



Seed Yield Stability Assessment in Advanced Breeding Lines of Chickpea (*Cicer arietinum* L.) using AMMI and GGE Biplot Analysis

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ABSTRACT

Background: Climate change has led to temperature variations affecting chickpea crops in dry and semi-arid regions. Late-sown crops are exposed to high temperatures during their reproductive phases, while early-sown crops experience low temperatures during their vegetative stages. A set of fourteen chickpea genotypes were evaluated for seed yield stability under five different sowing dates during 2022-23 to identify lines with heat and moisture stress tolerance. The results aim to determine the best sowing time for optimal growth and yield.

Methods: A study was conducted during the *Rabi* season of 2022-2023 to assess the yield performance of fourteen chickpea genotypes, including Advanced Breeding Lines and released varieties, at ZARS, Kalaburagi. The genotypes were sown on five dates and evaluated using the AMMI model and GGE biplot analysis to examine genotype-environment interactions and yield stability.

Result: Analysis of variance (ANOVA) across five environments (ENV-1 to ENV-5) revealed significant genotypic differences in all environments indicating the presence of substantial amount of variability among the evaluated genotypes. Further, the principal components (PCs) obtained from the genotype \times environment interaction studies were highly significant. The first principal component (PC1) accounts for 51.1% of the interaction variation, while PC2, PC3 and PC4 explain an additional 20.2%, 19.2% and 9.5%, respectively, together accounting for 100% of the interaction variation. Interaction principal component analysis (IPCA) scores from AMMI helped identify genotypes with consistent performance and those with specific adaptive responses. Based on all models, genotypes G1 (KCD-11) and G7 (GBM-2) emerge as the top performers, offering the highest yields and superior stability. Therefore, these genotypes could be recommended to farmers for various sowing dates.

Key words: AMMI, Chickpea, Environment, GGE, Stability, Wricke's ecovalence.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinating, annual diploid species ($2n = 2x = 16$) with a genome size of 738 Mb (Varshney *et al.*, 2018), commonly known as gram, Bengal gram, Egyptian pea, or garbanzo bean (Cobos *et al.*, 2007). As a member of the Fabaceae family, it remains a vital crop, grown in 57 countries and contributing over 20% of global pulse production. India dominates the market, producing 80-90% of the world's chickpeas, with 10.19 million hectares under cultivation, yielding 12.16 million tonnes at 1193 kg per hectare (Indiastat, 2023-24).

Climate change over the past two decades has introduced temperature fluctuations that negatively impact chickpea cultivation, especially in dry and semi-arid regions. Late-sown crops face high temperatures ($>35^{\circ}\text{C}$) during February and March, while early-sown crops encounter low temperatures in December and January, finding optimal sowing times is crucial (Ahmed *et al.*, 2024). The sowing window has extended from October to December, leading to increased temperature, humidity fluctuations and moisture stress, all of which affect crop yield and quality.

Identifying chickpea lines resilient to these changing conditions is essential. Testing genotypes under both normal and late-sown conditions can reveal those with

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heat and moisture stress tolerance. Genotype \times environment interaction (GEI) plays a significant role in crop yield variation and statistical methods like AMMI and GGE biplots are effective for analyzing GEIs and selecting stable genotypes (Saidiaiah *et al.*, 2024). This study uses multi-model

analysis to identify high yielding, stable chickpea genotypes adaptable to diverse environments, focusing on breeding varieties resilient to climate change.

MATERIALS AND METHODS

The experiment material consists of fourteen chickpea genotypes inclusive of Advanced Breeding Lines and released varieties (Table 1) were evaluated in a randomized complete block design (RCBD) with three replications during *Rabi*, 2022-2023 at Zonal Agricultural Research Station (ZARS), Kalaburagi. Each genotype was sown in four rows of four meters in length with a spacing of 30 cm × 10 cm. The genotypes were sown on five different dates: 9, October 2022; 21, October 2022; 5, November 2022; 19, November 2022 and 5, December 2022. All recommended cultural practices and plant protection measures were followed according to the University of Agricultural Sciences, Raichur guidelines to raise healthy crop.

To study the Genotype × Environment interaction (GEI) across all five environments, a combined analysis of variance was carried out. Since GEI effect was found significant, data was subjected to Additive Main Effects and Multiplicative Interaction (AMMI) analysis. AMMI model (Gauch and Zobel, 1998) was used to capture and characterise the pattern of G × E interaction. Genotype + Genotype × Environment (GGE) biplot analysis (Yan *et al.*, 2000) was used to graphically visualize which genotype performed best in specific environments and to identify high performing stable genotypes.

