CHICKPEA (*CICER ARIETINUM* L.) GENOTYPES' ASSESSMENT THROUGH DIVERSE ENVIRONMENTS

K.L. CHEEMA[1*], S. SARDAR[1*], M. AKHTAR[2], M.T. MAHMOOD[3], Z. QADEER[1], and S. AKBAR[1]

[1]Vegetable Research Institute, AARI, Faisalabad, Pakistan
[2]Pulses Research Institute, AARI, Faisalabad, Pakistan
[3]Gram Breeding Research Station, Kallurkot, Pakistan
Corresponding authors' emails: Klcheema@hotmail.com, sadiasardar636@yahoo.com
Email addresses of co-authors: directorpulses@yahoo.com, taqaisrani@gmail.com, zeeshanqadeer15@gmail.com, Sana.akbar2364@gmail.com

SUMMARY

Screening genotypes based on grain yield stability in different ecological zones is a prerequisite for developing a widely adapted genotype. For this purpose, 16 chickpea desi genotypes' evaluation through cooperative yield trial commenced during 2019–2020 at nine diversified locations across Punjab, Pakistan. Data underwent genotype by environment interaction (G × E) and mega environment analysis. Genotype plus genotype × environment (GGE) biplot view for yield depicted that G-4 (CH-21/13) was the ideal and superior genotype for stability and yield potential. GGE biplot 'what-won-where' for yield formed an irregular polygon showing interconnection among G-3 (CH-2016), G-4 (CH-21/13), G-8 (D-17003), G-11(D-17019), G-13 (TG-1427), G-14 (TG-1430), and G-16 (TG-1510), indicating these genotypes were comparatively more stable. Graphical representation of the mega environment analysis illustrated that E-1 (Pulses Research Institute, AARI, Faisalabad, Pakistan) was ideal and most discriminating for genotype screening. Results also revealed that the first mega environment's construction included the grouping of E-1 (Pulses Research Institute, AARI, Faisalabad, Pakistan), E-2 (Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan), E-3 (Gram Breeding Research Station, Kallurkot, Pakistan), and E-4 (Gram Breeding Research Station, Kallurkot, Barani, Pakistan), with G-4 (CH-21/13) as the winning genotype. Biplot also depicted that G-3 (CH-2016) was best in the second mega environment made by E-6 (Regional Agricultural Research Institute, Pakistan), and G-8 (D-17003) was a winner in E-4 (Gram Breeding Research Station, Kallurkot, Barani, Pakistan). Combined analysis showed that G-4 (CH-21/13), G-8 (D-17003), and G-13 (TG-1427) were the most stable and high-yielding; therefore, these genotypes may considerably be widely adaptive across environments.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) occupies an eminent place in the farming system of Pakistan (Akhtar *et al.*, 2021). Overstating its importance is unlikely due to its primary role in sustaining food security, generating revenue, and balancing the ecosystem (Jan *et al.*, 2020; Mahmood *et al.*, 2021). Chickpea is a major pulse crop and a rich source of proteins commonly called poor man's meat; therefore, it is crucial for food security (Merga and Haji, 2019). Chickpea's classification has two main types based on seed characteristics, i.e., desi and kabuli (Kumar *et al.*, 2021).

Chickpea desi types have rough seed coats with angular brown microsperma, and kabuli types have smooth seed coats and white or creamy macrosperma (Upadhyaya *et al.*, 2007; Foyer *et al.*, 2016). Unpredictable climatic changes and exposure of this legume to a wide range of environments are major causes of declining and unstable chickpea production (Considine *et al.*, 2017). Pakistan's average chickpea productivity per unit area is far below (444 kg ha^{-1}) the world's average production (962 kg ha^{-1}) (Bakhsh *et al.*, 2011). The national consumption is way higher than its annual production; therefore, addressing the gap between consumption and production by importing a substantial quantity of chickpeas (Jan *et al.*, 2020; Rafiq *et al.*, 2020).

The yield performance of genotypes in environments is a mixture of a genotype main effect (G), environment main effect (E), and the G × E interaction (Yan *et al.*, 2000, 2007; Gauch *et al.*, 2008). Ebdon and Gauch (2002) defined that the main effect of a genotype under a specific climatic zone is a genotype × environment interactions (GEI). Genotypic performances may be stable or vary under different surroundings due to changes in soil, temperature, humidity, and rainfall spells (Annicchiarico, 1997; Arshad *et al.*, 2003). It means that the performance of a genotype can fluctuate from one environment to another in such a way that a genotype superior in one environment may not be as much in another due to differing genotype interaction with the environment (G×E) (Makumbi *et al.*, 2015). In detecting the most stable and better-performing genotypes, several former researchers have extensively employed the GGE biplot and mega-environment analysis (Yan *et al.*, 2000; Abbas *et al.*, 2008; Gauch *et al.*, 2008; Farshadfar *et al.*, 2012 and Mahmood *et al.*, 2021). GGE biplot and mega-environment models have proven the most effective analysis methods for evaluating genotypes under multi-environments for further genetic improvement programs (Samonte *et al.*, 2005; Kaloki *et al.*, 2019).

The present status of chickpea productivity in Pakistan depicts a gloomy picture of this legume and the vulnerability of available chickpea cultivars to threats of climate change over a wide range of environments. In the current scenario, systematic breeding efforts are necessary to evolve genetically improved chickpea cultivars with a wider adaptability and higher yield potential. The pertinent research attempted to detect the most stable and high-yielding chickpea genotypes across environments.

MATERIALS AND METHODS

Plant material

In detecting the most stable and high-yielding chickpea genotypes, an experiment began during the Rabi season 2019–2020 under the Ayub Agricultural Research Institute, Faisalabad, at nine different geographic locations in Punjab, Pakistan. Sixteen advanced chickpea desi genotypes developed by various agricultural research organizations

Table 1. Chickpea genotypes used in the study.

No.	Code	Genotype name	Status
1	G-1	Bittal-16	Standard variety
2	G-2	BRC-474	Advance line
3	G-3	CH-2016	Standard variety
4	G-4	CH21/13	Advance line
5	G-5	CH28/13	Advance line
6	G-6	CH30/12	Advance line
7	G-7	CH39/13	Advance line
8	G-8	D-17003	Advance line
9	G-9	D-17006	Advance line
10	G-10	D-17015	Advance line
11	G-11	D-17019	Advance line
12	G-12	D-17028	Advance line
13	G-13	TG-1427	Advance line
14	G-14	TG-1430	Advance line
15	G-15	TG-1504	Advance line
16	G-16	TG-1510	Advance line

Table 2. Environments and experimental locations used for study.

No.	Codes used for environment	Experimental Sites
1	E1	PRI, (Pulses Research Institute, AARI, Faisalabad, Pakistan)
2	E2	NIAB (Nuclear Institute for Agriculture & Biology, Faisalabad, Pakistan
3	E3	GBRSS (Gram Breeding Research Station, Kallurkot, Pakistan)
4	E4	GBRSS (Gram Breeding Research Station, Kallurkot, Barani, Pakistan)
5	E5	AZRI (Arid Zone Research Institute, Bhakkar, Pakistan)
6	E6	RARI (Regional Agricultural Research Institute, Pakistan)
7	E7	Gram Breeding Research Sub-Station, Rakhutra, Khushab, Pakistan
8	E8	Farmer Field, Hyderabad Thal, Punjab, Pakistan
9	E9	Famer Field, Mankera, Thal, Punjab, Pakistan

bore codes, then packed and sent to nine locations with a uniform layout plan (Table 1).

Cultural and agronomic practices

Research material was sown in field using three replications under a randomized complete design. Sowing of all targeted experimental locations commenced during the last week of October 2019 by keeping four rows × rows with a 30 cm distance between rows and plant × plant with a 10 cm distance between plants. All cultural operations proceeded as per agronomic recommendations for the chickpea crop. At the pod formation stage, an insecticide application, Emamectin Benzoate @ 700 ml ha^{-1}, helped prevent pod borer attack.

Data collection

Data collection from all trials at diversified locations for grain yield per plot ensued(ensured) with set standards (Table 2).

Statistical analysis

Replicated yield data of chickpea genotypes underwent the GGE biplot analysis and genotype by environment interaction (GEI) through plant breeding tools (Version 1.4) for graphical illustration of results.
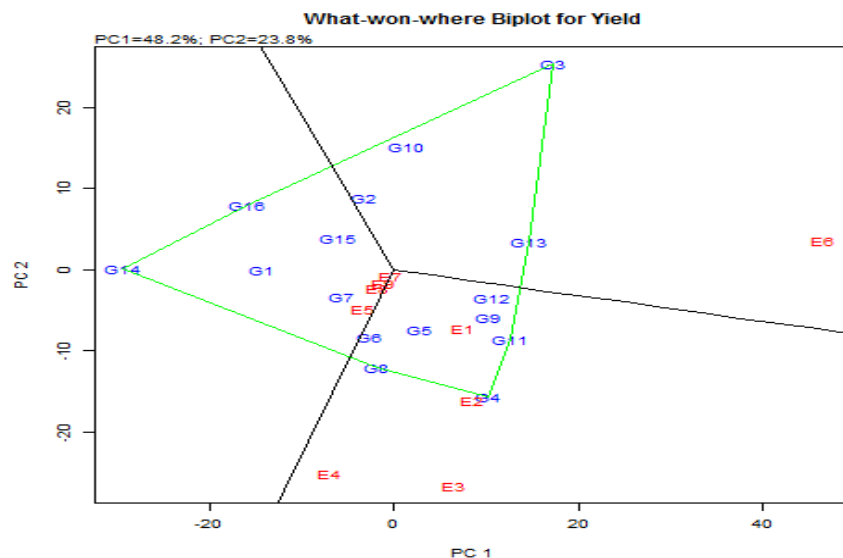
Figure 1. What-won-where Biplot for yield.

RESULTS AND DISCUSSION

The principal source of variation in evaluating different genotypes in diversified environments is the main effect of genotype (G) and the G × E interaction (Yan *et al.*, 2000, 2007). The said experiment proceeded to create variation and to select well-adapted chickpea cultivars. Engaging the genotype by environment interaction (G × E) and the mega-environment analysis constructed the graphical representation of data. GGE biplot analysis continued by plotting scores of the first principal component (PC1) against the respective second principal component (PC2) following the method of Yan *et al.* (2000) and Gauch *et al.* (2008).

GGE biplot ('what-won-where' pattern)

The biplot for what-won-where for yield mean illustrated an irregular polygon (Figure 1). The genotypes interconnected to each other in the vertex are winning genotypes in different mega environments for stable grain yield performances. The linked genotypes in this polygon were G-3 (CH-2016), G-4 (CH-21/13), G-8 (D-17003), G-11 (17019), G-13 (TG-1427), G-14 (TG-1430), and G-16 (TG-1510). It illustrated that these genotypes were comparatively more stable. The polygon intersections also indicated the assemblage of various environments to structure the mega environments (Yan *et al.*, 2001; Khan *et al.*, 2021). The first mega environment's construction grouped E-1 (Pulses Research Institute, AARI, Faisalabad), E-2 (Nuclear Institute for Agriculture and Biology, Faisalabad), E-3 (Gram Breeding Research Station, Kallurkot, Pakistan), and E-4 (Gram Breeding Research Station, Kallurkot, Barani, Pakistan), with G-4 (CH-21/13) as the winning genotype.

The biplot also depicted that G-3 (CH-2016) was superior in the second mega environment composed of E-6 (Regional Agricultural Research Institute, Pakistan). Similarly, E-7 (Gram Breeding Research Substation Rakhutra, Khushab, Pakistan), E-8 (Farmer Field, Hyderabad Thal, Punjab, Pakistan), and E-5 (Arid Zone Research Institute, Bhakkar, Pakistan) formed another mega environment with G-14 (TG-1430) as the winner. Likewise, G-8 (D-17003) won in E-4 (Gram Breeding Research Station, Kallurkot, Barani, Pakistan). Similar reports for mega-environment analysis were previous findings by Arshad *et al.* (2003), Getachew *et al.* (2015), and Erdemci (2018).
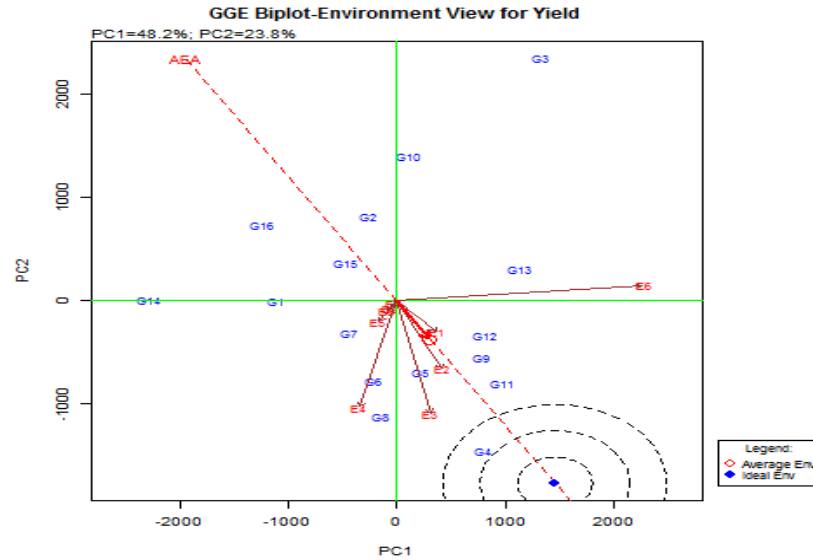
Figure 2. GGE Biplot-Environment view for yield.

Environment assessment for ideal environment

The GGE Biplot for environment view illustrated that E-1 (Pulses Research Institute, Faisalabad) revealed the ideal environment for screening of genotypes. The biplot for the environment view, formed by plotting the vectors, detected favorable environments (Figure 2). The length of vectors and their respective angles to the average environment axis (AEA) abscissa specifies the power of environments (Yan *et al.*, 2001; Yaghotipoor and Farshadfar, 2007; Rad *et al.*, 2013; Usharani and Kumar, 2016; Mahmood *et al.*, 2021). Based on the length of vectors, there were three main types of environments. Those having short vector lengths are type-1 environments with a minimum effect on the yield performance of test entries. The E5 (Arid Zone Research Institute, Bhakkar, Pakistan), E-7 (Gram Breeding Research Sub-Station, Rakhutra, Khushab, Pakistan), E-8 (Farmer Field Hyderabad Thal, Punjab, Pakistan), and E-9 (Farmer Field Mankera, Thal, Punjab, Pakistan) formed smaller vector lengths with no significant effect on the genotype's yield performance.

The environments with comparatively longer lengths than a type forming a smaller angle with the AEA abscissa are the type-2 environments. These are the most beneficial environments, i.e., E-1 (Pulses Research Institute, AARI, Faisalabad), E-2 (Nuclear Institute for Agriculture and Biology, Faisalabad, Pakistan), E-3 (Gram Breeding Research Station, Kallurkot, Pakistan), and E-4 (Gram Breeding Research Station, Kallurkot, Barani, Pakistan), which are more advantageous and ideal for selecting well-adapted genotypes (Funga *et al.*, 2017; Kaloki *et al.*, 2019; Hussain *et al.*, 2022). The environments with long vectors compared with the type-2 with a larger angle are the type-3, which are unfavorable with no significance in determining yield performances, i.e., E-6 (Regional Agricultural Research Institute, Pakistan).

Evaluation of genotypes and their mean performance

The biplot representing the genotypes' view for yield illustrated that G-4 (CH-21/13) was ideal for stability and higher yield potential across all studied environments (Figure 3). The mean performance of 16 chickpea genotypes for grain yield manifested in the following order: G-4 (CH-21/13) > G-9 (D-17006) > G-8 (D-17003) > G-13 (TG-1427) > G-5 (CH28/13) >
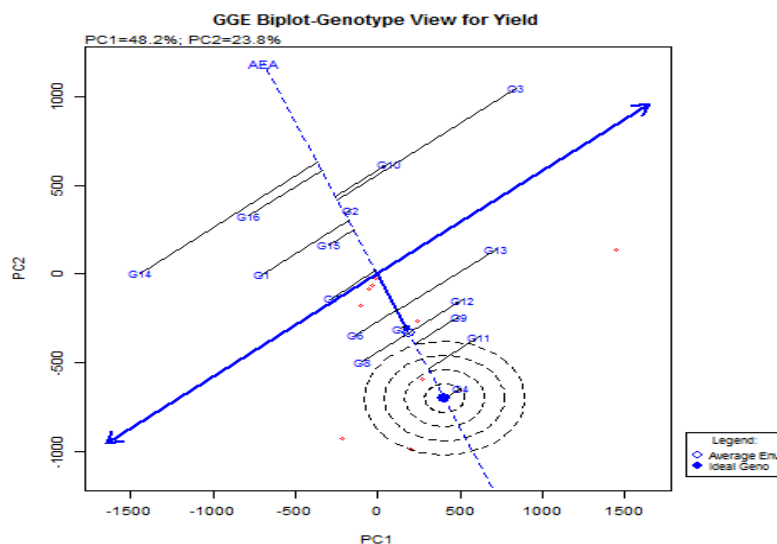
Figure 3. GGE Biplot-Genotype view for yield.

Table 3. Mean performance of the chickpea genotypes across all environments.

Code	Genotype name	Status	Breeding Center	Mean Yield (kg ha^{-1})
G-1	Bittal-16	Standard variety	PRI	1292
G-2	BRC-474	Advance line	RARI	1309
G-3	CH-2016	Standard variety	NIAB	1291
G-4	CH21/13	Advance line	NIAB	1625
G-5	CH28/13	Advance line	NIAB	1515
G-6	CH30/12	Advance line	NIAB	1460
G-7	CH39/13	Advance line	NIAB	1434
G-8	D-17003	Advance line	PRI	1525
G-9	D-17006	Advance line	PRI	1523
G-10	D-17015	Advance line	PRI	1253
G-11	D-17019	Advance line	PRI	1489
G-12	D-17028	Advance line	PRI	1511
G-13	TG-1427	Advance line	AZRI	1525
G-14	TG-1430	Advance line	AZRI	1224
G-15	TG-1504	Advance line	AZRI	1329
G-16	TG-1510	Advance line	AZRI	1285

PRI= Pulses Research Institute, AARI, Faisalabad, Pakistan; NIAB= Nuclear Institute for Agriculture & Biology, Faisalabad, Pakistan; AZRI= Arid Zone Research Institute, Bhakkar, Pakistan; RARI= Regional Agricultural Research Institute, Bahawalpur, Pakistan.

G-12 (D-17028) > G-11 (D-17019) > G-6 (CH30/12) > G-7 (CH39/13) > G-15 (TG-1504) > G-2 (BRC-474) > G-1 (Bittal-16) > G-16 (TG-1510) > G-3 (CH-2016) > G-10 (D-17015) > G-14 (TG-1430) (Table 3). The genotypes with a high yield potential and more stability are highly desirable (Yaan *et al.*, 2006). The present genotypes at the center of concentric circles in the figure indicate the minimum variability among environments and the most stable, i.e., G-4 (CH-21/13).

The genotypes closer to the ideal genotypes are less variable and more stable than others (Moreno *et al.*, 2003; Gauch *et al.*, 2008; Hasan and Deb, 2017; Qulmamatova, 2023). The order in the biplot showed G-11 (D-17019), G-9 (D-17006), G-8 (D-17003), G-13 (TG-1427), and G-6 (CH30/12) were closer,

thus, more stable; but, the genotypes G-11 (D-17019), G-9 (D-17006), and G-6 (CH30/12) have low yield potential, therefore are insignificant in a breeding program. On the other hand, the genotypes G-4 (CH-21/13), G-13 (TG-1427), and G-8 (D-17003) were highly significant (Bakhsh *et al.*, 2011; Farshadfar *et al.,* 2011 and Jan *et al.*, 2020).

CONCLUSIONS

Graphical data representations through the GGE biplot illustrated that G-4 (CH-21/13) was ideal and a winning genotype across all environments. Analysis of mega environments showed that E-1 (Pulses Research Institute, Faisalabad) was superior and the most discriminating environment for genotypes' screening. The GGE biplot also indicated that the genotypes G-4 (CH-21/13), G-13 (TG-1427), and G-8 (D-17003) have more stability and higher yield potential. Therefore, these genotypes may prove widely adapted chickpea genotypes recommended for general cultivation in similar agroecologies of the country.

REFERENCES

Abbas G, Atta BM, Shah TM, Sadiq MS, Haq MA (2008). Stability analysis for seed yield in mungbean, *Vigna radiata* L. Wilczek. *J. Agric. Res.* 46(3): 223-228.

Akhtar M, Muhammad TM, Kaiser LC, Mushtaq A, Muhammad JK, Amir A, Javed AS, Zeeshan Q, Zeeshan A (2021). Relative performance of promising chickpea (*Cicer arietinum* L.) lines under drought stress milieu. *Pak. J. Agric. Res.* 34(4):672-677.

Annicchiarico P (1997). Additive main effects and multiplicative interaction (AMMI) analysis of genotype-location interaction in variety trials repeated over years. *Theor. Appli. Genet.* 94(8): 1072-1077.

Arshad M, Bakhsh A, Haqqani AM, Bashir MH (2003). Genotype-environment interaction for grain yield in chickpea (*Cicer arietinum* L.). *Pak. J. Bot.* 35: 181-186.

Bakhsh A, Akhtar LH, Malik SR, Iqbal SM, Qureshi RU (2011). Grain yield stability in chickpea (*Cicer arientinum* L.) across environments. *Pak. J. Bot.* 43(5): 2947-2951.

Considine MJ, Siddique KHM, Foyer CH (2017). Nature's pulse power: Legumes, food security and climate change. *J. Exp. Bot.* 68(8): 1815-1818.

Ebdon JS, Gauch HG (2002). Additive main effect and multiplicative interaction analysis of national Turfgrass performance trials: I. Interpretation of genotype × environment interaction. *Crop Sci.* 42: 489-496.

Erdemci Ý (2018). Investigation of genotype × environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. *Turk. J. Field Crops.* 23: 20-26.

Farshadfar E, Gervandi M, Viasi Z (2012). Chromosomal location of QTLs controlling G × E interaction in barley. *Int. J. Agric. Crop Sci.* 4: 317-324.

Farshadfar E, Zali H, Mohammadi R (2011). Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot. *Ann. Biol. Res.* 2(6): 282-292.

Foyer CH, Lam HM, Nguyen HT, Siddique KHM, Varshney RK, Colmer TD, Cowling W, Bramley H, Mori TA, Hodgson JM (2016). Neglecting legumes has compromised human health and sustainable food production. *Nat. Plants.* 2: 1-10.

Funga S, Tadesse M, Eshete M, Fikre A, Korbu L, Girma N (2017). Genotype by environment interaction on yield stability of desi type chickpea (*Cicer arietinum* L.) at major chickpea producing areas of Ethiopia. *Aust. J. Crop Sci.* 11: 212-219.

Gauch HG, Piepho HP, Annicchiarico P (2008). Statistical analysis of yield trials by AMMI and GGE: Further considerations. *Crop Sci.* 48: 866-889.

Getachew T, Mekbib F, Fikre A, Eshete M (2015). Genotype × environment interaction and stability analysis for yield and yield related traits of Kabuli-type chickpea (*Cicer arietinum* L.) in Ethiopia. *Afr. J. Biotechnol.* 14(18):1564-1575.

Hasan MT, Deb AC (2017). Stability analysis of yield and yield components in chickpea (*Cicer arietinum* L.). *Horti. Int. J.* 1(1): 4-14.

Hussain T, Akram Z, Shabbir G, Manaf A, Rabbani G, Iqbal J, Javed U, Ahmad R, Akhtar J (2022). Identification of drought-tolerant kabuli chickpea (*Cicer arietinum* L.) genotypes at the early seedling stage. *SABRAO J. Breed. Genet.* 54(4): 885-896. http://doi.org/10.54910/sabrao2022.54.4.19.

Jan M, Haq T, Sattar H, Butt M, Khaliq A, Arif M, Rauf A (2020). Evaluation and screening of promising drought tolerant chickpea (*Cicer arietinum* L.) genotypes based on physiological and biochemical attributes

under drought conditions. *Pak. J. Agric. Res.* 33(3): 662-672.

Kaloki P, Trethowan R, Tan DKY (2019). Effect of genotype × environment × management interactions on chickpea phenotypic stability. *Crop Past. Sci.* 70: 453-462.

Khan MMH, Rafii MY, Ramlee SI, Jusoh M, Mamun MA (2021). AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdc.) genotypes under the multi-environmental trials (METs). *Nat. Portfolio.* 11: 22791.

Kumar N, Khurana SMP, Pandey VN (2021). Application of clove and dill oils as an alternative of salphos for chickpea food seed storage. *Nat. Portfolio.* 11:10390. 1-10.

Mahmood MT, Akhtar M, Cheema KL, Ahmad M, Khalid MJ, Zahid A, Kashif M, Ali Z (2021). Exploration of grain yield stability of advanced chickpea strains across environments. *Pak. J. Agric. Res.* 34(3): 608-613.

Makumbi D, Diallo A, Kanampiu K, Mugo S, Karaya H (2015). Agronomic performance and genotype × environment interaction of herbicide-resistant maize varieties in Eastern Africa. *Crop Sci.* 55: 540-555.

Merga B, Jema H (2019). Economic importance of chickpea: Production, value and world trade. Cogent Food & Agriculture. 5: 1615718. doi.org/10.1080/23311932.2019.1615718.

Moreno GJ, Crossa J, Cornelius PL (2003). Additive main effects and multiplicative interaction model-I. Theory on variance components for predicting cell means. *Crop Sci.* 43: 1967-1975.

Qulmamatova DE (2023). Chickpea (*Cicer arietinum* L.) genotypes evaluation for high yield through multivariate analysis. *SABRAO J. Breed. Genet.* 55(1): 107-114. http://doi.org/10.54910/sabrao2023.55.1.10.

Rad MRN, Kadir MA, Rafii MY, Jaafar ZEH, Naghavi MR, Ahmadi F (2013). Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. *A. J. Sci.* 7 (7): 956-961.

Rafiq M, Mahmood MT, Ahmad M, Ali I, Saleem M, Rasool I, Ali Z (2020). Differential response of elite chickpea genotypes under moisture stress conditions. *Pak. J. Agric. Res.* 33(3): 422-428.

Samonte SOPB, Wilson LT, McClung AM, Medley JC (2005). Targeting cultivars onto rice growing environments using AMMI and SREG GGE Biplot analyses. *Crop Sci.* 45: 2414-2424.

Upadhyaya HD, Dwivedi SL, Gowda CLL, Singh S (2007). Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.) core collection for use in crop improvement. *Field Crops Res.* 100: 320-326.

Usharani KS, Kumar CRA (2016). Estimation of variability, heritability and genetic advance in mutant populations of black gram (*Vigna mungo* L. Hepper). *SABRAO J. Breed. Genet.* 48(3): 258-265.

Yaghotipoor A, Farshadfar E (2007). Non-parametric estimation and component analysis of phenotypic stability in chickpea (*Cicer arientinum* L.). *Pak. J. Biol. Sci.* 10: 2646-2648.

Yan W, Cornelius PL, Crossa J, