Legume Science

WILEY

Legume Science

ORIGINAL ARTICLE OPEN ACCESS

Genotype-By-Environment Interaction and Yield Stability of Kabuli Chickpea (*Cicer arietinum* L.) in Northern Ethiopia

Alemnesh Eskezia[1] | Kelemu Nakachew[1] | Meseret Tadesse[1] | Mulusew Kassa[1,2]

[1]Department of Plant Science, College of Agriculture and Natural Resources, Debre Markos University, Debre Markos, Ethiopia | [2]Department of Agriculture, Environmental and Food Sciences, University of Molise, Campobasso, Italy

Correspondence: Alemnesh Eskezia (alemnesh_eskezia@dmu.edu.et)

Received: 30 August 2024 | **Revised:** 24 May 2025 | **Accepted:** 4 June 2025

Funding: The authors received no specific funding for this work.

Keywords: AMMI | chickpea | GEI | GGE | PCA stability | performance

ABSTRACT

Chickpea is a self-pollinated, diploid, and annual plant ($2x=2n=16$). After peas and beans, it is the most important legume in the world. Reduced chickpea production and productivity have been significantly influenced by the lack of improved and adaptable genotypes, poor management practices, biotic factors such as disease and pests, and abiotic factors including fluctuating rainfall and temperature. New chickpea genotypes introduced in Northern Ethiopia lack adaptability, stability, and performance evaluation, resulting in crop losses for farmers due to their susceptibility to the new and variable environment. To address these challenges, recently released high-yielding genotypes, alongside a standard check, were evaluated for adaptability, performance, and yield stability over 2 years (2022/2023 and 2023/2024) in three districts (Shebel, Awabel, and, Jabitenan) of Northern Ethiopia across six multienvironment field trials each employing a randomized complete block design with three replications. SAS 9.4 and R software were used, showing significant differences in crop phenological stages, growth, and yield parameters across years and locations for test traits. Genotype, location, and year interactions significantly influenced all Kabuli chickpea genotypes. The highest combined mean grain yield was obtained from genotype "Arerti" (2.42 t ha^{-1}) followed by "Yelbie" (2.18 t ha^{-1}), which explained their best performance among the tested genotypes. Analysis of variance revealed significant interactions and differences between genotypes and environments, with 15.6% of the variation in grain yield attributed to environmental factors, 6.4% to genotype differences, and 11.4% to genotype-by-environment interactions. The Genotype and Genotype × Environment biplot and Additive Main Effect and Multiplicative Interaction analysis identified stable genotypes, representative environments, and interesting genotype–environment interactions. Genotypes Arerti, Chefe, and Yelbie were identified as stable based on Genotype and Genotype × Environment biplot and Additive Main Effect and Multiplicative Interaction analysis. Environments Shebel and Jabitenan were identified as representative among all environments considered.

1 | Introduction

Chickpea (*Cicer arietinum* L.) is a self-pollinated, diploid, and annual plant ($2x=2n=16$). After peas and beans, it ranks as the third most important legume globally. For breeding purposes, chickpeas are primarily categorized into two types: desi and kabuli, which are distinguished mainly by seed size and color. Kabuli chickpeas, characterized by their larger and lighter colored seeds, are believed to have originated from spontaneous mutations, whereas the desi type, featuring smaller and darker seeds, likely predates kabuli genotypes. These two types exhibit genetic compatibility despite their distinct characteristics, facilitating gene flow between them. This genetic exchange supports ongoing efforts in chickpea breeding aimed at enhancing agronomic traits and improving environmental tolerance (Shibeshi 2019).

Chickpeas are a crop of significant relevance due to their high nutritional content; on average, one cup of chickpeas contains approximately 2.7% ash, 63% carbohydrate, 4.5% fat, 8% crude fiber, and 22% protein (Purewal et al. 2023). In addition to being a vital food source for humans and livestock, chickpeas also play an essential role in soil fertility by fixing atmospheric nitrogen. Environmental factors such as temperature, photoperiod, sowing time, and soil moisture significantly influence the various growth stages of the plant (Fick et al. 1988; Richards et al. 2020). This comprehensive nutritional profile and beneficial environmental impact underscore the importance of chickpeas in agricultural systems and food systems worldwide.

The production of chickpeas in Ethiopia is significantly below its potential, which has a potential exceeding 2.7 t ha^{-1} (Alemu et al. 2021). Despite the country's vast agricultural land and the crop's essential role in ensuring food security, supporting farmers, and enhancing foreign exchange earnings (Bakala et al. 2022), Ethiopia ranks as the sixth-largest producer of chickpeas in the world. The country contributes 90% of sub-Saharan Africa's chickpea output and accounts for 3% of global production (Gebeyaw et al. 2024; Getahun et al. 2021). The Amhara region had coverage and production of chickpeas of 689,614.06 ha, yielding about 1.92 million tons, yielding an average productivity of 2.6 t ha^{-1} (ESS 2022). However, the productivity of chickpeas often falls short when compared with the potential yield of improved genotypes. Various yield-limiting factors contribute to this issue, including lack of stability, diseases, pest infestations, waterlogging, and adverse weather conditions (Bakala et al. 2022; Chichaybelu et al. 2021; H. K. Singh et al. 2021). Addressing these constraints is crucial for improving chickpea yield and maximizing its potential as a vital crop for food security and economic development in Ethiopia.

The varying responses of chickpea genotypes to different environmental conditions present significant challenges in evaluating production and quality, as pronounced environmental changes can lead to yield instability (Kaloki et al. 2019). Stability in plant breeding is essential for identifying genotypes that consistently perform well across diverse environments, particularly with regard to genotype-by-environment interactions (GEI). Statistical measures of stability have received much attention (Lin et al. 1986). For example, Shukla (1972) proposed a stability variance that quantifies the contribution of each genotype to GEI, with smaller values indicating greater stability. Finlay and Wilkinson (1963) introduced a regression-based method that evaluates genotype performance across environments to assess sensitivity and adaptability.

Genotypic stability is commonly categorized into two forms: static stability, where genotype performance remains relatively constant across environments, and dynamic stability, where performance changes in a consistent and predictable manner in response to environmental variation (Carvalho et al. 2024). These complementary concepts are critical for identifying genotypes that combine high productivity with reliable performance across diverse environmental conditions.

Crop production consistency across diverse conditions is significantly influenced by GEI. This interaction complicates the selection process, as certain genotypes may excel in specific environments but perform poorly in others. To mitigate these challenges and enhance productivity and reliability, breeding efforts should prioritize the development of stable genotypes that consistently yield high outputs across various situations (Beksisa 2021). Multienvironment trials (METs) employing stability analysis techniques such as biplot graphical representation, which classifies genotypes based on principal component values, are essential for the evaluation of yield stability (De Vita et al. 2010; Gebeyaw et al. 2024). METs are crucial for assessing genotype stability and adaptability in various settings (Asefa 2022; Danakumara et al. 2023). Ethiopian chickpea breeding initiatives primarily focus on developing improved cultivars that exhibit high and consistent yields while resistant to both biotic and abiotic stresses, thereby enhancing overall production (Haider et al. 2017).

Genotype performance can vary across locations due to environmental factors (Abraha et al. 2019). Therefore, METs employing stability analysis techniques such as biplot graphical representation, which classifies genotypes based on principal component values, are essential for the evaluation of yield stability (De Vita et al. 2010; Gebeyaw et al. 2024). Environmental conditions vary across time and space, necessitating crop genotype evaluation at different locations to assess performance based on yield and stability (Daemo 2024; Delesa et al. 2022). GEI analysis of chickpeas in Ethiopia is essential yet underexplored. It provides insights into how various chickpea genotypes respond to environmental conditions, especially in Northern Ethiopia. This research could bridge knowledge gaps and help identify optimal chickpea genotypes for specific regions, enhancing yield stability and agricultural productivity (Derbew et al. 2024). Increased genetic yield gains can be achieved by improving genotype adaptations and leveraging the interplay between genotype and environment (Tadesse, Bishaw, and Assefa 2018; Xu et al. 2017).

The current study employs Additive Main Effects and Multiplicative Interaction (AMMI) (Gauch and Zobel 1988) and Genotype and Genotype × Environment (GGE) biplot analysis (Yan et al. 2000) to investigate GEI and stability. This approach is particularly suited to the limited number of genotypes and environments available, aligning well with the assumptions of these methods. While AMMI and GGE offer intuitive graphical outputs that enhance their utility in resource-limited breeding programs, they carry inherent limitations, such as overfitting risk (Smith et al. 2014). Results were thus interpreted cautiously within these constraints. The AMMI model, a statistical method for analyzing genotype-by-environment interactions (GEI) in crop performance studies, demonstrates this balance. It integrates analysis of variance (ANOVA) with principal component analysis (PCA) to differentiate the effects of genotypes and environments from their interactions, thereby helping identify stable genotypes suited to specific environments GEI (Negash et al. 2013;

Scavo et al. 2023). Similarly, the GGE biplot is a powerful tool for analyzing MET, focusing on genotype performance and GEI while excluding environmental main effects (C. Singh et al. 2019). This two-dimensional representation aids in identifying stable, high-yielding genotypes. Both AMMI and GGE-biplot analyses are effective statistical methods for evaluating GEI (Negash et al. 2013; Scavo et al. 2022), assisting in identifying high-yielding and stable genotypes suitable for different environmental conditions.

In Ethiopia, particularly in northern Ethiopia, there is a lack of sufficient data regarding how GEI impacts chickpea yield and related traits. Strong GEI can significantly limit selection gains of superior genotypes for cultivar improvement, particularly for quantitative characteristics such as seed production (Gebeyaw et al. 2024). Addressing this gap is crucial for improving chickpea breeding efforts and ensuring food security in the region. Therefore, the objective of this experiment was to evaluate and select the best-adapted, stable, and high-yielding kabuli chickpea genotypes to improve the crop yield in the northern part of Ethiopia.

2 | Material and Methods

2.1 | Description of the Study Area

The study was conducted across three key chickpea-producing districts in northern Ethiopia: Shebel, Jabitenan, and Awabel. Specifically, it took place at the Farmers Training Centers (FTCs) during the main cropping seasons of 2022/2023 and 2023/2024. The locations were purposively selected based on their high potential for chickpea production. The study location's agroecological data are summarized in Table 1, and the study map is presented in Figure 1.