Yield stability was assessed using various stability parameters and the AMMI and GGE biplot analyses were carried out by using R statistical software version 4.2.0.

RESULTS AND DISCUSSION

Chickpea's sowing window has been extended from October to December in major crop growing districts of

Table 1: Genotypes used in the study along with their parentage and characteristic features.

Code	Genotype	Parentage	Characteristic features
G1	KCD-11	JG-11 × WR-315	High yielding, wilt resistant desi genotype.
G2	KCD-134	ICCV 03112 × ICCV 10	High yielding, wilt resistant variety, suitable for irrigated condition.
G3	KCMH-2	GBM-2 × WR-315	High yielding wilt resistant and suitable for mechanical harvest.
G4	KCMH 20-17	ICCV 10/ICCV 11601	High yielding wilt resistant, medium sized seeds, suitable for mechanical harvest.
G5	SA-1	Annigeri-1 × WR-315	High yielding, wilt resistance desi variety (MABC line)/ Zonal and regional check.
G6	JG-11	ICCV 93954	High yielding wilt resistant desi variety (National check).
G7	GBM-2	Mutant of Annigeri 1	High yielding suitable for mechanical harvest (National / zonal check).
G8	KCD 21-6	NBeG-857	High yielding, wilt resistance medium sized seeds.
G9	KCD 20-8	ICCV 93954//ICCV 93954// ICCV 96029/ICCV 93954	High yielding, wilt resistance, medium seedsize desi genotype.
G10	KCD 20-03	GG 2/ICC 1205	High yielding, wilt resistance medium seed size desi genotype.
G11	ICC 4958	ICRISAT collection	Bold seeded, check variety for drought trial.
G12	JG-14	(GW 5/7×P327) ×ICCL83149	Heat stress check.
G13	BGD 111-1	JG-62 × ICC 12237//JG-62	High yielding, wilt resistance, desi variety.
G14	GJG 1913	PG 07104 × WR-315	High yielding variety suitable for irrigated condition and mechanical harvesting.

Table 2: Analysis of variance, mean performance and heritability of five different dates of sowing.

ENV	ENV-1	ENV-2	ENV-3	ENV-4	ENV-5
DF			13		
MEAN	2316.89	1804.42	1587.33	1017.73	705.16
MSG	150134.00***	345840.76***	269535.26***	45702.89***	98109.20***
MSB	5225.93	4973.20	66766.42	12468.85	14095.63
MSE	25986.99	18678.96	20154.94	11957.18	4135.07
CV	6.96	7.57	8.94	10.74	9.12
h ²	0.83	0.95	0.93	0.74	0.96

Karnataka due to climatic changes in recent years. Due to the prolonged cropping season, crops are exposed to variations in temperature, relative humidity and moisture levels (Richards *et al.*, 2020). These environmental fluctuations influence crop phenology, yield-contributing traits and quality characteristics. Therefore, it is crucial to identify chickpea genotypes that can consistently produce stable yields under changing environmental conditions.

The ANOVA analysis across five environments (ENV-1 to ENV-5) reveals significant differences among the genotypes, indicating variability among the genetic materials being studied (Table 2). The mean values varied, with ENV-1 recording the highest average of 2316.89, while ENV-5 had the lowest at 705.16. The coefficient of variation (CV) indicated that ENV-4 exhibited the greatest relative variability at 10.74%, whereas ENV-1 showed the least variability at 6.96%. Broad-sense heritability (h^2) is high across all environments, ranging from 0.74 to 0.96, indicating that genetic factors significantly influence the phenotypic traits. This suggests a strong genetic control over the traits studied, with relatively stable genetic influence despite environmental differences.

The Pooled ANOVA (Table 3) across five environments revealed highly significant differences in the $G \times E$ interactions, indicating that the grain yield of the 14 genotypes varied significantly across the different environments. Environment mean squares were highly significant across the five environments with 82.90% contribution to the total variance. The interaction between genotype and environment mean squares were also significant with contribution 6.55% to the total variance. The replication within environments

mean squares were non-significant with a minimal contribution of 0.25%. The residual mean squares contribute 2.55% to the total variance. These results registered the predominant influence of environmental factors on the yield attributing traits of chickpea.

