



PLANT BREEDING &
GENETICS

GGE BIPLLOT ANALYSIS FOR THE SELECTION OF STABLE CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES UNDER DIFFERENT ENVIRONMENTAL CONDITIONS OF PAKISTAN

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ABSTRACT

Chickpea is reckoned as one of the most important pulse crops globally, valued for its high protein content. However, the productivity of chickpeas is often challenged by various biotic and abiotic stresses. Identifying and selecting stable genotypes is critical for addressing these issues and ensuring sustained chickpea yield. The GGE biplot analysis is a powerful tool for dissecting genotype-environment interactions and identifying stable genotypes across diverse environments. This present study was aimed to explore this tool for selecting stable chickpea genotypes by conducting field trials across multiple environments. Studied chickpea genotypes were tested at ten different locations in Pakistan. The experiments were carried out in a randomized complete block design using three repeats at each location. In the present study genotype by environment interaction effect was significant ($P < 0.001$) along with main effects of environment and genotype. GGE Biplot cumulatively explains 61.21 % of the total variation in the 1st year and 79.74% in the 2nd year. Principal component 1 of the GGE Biplot contributed 35.62%, and 60.37% while principal component 2 contributed 25.59% and 19.37% to the total variation respectively in both years. Through GGE Biplot, G1(BRC-408), and G3 (15FCK16) were identified as highly stable and well-adapted genotypes that could be released as a variety for general cultivation throughout Pakistan in both years. For highly variegated environments or mega environments, specific genotypes that were well performed in these environments such as G2, (15KCC-112), G7(CH64/11), and G14(CH53/12) should be recommended.

KEYWORDS: *Cicer arietinum*; multi environment testing; genotype-environment interaction; GGE Biplot; Pakistan

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INTRODUCTION

Chickpea (*Cicer arietinum* L.) is well reckoned among the pulse crops globally, valued for its high protein content, dietary fiber, and essential nutrients (Koul *et al.*, 2022). However, the productivity of chickpeas is often challenged by various abiotic and biotic stresses, including pests, diseases, and adverse environmental conditions (Arriagada *et al.*, 2022). To address these challenges and ensure stable chickpea yields, the identification and selection of resilient genotypes is imperative (Hussain *et al.*, 2021).

Traditional methods of evaluating chickpea genotypes typically involve field trials conducted across multiple environments. However, these methods often overlook the complex genotype-environment interactions that significantly influence crop performance (Fox *et al.*, 1997). GGE (main effects of genotypes plus Genotype $\times$ Environment interaction) biplot analysis has emerged as a powerful tool for dissecting

genotype-environment interactions and identifying stable genotypes across diverse environments. (Kindie *et al.*, 2022; Liu *et al.*, 2022).

The GGE biplot method integrates both genotype and environmental data into a graphical representation, allowing researchers to visualize genotype-environment interactions and identify stable genotypes that exhibit consistent performance under varying environments (Yan *et al.*, 2000). By analyzing the main effects of genotypes, the magnitude of genotype-by-environment interactions, and the response of genotypes to specific environmental conditions, GGE biplot analysis provides valuable insights into genotype stability and adaptability (Yan and Tinker, 2006). GGE biplot analysis was used to identify genotypes with broad adaptation, capable of performing well across diverse agro-climatic conditions in various pulses e.g., *C. arietinum* L. (Azam *et al.*, 2020), *Lens culinaris* M. (Hossain *et al.*, 2023), *Vigna radiata* L. (Ullah *et*

al., 2012), *V. unguiculata* L. (Kindie *et al.*, 2022), and *V. subterranea* L. (Khan *et al.*, 2022). It allowed the breeders to develop region-specific cultivars of chickpea which were tailored to local conditions (Azam *et al.*, 2020; Rao *et al.*, 2023). Additionally, it also assisted in the identification of mega-environments, grouping similar environments together based on genotype performance patterns (Azam *et al.*, 2020; Rao *et al.*, 2023; Kindie *et al.*, 2022; Hossain *et al.*, 2023).

This present study aims to explore the application of GGE biplot analysis for selecting stable chickpea genotypes. By conducting field trials across multiple environments and employing GGE Biplot analyses, this study seek out to demonstrate the use of GGE biplot analysis for identifying stable chickpea genotypes having enhanced adaptability and yield stability under different environmental conditions of Pakistan.