2.2 | Experimental Plant Materials

Nine improved and high-yielding kabuli chickpea genotypes (Table 2) were selected for this study, with their seeds collected from the Debre Zeit Agricultural Research Center (DZAR), Ethiopian Institute of Agricultural Research. In addition, the Akuri genotype was selected as a standard check because of its

TABLE 1 | Geographical description of the study areas.

Location	Code		Alt. (masl)	Temp. max and min (°C)	RF. Ave. (mm)	Soil type	Geographic location	
	2022/2023	2023/2024					Latitude	Longitude
Shebel	E1	E4	800–2220	18–27	1150	Vertisol	10°22′ N	37°47′ E
Jabitenan	E2	E5	2250	15–17	900–1200	Vertisol	10°38′ N	10°37′ E
Awabel	E3	E6	2446	15–22	1380	Vertisol	10°21′ N	37°43′ E

Abbreviations: Alt: altitude, RF.: rainfall, Temp.: temperature.
Source: District administrative office.

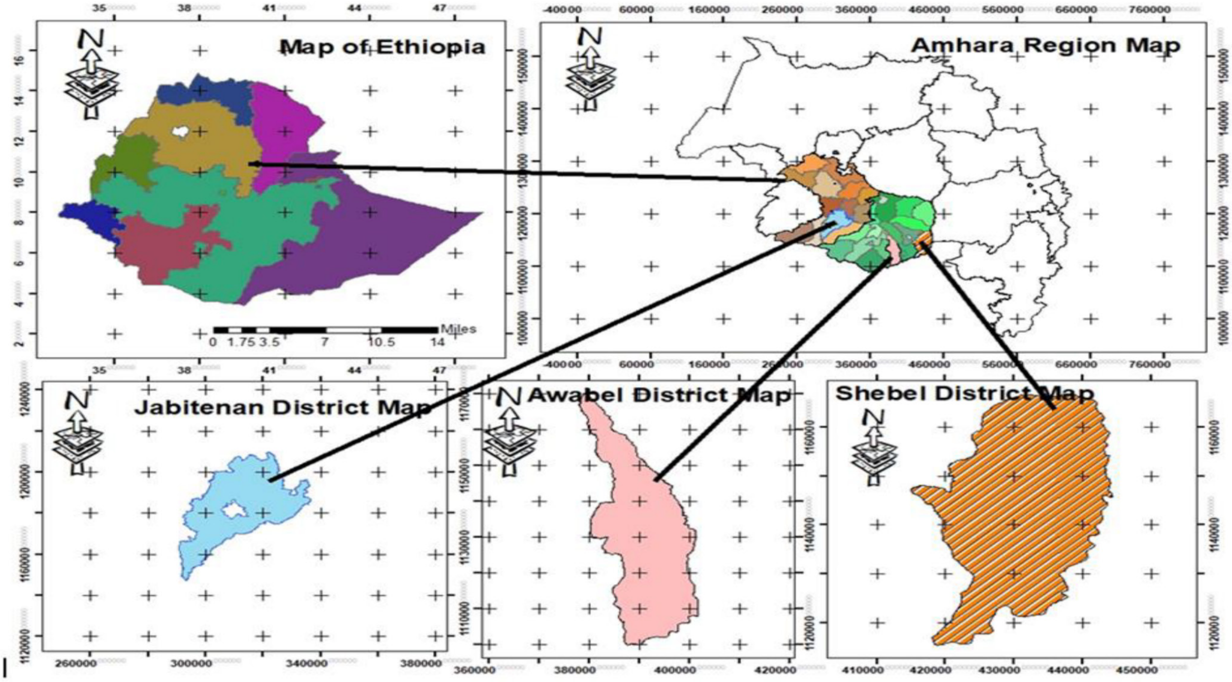


FIGURE 1 | Schematic map of the study area.

TABLE 2 | The descriptions of the Kabuli chickpea genotypes used in the experiment.

Genotype	Type	Code	Origin	Breeding method	Year of released
Arerti	Kabuli	G5	ICARDA	Introduction & hybridization	1999
Habru	Kabuli	G6	ICRISAT	Introduction & hybridization	2004
Chefe	Kabuli	G1	ICARDA	Introduction & hybridization	2004
Ejere	Kabuli	G8	ICARDA	Introduction & hybridization	2005
Yelbie	Kabuli	G9	ICRISAT	Introduction & hybridization	2006
Akuri	Kabuli	G7	ICRISAT	Introduction & hybridization	2012
Hora	Kabuli	G3	ICARDA	Introduction & hybridization	2016
Dhera	Kabuli	G2	ICARDA	Introduction & hybridization	2016
Koka	Kabuli	G4	ICRISAT	Introduction & hybridization	2019

Note: ICRISAT and ICARDA are the International Crop Research Institute for the Semi-Arid Tropics and the International Center for Agriculture Research in the Dry Areas, respectively.
Source: EAA (2022).

wider adoption by farmers and the availability of seeds in the study area. The detailed descriptions and passport data of the genotypes used in the experiments are summarized below. This selection aims to enhance chickpea production by leveraging improved genetic traits that align with local agricultural practices and market demands.

2.3 | Experimental Design and Procedure

The experiment was laid out in a randomized complete block design with three replications in a plot size of $4.2\,m^2$ ($2\,m \times 2.1\,m$). A plot consisted of seven rows of 2 m long and 2.1 m width with 0.3 m between rows, 0.5 m between plots, and 1 m between blocks. Seeds of each chickpea genotype were used at one seed on one hole and seeds were sown manually (hand drill) in rows. All other preagronomic and postagronomic management practices (weeding, insect pest monitoring, and chemical application) were applied as per recommendations made for the chickpea production manual uniformly for all plots.

2.4 | Data Collected

Data on various agronomic traits were collected at appropriate intervals according to standard procedures for each parameter. The recorded traits included days to 90% maturity, plant height, number of productive branches, number of pods per plant, number of seeds per pod, biomass yield, grain yield, hundred-seed weight, and harvest index. This comprehensive data collection aimed to evaluate the performance of the selected chickpea genotypes and their adaptability to the environmental conditions of the study area.

2.5 | Data Analysis

ANOVA was conducted to test for significant differences among genotypes for different traits, considering the effects of year and location. The data collected for each trait were analyzed using the PROC GLM procedure of SAS version 9.4 (SAS 2013). Then, after testing the ANOVA, Fisher's least significant difference (LSD) test at a 5% significance level was used for mean comparisons among genotypes whenever genotype differences were significant. Additionally, the GEI was further partitioned using GGE biplot and the AMMI statistical model, using R software. This comprehensive approach allows for a detailed understanding of the performance of different chickpea genotypes across varying environmental conditions, facilitating the identification of stable and high-yielding genotypes suitable for diverse agricultural settings.

2.6 | AMMI and GGE Biplot Analysis

The studies were conducted using the AMMI and GGE biplot packages in R software, along with MET (metan) version 1.18.0 (Mwendo et al. 2025). The AMMI method integrates PCA and ANOVA into a single analysis that encompasses both additive and multiplicative properties (Gauch and Zobel 1997). In the initial phase of AMMI, conventional ANOVA techniques are used to evaluate the main effects of genotype (G) and environment (E). Subsequently, PCA is performed on the interaction effects after eliminating the main effects. The interaction effects between genotype and environment are analyzed within the AMMI framework to better identify chickpea genotypes that are well-adapted to various habitats (Gauch 2013). It is important to note that genotypes exhibiting the highest stability may not always yield the best results, indicating that stability alone should not be the sole criterion for selection (Bose et al. 2014). To categorize stable genotypes effectively, yield and stability are often combined into a single index (Grüneberg et al. 2005).

The GGE-biplot methodology was used to analyze the MET results visually by integrating the biplot concept (Jifar et al. 2019). This method illustrates the significant components of GGE relevant to genotype evaluation and identifies sources of variance in the GEI analysis of METs data (Farshadfar et al. 2013).

In this context, lines connecting the test environment to the biplot origin are referred to as environment vectors. The angle between the environment vector, specifically its cosine, estimates the correlation between environments. An acute angle indicates a high correlation between environments, whereas a larger angle suggests a decreasing relationship (Fekadu et al. 2023). This comprehensive approach allows researchers to effectively analyze GEI and select chickpea genotypes that are both high-yielding and stable across different environmental conditions. Assessed genotype adaptability using Eberhart and Russell's model by calculating regression coefficients (bi) and deviation from regression (S^2di), complemented by the coefficient of determination (R^2) to confirm stability in yield performance across environments.

3 | Results and Discussion

3.1 | Combined ANOVA

The results of the ANOVA for the data combined across locations and over the years are presented in Table 3. The combined analysis showed a highly significant ($p < 0.01$) difference among genotypes for the traits considered in the experiment. The location had a highly significant effect ($p < 0.01$) on days to maturity, plant height, number of branches per plant, number of seeds per plant, number of seeds per pod, hundred-seed weight, and grain yield. Similarly, the year also exhibited a highly significant difference ($p < 0.01$) in days to maturity, plant height, number of seeds per plant, hundred-seed weight, and grain yield. The interaction between genotype and location (G × L) was highly significant ($p < 0.01$) for days to maturity, number of branches per plant, number of seeds per plant, hundred-seed weight, and grain yield. Additionally, the interaction between genotype and year (G × Y) was also highly significant ($p < 0.01$) for days to maturity, plant height, hundred-seed weight, and grain yield. Takele et al. (2024) reported that the genotype × year (G × Y) interactions were significant for all the studied characters. Furthermore, the interaction between location and year (L × Y) was highly significant ($p < 0.01$) for days to maturity, number of branches per plant, hundred-seed weight, and grain yield. These findings align with numerous research outputs that have observed a significant difference in genotypes × location (G × L) interactions (Takele et al. 2024; Taye and Ayenew 2023). This underscores the importance of considering both environmental factors and their interactions when evaluating chickpea genotypes for improved performance across diverse conditions.

