Heliyon 10 (2024) e28764

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon

Research article

Stability analysis and nutritional quality of soybean (*Glycine max* (L).*Merrill*.) genotypes for feed in southwestern Ethiopia

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ARTICLE INFO

Keywords:
Dry matter yield
Environment
GGE biplot
Nutritive values
And soybean genotypes

ABSTRACT

Soybean is a leguminous crop known for its multiple utilizations both as food and feed for humans and livestock. The objectives of the study were to identify high dry matter yielder and stable genotypes across environments in southwestern Ethiopia. The effect of genotype environment (G x E) interaction on dry matter yield of soybean genotypes were evaluated in two cropping seasons (2019–2020) under rain fed condition. Eight pre tested soybean genotypes with two checks were used as treatment in a randomized complete block design with three replications. Collected data were recorded and analyzed using GGE biplot models using R software. The combined analysis of variance showed that dry matter yield of soybean genotypes was significantly affected by genotype, environment and genotype-environment (G x E) interaction. The genotype, environment, and genotype-environment interaction, respectively, accounted for 11.4%, 49.5%, and 38.8% of the observed variation to the dry mater yield. This indicates that dry matter yield was significantly more affected by environments and G × E interaction than genotypes. The GGE biplot analysis revealed that six environments used in the current study were grouped into four mega-environments. The mega-environments were identified for genotype evaluation. The biplot showed that the vertex genotypes were G4, G10, and G9 and considered as optimum performance in their respective mega-environments and more responsive to environmental changes. The biplot also showed that ENV5 (Kersa 2020) was an ideal and the most discriminating and representative environment. Genotype G4 (TGX1990-114FN) was the ideal genotype and overall winner in dry matter yield and stability in the findings. Therefore, genotype G4 (TGX-1990-114FN) is the better option to be used as forage soybean in Ethiopia. Further demonstration of the feeding values of high yielders and stable genotypes on animal performances should be done.

1. Introduction

The major constraints to livestock productivity are shortage of feed in quantity and quality particularly in dry season [37]. This situation prone animal's poor performance, low growth rates, reduced reproductive efficiency and high mortality [4]. The source of livestock feed in Ethiopia are mainly natural pasture and crop residues. The natural pastures decline from time to time because of the increase in the size of croplands [5]. However, the contribution of these feed depends on the agro-ecology, the type of crop produced, accessibility and production systems [8]. Production of adequate and quality forage to supplement crop residues and pasture

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https://doi.org/10.1016/j.heliyon.2024.e28764
Received 16 October 2023; Received in revised form 22 March 2024; Accepted 24 March 2024
Available online 29 March 2024

roughages is the way to economically mitigate the dry season shortage affecting livestock production in Ethiopia. Almost all small scale farmers' livestock are highly dependent on grazing lands and crop residues for few period of times [16]. However, most of the areas have no communal grazing lands and no forage conservation management practices [5]. The livestock productivity under such type of production system will not maximize unless quantitative and quality feed supplied even if the maintenance requirement fulfill. Supplying balanced nutrition to livestock improves animal productivity as well as reduces production costs and decrease emission of greenhouse gases per unit of animal product [22]. Therefore, evaluating nutrient enriches forage genotypes to supplement crop residues and pasture feeding practice is the best options to mitigate feed shortage and climate change impacts [4,23,24].

Soybean is a leguminous crop known for its multiple utilizations both as food and feed for humans and livestock [25]. Literature indicates that soybean grain, steam, and leaf have a tremendous advantage in supplementing livestock for their maximum production, unlike most legume crops [33]. When soybean forages are alternated with corn (Zea mays L.) or other non-legume crops, benefits are gained in the form of lingering nitrogen in the soil. Furthermore, because land is not committed for many years, forage soybeans are preferred in crop rotations over perennial legumes [36]. Soybean forages are either grazed or harvested from the flowering stage to near maturity for use as high-quality forage [25]. It can also be grown as silage in pure culture or intercropped with corn or sorghum [18]. The performance of soybean genotypes differ over environments and their dry matter yield performance is determined by genotype, environment and genotype x environment (G x E) interaction. The soil types, temperature and amount of rainfall distribution in different environments also determine dry matter yield performance of forage soybean genotypes.

Testing the most adaptable and high-yielding potential of different forage crops in different environments and growing seasons are important to identify the best-bet genotypes for utilization. The G × E interaction is significant in plant breeding programs since the G × E interaction impairs efforts in the selection of genotypes [49]. In multi-environmental experiments, G × E interactions develops as a result of unpredictable macro- and micro-environmental effects such as temperature, rainfall, and humidity [45]. Understanding the nature of G × E interaction is used to determine whether to develop genotypes for all locations or to develop specific genotypes for specific target locations [19]. There are several approaches for determining G × E interactions and identifying stable genotypes, including parametric, non-parametric, and graphical estimates Graphical estimation methods, such as additive main effects and multiplicative interaction (AMMI) and genotype and genotype by environment interaction (GGE), are used to measure and interpret G × E interactions for multi-environmental trials for the investigation of yield stability [26]. The GGE biplot analysis is used to identify ideal genotypes for specific environments, the stability of the genotypes, potential mega-environments (which-won-where), and cross-over and non-cross-over genotype by environment interactions [7]. The GGE biplot is superior to the AMMI model in mega-environment analysis and genotype evaluation because it explains more genotype and GxE interactions and has the inner--product property of the biplot. The discriminating power versus representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis [48]. Therefore, GGE model was used to evaluate and identify soybean genotypes in order to study genotype-environment interaction effects and to select high-yielding and stable genotypes across environments. Therefore, the study's aims were to evaluate soybean genotypes for dry matter production, and to identify stable genotypes

