describe genotype by environment interaction and stability in winter wheat* [PhD thesis, Department of Agronomy, Faculty of Agriculture, University of the Orange Free State].
- Purchase, J. L., Hatting, H., & Van Deventer, C. S. (2000). Genotypex environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South African Journal of Plant and Soil*, 17(3), 101–107. <https://doi.org/10.1080/02571862.2000.10634878>
- Qasemi, S. H., Mostafavi, K., Khosroshahli, M., Bihamta, M. R., & Ramshini, H. (2022). Genotype and environment interaction and stability of grain yield and oil content of rapeseed cultivars. *Food Science & Nutrition*. <https://doi.org/10.1002/fsn3.3023>
- Qin, P., Wang, T., & Luo, Y. (2022). A review on plant-based proteins from soybean: Health benefits and soy product development. *Journal of Agriculture and Food Research*, 7, 100265. <https://doi.org/10.1016/j.jafr.2021.100265>
- Ranjekesh, N., & Talubaghi, M. J. (2023). Agronomic characteristics and grain yield of 30 Iranian rice genotypes as affected by genotype x environment interaction. *Ecological Genetics and Genomics*, 26, 100153. <https://doi.org/10.1016/j.egg.2022.100153>
- Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*, 41(8), 353–359. <https://doi.org/10.2134/agronj1949.00021962004100080005x>
- Sritongtae, C., Monkham, T., Sanitchon, J., Lodthong, S., Srisawangwong, S., & Chankaew, S. (2021). Identification of superior soybean cultivars through the indication of specific adaptabilities within duo-environments for year-round soybean production in northeast Thailand. *Agronomy*, 11(3), 585. <https://doi.org/10.3390/agronomy11030585>
- Tesfaye, A., Adane Arega, B. A., Degu, T., & Hailemariam, M. (2018). Progresses in breeding and genetic improvement of soybean in Ethiopia: A review. *Ethiopian Journal of Crop Science*, 6(3), 129–152.
- VSN. (2011). *GenStat for Windows* (14th ed. Release 16.1) [Computer software]. VSN International.
- Whaley, R., & Eskandari, M. (2019). Genotypic main effect and genotype-by-environment interaction effect on seed protein concentration and yield in food-grade soybeans (*Glycine max* (L.) Merrill). *Euphytica*, 215, 33. <https://doi.org/10.1007/s10681-019-2344-2>
- Yan, W. (2002). Singular-value partitioning in biplot analysis of multi-environment trial data. *Agronomy Journal*, 94(5), 990–996. <https://doi.org/10.2134/agronj2002.9900>
- Yan, W. (2015). Mega-environment analysis and test location evaluation based on unbalanced multiyear data. *Crop Science*, 55(1), 113–122. <https://doi.org/10.2135/cropsci2014.03.0203>
- Yan, W., Cornelius, P. L., Crossa, J., & Hunt, L. A. (2001). Two types of GGE biplots for analyzing multi-environment trial data. *Crop Science*, 41(3), 656–663. <https://doi.org/10.2135/cropsci2001.413656x>
- Yan, W., Hunt, L. A., Sheng, Q., & Szlavniks, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, 40(3), 597–605. <https://doi.org/10.2135/cropsci2000.403597x>
- Yan, W., & Tinker, N. A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian journal of plant science*, 86(3), 623–645. <https://doi.org/10.4141/P05-169>
- Yan, W., & Wu, h. (2008). Application of GGE biplot Analysis to Evaluate Genotype (G), Environment (E), and GxE interaction on *pinus radiata*: A case study. *New Zealand Journal of Forestry Science*, 38(1), 132–142. <https://hdl.handle.net/1959.11/3557>
- Yirga, M., Sileshi, Y., Tesfaye, A., & Hailemariam, M. (2022). Genetic variability and association of traits in soybean (*Glycine max* (L.) genotypes in Ethiopia. *Ethiopian Journal of Crop Science*, 9(2), 49–74.
- Zobel, R. W., Wright, M. J., & Gauch, H. G. (1988). Statistical analysis of a yield trial. *Agronomy Journal*, 80, 388–393. <https://doi.org/10.2134/agronj1988.00021962008000030002x>
- Zuffo, A. M., Steiner, F., Aguilera, J. G., Teodoro, P. E., Teodoro, L. P. R., & Busch, A. (2020). Multi-trait stability index: A tool for simultaneous selection of soya bean genotypes in drought and saline stress. *Journal of Agronomy and Crop Science*, 206(6), 815–822.

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