The G × L × Y effect was highly significant ($p < 0.01$) for days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per plant, hundred-seed weight, and grain yield. A similar finding was reported by Kumar et al. (2023), where genotypes tested in eight environments showed highly significant differences ($p < 0.01$) for environments (E), genotypes (G), and environments by genotypes interaction in major chickpea production areas in Ethiopia. This indicates that the performance of chickpea genotypes is greatly influenced by the combined effects of genotype, location, and year, emphasizing the complexity of breeding programs aimed at improving chickpea yields under varying environmental conditions. The significant G × L × Y interaction highlights the necessity for breeders to consider these interactions when selecting genotypes for specific environments to ensure optimal performance and stability across different growing conditions.

According to Takele et al. (2024), both environment and GEI were found to be significant for all the studied traits. Similarly, Atta and Shah (2009), Daemo et al. (2024), Danakumara et al. (2023), and Mohammadi and Amri (2012) reported highly significant mean squares due to genotypes, environments, year, GEI, genotype-by-year interaction, environment-by-year interaction, and genotype-by-environment and by year interaction for the traits such as days to maturity, plant height, number of pods per plant, and number of branches per plant. These findings emphasize the critical role of GEI in influencing the performance of chickpea genotypes across different environmental conditions, highlighting the need for

TABLE 3 | The two cropping seasons (2022/2023 and 2023/2024) combined ANOVA results of nine quantitative traits from six locations.

	Mean squares									
SOV	**DF**	**DM**	**PH**	**NB**	**NPP**	**SPD**	**SEW**	**BY**	**GY**	**HI**
Genotype	8	86.15**	46.80*	11.21**	563.85*	0.10**	129.44**	3.996**	0.794**	94.772*
Location	2	288.38**	560.98**	711.40**	424.81**	0.02**	323.69**	29.95**	2.79**	343.45**
Year	1	82.98**	1227.88**	176.47**	123.06 ns	0.09**	64.09**	191.149**	7.236**	1921.95**
G*L	16	28.81**	90.57**	14.58**	747.87 ns	0.07**	2.744**	5.211**	0.493**	49.78 ns
G*Y	8	6.39**	105.74**	7.84 ns	716.68 ns	0.04 ns	0.623**	1.774**	0.031**	43.95 ns
L*Y	2	137.08**	433.32 ns	174.88**	651.19 ns	0.13*	1.327**	52.60**	1.362**	40.248 ns
L: G	6	0.54 ns	19.53 ns	9.27*	572.18 ns	0.02 ns	0.189 ns	1.35*	0.03**	46.654 ns
G*L*Y	16	8.95**	50.42**	8.17**	696.29**	0.05**	0.479**	1.646**	0.203**	67.567**
Residuals	102	0.37	19.65	4.05	683.86	0.03	0.19	0.47	0.11	45.74

Abbreviations: BY: biomass yield; DF: degrees of freedom; DM: days to 90% maturity; G: genotype; GY: grain yield; HI: harvest index; HSW: hundred-seed weight; L: location; NB: number branch; NPP: number pod per plant; ns: nonsignificant; PH: plant height; SOV: source of variation; SPP: seed per pod; Y: year.
**: highly significant at $P \leq 0.01$, *: significant at $P \leq 0.05$.

targeted breeding strategies that consider these interactions to improve yield stability and adaptability in various agroecological settings.

The significant GEI effects indicated the inconsistent performance of genotypes across the tested environments and highlighted the varying discriminating abilities of these environments. This suggests that it is possible to identify high-yielding and stable genotypes, as the same crop variety may perform well in one environment but poorly in another due to differences in climate, soil, or management practices. These findings align with previous studies by Negash et al. (2021), Kizilgeci et al. (2019), and Misganaw (2016), which reported significant differences ($p < 0.05$) among bread wheat genotypes for grain yield across all the individual test locations in METs. The differential performance underscores that plant productivity is directly influenced by environmental conditions (Ejara et al. 2020). The combined analysis revealed significant differences in grain yield among the genotypes. Arerti recorded the highest grain yield (2.42 t ha^{-1}), followed by Yelbie (2.28 t ha^{-1}) and Akuri (2.18 t ha^{-1}), whereas Hora had the lowest grain yield (1.75 t ha^{-1}) (Table 4).

3.2 | Mean Performance of Agronomic Traits in Each Test Location

Among the testing locations, grain yields were the highest at Shebl in the 2023 cropping season as compared with the other three testing locations with a mean grain yield of 2.68 t ha^{-1} followed by Shabel 2022 cropping seasons (2.10 t ha^{-1}). The lowest grain yield was obtained at Awabel 2022 with a mean yield of 1.05 t ha^{-1}. The superior performance of genotypes at Shabel 2023 (2.68 t ha^{-1}) and Shebel 2022 (2.10 t ha^{-1}) can be attributed to the uniform distribution of rainfall and other cropping seasons and suitable environmental conditions for genotypes. The tested genotypes showed inconsistent yield advantages across environments. The mean grain yield of genotypes over environments indicated that Arerti (2.71 t ha^{-1}), Yelbie (2.48 t ha^{-1}), and Ejere (2.15 t ha^{-1}) were the highest yielding varieties, whereas variety Hora (1.72 t ha^{-1}) and Koka (1.74 t ha^{-1}) are low yielding varieties (Table 5). The mean grain yield across environments ranged from 2.68 t ha^{-1} for Shebel to 1.21 t ha^{-1} for Awabele. Shebel was a relatively high-yielding environment compared with Jabitenan. All chickpea varieties have higher grain yield at Shebel. The variety Arerti performed best in most of the environments followed by the variety Ylibie. The high variation in grain yield among the nigh chickpea varieties at the four locations might be due to extensive variability in climatic and soil conditions. Similarly, inconsistent grain yield performances of variety have been found across locations (Wang et al. 2023).

3.3 | Additive Main Effect and Multiplicative Interaction Analysis

AMMI ANOVA for grain yield of kabuli chickpea genotypes evaluated across six environments is presented in Table 6. Genetic variation and the potential selection of stable genotypes were revealed by AMMI analysis. The analysis revealed substantial variation among environments (E), genotypes (G), and their GEI ($p < 0.01$). The sum of squares (SS) partitioning identified environmental influence as the primary cause of variation, followed by GEI and the main effects of genotype. This suggests that changes in G and GEI are relatively minor, with

TABLE 4 | The combined mean performance of grain yield and yield-related parameters of six locations in the 2022/2023 and 2023/2024 cropping seasons.

	Mean values								
Genotype	**DM**	**PH**	**NB**	**NPP**	**SPP**	**HSW**	**BY**	**GY**	**HI**
Chafe	177.67c	45.38ab	11.68a	152.02a	1.15bcd	34.23c	4.93b	2.11bc	36.38cd
Dhera	176.61e	47.41a	9.74bc	151.19a	1.06d	31.49e	4.79bc	1.87d	38.97abcd
Hora	175.92f	43.86b	9.29c	153.38a	1.17bcd	28.07h	4.34cg	1.75d	40.61abc
Koka	177.09d	46.04ab	10.3bc	155.51a	1.16bcd	30.2f	4.84b	1.92cd	36.12d
Arerti	176.05f	47.45a	11.02ab	157.1a	1.31a	36.26a	5.78a	2.42a	36.69bcd
Habru	172.89g	43.68b	9.41c	204.41a	1.15cd	30.45f	5.21b	2.18b	37.69bcd
Akuri	179.38b	44.75ab	10.58abc	177.96a	1.26ab	29.87g	4.84b	2.18b	36.66a
Ejera	176.28ef	43.29b	9.72bc	156.64a	1.25abc	33.02d	4.14d	1.95cd	42.26ab
Yelbie	180.54a	43.68b	9.96bc	153.72a	1.24abc	34.75b	4.88b	2.28ab	40.92bcd
Mean	0.37	19.65	4.05	6853.86	0.027	0.187	0.46	0.11	0.37
LSD	176.93	45.06	10.18	162.43	1.19	32.03	4.86	2.06	176.93
CV	0.34	9.83	19.76	50.96	13.82	1.35	14.04	16.15	0.34

Note: Similar letters indicate nonsignificant differences, whereas different letters signify significant differences among varieties for each tested trait.
Abbreviations: BY: biomass yield; CV: coefficient of variation; DM: days to 90% maturity; GY: grain yield; HI: harvest index; HSW: hundred-seed weight; LSD: least significant difference; NB: number of branches; NPP: number of pods per plant; PH: plant height; SPP: seed per pod.

TABLE 5 | Mean performance of agronomic traits in each test location.

Tested genotypes	Locations and years								Overall	
	2022				2023					
	Jabitenan	Shebel	Awabel	Mean	Jabitenan	Shebel	Awabel	Mean	Mean	Rank
Chefe	1.37bc	2.36b	1.20bc	1.64ab	1.88c	2.88ab	1.23bc	2.38abc	2.12bc	5
Dhera	1.50b	1.62e	1.31b	1.14cd	2.05bc	2.30bc	1.30b	2.18bc	1.87cd	7
Hora	1.47b	1.53e	1.21b	1.05cd	1.74c	2.16c	1.26b	1.95c	1.72d	9
Koka	1.17c	1.77de	1.03c	1.32d	1.24d	2.79ab	1.08c	2.02c	1.74d	8
Arerti	2.38bc	2.86a	2.06bc	2.43a	2.61a	3.22a	2.09bc	2.80a	2.71a	1
Habru	1.38bc	2.29bc	1.08c	1.58bcd	2.21abc	2.68abc	1.11c	2.44abc	2.14bc	4
Akuri	1.16c	1.99cd	1.05c	1.4cd	2.01bc	2.47bc	1.07c	2.24abc	1.90cd	6
Ejere	1.57b	2.30bc	1.27b	1.71ab	1.96bc	2.77abc	1.19b	2.36abc	2.15bc	3
Yelbie	2.30a	2.18bc	2.13a	2.24bc	2.39ab	2.85ab	2.18a	2.73ab	2.48ab	2
Mean	1.59	2.10	1.21	1.84	2.01	2.68	1.18	2.34	2.09	
F-test	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	
CV	8.58	9.99	0.81	11.08	13.42	13.29	0.91	17.61	12.01	
LSD	0.23	0.36	0.21	0.45	0.46	0.61	0.20	0.79	0.36	
R^2	0.94	0.85	0.82	0.89	0.76	0.68	0.86	0.60	0.92	

the environment being the predominant factor explaining variations in genotype performance (Yan et al. 2007). Furthermore, the first two IPCAs of the AMMI model were found to be highly significant ($p < 0.01$) when applied to the partitioning of GEI. This highlights the importance of these components in understanding the interactions between genotypes and their environments, thereby aiding in the identification of stable and high-yielding chickpea genotypes across varying conditions. The AMMI model, using IPCA1 and IPCA2, effectively predicts GEI-driven yield variation, especially with limited data. AMMI performs well when GEI is simple, IPCAs capture the most variation, and datasets are balanced. GGE biplot is better for ranking genotypes and identifying mega environments, whereas mixed models excel in complex GEI, large datasets, or when high prediction accuracy is needed (Mohammadi and Amri 2012; Tadesse, Zegeye, et al. 2018). Variations in the grain yield components from the AMMI indicated that genotype, environment, and GEI all had significant ($p < 0.01$) effects, explaining variability in both environments and genotypes. As a result, there are possibilities for selection of genotypes that are high-yielding, stable, and well-performing.