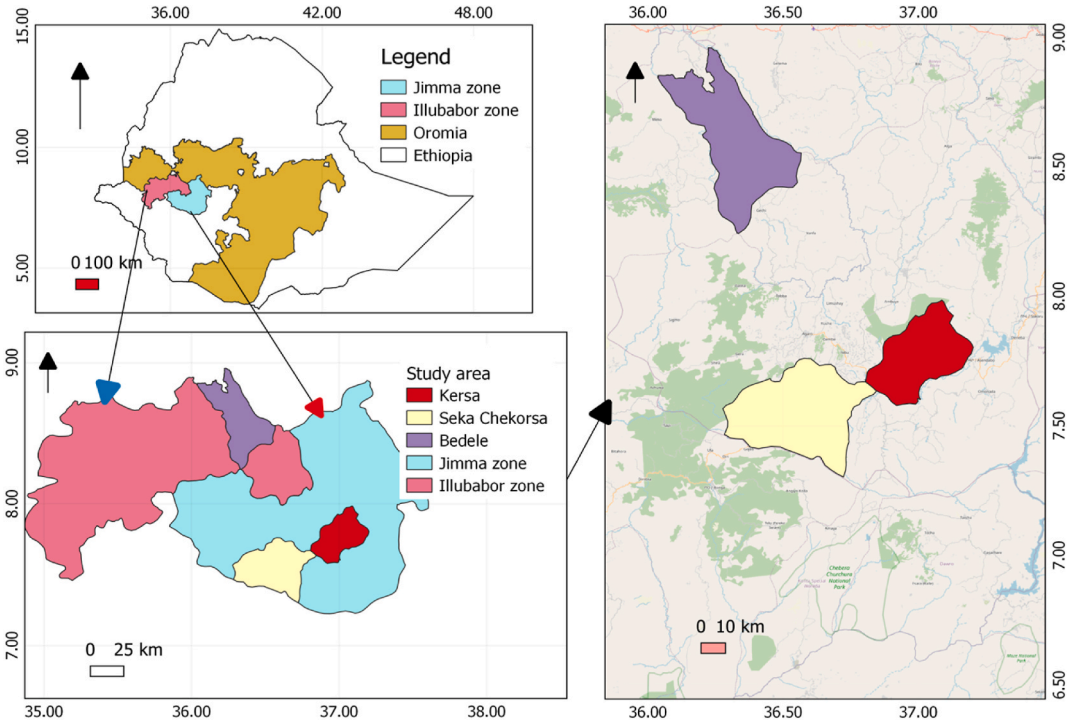

Fig. 1. Study area map.

across environments in southwestern part of Ethiopia. The nutritional quality of forage soybeans was also determined.

2. Materials and methods

2.1. Study area

The study was conducted in 2019–2020 at three locations in southwest Ethiopia: Jimma (Melko), Bedele (Banchure kebele), and Kersa (Kitble kebele) during two consecutive cropping seasons (Fig. 1, Table 1). The soil type of Jimma (Melko), Kersa and Bedele are Nitosol with a pH of 5.1, 5.38 and 5.48, respectively. The study sites were selected purposively to evaluate forage soybean genotypes across different agro-ecologies and climatic zone. The study area practices mixed farming system.

2.2. Experimental design and lay out

The introduced soybean genotypes were collected based on secondary information from the records of the last two (2017–2018) cropping seasons undertaken at the nursery and field conditions of the Jimma Agriculture Research Center. Genotypes were evaluated via split lattice design. The selected soybean genotypes were planted in randomized complete block design (RCBD) with three replications. Eight soybean accessions with two checks (lablab and Afgat) were used for the experiment. The planting materials of soybean genotypes were obtained from (pulse, oil and fiber crops case team working at Jimma Agriculture Research Center.

2.3. Planting and field management

Before planting, the experimental land was first cleared from weeds and ploughed three times, and then 2.16 kg of soybean seeds were sowed at the beginning of the main rain season in June 2019. The seeding rate of soybean genotypes was 60 kg/ha [6]. The experimental plot size was 12 m^2 (4 × 3 m) for each treatments. The spacing between rows, plots and blocks were 0.6 m, 1 m, and 1.5 m, respectively. The spacing between plants was 5 cm, and the number of rows per plot was six. Nitrogen, phosphorus and sulfur (NPS) fertilizer was uniformly applied to all treatments at the rate of 100 kg/ha. Then all agronomic practices such as weeding and tinning were done as required. Harvesting for forage green yield was made manually by sickle at 50% flowering stage of the forage. All the field and agronomic data and samples required were collected from planting to harvesting date.

2.4. Data collection and measurement

The green herbage yield and dry matter yield of forage soybean genotypes were collected during 50 % flowering stage of the forage. A 500-g fresh representative sample was taken from each plot using paper bags and placed in an oven at 65 °C for 72 h. The dried sample was measured in each plot and converted to hectares to calculate dry matter yield.