MATERIALS AND METHODS

A total of sixteen chickpea genotypes along with check variety Noor-13 were tested at ten different locations in Pakistan during 2019-2021. These 10 locations were represented as ten different environments and coded as E1: Pulses Research Institute, AARI, Faisalabad. E2: Agriculture Research Station, Karak. E3: Arid

Zone Research Institute, Bhakkar, E4: Arid Zone Research Center, D. I. Khan, E5: Barani Agricultural Research Station, Fatehjang, E6: Gram Research Center, KlurKot, E7: National Agricultural Research Center, Islamabad, E8: National Institute of Agriculture Biology, Faisalabad, E9: Quaid-Awam Agriculture Research Institute, Larkana, E10: Regional Agricultural Research Institute, Bahawalpur. Mean performance of the genotypes in both years along with ID and source of genotype is given in Table 1.

This experiment was carried out in a randomized complete block design using three repeats at all locations. Sowing was completed during the last week of October and harvesting was carried out in the first night of April for all the locations. Sowing and crop management in all regions were done according to chickpea production technology for the respective region. The crop was raised on rainfed conditions at all the sites. Finally, grain yield (GY) was estimated by converting experimental unit data to kg per hectare.

Statistical analysis: To check the significance of environment, genotype and the interaction of genotype $\times$ environment, the combined ANOVA was used for the grain yield data of 16 chickpea genotypes from 10 different locations. The data were further analyzed using the GGE analysis as per the statistical model given by

Table 1. Mean performance of the studied genotypes in both years

Genotype Name	ID	Source of genotype	2019-20	2020-21
BRC-408	G1	Regional Agricultural Research Institute, Bahawalpur	1334	1729
15KCC-112	G2	Barani Agricultural Research Institute, Chakwal	1296	1535
15FCK16	G3	Barani Agricultural Research Station, Fatehjang	1291	1612
TGK-1504	G4	Arid Zone Research Institute, Bhakkar	1255	1499
TGK1508	G5	Arid Zone Research Institute, Bhakkar	1254	1538
NCK-1801	G6	National Agricultural Research Center, Islamabad	1239	1169
CH64/11	G7	National Institute of Agriculture Biology, Faisalabad	1237	1313
CH66/10	G8	National Institute of Agriculture Biology, Faisalabad	1237	-
PCK-15001	G9	Pulses Research Institute, AARI, Faisalabad	1229	1457
CH47/12	G10	National Institute of Agriculture Biology, Faisalabad	1210	-
NOOR 13	G11	Barani Agricultural Research Institute, Chakwal	1208	1228
14FCK02	G12	Barani Agricultural Research Station, Fatehjang	1162	1334
CH48/12	G13	National Institute of Agriculture Biology, Faisalabad	1124	-
TGK1503	G14	Arid zone Research Institute, Bhakkar	1120	-
PCK-15019	G15	Pulses Research Institute, AARI, Faisalabad.	1105	1480
CH53/12	G16	National Institute of Agriculture Biology, Faisalabad	1054	-

(Yan and Tinker, 2006). Analysis of the stability models presented in this paper was performed in R-software (R 4.5.1) using the Metan multi environment trial analysis Package developed by Olivoto & Lúcio, (2020).

RESULTS AND DISCUSSION

Combined ANOVA: Combined Analysis of variance was performed to check the significance of main effects of genotype, environment and their interaction. The main effects of genotype (GEN), environment (ENV) and their interaction (GEI) were significant ($P < 0.001$) for the grain yield in both years (Table 2). In total

variation, the environmental contribution was 85% in the 1st year but it was 0.47% in the 2nd year while the share of GEI was 14% in the 1st year while 88.81 % in the 2nd year. Further, the sum square of GEI was 8.51 times (SSGEI/SSG) more than that for the genotype effect in the 1st year while in the 2nd year it was 8.62 % in 2nd year (Table 2). Hence, there was a considerable amount of differential response among the genotype's performance for grain yield in respect to the change in environment in both years.