The total sum of squares analysis reveals that 15.6 of the variation in grain production is attributed to environmental factors, 6.4 to genotype differences, and 11.4 to GEI. Analysis of the sum of squares for environments (Table 6) confirms significant diversity among test environments, with environmental differences predominantly influencing grain yield variations. This emphasizes the purpose of carrying out studies in MET. Variations in soil type, fertility, temperature, precipitation, and moisture availability are probably the main causes of these environmental variations (Mehari et al. 2015).

According to the AMMI analysis, the first and second interaction principal components (IPCA1 and IPCA2) explained 65.96% and 24.31% of the interaction sum squares, respectively. This indicates that 90.27% of the total GEI was contributed by IPCA1 and IPCA2 collectively (Figure 2a,b). The model effectively explained the GEI component, allowing for the ranking of genotypes based on their AMMI stability value (ASV) scores, with lower scores indicating more stable genotypes.

The model effectively explained the GEI component, allowing for the ranking of genotypes based on their ASV scores, with lower scores indicating more stable genotypes. Based on ASV, the most stable genotypes for grain yield were G6, G4, and G2, which had the lowest ASV scores. Genotypes G5, G2, and G3 exhibited the highest stability, characterized by the lowest ASV ranks. In contrast, genotypes G7, G9, and G4 were less stable but demonstrated higher dry matter content (Table 6).

3.4 | Stability Analysis and Mega Environment Classification Using GGE Biplot

3.4.1 | GEI Analysis for Which-Won-Where Patterns Using GGE Biplot

Based on the findings regarding the first two principal components, a GGE biplot was constructed (Yan 2001). In the current research, the first two principal components of the GGE biplot explained 79.49% of the total variation with PC1 accounting for 46.93% and PC2 for 32.56% (Figure 3). According to (Yan and Tinker 2006), the vertex genotypes with the highest yield in a given sector are those found furthest from the origin in the

TABLE 6 | Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of chickpea genotype across environments.

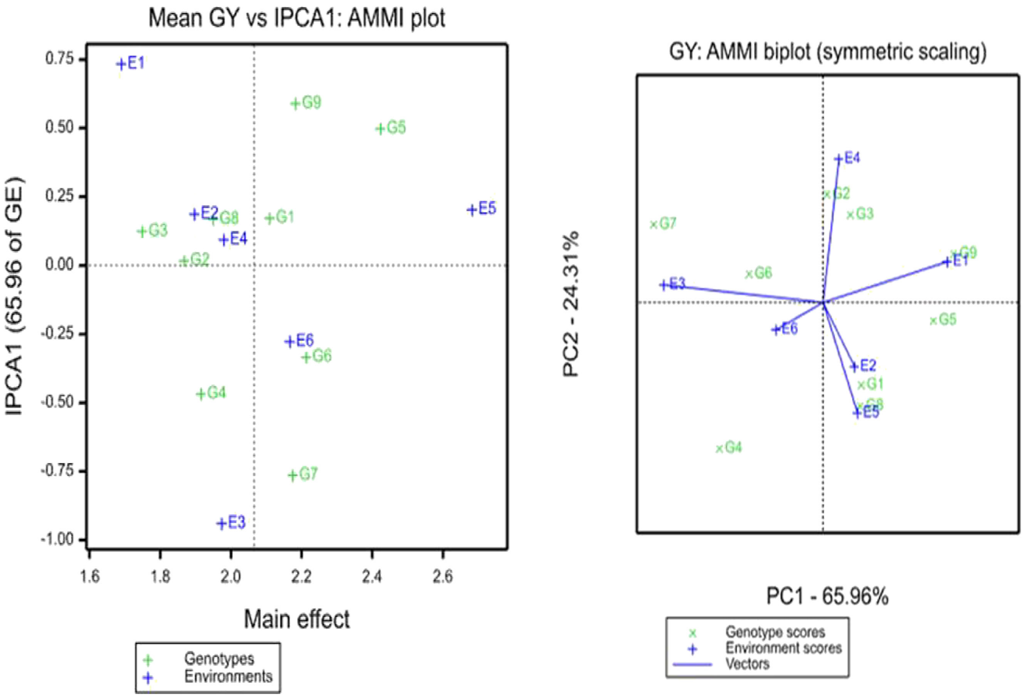
Source	DF	Sum sq	Mean sq	*F* values	*Pr* (> *f*)	Proportion	Accumulated
ENV	5	15.6	3.10**	44.43	2.48	NA	NA
REP (ENV)	12	0.84	0.069**	0.62	8.14	NA	NA
GEN	8	6.4	0.79**	7.11	2.34	NA	NA
GEN:ENV	40	11.4	0.28**	2.55	9.72	NA	NA
PC1	12	7.52	0.62	5.62	0.00	66.0	66
PC2	10	2.77	0.27	2.49	1.06	24.3	90
PC3	8	0.86	0.10	0.97	4.64	7.6	97
PC4	6	021	0.035	0.32	9.25	1.9	99
PC5	4	0.03	0.079	0.70	9.90	0.3	100
Residual	96	10.71	0.11	NA		NA	NA
Total	201	44.86	0.28	NA		NA	NA
Genotype rank based on AMMI stability value							
Number	**Genotype**	**Mean yield**	**ASV**	**IPCA 1**	**IPCA 2**	**YSI**	**Rank**
1	Chafe	2.13	0.49	0.171	−0.310	8	5
2	Dhera	1.87	0.41	0.017	0.406	9	7
3	Hora	1.73	0.43	0.123	0.330	11	9
4	Koka	1.75	1.18	−0.468	−0.550	14	8
5	Arerti	2.42	0.14	0.497	−0.068	7	1
6	Habru	2.14	0.75	−0.334	0.106	7	4
7	Akuri	1.91	1.73	0.764	0.293	13	6
8	Ejera	2.15	0.54	0.167	−0.390	10	3
9	Yelbie	2.18	1.32	0.589	0.182	11	2

Abbreviations: ENV: environment, GEN: genotype, PC: principal component, REP: replication.

polygon view. This assertion is further supported by Farshadfar et al. (2013), who also emphasize that the best-performing genotypes are typically positioned at the vertices of the sectors in the GGE biplot.

The GGE biplot is a powerful tool for visualizing genotype performance across multiple environments, helping to identify stable and high-yielding genotypes. By analyzing the positions of genotypes relative to one another and their environments, researchers can make informed selection decisions. This graphical representation facilitates comparisons of genotype performance under varying conditions and highlights GEI. Ultimately, the GGE biplot enhances breeding programs by guiding the selection of productive and adaptable genotypes.

Vertex genotypes in the current investigation include G9, G3, G5, G7, and G4. To effectively split the testing environments and genotypes in a GGE biplot graph, lines emerging from the origin that are perpendicular to the line connecting the vertex genotypes are utilized. Therefore, the six testing environments were divided into two mega environments, whereas the nine genotypes were divided into five genotypic groups (Figure 3). The two mega environments consisted of Group I (E1, E2, E4, and E5) and Group II (E3 and E6). To explore the adaptation of genotypes in a particular or across all test environments, the illustration of a which-won-where pattern in MET is crucial (Yan and Tinker 2006). Despite being the furthest from the biplot origin, the vertex genotypes were the most sensitive. Yan and Tinker (2006) defined responsive genotypes as those that performed either best or worst in one or all situations. The GGE biplots of the graph findings showed the relative performance of each genotype in a particular environment. It is more typical and ideal for other test settings to have a small angle with AEC, that is, to be at the center of concentric circles (Yan 2001). Related to this result, Shunbura et al. (2024); Tadesse, Zegeye, et al. (2018); and Takele et al. (2024) identified different chickpea, bread wheat, and faba bean genotypes, respectively, growing in mega environments. The genotypes Arerti and Chefe perform well at Shebel 2023/2024, Jabitenan 2022/2023, and Jabitenan 2022/2023 and Yelbie at Shebel 2022/2023. Additionally, Akuri excelled at Awabel 2022/2023, whereas Arerti again showed strong performance at Awabel 2023/2024, with Chefe and Ejere



a. AMMI 1 graphs **b**. AMMI 2 graphs

FIGURE 2 | AMMI-1 and AMMI-2 analysis model biplot for grain yield of chickpea genotype evaluated at six environments. G1: Chefe, G2: Dhera, G3: Hora, G4: Koka, G5: Arerti, G6: Habru, G7: Akuri, G8: Ejere, G9: Yelbie genotype, GE: Genotype × Environment interaction, GY: grain yield, IPCA: principal component axis (E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season).