2.5. Nutritional value

Nutritional compositions were determined at the Holeta Agricultural Research Center (HARC) in the Animal Nutrition Laboratory. To determine the chemical constituents, 500 g of fresh samples were taken, stored in an airtight bag, and subjected to a forced air draft oven at 650 °C for 72 h [29]. Then the dried samples were then ground and passed through a 1 mm-wide sieve. All samples were subjected to chemical analysis for the determination of organic matter following the methods of [9]. Crude protein (CP) (Kjeldhal method), acid detergent fiber (ADF), neutral detergent fiber (NDF), and acid detergent lignin (ADL) were analyzed using the procedure of the Van Soest method. Ash was determined by igniting at 550 °C overnight [9]. [41] Tilley and Terry's procedure was used to determine in vitro dry matter digestibility.

2.6. Data analysis

The collected data were subjected to combined analysis of variance using R software after testing the ANOVA assumption to examine the main effect of environment and genotype. Least significant difference (LSD) at 5% level of probability was used for comparison of means among treatments. Genotype main effect and genotype × environment interaction effect (GGE) biplot analysis were used to determine the effects of G × E interaction on dry matter yields [46]. The GGE model used was:

Table 1
Description of experimental sites where trials were conducted.

Sites	Altitude	Latitude	Longitude	Temperature(°C)		annual rain fall (mm)	
				2019	2020	2019	2020
Melko/Jarc	1763 masl	7°40′N	36° 47′E	27.4	27.6	2272.5	1529.8
Bedele	2087 m asl	8°27′N	36° 21′E	30.0	28.23	1461.1	1500.1
Kersa	2784 m asl	7°44′N	37° 04′E	28.3	27.02	1487.8	1654.1

$$Yij - \mu - \beta j = \lambda 1 \xi i 1 \eta j 1 + \lambda 2 \xi i 2 \eta j 2 + \varepsilon ij \quad (1)$$

Where *Yij* is measured mean of genotype *i(=1,2, ….,n)* in environment *j(=1,2 …,m)*, μ is the grand mean, βj is the main effect of environment *j*, $\mu + \beta j$ being the mean yield across all genotypes in environment *j*, $\lambda 1$ and $\lambda 2$ are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, $\xi i1$ and $\xi i2$ are eigenvectors of genotype I for PC1 and PC2, respectively, $\eta 1j$ and $\eta 2j$ are eigenvectors of environment *j* for PC1 and PC2, respectively, εij is the residual associated with genotype *i* in environment *j*.

3. Results and discussion

3.1. Combined analysis of variance

The combined mean square values of soybean genotypes for dry matter yield were presented in Table 2. The result indicated that dry matter yield was significantly affected ($P < 0.05$) by genotypes, environments and genotype x environment (G x E) interaction. The considerable variation between tested genotypes demonstrates that genetic variability exists among soybean genotypes. The analysis result also showed that principal component 1 (PC1) and principal component 2 (PC2) had significant differences. This showed that strong genotype-environment interactions caused considerable differences in dry matter yield among soybean genotypes across the investigated environments. The significant differences in G × E interaction for the DM yield of genotypes are an indication of different performances of genotypes across environments. This necessitates the investigation of the nature of the different responses of the genotypes to environments. The genotype, environment, and genotype-environment interaction, respectively, accounted for 11.4%, 49.5%, and 38.8% of the observed variation to the dry mater yield. The PC 1 and PC2 principal components were explained by 48.9 % and 32.8 % of the G × E interaction (Table 2). The degree of variation of environment had greater influence on soybean dry matter yield performances. This finding is in line with previous studies reported by Refs. [7,17,20,27]. The interplay between genotype and environment is significant for plant breeding because it has an impact on genetic gain and the selection of cultivars with a wide range of adaptation [39]. The interaction is a result of variations in cultivar performance in various environments brought on by genotype-specific responses to biotic, edaphic, and climate-related factors [21]. For optimum management and exploitation, it is crucial to assess the yield performance and adaption patterns of different soybean genotypes across location.

3.2. Dry matter yield performance of soybean genotypes in location

The highest mean dry matter yield of soybean genotypes (t/ha) was recorded from G3 (9.7) and G4 (9.4), with a grand mean of 8.1 (Table 3). Genotype six (G6), on the other hand, gave the lowest dry matter yield (6.9 t/ha) compared to others. Checks G2 (lablab) and G 10 (Afgat) were given relatively lower dry matter yields compared to the tested genotypes, particularly G3 and G4. The current study found a slightly similar dry matter yield (t/ha) to the findings of [25,35,36] conducted in different parts of the world. The current studies' mean dry matter yield (8.1 t/ha) was lower than that reported by Ref. [2] (15.1 t/ha) [3], (18.6 t/ha), and [1] (11.0 t/ha). On the other hand, a higher dry matter yield of soybean was found in the current finding than in the study reported by Ref. [31],who reported a low dry matter yield of lablab genotypes. This discrepancy is caused by differences in testing fodder soybean genotypes, soil type, sowing rate, row spacing, harvesting stage, agro-ecology differences, and other associated factors. The higher mean dry matter yields were found at ENV2 (Kersa 2019) and ENV5 (Kersa 2020) experimental sites (Table 3). Soybean genotypes G4 and G3 showed better performance in DM yields in all locations compared to checks (Lablab and Afgat). Genotype G9, G3, G4, and G7 gave a higher dry matter yield at ENV2 (Kersa 2019), while G3, G7, and G5 recorded a better dry matter yield at ENV5 (Kersa 2020). Genotype G7, G4, G3, and G10 genotypes had significantly high dry matter yields at ENV1 (Melko2019) and ENV4 (Melko 2020). These different dry matter yields across tested environments showed the existence of cross-over GEI.