AMMI analysis of 14 genotypes evaluated across five environments

The analysis of variance for grain yield of 14 chickpea genotypes evaluated across five environments (Table 4) through AMMI model revealed that chickpea genotypes were significantly ($P \leq 0.01$) affected by different environments. The genotype by environment interaction also showed highly significant, suggesting that the performance of genotypes varies significantly across different environments. This interaction is crucial for identifying genotypes that perform well under specific conditions.

The principal components (PCs) derived from the genotype by environment interaction are highly significant. The first principal component (PC1) explains 51.1% of the interaction variation, while PC2, PC3 and PC4 explain an additional 20.2%, 19.2% and 9.5% respectively, cumulatively explaining 100% of the interaction variation. This reveals that these components effectively capture the variation due to genotype by environment interactions at different environments. According to the AMMI model, the genotypes which are characterized by means greater than grand mean and the IPCA score nearly zero are considered as adaptable genotypes across the environment (Rashidi *et al.*, 2013). However, the genotypes with high mean performance and large value of IPCA score suggests that these genotypes were adaptable to the specific environments.

Table 3: Pooled analysis of variance of genotypes across five environments.

Source	Df	Sum Sq	Mean Sq	F value	Pr (>F)	% Contribution
ENV	4	68503049	17125762	1058.281	4.23E-98	82.90
REP(ENV)	10	207060	20706	1.279521	0.248488	0.25
GEN	13	6405713	492747.1	30.44914	3.25E-33	7.75
GEN: ENV	52	5415475	104143.7	6.435527	4.1E-18	6.55
Residuals	130	2103742	16182.63			2.55
Total	209	82635038				
CV (%)	8.558867					
OV mean	1486.306					

Table 4: AMMI analysis of variance for grain yield (kg/ha) of 14 chickpea genotypes for five different dates of sowing.

Source	Df	Sum Sq	Mean Sq	F value	Pr (>F)	Proportion	Accumulated
ENV	4	68503049.10	17125762.28	827.09	0.00		
REP (ENV)	10	207060.05	20706.00	1.28	0.25		
GEN	13	6405712.87	492747.14	30.45	0.00		
GEN: ENV	52	5415474.56	104143.74	6.44	0.00		
PC1	16	2765275.12	172829.69	10.68	0.00	51.1	51.1
PC2	14	1095778.02	78269.86	4.84	0.00	20.2	71.3
PC3	12	1039339.32	86611.61	5.35	0.00	19.2	90.5
PC4	10	515082.10	51508.21	3.18	0.00	9.5	100
Residuals	130	2103741.53	16182.63				
Total	261	88050512.67	337358.29				

The AMMI 1 biplot for grain yield of the 14 chickpea genotypes at five environmental conditions is shown in Fig 1. The main effects (genotypes and environments) accounted for 90.65% of the total variation and IPCA 1 accounted for 51.1% of the total variation due to genotype by environment interaction alone. For instance, ENV-1 and ENV-2, located on the right side with higher yield values revealed that G1, G7 and G9 may perform well in these environments. Conversely, ENV-5, positioned on the upper left, suggests that G12 and G13 are more adapted to this environment. ENV-3 and ENV-4, near the plot centre, show moderate interactions with several genotypes like G3, G4 and G10. This biplot effectively illustrates which genotypes are best suited to specific environments, aiding in targeted breeding and selection efforts. The AMMI1 biplot shows that genotypes G1, G7 and G9 perform best in high-yield environments ENV-1 and ENV-2, while G12 and G13 are better suited for ENV-5.

The AMMI 2 biplot provides a visual representation of the interactions between genotypes (G1 to G14) and environments (ENV-1 to ENV-5) based on the first two principal components (PC1 and PC2), which together accounts 71.3% of the total interaction variation (51.1% by PC1 and 20.2% by PC2). ENV-3 is unique and highly interactive, with genotypes G6 and G10 thriving in this environment. In contrast, ENV-2 is more compatible with genotypes G5 and G7. While, ENV-1, ENV-4 and ENV-5 cluster near the centre, indicating a moderate interaction with multiple genotypes, such as G3, G4, G8 and G13 shown in Fig 2. These results highlight the specific adaptation of certain genotypes to particular environments, which is crucial for targeted breeding programs to enhance yield stability and performance across varying conditions.