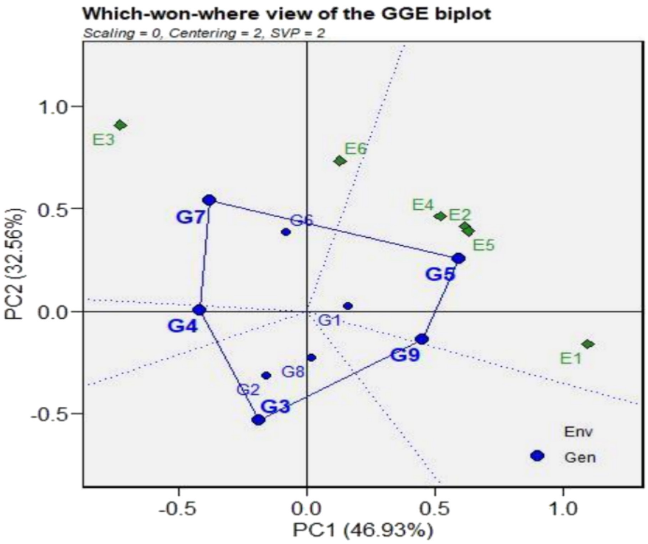


FIGURE 3 | Which-won-where view of GGE biplot for grain yield of chickpea genotypes. G1: Chefe, G2: Dhera, G3: Hora, G4: Koka, G5: Arerti, G6: Habru, G7: Akuri, G8: Ejere, G9: Yelbie genotype (E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season). The blue numbers connected with the polygon represent the genotypes, whereas the green numbers represent locations/environments.

also performing reasonably well at Shebel 2022/2023. The other genotypes located at the vertices of the polygon, which do not include any of the six environments, were unfavorable across all test environments, exhibiting low responsiveness and yields due to their proximity to the origin. Consequently, in the Kabuli chickpea genotypes, the test environments were divided into five sectors, with three of these sectors lacking any test environments. The best-performing genotype in yield was Arerti.

3.4.2 | Mean Grain Yield and Stability Performance of Genotypes

The average yield produced by a genotype across environments and stability performance of genotypes are visually represented using the average environment coordination (AEC) approach (Figure 4). This technique combines grain yield and genotype stability performance to identify genotypes that yield the highest and are the most stable. The genotype with the highest mean performance and greatest stability across all test conditions is considered stable (Shahir et al. 2022). Desired genotypes are positioned closer to the ideal genotype at the center of the AEC biplot. The best-performing genotypes are characterized by long vectors and high yields. In this biplot, the Y-axis (PC2) represents stability, whereas the X-axis (PC1) reflects mean performance. Genotypes that are farther from the origin on the positive side yield higher outputs, whereas those on the negative side produce lower yields. The genotypes were split into two groups for this study. The first group, consisting of G5, G1, G9, G6, and G7, has stable performance that is above average. In contrast, the remaining genotypes (G4, G8, G2, and G3) exhibited below-average performance. An ideal genotype is completely stable in a wide range of conditions and has the highest performance of any genotype (Mohammadi and Amri 2012; Sharma et al. 2010; Yazachew et al. 2021). Consequently, G5, G1, and G9 were identified as more stable and relatively high-yielding in terms of grain production when considering both yield and stability performance. These genotypes might be thought of as the most advantageous ones. This result is in line with previous studies (Behera et al. 2023; Gebeyaw et al. 2024). Furthermore, it is noted that the longer a genotype is in absolute terms, the less stable its projection (Kaya et al. 2006). The main causes of yield variation were the environment (34.6%) and the GEI (25.4%), with genotype accounting for 14.2%. The differential performance of varieties across habitats is indicated by the substantial GEI (Table 7).

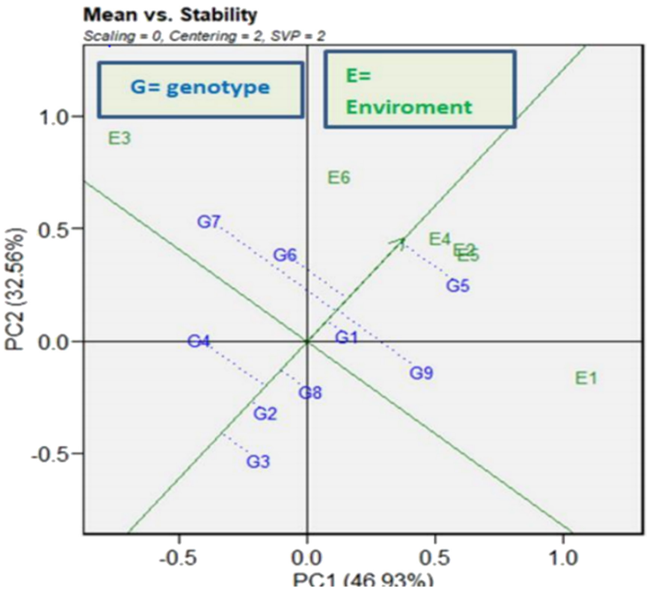


FIGURE 4 | Which genotype was more stable across the tested environments. G1: Chefe, G2: Dhera, G3: Hora, G4: Koka, G5: Arerti, G6: Habru, G7: Akuri, G8: Ejere, G9: Yelbie genotype (E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season). The blue numbers connected with the polygon represent the genotypes, whereas the green numbers represent locations/environments.

3.4.3 | Evaluation of Environments Relative to the Ideal Environments

For an ideal setting, two essential requirements must be successfully met simultaneously. First, it should differentiate between different genotypes, illustrating how distinct genetic compositions respond to their surroundings. This differentiation is crucial for understanding the performance of various genotypes under varying conditions. Second, the setting must accurately represent the conditions found in the target environments to ensure that research or experiments conducted there are relevant and applicable to real-world scenarios. Meeting both of these requirements allows for more effective evaluation and selection of genotypes that are well-suited for specific agricultural contexts. This dual ability guarantees that scientific discoveries are both particular to genetic variations and generally applicable to the environments in which these variations exist, thus improving the reliability and practicality of the study carried out (Yan and Holland 2010). According to Megerssa et al. (2024), the ideal environment has the most discriminating power and is the most representative. Like the perfect genotype, the ideal environment is located in the first concentric circle of the environment-focused biplot, and favorable environments are situated near the ideal environment. Accordingly, Figure 5 shows that the discriminating ability and representative environments for Kabuli chickpea among Shebel 2023/2024, Jabitenan 2023/2024, and Jabitenan 2022/2023 were closest to the ideal environment. These environments were the most representative of the overall environments and had the strongest power in discriminating genotypes; consequently, they were identified as more desirable environments than the others. Furthermore, Awabel 2023/2024 was closer to the ideal environment and was considered the second most powerful for discriminating genotypes. On the other hand, Shebel 2022/2023 and Awabel 2022/2023 were far from the ideal environment and considered less powerful in discriminating between genotypes (Figure 5). The discriminating ability of a location is influenced by the composition of genotypes; however, the presence of GEI complicates the selection of the best test site (Nkalubo et al. 2024). According to Dabi et al. (2023), test environments should have small PC2 scores in absolute value to be more representative of the overall locations, whereas large PC1 scores are necessary to effectively discriminate genotypes based on their main effect.

TABLE 7 | The GGE analysis of the variance table/the sum of squares, mean squares, and percent of variance explained by different sources of variation from the analyses of variance of grain yield of nine chickpea genotypes tested at six environments.

Source of variation	DF	SS	MS	Explained variance (%)	*Pr* > *F*
Environment (E)	5	15.6	3.10	34.65	< 0.001
Blocks (environments)	12	0.83	0.07	1.87	0.024
Genotype (G)	8	6.4	0.79	14.2	< 0.001
G*E	40	11.4	0.28	25.4	< 0.001
Error	96	10.71	0.11	23.88	
Total	161	44.87		100	
Mean = 2.07			CV (%) = 16.6		

Abbreviations: CV: coefficient of variance, DF: degree of freedom, MS mean squares, SS: sum of squares.

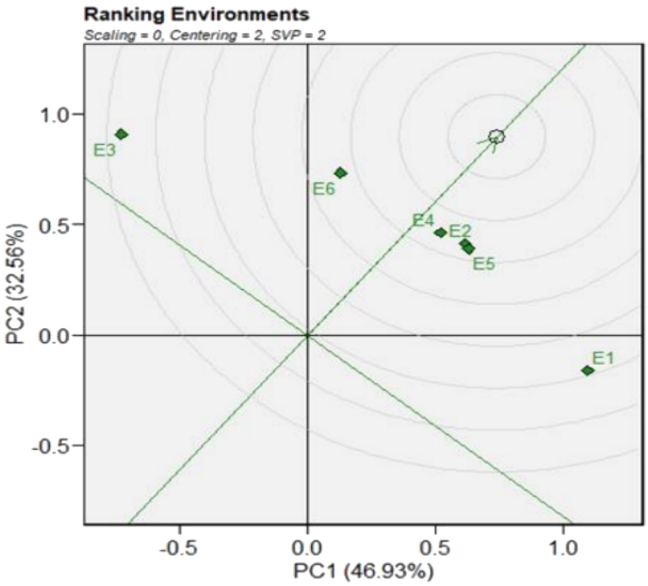


FIGURE 5 | Ranking of the six test environments—to identify which environment was good for the tested genotypes. E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season.

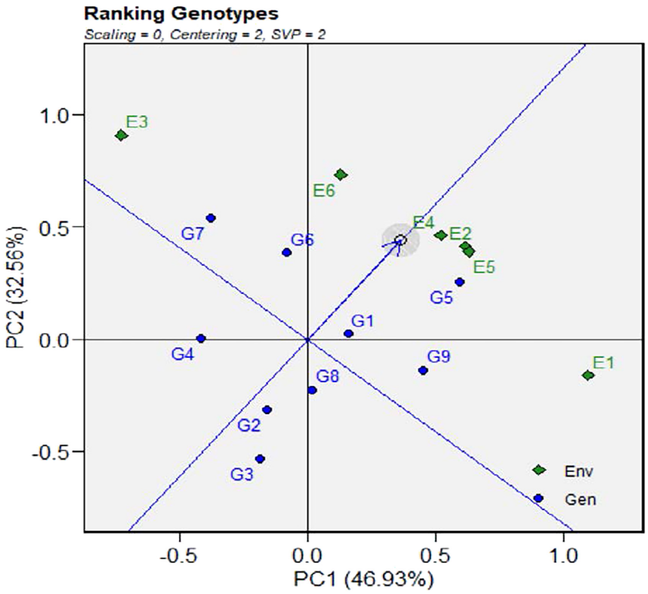


FIGURE 6 | Ranking of the genotypes based on the yield performance and stability ability (which genotype was good). G1: Chefe, G2: Dhera, G3: Hora, G4: Koka, G5: Arerti, G6: Habru, G7: Akuri, G8: Ejere, G9: Yelbie genotype (E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season). The blue numbers connected with the polygon represent the genotypes, whereas the green numbers represent locations/environments.

3.4.4 | Evaluation of Genotype Relative to Ideal Genotype

In plant breeding, identifying an ideal genotype with high mean grain yield and stability across environments is crucial for developing superior cultivars. Farshadfar et al. (2013) emphasized the significance of this ideal genotype concept, which serves as a benchmark for selection. To visualize differences among genotypes, Dabi et al. (2023) employed concentric circles in biplots, where genotypes positioned closer to the center indicate greater proximity to the ideal genotype. This method allows breeders to easily identify genotypes that not only perform well but also exhibit stability across varying environmental conditions, facilitating more informed decisions in cultivar development. Bekana (2023) suggested using the ideal genotype as a reference for selection, rejecting genotypes that are far from it early in the breeding cycles while advancing those closer for further evaluation. Karimizadeh et al. (2023) emphasized the desirability of genotypes that are more similar to the ideal based on their performance metrics. According to Figure 6, Arerti (G5), being at the center of the concentric circle, can be considered the ideal genotype for chickpea grain production because of its higher mean yield and stable characteristics. Likewise, Chefe (G1), Ejere (G8), and Yelbie (G9) were close to the ideal genotypes and are considered good genotypes based on their performance and stability. On the other hand, Koka (G4), Hora (G3), Dhera (G2), and Akuri (G7), which are found farther from the concentric circle, are unstable and low-yielding genotypes (Figure 6). Similar findings were observed by Seyoum (2021) in sorghum, affirming the efficacy of this approach in identifying outstanding genotypes. This study also confirms the results of Atta and Shah (2009) and Fekadu et al. (2023), who found outstanding genotypes near the ideal genotype in sorghum for two consecutive years. The relative contribution of stability and grain yield for identifying desirable genotypes, as found in this study using the ideal genotype procedure of the GGE biplot, were also similar to those reported by Fan et al. (2007) in maize hybrids stability studies.

3.4.5 | Relationship Among Environment

Interrelationships among the six test environments are shown in Figure 7. The environment vectors are the lines that connect the biplot origin to the surroundings markers, and the correlation coefficient between the two environments is indicated by the angle formed between their vectors. According to Otieno and Owuor (2019), this correlation coefficient is estimated using the cosine of the angle between the vectors. Yan and Tinker (2006) further explained that two environments are positively linked when the angle between their vectors is less than 90°, independent when the angle equals 90°, and negatively correlated when the angle is more than 90°. In this analysis, Shebel 2023/2024, Jabitenan 2023/2024, Jabitenan 2022/2023, and Awabel 2023/2024 environments were found to be positively correlated with each other, as all angles among their vectors were smaller than 90°. Conversely, Awabel 2022/2023 and Shebel 2022/2023 exhibited a negative correlation, as all angles among their vectors were greater than 90°.

3.4.6 | Stability Parameter

3.4.6.1 | The Regression Coefficient. The performance of a genotype in an environment is determined by its mean performance, environment-responsiveness as a linear function, and departure from regression. Eberhart and Russell

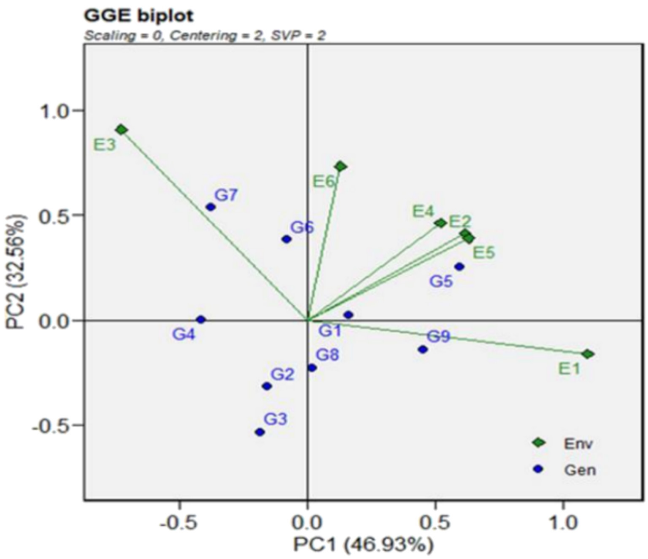


FIGURE 7 | Interrelationships between the six test environments. G1: Chefe, G2: Dhera, G3: Hora, G4: Koka, G5: Arerti, G6: Habru, G7: Akuri, G8: Ejere, G9: Yelbie genotype (E1: Shebel, E2: Jabitenan, and E3: Awabel, in 2022/2023 cropping season, and E4: Shebel, E5: Jabitenan, and E6: Awabel, in 2023/2024 cropping season). The blue numbers connected with the polygon represent the genotypes, whereas the green numbers represent locations/environments.

TABLE 8 | The various models of stability used to partition the G × E for grain yield in the test chick pean genotypes.

Genotypes	Mean	Bi	S^2di	R^2
G1	2.13	0.50	0.112	0.940
G2	1.87	0.53	0.185	0.706
G3	1.73	0.41	0.081	0.817
G4	1.75	1.19	0.310	0.877
G5	2.72	0.34	0.139	0.813
G6	2.14	0.35	0.153	0.888
G7	1.91	0.29	0.123	0.907
G8	2.15	0.11	0.0458	0.960
G9	2.49	0.87	0.201	0.520

Abbreviations: bi: Eberhart and Russell (1966) stability value of regression coefficient, Wi; G1: Chefe; G2: Dhera; G3: Hora; G4: Koka; G5: Arerti; G6: Habru; G7: Akuri; G8: Ejere; G9: Yelbie genotype; R^2: coefficient of determination; S^2di: Eberhart and Russell (1966) stability deviation value from regression.

suggested using a linear regression coefficient and the variance of the regression deviations to evaluate crop responses to environmental changes. The average stability is indicated by a regression coefficient (bi) that approaches one and a deviation from regression (S^2di) of zero. In this model, regression scores above one indicate genotypes that are more sensitive to changes in the environment (below-average stability) and are specifically adaptable to high-yielding environments (Mansour et al. 2018). Conversely, regression coefficients below one enhance the specificity of adaptability to low-yielding environments by demonstrating greater resistance to environmental change (above-average stability). The present results indicated that linear regression for the average grain yield of a single genotype on the average yield of all genotypes in each environment resulted in regression coefficients (bi values) ranging from 0.11 to 1.29. This variation in the regression coefficients indicates different responses of the genotypes to environmental changes (Table 8). A mean regression coefficient (bi) that is close to one, minimum values for deviation from regression, and grain yields higher than the grand mean indicate that the aforementioned genotypes G9, G5, and G1 are well adapted to all environments, indicating broader adaptation across different environments. In contrast, G3, G2, and G8 are poorly adapted to all environments. It is recommended that these genotypes be cultivated under unfavorable conditions, as they demonstrate resilience to environmental variations. Several researchers reported similar findings (Delesa et al. 2022).

3.5 | Limitation of the Study

Although the findings provide valuable insights into genotype performance and stability, it is important to acknowledge certain limitations. The study is based on data collected over only 2 years and across six environments, which may not fully capture the wide range of environmental variability impacting chickpea production. Additionally, the statistical methods applied, though robust, have inherent assumptions and constraints that may influence the interpretation of GEI. These factors suggest that recommendations for commercial cultivation should be considered with caution, and further multiyear, multilocation trials would strengthen the reliability of these findings.

4 | Conclusions and Recommendation

The development of kabuli-type chickpea genotypes, which are adapted to a wide range of diversified environments, is the ultimate aim of breeders in crop improvement programs. The adaptability of genotypes over diverse environments is commonly evaluated by the degree of their interaction with different environments in which it is grown. The combined ANOVA revealed significant differences among the genotypes for all of the studied traits. Grain yield is an important character to be considered for genotype selection to address the objective of the conducted activity as long as its economic yield is grain yield in Ethiopia. Genotypes Arerti (G5) and Yelbie (G9) were the first and second highest-yielding genotypes with a yield of 2.42 and 2.18 t ha^{-1}, respectively. Arerti is a wide-adapted genotype, performing well across multiple environments, whereas Hora and Koka are more specifically adapted to particular locations with favorable conditions. GGE biplot analysis shows the best-suited genotype for each specific environment. Considering simultaneous average yield and stability, Arerti (G5), Chefe (G1), and Yelbie (G9) genotypes were the best and most stable genotypes across all tested environments. The six testing environments were divided into two mega environments, whereas the nine genotypes were divided into five genotypic groups. Environments Shebel and Jabitenan were more representative environments. Therefore, after receiving approval, this genotype would be used as a commercial genotype for possible chickpea growing places to increase chickpea productivity and production well as used as parent material for kabuli chickpeas breeding. Cultivating Arerti and Yelbie in Northern Ethiopia and other similar chickpea growing areas is recommended because of their high yield and moderate stability. Further exploration of GEI can help refine the genotype selection for optimal performance in specific environments.

Author Contributions

Alemnesh Eskezia: investigation, methodology, supervision, visualization, writing – original draft, writing – review and editing. **Kelemu Nakachew:** conceptualization, data curation, supervision, validation. **Meseret Tadesse:** resources, software, supervision. **Mulusew Kassa:** data curation, formal analysis, visualization.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Datasets generated in this study are available from the corresponding author upon reasonable request.

References

Abraha, M. T., H. Shimelis, T. Solomon, and A. Hailu. 2019. "Genotype-By-Environment Interaction and Selection of Elite Wheat Genotypes Under Variable Rainfall Conditions in Northern Ethiopia." *Journal of Crop Improvement* 33, no. 6: 797–813.

Alemu, G., N. Geleta, A. Dabi, A. Delessa, and R. Duga. 2021. "Stability Models for Selecting Adaptable and Stable Bread Wheat (*Tritium aestivum* L.) Varieties for Grain Yield in Ethiopia." *Journal of Agricultural Science and Engineering* 7: 14–22.

Asefa, G. 2022. "GGE Biplot Analysis of Genotype by Environment Interaction and Yield Stability Analysis of Arabica Coffee (*Coffea arabica* L.) Diallel Genotypes in South Western Ethiopia." *GSJ* 10, no. 3: 1082–1100.

Atta, B. M., and T. M. Shah. 2009. "Stability Analysis of Elite Chickpea Genotypes Tested Under Diverse Environments." *Australian Journal of Crop Science* 3, no. 5: 249–256.

Bakala, N., I. Jibat, and B. Idao. 2022. "Agro-Morphological Evaluation of Improved Bread Wheat (*Triticum aestivum* L) Varieties for Highland Areas of Western Guji, Southern Oromia." *Scholarly Academic Journal of Biosciences* 1: 5–10.

Behera, K., A. Babbar, R. G. Vyshnavi, T. Patel, and S. S. Prajapati. 2023. "Exploring the Chickpea Genotypes Through Morphological Characterization for Improved Breeding." *International Journal of Plant & Soil Science* 35, no. 18: 551–563.

Bekana, G. 2023. "Genotype X Environment Interactions and Yield Stability of Tef (*Eragrostis tef*) Genotypes Grown in Central Parts of Ethiopia." *American Journal of BioScience* 11, no. 4: 104–110.

Beksisa, L. 2021. "Genotype x Environment Interaction and Its Stability Measures in Plant Breeding; Major Emphasis on Arabica Coffee (*Coffea arabica* L.): A Review." *International Journal of Research Studies in Science, Engineering and Technology* 8, no. 3: 27–37.

Bose, L. K., N. N. Jambhulkar, K. Pande, and O. N. Singh. 2014. "Use of AMMI and Other Stability Statistics in the Simultaneous Selection of Rice Genotypes for Yield and Stability Under Direct-Seeded Conditions." *Chilean Journal of Agricultural Research* 74, no. 1: 3–9. https://doi.org/10.4067/S0718-58392014000100001.

Carvalho, R. F., T. S. Silva, A. K. D. S. Pereira, G. S. Cavallini, and D. H. Pereira. 2024. "Theoretical and Experimental Study of the Stability of Thiamethoxam Under Different Environmental Conditions." *Processes* 12, no. 11: 2328.

Chichaybelu, M., N. Girma, A. Fikre, et al. 2021. "Enhancing Chickpea Production and Productivity Through Stakeholders' Innovation Platform Approach in Ethiopia." In *Enhancing Smallholder Farmers' Access to Seed of Improved Legume Varieties Through Multi-Stakeholder Platforms: Learning From the TLIII project Experiences in Sub-Saharan Africa and South Asia*, 97–111. Springer.

Dabi, A., G. Alemu, B. Sime, et al. 2023. "Genotype× Environment Interaction and Stability Analysis Using GGE Biplot for Grain Yield of Bread Wheat (Triticum Aestivum) Genotypes Under Low Moisture Stress Areas of Ethiopia." *International Journal of Bio-Resource and Stress Management* 14, no. 7: 1089–1098.

Daemo, B. B. 2024. "Genotype by Environment Interaction and Performance Stability of Common Bean (*Phaseolus vulgaris* L.) Cultivars Grown in Dawuro Zone, Southwestern Ethiopia." *Open Agriculture* 9, no. 1: 20220288. https://doi.org/10.1515/opag-2022-0288.

Daemo, B. B., G. B. Wolancho, Z. A. Arke, D. D. Wakalto, and M. H. Onu. 2024. "Performance Evaluation and Stability of Maize (*Zea mays* L.) Genotypes for Grain Yield Using AMMI and GGE Biplot." *International Journal of Agronomy* 2024, no. 1: 8801999. https://doi.org/10.1155/2024/8801999.

Danakumara, T., T. Kumar, N. Kumar, et al. 2023. "A Multi-Model Based Stability Analysis Employing Multi-Environmental Trials (METs) Data for Discerning Heat Tolerance in Chickpea (*Cicer arietinum* L.) Landraces." *Plants (Basel)* 12, no. 21: 3691. https://doi.org/10.3390/plants12213691.

De Vita, P., A. M. Mastrangelo, L. Matteu, et al. 2010. "Genetic Improvement Effects on Yield Stability in Durum Wheat Genotypes Grown in Italy." *Field Crops Research* 119, no. 1: 68–77. https://doi.org/10.1016/j.fcr.2010.06.016.

Delesa, A., G. Alemu, N. Geleta, et al. 2022. "Stability and Performance Evaluation of Advanced Bread Wheat (*Triticum aestivum* L.) Genotypes in Optimum Areas of Ethiopia." *International Journal of Bio-Resource and Stress Management* 13, no. Jan, 1: 69–80. https://doi.org/10.23910/1.2022.2723.

Derbew, S., F. Mekbib, B. Lakew, A. Bekele, and Z. Bishaw. 2024. "AMMI and GGE Biplot Analysis for Barley Genotype Yield Performance and Stability Under Multi Environment Condition in Southern Ethiopia." *Agrosystems, Geosciences & Environment* 7, no. 3: e20565. https://doi.org/10.1002/agg2.20565.

EAA. 2022. "Ethiopian Agriculture Authority, Plant Variety Release, Protection and Seed Quality Control Directorate, Crop Variety Register, Issue No. 25, June 2022, Addis Ababa, Ethiopia."

Eberhart, S. T., and W. Russell. 1966. "Stability Parameters for Comparing Varieties 1." *Crop Science* 6, no. 1: 36–40.

Ejara, E., K. Kitaba, Z. Misganaa, and G. Tesama. 2020. "Performance Evaluation of Chickpea Varieties (*Cicer arietinum* L.) at Bule Hora and Abaya Southern Ethiopia." *Journal of Biotechnology Research* 6, no. 5: 34–40.

ESS. 2022. "Report on Area and Production of Major Crops (Private Peasant Holdings, Meher Season)." Volume I, Statistical Bulletin 593, Addis Ababa, Ethiopia.

Fan, X.-M., M. S. Kang, H. Chen, Y. Zhang, J. Tan, and C. Xu. 2007. "Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China." *Agronomy Journal* 99, no. 1: 220–228. https://doi.org/10.2134/agronj2006.0144.

Farshadfar, E., M. Rashidi, M. M. Jowkar, and H. Zali. 2013. "GGE Biplot Analysis of Genotype× Environment Interaction in Chickpea Genotypes." *European Journal of Experimental Biology* 3, no. 1: 417–423.

Fekadu, W., F. Mekbib, B. Lakew, and B. I. G. Haussmann. 2023. "Genotype× Environment Interaction and Yield Stability in Barley (*Hordeum vulgare* L.) Genotypes in the Central Highland of Ethiopia." *Journal of Crop Science and Biotechnology* 26, no. 2: 119–133.

Fick, G. W., D. A. Holt, and D. G. Lugg. 1988. "Environmental Physiology and Crop Growth." *Alfalfa and Alfalfa Improvement* 29: 163–194.

Finlay, K. W., and G. N. Wilkinson. 1963. "The Analysis of Adaptation in Plant-Breeding Programme." *Australian Journal of Agricultural Research* 14: 742–754.

Gauch, H. G., Jr. 2013. "A Simple Protocol for AMMI Analysis of Yield Trials." *Crop Science* 53, no. 5: 1860–1869. https://doi.org/10.2135/cropsci2013.04.0241.

Gauch, H. G., and R. W. Zobel. 1988. "Predictive and Postdictive Success of Statistical Analyses of Yield Trials." *Theoretical and Applied Genetics* 76, no. 1: 1–10. https://doi.org/10.1007/BF00288824.

Gauch, H. G., Jr., and R. W. Zobel. 1997. "Identifying Mega-Environments and Targeting Genotypes." *Crop Science* 37, no. 2: 311–326. https://doi.org/10.2135/cropsci1997.0011183X003700020002x.

Gebeyaw, M., A. Fikre, A. Abate, et al. 2024. "Genotype by Environment (G× E) Interaction and Yield Stability of Chickpea (*Cicer arietinum* L.) Varieties Across Agroecological Regions of Ethiopia." *Legume Science* 6, no. 2: e227. https://doi.org/10.1002/leg3.227.

Getahun, T., K. Tesfaye, A. Fikre, et al. 2021. "Molecular Genetic Diversity and Population Structure in Ethiopian Chickpea Germplasm Accessions." *Diversity* 13, no. 6: 247.

Grüneberg, W. J., K. Manrique, D. Zhang, and M. Hermann. 2005. "Genotype× Environment Interactions for a Diverse Set of Sweetpotato Clones Evaluated Across Varying Ecogeographic Conditions in Peru." *Crop Science* 45, no. 6: 2160–2171.

Haider, Z., M. Akhter, A. Mahmood, and R. A. R. Khan. 2017. "Comparison of GGE Biplot and AMMI Analysis of Multi-Environment Trial (MET) Data to Assess Adaptability and Stability of Rice Genotypes." *African Journal of Agricultural Research* 12, no. 51: 3542–3548.

Jifar, H., K. Assefa, K. Tesfaye, K. Dagne, and Z. Tadele. 2019. "Genotype-By-Environment Interaction and Stability Analysis in Grain Yield of Improved Tef (*Eragrostis tef*) Varieties Evaluated in Ethiopia." *Journal of Experimental Agriculture International* 35, no. 5: 1–13.

Kaloki, P., R. Trethowan, and D. K. Y. Tan. 2019. "Effect of Genotype× Environment× Management Interactions on Chickpea Phenotypic Stability." *Crop and Pasture Science* 70, no. 5: 453–462. https://doi.org/10.1071/CP18547.

Karimizadeh, R., P. Pezeshkpour, A. Mirzaee, M. Barzali, P. Sharifi, and M. R. S. Motlagh. 2023. "Stability Analysis for Seed Yield of Chickpea (*Cicer arietinum* L.) Genotypes by Experimental and Biological Approaches." *Vavilov Journal of Genetics and Breeding* 27, no. 2: 135.

Kaya, Y., M. Akçura, and S. Taner. 2006. "GGE-Biplot Analysis of Multi-Environment Yield Trials in Bread Wheat." *Turkish Journal of Agriculture and Forestry* 30, no. 5: 325–337.

Kizilgeci, F., O. Albayrak, M. Yildirim, and C. Akinci. 2019. "Stability Evaluation of Bread Wheat Genotypes Under Varying Environments by AMMI Model." *Fresenius Environmental Bulletin* 28, no. 9: 6865–6872.

Kumar, K. N. R., M. J. M. Reddy, and S. C. Babu. 2023. "Climate Change Effects on Chickpea Yield and Its Variability in Andhra Pradesh, India." *Journal of Applied and Natural Science* 15, no. 1: 178–193. https://doi.org/10.31018/jans.v15i1.4102.

Lin, C.-S., M. R. Binns, and L. P. Lefkovitch. 1986. "Stability Analysis: Where Do We Stand? 1." *Crop Science* 26, no. 5: 894–900.

Mansour, E., E. S. A. Moustafa, N. Z. A. El-Naggar, A. Abdelsalam, and E. Igartua. 2018. "Grain Yield Stability of High-Yielding Barley Genotypes Under Egyptian Conditions for Enhancing Resilience to Climate Change." *Crop and Pasture Science* 69, no. 7: 681–690. https://doi.org/10.1071/CP18144.

Mehari, M., M. Tesfay, H. Yirga, et al. 2015. "GGE Biplot Analysis of Genotype-by-Environment Interaction and Grain Yield Stability of Bread Wheat Genotypes in South Tigray, Ethiopia." *Communications in Biometry and Crop Science* 10, no. 1: 17–26.

Megerssa, S. H., Y. S. Ishetu, M. Hailu, and A. Z. Lemma. 2024. "Genotype by Environment Interaction and Stability Analyses of Durum Wheat Elite Lines Evaluated in Ethiopia." *Crop Breeding and Applied Biotechnology* 24, no. 1: e45542417.

Misganaw, F. 2016. "Stability Analysis in Bread Wheat (*Triticum aestivum* L.) Genotypes in North-Western Ethiopia." *East African Journal of Sciences* 10, no. 1: 15–22.

Mohammadi, R., and A. Amri. 2012. "Analysis of Genotype× Environment Interaction in Rain-Fed Durum Wheat of Iran Using GGE-Biplot and Non-Parametric Methods." *Canadian Journal of Plant Science* 92, no. 4: 757–770.

Mwendo, M. M., E. R. Mbega, J. Ndunguru, and M. Philipo. 2025. "AMMI and GGE Biplot Analysis of Maize Genotypes for Seed Yield Across Different Maize Growing Location in Tanzania." *Cogent Food & Agriculture* 11, no. 1: 2438909. https://doi.org/10.1080/23311932.2024.2438909.

Negash, A. W., H. Mwambi, T. Zewotir, and G. Taye. 2013. "Additive Main Effects and Multiplicative Interactions Model (AMMI) and Genotype Main Effect and Genotype by Environment Interaction (GGE) Biplot Analysis of Multi-Environmental Wheat Variety Trials." *African Journal of Agricultural Research* 8, no. 12: 1033–1040.

Negash, G., B. Alemu, and W. Raga. 2021. "Multi-Location Evaluation of Yield and Yield Related Trait Performance in Bread Wheat Genotypes at Western Oromia, Ethiopia." *International Journal of Applied Agricultural Sciences* 7, no. 3: 119. https://doi.org/10.11648/j.ijaas.20210703.12.

Nkalubo, S. T., A. Namayanja, A. Namusoke, et al. 2024. "Agronomic Performance, Stability Analysis and Evaluation of Anthracnose Disease Resistance of Common Bean Lines Derived by Marker-Assisted Backcrossing in Uganda." *Agricultural Sciences* 15, no. 3: 376–397.

Otieno, O. V., and O. N. Owuor. 2019. "Multivariate Genotype and Genotype by Environment Interaction Biplot Analysis of Sugarcane Breeding Data Using R." *International Journal of Statistics and Distribution Applications* 5: 22.

Purewal, S. S., P. Kaur, and R. K. Salar. 2023. *Chickpea and Cowpea: Nutritional* Profile, *Processing, Health Prospects and Commercial Uses*. CRC Press.

Richards, M. F., A. L. Preston, T. Napier, L. Jenkins, and L. Maphosa. 2020. "Sowing Date Affects the Timing and Duration of Key Chickpea (*Cicer arietinum* L.) Growth Phases." *Plants* 9, no. 10: 1257.

SAS. 2013. *System Analysis Software*. Institute: Chapman and Hall/CRC.

Scavo, A., G. Mauromicale, and A. Ierna. 2022. "Dissecting the Genotype × Environment Interaction for Potato Tuber Yield and Components." *Agronomy* 13, no. 1: 101. https://doi.org/10.3390/agronomy13010101.

Scavo, A., G. Mauromicale, and A. Ierna. 2023. "Genotype× Environment Interactions of Potato Tuber Quality Characteristics by AMMI and GGE Biplot Analysis." *Scientia Horticulturae* 310: 111750.

Seyoum, A. 2021. "Multi-Environment Evaluation and Genotype x Environment Interaction Analysis of Sorghum [Sorghum Bicolor (L.) Moench] Genotypes in Highland Areas of Ethiopia." *Journal of Environmental Geology* 5, no. 3: 1.

Shahir, A. A., Francesco, F., and Ali, A. M.. 2022. Ethiopia.

Sharma, R. C., A. I. Morgounov, H. J. Braun, et al. 2010. "Identifying High Yielding Stable Winter Wheat Genotypes for Irrigated Environments in

Central and West Asia." *Euphytica* 171, no. 1: 53–64. https://doi.org/10.1007/s10681-009-9992-6.

Shibeshi, S. 2019. "Performance Evaluation of Released Bread Wheat Varieties at Mid Altitude Areas of Southern Ethiopia." *Ukrainian Journal of Ecology* 9, no. 4: 661–664.

Shukla, G. K. 1972. "Some Statistical Aspects of Partitioning Genotype-Environmental Components of Variability." *Heredity, UK* 29, no. 2: 237–245.

Shunbura, A. K., S. A. Rorisa, and K. K. Gedefa. 2024. "Genotype by Environment Interaction and Stability Study in Bread Wheat (*Triticum Aestivum* L.) Genotypes in Guji Zone, Southern Ethiopia." *GSC Advanced Research and Reviews* 19, no. 2: 85–92.

Singh, C., A. Gupta, V. Gupta, et al. 2019. "Genotype x Environment Interaction Analysis of Multi-Environment Wheat Trials in India Using AMMI and GGE Biplot Models." *Crop Breeding and Applied Biotechnology* 19, no. 3: 309–318. https://doi.org/10.1590/1984-70332019v19n3a43.

Singh, H. K., P. K. Ray, S. S. Solankey, and R. N. Singh. 2021. "Impact of Climate Change on Leguminous Vegetables Productivity and Mitigation Strategies." *Advances in Research on Vegetable Production Under a Changing Climate* 1: 149–161.

Smith, B., D. Wårlind, A. Arneth, et al. 2014. "Implications of Incorporating N Cycling and N Limitations on Primary Production in an Individual-Based Dynamic Vegetation Model." *Biogeosciences* 11, no. 7: 2027–2054.

Tadesse, W., Z. Bishaw, and S. Assefa. 2018. "Wheat Production and Breeding in Sub-Saharan Africa: Challenges and Opportunities in the Face of Climate Change." *International Journal of Climate Change Strategies and Management* 11, no. 5: 696–715.

Tadesse, Z., H. Zegeye, D. Asnake, T. Solomon, Y. Shewaye, and T. Debele. 2018. "Identification of Stable Bread Wheat (*Triticum aestivum* L.) Genotypes Using AMMI Analysis in Ethiopia." *International Journal of Research in Agriculture and Forestry* 5: 6–14.

Takele, E., N. Kefelegn, D. Admasu, et al. 2024. "Performance of Genotype by Environmental Interaction and Stability of Faba Bean (*Vicia faba* L.) Genotypes in Vertisol Areas of Amhara Region, Ethiopia." *Advances in Agriculture* 2024, no. 1: 7574274.

Taye, Y. and A. Ayenew. 2023. "Performance Evaluation of Desi Chickpea (*Cicer arietinum* L.) Varieties Through Participatory Variety Selection South Gonder Zone, North Western Ethiopia."

Wang, R., H. Wang, S. Huang, et al. 2023. "Assessment of Yield Performances for Grain Sorghum Varieties by AMMI and GGE Biplot Analyses." *Frontiers in Plant Science* 14: 1261323. https://doi.org/10.3389/fpls.2023.1261323.

Xu, Y., P. Li, C. Zou, et al. 2017. "Enhancing Genetic Gain in the Era of Molecular Breeding." *Journal of Experimental Botany* 68, no. 11: 2641–2666. https://doi.org/10.1093/jxb/erx135.

Yan, W. 2001. "GGEbiplot—A Windows Application for Graphical Analysis of Multienvironment Trial Data and Other Types of Two-Way Data." *Agronomy Journal* 93, no. 5: 1111–1118.

Yan, W., and J. B. Holland. 2010. "A Heritability-Adjusted GGE Biplot for Test Environment Evaluation." *Euphytica* 171, no. 3: 355–369.

Yan, W., L. A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. "Cultivar Evaluation and Mega-Environment Investigation Based on the GGE Biplot." *Crop Science* 40, no. 3: 597–605.

Yan, W., and N. A. Tinker. 2006. "Biplot Analysis of Multi-Environment Trial Data: Principles and Applications." *Canadian Journal of Plant Science* 86, no. 3: 623–645.

Yan, W., M. S. Kang, B. Ma, S. Woods, and P. L. Cornelius. 2007. "GGE Biplot vs. AMMI Analysis of Genotype-by-Environment Data." *Crop Science* 47, no. 2: 643–653.

Yazachew, G., S. Ch, F. Tsion, et al. 2021. "Genotype by Environment Interaction and Grain Yield Stability Analysis of Advanced TEF Genotypes for High Potential TEF Growing Areas of Ethiopia." *Journal of Advanced Plant Sciences* 3: 204.