3.3. Genotype and genotype by environment interaction (GGE) biplot analysis

The first two principal components (PC), the biplot explained 66.41% of the total variation observed. The first and second interaction principal components (axis 1 and 2) explained 40.98% and 25.43% variation, respectively.

The genotypes located within the polygon and close to the center of axis are least responsive to the stimuli of the environment (Fig. 2). Genotypes including G1, G8, G3, and G6 were found within the polygon and showed less response to environmental changes.

Table 2
Mean square analysis of variance for dry matter yield of soybean genotypes.

Source of variation	Df	DMY t/ha	% explained for DMY
Genotype (G)	9	16.1[a]	11.4
Environment (E)	5	126.8[b]	49.7
G[a] E	45	38.8[a]	38.8
PC1	13	18.6[b]	48.9
PC2	11	14.7[a]	32.8

[a] Significant at the 0.05 probability level.
[b] Significant at the 0.01 probability level, ** Significant at the 0.0001 probability level, DMY = Dry matter yield and t/h = tone per hectare.

Table 3
Mean dry matter yield performance of soybean genotypes over environments.

Code	Genotypes	Environments						
		ENV1	ENV2	ENV3	ENV4	ENV5	ENV6	Mean
G1	TGX1990-111FN	7.1	11.74	7.2	6.5	7.5	5.0	7.5^{b}
G2	Lablab (Check)	8.3	8.7	7.7	6.2	7.8	8.5	8.2^{ab}
G3	PI567069A	8.8	14.8	7.8	4.9	14.2	6.2	9.7^{a}
G4	TGX1990-114FN	8.8	14.3	9.1	7.9	7.6	10.8	9.4^{a}
G5	TGX1990-110FN	8.1	8.1	5.1	6.6	8.4	7.8	7.3^{b}
G6	TGX1989-FN	5.8	10.0	6.7	5.8	6.8	6.7	6.9^{b}
G7	TGX1990-57F	9.3	13.1	5.6	7.1	10.6	5.3	8.5^{ab}
G8	PI567056A	7.6	12.6	5.2	4.9	8.4	7.1	7.6^{b}
G9	TGX1987-62F1	4.5	15.3	4.8	6.0	4.9	7.7	7.2^{b}
G10	AFGAT (Check)	7.4	11.1	4.3	8.1	7.2	11.7	8.3^{ab}
Mean	–	7.5^{cbd}	12.0^{a}	6.4^{d}	6.6^{cd}	8.3^{b}	7.6^{bc}	8.1

ENV1 = Melko 2019, ENV2 =Kersa 2019, ENV3= Bedele 2019, ENV4 = Melko 2020, ENV5 =Kersa 2020 and ENV6= Bedele 2020.

Genotype G1 was close to the center of the axis, indicating genotype stability under different environmental conditions. The genotypes had small G × E interactions. This finding is consistent with the study carried out by Refs. [34,45] using GGE biplot. A genotype that is connected to a vertex of a polygon when no environmental indicator is present in the sector may not be operating as well as it could [48]. Therefore, four mega-environments were identified. ENV1, ENV3, ENV5 with G4 vertex genotypes are categorized as one environment, whereas ENV2, ENV4, and ENV6 are grouped as second, third, and fourth mega-environments, respectively. The genotypes located at the sector apex had the optimum performance in their respective mega-environments. The environment group within each sector and the genotypes at the polygon's extremity characterized the mega environment [49]. Apex genotypes, which are found on the edge, were the most yielding in the given environment [32]. The apex of the polygon is formed by the genotypes G4, G9, and G10. These genotypes are classified as the most responsive, showing better or worse performance in environments. Genotypes G9 and G10 were higher dry matter yielders at ENV2 and ENV6, respectively. Whereas G4 was the top dry matter yielder at ENV1, ENV3, and ENV5, with G1 and G7 performing well in these environments as well. The genotypes within the polygon perform better in their respective environments [7]. Therefore, G8 and G4 had better performance in ENV2. Genotypes G5, G2, and G6 had no environmental indicator; this indicates that those genotypes in the vertex and sector without environment performed poorly in all test environments [45] conducted a similar study, finding that vertex genotypes in the sector without environment performed poorly in all test environments. Genotypes including G1, G8, G3, G7, and G6 were found within the polygon and showed less response to environmental