Which won where the view of GGE biplot: The which won where view of the GGE biplot was

Table 2. Combined analysis of variance of chickpea grain yield

Source	Df	Sum sq	p Value	SS%	Df	Sum sq	P value	SS%
2019-20					2020-21			
ENV	9	1.42E+08	0.0000**	85	9	1.01E+05	0.0000**	0.47%
REP(ENV)	20	15750.13	0.0382 ^{ns}	0	20	9876.098	0.06	0.05%
GEN	15	2672464	0.0000**	2	10	2230121	0.0000**	10.3%
GEN: ENV(GEI)	135	22746299	0.0000**	14	90	19228867	0.0000**	88.81%
Residuals	300	92975.87			200	81233.21		
Total	479	1.68E+08			329	2.17E+07		

** Results are significant at 0.01 & 0.05 level, Df= degree of freedom, ns= non-significant, Sq= Square, SS= Sum Square

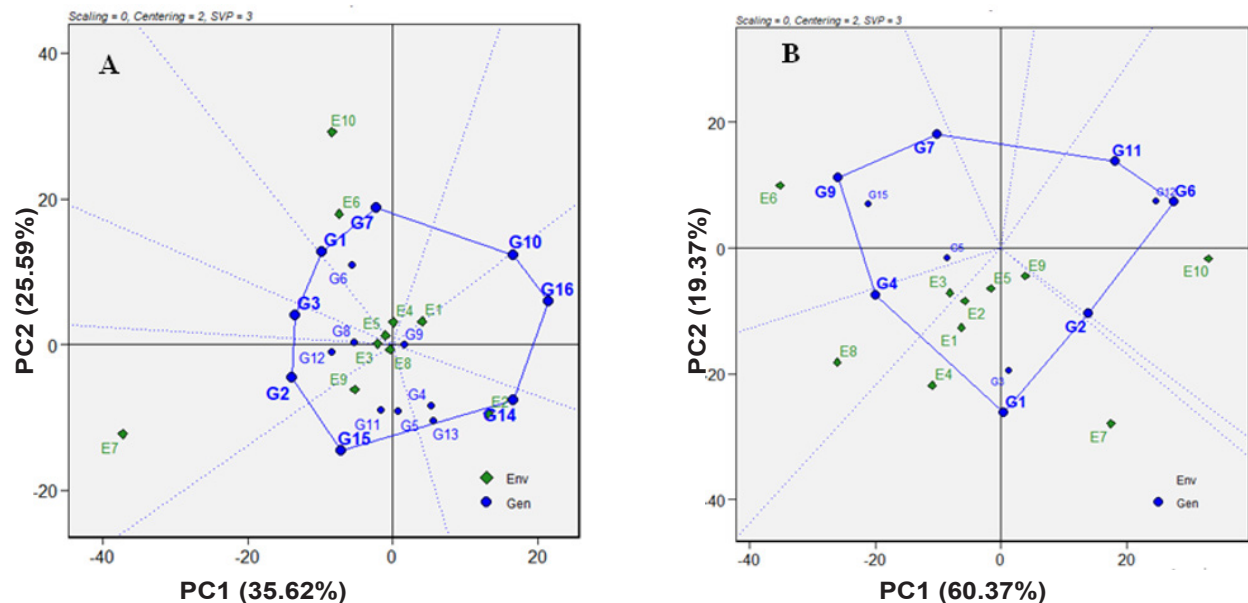


Fig. 1. The "Which-won-where" view of GGE biplot explaining vertex genotypes along with mega environments PC1 on X-axis and PC2 on Y-axis in both years A (2019-20) and B (2020-21). Genotypes are represented by blue dots along with the ID presented in Table1 e.g. G1, G2 and Locations/Environments are represented by green diamonds with environmental ID e.g. E1, E2

established with symmetrical preserving (SVP = 3) partitioned equally with the genotype and environment eigenvector (represented with blue dots and green diamonds respectively on biplot) for both years. GGE

Biplot cumulatively explained 61.21 % of the total variation in the 1st year and 79.74 in the 2nd year. PC1 contributed 35.62% while PC2 contributed 25.59% to the total variation in 1st year while in 2nd year PC1

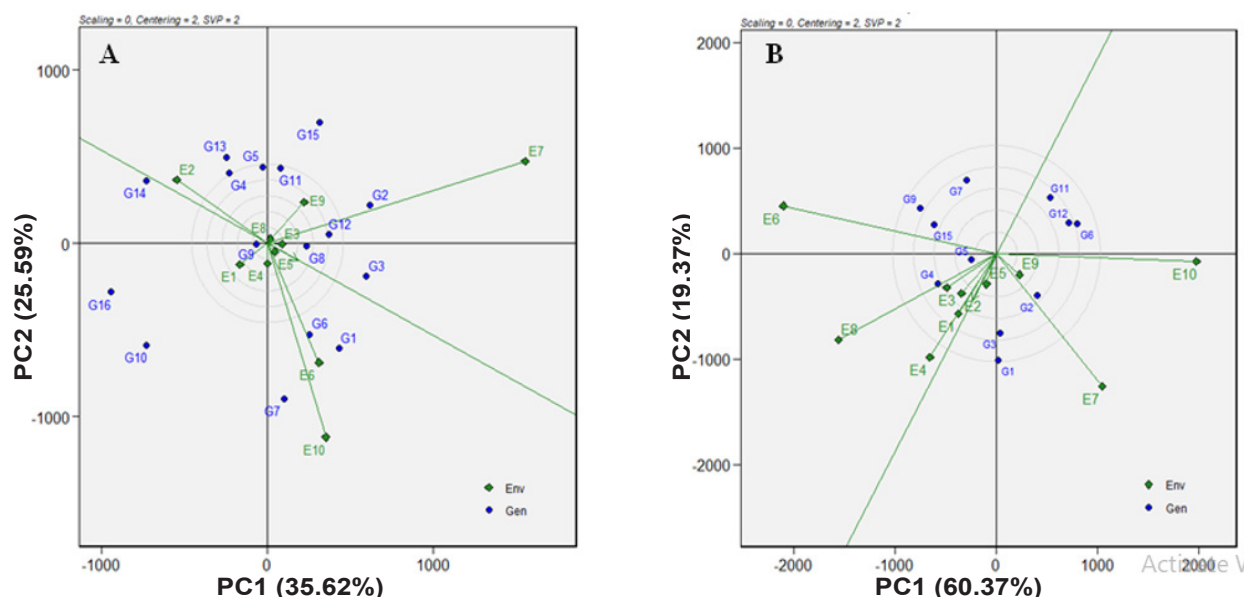


Fig. 2. Discriminative vs. representative of 10 tested environments showed by using 2 PCs, PC1 on X-axis and PC2 on Y-axis in both years A (2019-20) and B (2020-21). Genotypes are represented by blue dots along with the ID presented in Table 1 e.g. G1, G2 and Locations/Environments are represented by green diamonds with environmental ID e.g. E1, E2.

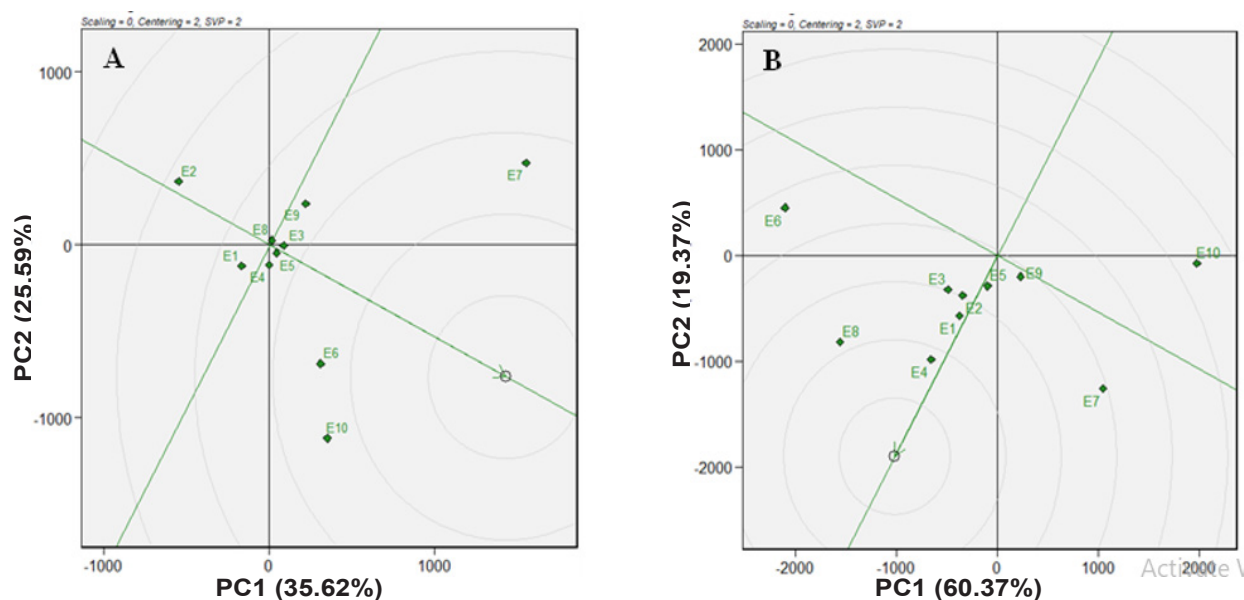


Fig. 3. Identification of ideal environment along with ranking of studied environments based on representativeness and discriminating ability in both years A (2019-20) and B (2020-21). Environments are represented by green diamonds e.g. E1, E2.

contributed 60.37% and PC2 19.37% (Figure 1). The apex entries lying outermost from the biplot origin were connected to create the polygon outlook of the GGE Biplot. Vertical lines drew on either side of the polygon divided it into multiple sections (denoted by blue dotted lines). The apex genotype in each section i.e., G1, G7, G10, G16, G14, G15, G2, and G3 showed the maximum or minimum yield concerning environments present in each section.

The biplot analysis revealed the presence of three distinct mega-environments. In the first year (Figure 1A), environments E6 and E10 grouped together to form the first mega-environment, E2 represented the second, and E7 formed the third. In the second year, E6 continued to represent the first mega-environment, while E10 separated to form a distinct second mega-environment. Unlike the first year, E8 replaced E2 to become part of the third mega-environment, along with E7.

To the first mega-environment (E6) G1 was the winning genotype in 2019-20 and G9 in 2020-21 while G7 showed broad adaptation in both years. G14 was specifically adapted to E2 (mega-environment 2 of the first year), while G2 performed best in the third mega-environment (E7) across both years.

Environment-vector view of the GGE biplot: The GGE biplot's environment-vector view was established on an environment-centered $G \times E$ (SVP = 2) rather than genotype and was better for the evaluation of environment (Figure 2 A & B). The environment's

vector length represented their degree of discriminating ability. Hence, among the ten environmental conditions, E10, E6, and E7 with large vector lengths were utmost discerning and E1, E3, E5 and E9 with very short vectors were least/non-discriminating in both years. These least/non-discriminating environments are practically less beneficial as they are not able to provide reliable discriminating information about the genotypes in both years.

In Figure 3, small circle at the end of the arrow had the mean coordinates of all tested locations known as the average environment and the "Average Environment Axis" (AEA) is the line that is passing through the average environment and the biplot origin used for checking the representativeness of environments. E1, E5 and E4 environments that had a minor angle with the AEA were more representative than that of other tested environments whereas E7 was least/non-representative. According to the environmental view of GGE biplots environments E7 discriminating but with non-representative powers was suitable for choosing precisely adapted genotypes and for discarding unstable genotypes. While the E6 and E10 test environments with both discriminating and representative powers in 1st year were considered better-tested environments for selecting adapted genotypes for general cultivation. Figure 3 A identified E6 as the ideal test environment as it was contiguous to the center of the concentric circles whereas the E2 environment farthest from the concentric circles had

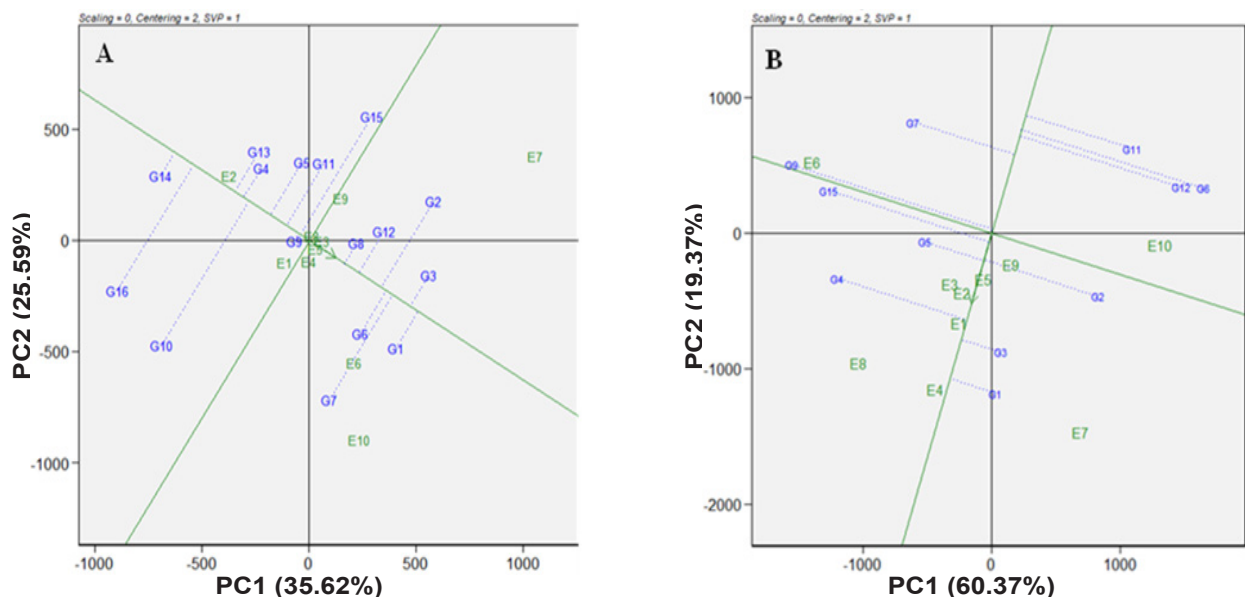


Fig. 4. Ranking of the 16 chickpea genotypes based on mean performance and stability in both years A (2019-20) and B (2020-21). Genotypes are represented by blue dots along with the ID presented in Table1 e.g. G1, G2 and Locations/Environments are represented by green diamonds with environmental ID e.g. E1, E2.

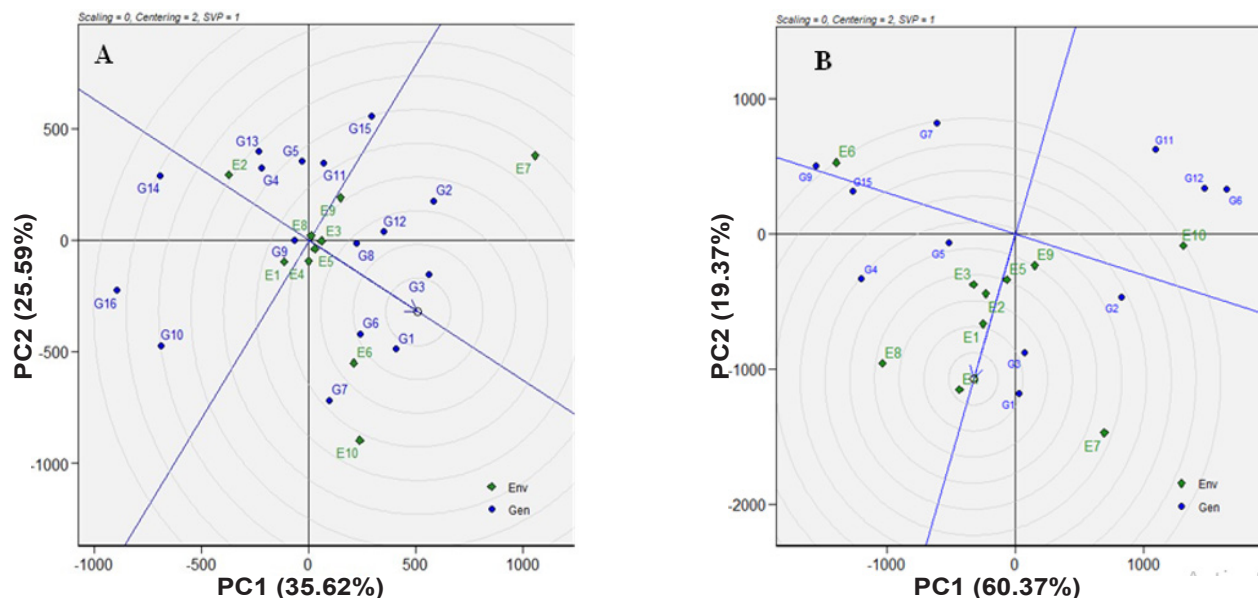


Fig. 5. Identification of ideal genotype along with ranking of the genotypes regarding yield and stability in both years A (2019-20) and B (2020-21). Genotypes are represented by blue dots along with the ID presented in Table1 e.g. G1, G2 and Locations/Environments are represented by green diamonds with environmental ID e.g. E1, E2.

the greatest $G \times E$ and was the poorest for choosing genotypes adapted to the whole region.

The average-environment coordination (AEC) view of the GGE biplot was established with genotype-metric preserving (SVP = 1) rather than environment and was better for the evaluation of genotype in both studied years (Figure 4 A & B).

The GGE Biplot's AEC view showed that G1 had the maximum average yield, followed by G3 in both years. G9 had an average yield near the mean in the 1st year but in the 2nd year its performance was below average and G14 and G16 had the minimum average yield in the 1st year. The AEC ordinate/double-arranged line showed a higher variation (inferior stability) in either direction. The G10 genotype was thus unstable in both years whereas G1 and G3 proved to be highly stable genotypes in both year (Figure 4 A & B).

The concentric circles in the GGE biplot not only showed the distance from the ideal genotype but also the distance between each genotype. The first concentric circle of the GGE biplot graph contained the optimum/ideal genotype. Likewise, the genotypes close to the ideal one were considered as "desirable genotypes" and thus can be considered for the breeding purpose. G1 present near the center of the concentric with greater average performance regarding yield and high stability was identified as the ideal genotype followed by G3 even though G2 had a higher average yield as G3 was a more stable and high yield performer. G10 was the poorest genotype because it was constantly meagre in both years (Figure 5 A & B).

CONCLUSION

The GGE biplot analysis provides a holistic view of genotype into environment interactions by simultaneously considering genotype main effects and genotype-by-environment interactions. This comprehensive assessment allows breeders to identify genotypes that exhibit stable performance across diverse environmental conditions (Yan *et al.*, 2007).

In this study, significant effect of GEI ($p < 0.01$ and 0.05) suggested that the selection of genotype merely on the basis of higher yield may be misleading. Therefore, genotypes with stable performance across multiple environments must be selected to release it for general cultivation. Like, the GGE biplot identified G9 as a stable genotype in our study but it was below average yielder while genotype G1 was identified as the ideal genotype followed by G3 as both were more stable and had high yield performance. Multiple researchers also found GGE Biplot analysis as an important and useful tool for identifying stable and higher yielder genotypes. Rao *et al.* (2023) used GGE Biplot analysis to identify a stable, drought-tolerant chickpea genotype for targeted environments in India. Azam *et al.* (2020) found that GGE Biplot results were additionally bolstered in identifying stable and well-adapted chickpea genotypes compared to the AMMI and Eberhart and Russell models.

Another advantage of GGE biplot analysis is its ability to visualize mega-environments, grouping similar environments based on genotype performance patterns. This facilitates the targeted selection of

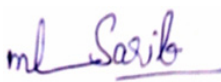
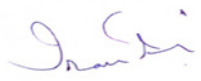
genotypes tailored to specific agro-climatic regions, thereby maximizing productivity and adaptability. In the present study, three mega environments were identified in almost all the studied regions of Pakistan. Genotypes which were well adapted to these regions were also identified. GGE biplot analysis was also found useful in identifying mega environment for different crops. Azam *et al.*, (2020); Rao *et al.*, (2023) found GGE Biplot useful for mega environment identification in *C. arietinum* L., while Hossain *et al.* (2023) reported similar findings for *L. culinaris* L., Kindie *et al.*, 2022 for *V. unguiculata* L. and Khan *et al.*, 2022 for *V. subterranea* L.

In conclusion, the adoption of GGE biplot analysis for selecting stable chickpea genotypes help in the release of a cultivar with broader adaptability hence per unit yield of chickpea will be improved. By a more comprehensive understanding of genotype-environment interactions, and visualization of mega-environments, chickpea genotypes specific to highly variegated environments were also identified. In the present study G1(BRC-408), and G3 (15FCK16) were identified as highly stable and well adapted genotypes which could be released for general cultivation. While for highly variegated environments or mega environments specific genotypes which were well performed in these environments such as G2 (15KCC-112), G7 (CH64/11), and G14 (CH53/12) should be recommended.

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CONTRIBUTION OF AUTHORS

Sr. No.	Authors' name	Contribution	Signature
1.	Muhammad Zeeshan	Planned and supervised the experiment	
2.	Waheed Arshad	Conducted the research work	
3.	Saba Aleem	Conducted data analysis and prepared the draft of research paper	
4.	Muhammad Imran Khan	Conducted the research work	
5.	Muhammad Saqib	Assisted to write up the manuscript	
6.	Ayesha Malik	Proof read the manuscript	
7.	Iram Sharif	Contributed in data analysis	
8.	Muqadas Aleem	Contributed in data analysis	