Test environment evaluation

The persistence of test-environment evaluation is to identify environments that are effective in distinguishing superior genotypes within a mega-environment. An "ideal" test environment should be both discriminating of the genotypes and representative of the mega-environment and it is based on environment-focused scaling (Yan, 2002), that is, the singular values were entirely partitions the environment scores ("SVP = 2") so that it is appropriate for studying the relationships among test environments. This type of AEC can be referred to as the "Discriminating power vs. Representativeness" view of the GGE biplot.

Test environments with longer vectors are more effective at distinguishing between genotypes, while test environments with smaller angles are more representative of the mega-environment compared to those with larger angles. ENV-2 is having the longest vector, hence discriminating all the 14 genotypes and ENV-4 exhibits small angle among the all-test environment indicating ENV-4 is representative of all the 14 genotypes as in Fig 3.

Hence, ENV-4 may be regarded as an ideal test location. Hence, this biplot elucidates the differential performance of genotypes across various environments, highlighting which environments are most effective for

Table 5: Evaluation of 14 genotypes based on different stability models.

GEN	Y	Y_R	CV	CV_R	ACV	Shukla	Shukla_R	Wl_g	Wl_g_R	Wl_f	Wl_f_R	Wl_u	Wl_u_R	Ecoval	Ecoval_R	bij	Sij	Sij_R	R2	R2_R	Pl_a	Pl_a_R	Pl_f	Pl_f_R	Pl_u	Pl_u_R
G1	1724	2	41	3	43	23257	3	104	1	101	2	112	1	268969	3	1	19903	5	1	4	8074	2	8654	3	7205	1
G2	1554	5	43	7	43	45172	12	78	7	81	6	78	7	494386	12	1	49505	13	1	14	79082	6	124763	8	10561	4
G3	1297	12	35	1	34	42010	11	76	9	76	11	96	3	461860	11	1	-1606	1	1	1	174545	12	270541	12	30551	7
G4	1245	13	47	11	45	13540	1	65	13	75	12	48	13	169021	1	1	8587	2	1	2	197768	13	277644	13	77954	13
G5	1700	4	47	10	49	74762	14	78	8	98	4	51	12	798737	14	1	61249	14	1	12	20004	4	6569	1	40156	9
G6	1539	6	45	8	46	32097	8	82	4	88	5	70	9	359891	8	1	33019	11	1	9	56307	5	65687	5	42237	10
G7	1731	1	42	5	43	34930	9	101	2	99	3	103	2	389039	9	1	32626	10	1	6	7741	1	7275	2	8440	2
G8	1472	7	46	9	46	30278	5	82	5	78	8	87	5	341189	5	1	32225	9	1	10	97263	9	148609	9	20245	6
G9	1701	3	42	6	44	24617	4	93	3	105	1	73	8	282964	4	1	19317	4	1	3	16884	3	17619	4	15782	5
G10	1399	10	41	4	41	18570	2	81	6	79	7	80	6	220763	2	1	12415	3	1	5	113728	10	163719	10	38742	8
G11	1428	9	49	13	48	30583	6	69	11	77	10	52	11	344327	6	1	31125	7	1	7	95487	8	121964	7	55771	12
G12	1385	11	37	2	36	48823	13	69	12	75	13	91	4	531939	13	1	23285	6	1	13	147022	11	239065	11	8958	3
G13	1178	14	59	14	55	30932	7	47	14	58	14	27	14	347912	7	1	31673	8	1	8	248231	14	327256	14	129694	14
G14	1456	8	48	12	48	36431	10	75	10	77	9	63	10	404478	10	1	37911	12	1	11	84752	7	108814	6	48659	11

distinguishing genotypic performance and which genotypes show specific adaptation to particular environmental conditions.

Genotype evaluation

An ideal stable genotype should have high mean performance coupled with high stability within a mega environment.

Genotype evaluation is only useful for a particular mega-environment. Yan (2002) defined an “ideal” genotype on the basis of both mean performance and stability and the genotypes can be ranked based on their biplot distance from the ideal genotype. Fig 4 reveals that the biplot involves five environments with the “Average Environment

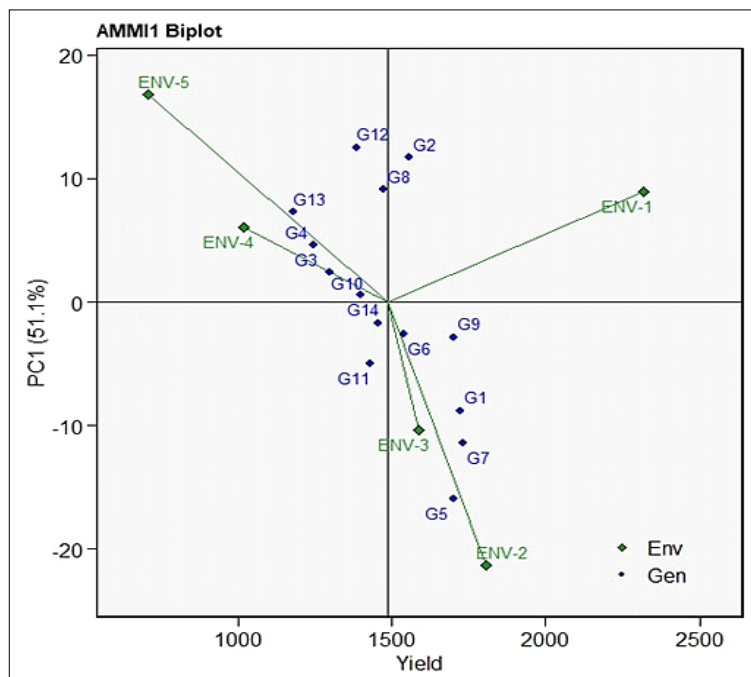


Fig 1: AMMI 1 biplot analysis of IPCA scores and environment means for grain yield of 14 chickpea genotypes.

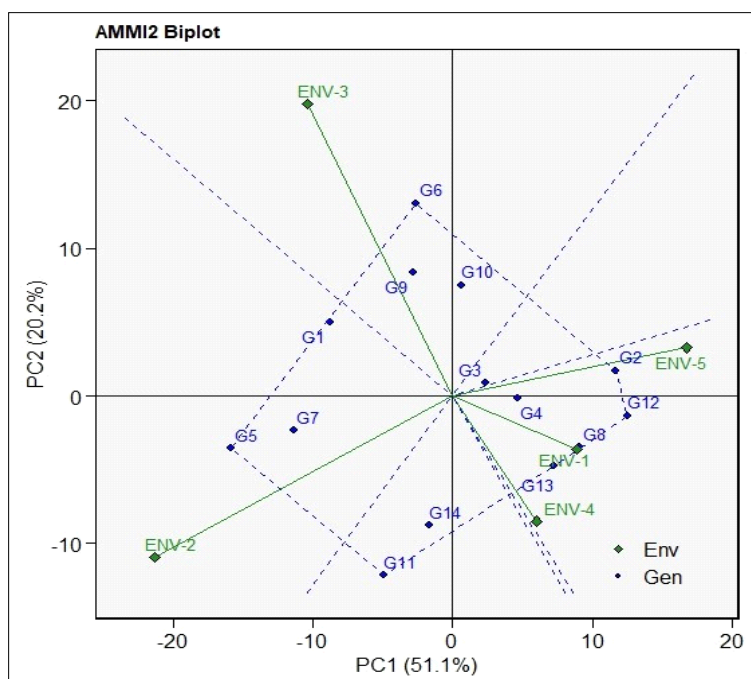


Fig 2: Biplot analysis of GE interaction using the AMMI2 model based on the first two principal component scores.

Coordination" (AEC) axis. The genotype-focused singular value partitioning (SVP), which divides the singular values completely into genotype scores is the basis of this AEC axis. The AEC view with SVP = 1 is commonly known as the "Mean vs. Stability" view due to its ability to compare

genotypes between environments based on mean performance and stability within a mega-environment.

The genotype on the extreme left of AEC axis indicates the higher mean performance and thus, the genotypes are ranked as $G9 = G1 > G7 > G5 > G6 > G2 > G14 > G11 > G10$

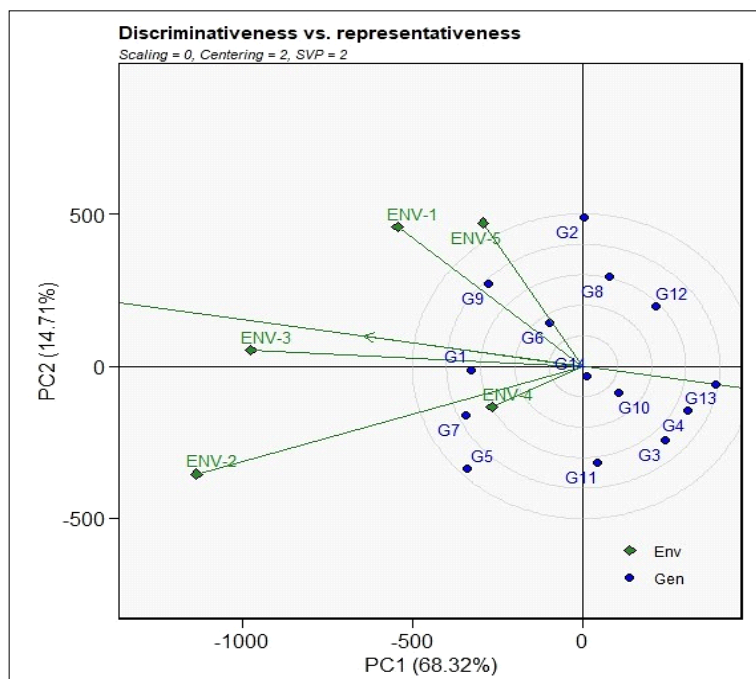


Fig 3: Discriminating power and representativeness of the test environments.

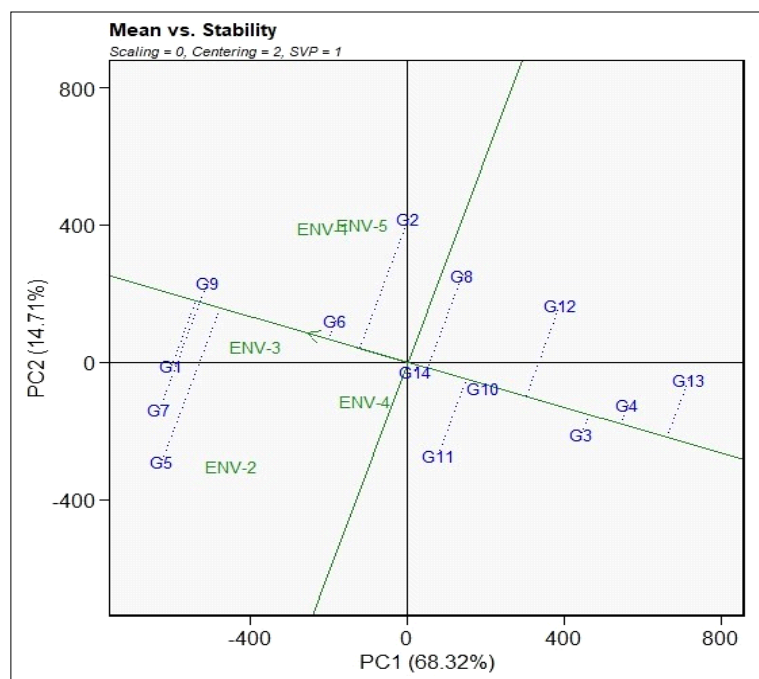


Fig 4: Mean performance and stability of 14 chickpea genotypes.

> G12 > G3 > G4 > G13. The genotypes which closure to the AEC ordinate indicates most stable genotypes. Among 14 genotypes, G4 and G10 are closure to the AEC ordinate compared to other genotypes. Hence, G4 and G10 are more stable genotypes.

Mega-environment analysis

The first principal component (PC1) scores of the genotypes and the environments are plotted against the corresponding scores for the second principal component (PC2) that derived from the SVD of environment-centred GGE biplot. This mega-environment analysis exhibits the which-won-where view of the biplot (Yan and Kang, 2002).

The biplot is divided into sectors by the perpendicular lines to the polygon sides, each of which has a distinct winning cultivar. The genotypes at the vertex of the polygon sides in the sector's boundary is the winning cultivar for that sector. In which-won-where view of the biplot shown in Fig 5, the five environments fell into two sectors with different winning cultivars. Specifically, G2, G9 and G1 were the highest yielding cultivar in first mega-environment (E1, E3 and E5). Whereas, G7 and G5 recorded highest yielding cultivar in the second E2 and E4 mega-environments. Therefore, identification of specific genotypes that perform well in certain environments can help in developing targeted breeding programs (Das *et al.*, 2024).

The comprehensive evaluation of 14 genotypes (G1 to G14) based on various metrics such as yield (Y), coefficient of variation (CV), adjusted coefficient of variation (ACV), Shukla's stability variance (Shukla), Wricke's ecovalence (Wi_g, Wi_f, Wi_u) and other stability parameters (Table 5)

reveals significant variations in yield performance, stability and adaptability across different environments. Genotypes G1 and G7 emerge as the top performers with the highest yield (1724 and 1731) and stability, as indicated by low coefficients of variation (CV), Wricke's ecovalence (Wi_g, Wi_f, Wi_u) and Shukla's stability variance. These genotypes also show excellent adaptability and predictability, with low Pi_a and Pi_u values, making them ideal candidates for diverse and variable growing conditions. Conversely, genotypes G13 and G4 exhibit the lowest yields and highest variability, marked by high CV and Shukla's variance, indicating their poor performance and instability. G3 stands out for its exceptional stability, with the lowest CV and ACV values, despite its lower yield, suggesting its suitability for environments where stability is prioritized. Overall, this analysis highlights G1 and G7 as the most promising genotypes for both high yield and stability, while G13 and G4 are less favourable due to their lower performance and higher variability similar finding was reported by Tiwari *et al.* (2018).

By integrating all the models, genotypes G1 and G7 consistently recorded high yield, low variability and constant stability across different environments. Genotypes G13 and G4, despite showing stability, generally have low yields and high variability, making them less favourable. While, Genotype G3 shows excellent stability (low CV, ACV) but lower yield, suggesting it could be suitable in environments where stability is prioritized over yield and Genotype G5 is high-yielding but shows high variability and instability suggests that it might perform well in favourable coupled with consistent environments (Laxuman *et al.*, 2025).

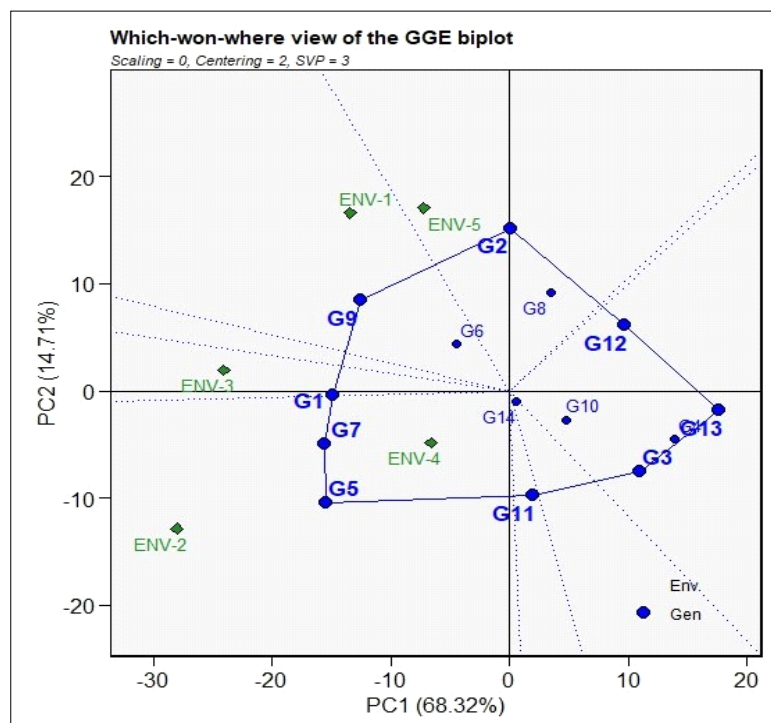


Fig 5: The "which-won-where" view of the GGE biplot based on the $G \times E$ interaction.

Overall, this comprehensive analysis provides a detailed performance and stability profile of each genotype, assisting in selecting the best-performing and most stable genotypes for particular environmental conditions.

CONCLUSION

The GGE biplot and AMMI model effectively highlighted the significance of genotype \times environment interactions (GEI) in chickpea breeding. Genotypes G1 (KCD-11) and G7 (GBM-2) emerged as top performers, combining high yield and stability across diverse environments, making them ideal for cultivation under varying conditions. Conversely, G13 (BGD-111-1) and G4 (KCMH-20-17) showed lower yields and higher variability, indicating less favourable adaptability. Genotype G3 (KCMH-2), while lower in yield, exhibited exceptional stability, crucial for environments prioritizing consistent performance. These insights underscore the importance of GEI in guiding targeted breeding strategies for enhanced chickpea production and agricultural sustainability.

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Disclaimers

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Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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