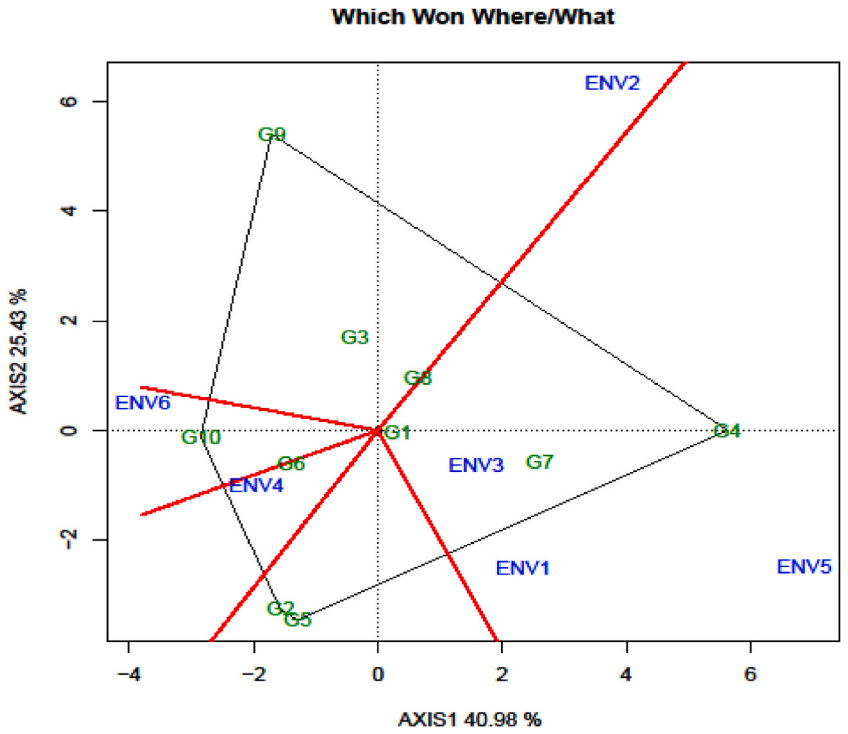

Fig. 2. GGE (Genotype and genotype by environment interaction) biplot (which-won-where model) of soybean genotypes in six environments.

changes. Distinct genotypes perform better in various environments if the environments are classified into distinct sectors [31].

3.4. Ranking of environments and genotypes based on relative to ideal environments and genotypes

The ideal environment is located in or near the concentric circle. Fig. 3 indicates the ideal environment is ENV5 (Kersa 2020). Therefore, this environment is most powerful for discriminate widely adapted genotypes. ENV3 and ENV1 were close to the ideal environment, and this environment has been identified as a representative and the most powerful environment to discriminate genotypes. In general, environments were ranked in the following order relative to the ideal environment: ENV3>ENV1>ENV2>ENV4>ENV6 (Fig. 3). GGE biplot analysis is used to evaluate genotypes and environments relative to an ideal genotype and environment.

The ideal genotype is always located in the innermost circle and near the head of the arrow at the center of the circular ring (Fig. 3). As a result, G4 is the ideal genotype. The genotypes G7, G1, G8, and G3 were closer to the ideal genotypes and performs better in terms of dry matter yield. Genotypes should be high-yielding and stable for efficient selection. While genotypes (G9 and G10) were unfavorable since they are too far from the ideal genotype. The ideal genotype has high mean yields across test settings and consistent performance [49]. The ideal genotype is characterized as having the longest vector length among the high-yielding genotypes with low GEI [48].

3.5. Discriminating and representativeness of the test environment

The ability to discriminate and the representativeness of tested environments are important features of GGE biplot [46]. An ideal environment should be highly distinguishing for the genotypes being tested and typical of the intended location [49]. An environment that has a smaller angle with AEA is more representative than other environments [49]. Thus, ENV5 and ENV6 had a lesser angle with AEA in this regard, but ENV2 and ENV1 had a larger angle (Fig. 4). Additionally, a significant level of genotype discrimination is conferred by vector length [48]. Environments with longer vectors are more discriminating against genotypes, whereas environment indicators with short vectors give little or no information about genotype variations [48]. The current findings, ENV2 and ENV5, had longer vector lengths from the origin and provided the most discriminating or holding more information about the genotypes. ENV1 and ENV6, on the other hand, had medium discriminating ability among the genotypes (Fig. 4). Non-discriminating test environments provide little information regarding genotypes and should not be used for testing. Having short vectors and being close to the origin,

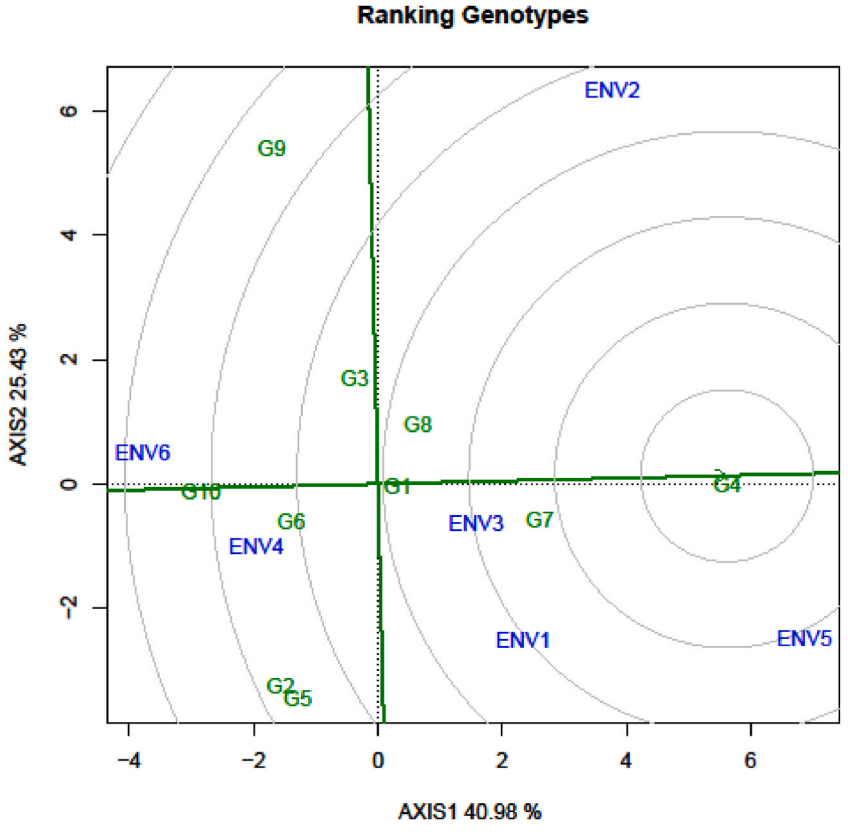

Fig. 3. Ranking of genotypes and environments relative to ideal genotype and environment.

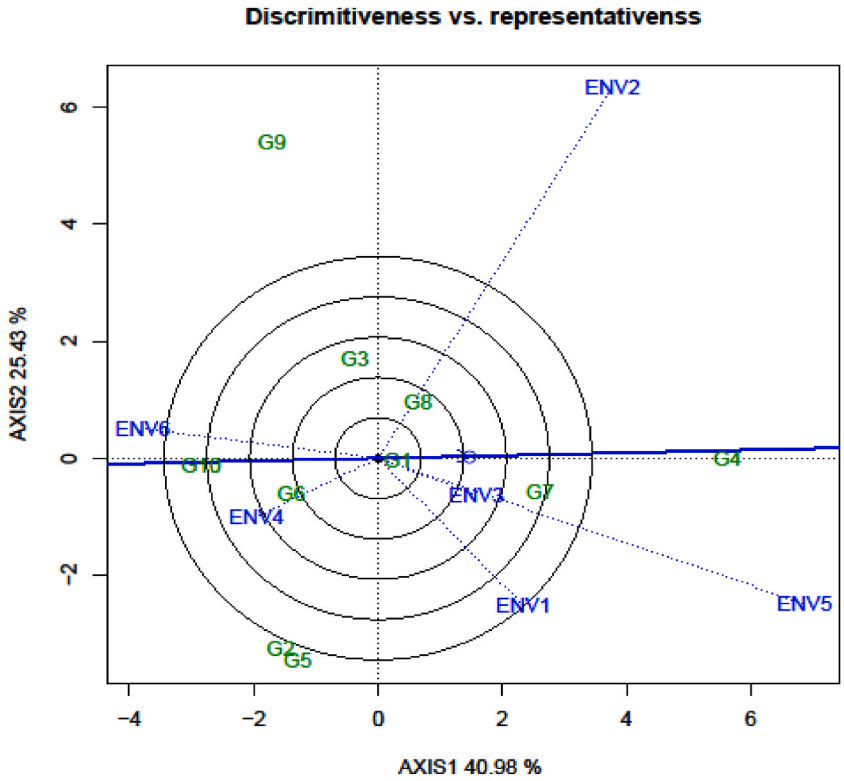

Fig. 4. Discriminative capability and representativeness of environments.

ENV3 and ENV4 offered less distinct information on the genotypes. As a result, ENV5 had a longer vector and a smaller angle with AEA, which was an ideal environment that allowed for the selection of superior genotypes in the most accurate and discriminating manner. These findings are congruent with the study conducted by Ref. [34], who used the GGE biplot to identify represented environments.

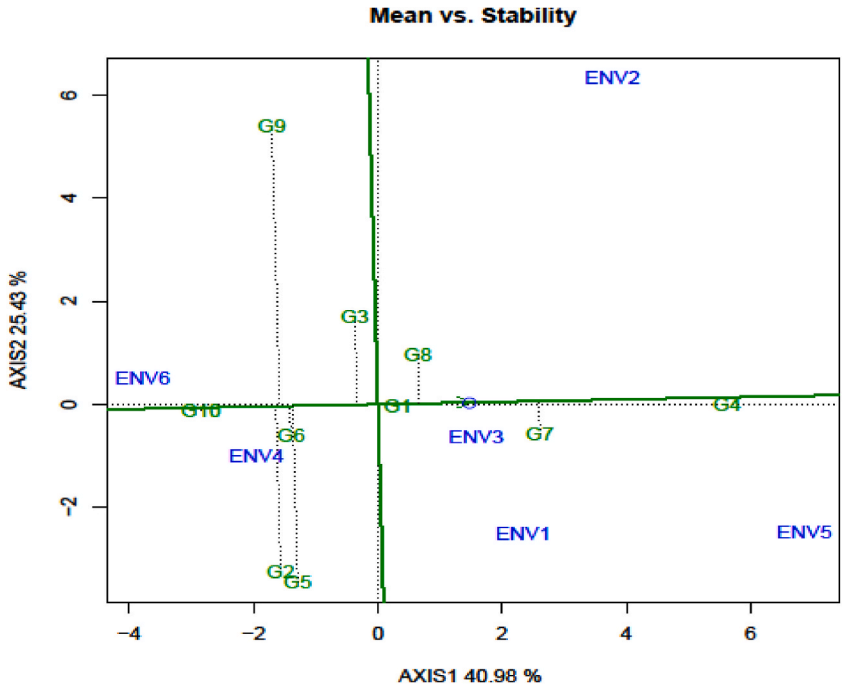

Fig. 5. GGE biplot for mean versus stability using PC1 and 2 of soybean genotypes across six environments.

3.6. Mean and stability analysis of GGE biplot

Mean performance and stability of genotypes assessed under a wide range of environments in GGE biplot model using AEC (Fig. 5) [17]. The AEC is defined by the average PC1 and PC2 scores for all the environments [47]. The mean vs stability pattern of the GGE biplot showed that 66.41% of dry matter yield per hectare of G + G x E variation (Fig. 4). The AEC X-axis (PC1) line passes through the biplot origin with an arrow pointing the positive end of the axis or the arrow and shows the mean yield performance of genotypes. The line that passes through the origin and perpendicular to the AEC, on the other hand, measures the stability of genotypes (PC2) in either direction. Stable genotypes close to AEC (PC1) with PC2 scores of almost zero. On the contrary, any direction on the axis away from the biplot origin suggests increased GE interaction and decreased stability. The best genotypes for selection criteria are those with high yield and high stability. The arrow sign on the AEC line directed the ranking of genotypes in the increasing order of mean dry matter yield. Genotypes with above average dry matter yield in increasing order are G4, G7, G8 and G1. Therefore, genotype four (G4) is the highest yielding genotype on average while G10 (check) was lowest yielding genotype. Genotypes, including G1, G4, G6 and G10 showed shorter projections were more stable across environments whereas G2, G5, and G9, were highly unstable genotypes since they had longer projection from AEA (Fig. 5). The genotypes that combined good performance with stability was G4 because it had higher mean dry matter yield and short projection of the genotype marker lines. The current finding is in line with the study reported by Refs. [13,31,49]. Based on average performance and stability across conditions, they ranked genotypes.

3.7. Chemical composition and in vitro dry matter digestibility of soybean genotypes

The combined analysis of variance revealed that absolute dry matter (DM), ash, crude protein (CP), neutral detergent fiber (NDF), and in vitro-dry matter digestibility (Invitro) traits have significant differences ($P < 0.05$) among genotypes (Table 4). However, acid detergent fiber (ADF) and lignin parameters showed non-significant differences among soybean genotypes. Only ash and lignin traits showed significant differences across locations. The overall mean values of DM, ash, CP, NDF, ADF, Lignin, and Invitro were 90.4, 10.3, 15.7, 45.4, 31.9, 7.8, and 59.98, respectively. The highest and lowest DM values were recorded from genotypes TGX1990-114FN (94.6%) and PI567069A (87.8%), respectively, with a mean of 90.4% as compared to the rest of the genotypes.

The genotypes TGX1990-114FN (21.56%) and TGX1990-111FN (17.5%) gave the highest CP content among testing genotypes. The lowest (14%) CP content recorded from PI567056A soybean genotypes. The current findings' mean value of CP content was similar to the findings of [1], who reported a mean value of 15.1% CP content. The CP content values found in the current study is satisfactorily supply CP acquirement of ruminant animals. Forage soybean has a high CP value, which can supplement low-quality roughages that attain the CP requirement of ruminant livestock like natural pasture (5.5%), Napier grass (6.12%) [11], Desho grass (8.4%) [12], and Bracharia grass (6.7%) [44], respectively. The CP yield of forage soybean showed non-significant differences among genotypes but significant differences among locations. The present findings of CP yield higher than findings of [2], who founds less than 1 t/ha. The higher CP yield was found at Kersa experimental site compared to Melko and Bedele. The CP content is not the only trait to be considered when evaluating forage crops since the CP yield and content describe the overall and actual productivity of quality forage. The nutritional quality of soybean forage is significantly affected by harvesting stages. The CP content decreased significantly with advancing maturity stages [2,35,40].

The ash content of soybean genotypes showed differences both at locations and among genotypes. The ash content was highest in TGX1987-62F1, followed by TGX1990-5757F and TGX1990-110, and lowest in TGX1989-FN soybean genotypes. The high ash content in forage is an indication of high mineral concentration. The ash content of most herbaceous plants was reduced with increased stage of maturity [14]. According to studies, the concentration of ash in fodder varies based on plant developmental stage, morphology fractions, meteorological circumstances, and soil factors.

In-vitro dry matter digestibility (IVDMD) revealed significant differences among genotypes. TGX1990-114FN soybean genotypes had the highest IVDMD (90.4%), followed by TGX1990-111FN (79.15%) and TGX1990-110FN (73.1%), and AFGAT (59.9%) genotypes gave the lowest IVDMD. The current findings of IVDMD percentage were significantly higher than the studies reported by Ref. [1]. Chemical composition and digestibility of soybean forages are significantly affected by climate, soil fertility, harvesting stage, and other management practices. IVDMD decreased with advancing maturity of plants [1].The nutritional value of forages is primarily determined by voluntary consumption, crude protein, and structural carbohydrates. Forage consumption is influenced by digestible DM and CP content [30]. Ruminant maintenance necessitates a dry matter digestibility of around 550 g/kg DM [38]. For dairy cows, 600–700 g/kg DM are necessary for moderate milk production (10–15 kg/cow/day) [10].

Neutral and acid detergent fiber: The result showed that measurements of ADF and NDF are inversely associated with CP content (Table 4). The NDF content of soybean legumes showed significant differences among genotypes, whereas the ADF content showed non-significant differences in both location and genotype. AFGAT (check) had the highest NDF (51.1%), followed by PI567056A (50.5%) and PI567069A (49.0%), whereas TGX1990-114FN (34.8%) gave the lowest NDF content. The current result showed that the mean NDF (45%) and ADF (31.9%) content of the soybean genotypes were higher than that reported by Refs. [2,42]. On the contrary, the current finding revealed that the mean of NDF and ADF content were lower than that reported by Ref. [43]. This suggests that the soybeans used in this study were high in fiber fractions (NDF and ADF). The fiber content of a feed is particularly important for determining quality in terms of digestion. NDF content represents most of the cell wall/fiber of soybeans seeds [42], while ADF content consists of primary lignocellulose structure and is resistant to microbial fermentation in the rumen [28]. NDF levels have a negative correlation with feed intake, while ADF has a negative correlation with digestibility values of feedstuffs [43]. Harvest stage affected ADF and NDF traits [2]. Soybean forage quality differs by genotypes, harvesting stage and environmental factors [3]. Progress of plants to maturity accumulating indigestible lignin and decrease CP content in plants [15]. Therefore, soybean genotypes that maximize seed

Table 4
Quality traits of Soybean genotypes.

Genotypes Code		Nutritional qualities (g/kg DM)							
		DM %	Ash %	CP %	CPY t/ha	NDF %	ADF %	Lignin %	Invitro %
TGX1990-111FN	G1	91.4 ab	10.4 abc	17.5b	1.5a	40.6cd	24.3BCE	7.4a	79.15 ab
PI567069A	G3	87.8b	8.4c	14.4b	1.4a	49.0 ab	37.4a	8.2a	66.7BCE
TGX1990-114FN	G4	94.6a	9.4BCE	21.56a	1.6a	34.8d	22.7c	7.6a	90.4a
TGX1990-110FN	G5	91.2 ab	11.3 ab	15.2b	1.5a	46.2abc	33.9 ab	8.3a	73.1BCE
TGX1989-FN	G6	89.6b	8.8BCE	15.4b	1.4a	48.2abc	32.5 abc	7.8a	67.1BCE
TGX1990-57F	G7	88.4b	11.4 ab	14.0b	1.5a	43.1BCE	35.4a	7.8a	68.1BCE
PI567056A	G8	90.7b	9.5BCE	14.0b	1.3a	50.5 ab	34.8 ab	8.2a	69.7BCE
TGX1987-62F1	G9	88.3b	12.4a	14.5b	1.3a	44.8 abc	34.8 ab	7.5a	70.9BCE
AFGAT	G10	90.7b	10.9 abc	14.4 b	1.6a	51.1a	31.6 abc	7.8a	59.98c
GM		90.4	10.3	15.7	1.5	45.4	31.9	7.8	71.7
Genotype		*	*	*	Ns	**	Ns	Ns	*
Environment		Ns	**	Ns	***	Ns	Ns	***	Ns
CV		2.4	15.4	13.9	15.6	9.6	19.2	8.3	12.1
Lsd (0.05)		3.8	2.7	3.8	0.4	7.5	10.6	0.6	15.0

DM = dry matter, CP = crude protein, CPY = crude protein yield, NDF = neutral detergent fiber, ADF = acid detergent fiber.

yield may not be suitable for forage use regardless of plant height, which does not correlate with DM yield [3].

4. Conclusion and recommendation

The current findings demonstrated that the dry matter yield of soybean genotypes was significantly affected by the environment, followed by genotype-environment interaction and genotype effects due to the differential responses of genotypes to environmental and climatic factors. The degree of variation in the environment had a greater influence on soybean dry matter yield performances. The GGE biplot model was a good tool for visual multi-environment trail data analysis and allowed the estimation of the interaction effect of genotype and environment. Four mega-environments were identified for genotype evaluation and productivity breeding. ENV5 (Kersa 20120) was the ideal and most representative environment-based GGE biplot analysis. Genotype G4 was the ideal genotype and overall winner in dry matter yield and stability, depending on different stability parameters and models. The findings also showed that genotype G4 (TGX-1990-114FN) had higher crude protein content, in vitro dry matter digestibility, and relatively lower NDF and ADF concentrations. This attracts genotype-potential adaptors and improves the quality of forage for livestock. Therefore, genotype G4 (TGX-1990-114FN) is the better option to be used as forage soybean in Ethiopia. Further demonstration of the feeding values of high-yielders and stable genotypes on animal performances should be done.

Funding statement

We are grateful to the Ethiopian Institute of Agriculture Research for the financial support of the study.

Data availability statement

All data from this study is included in this published article. Requests for the data should be directed to the corresponding author.

Ethics approval

This is not applicable since the work does not use either humans or animals by any of the listed authors.

CRediT authorship contribution statement

Tesfa Mossie: Writing – review & editing, Writing – original draft, Software, Methodology, Formal analysis. **Kasa Biratu:** Writing – review & editing, Visualization. **Helina Yifred:** Methodology, Data curation. **Yechalew Silesh:** Validation, Supervision. **Abush Tesfaye:** Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgement

We are grateful to the Ethiopian Institute of Agriculture Research for the financial support of the study.

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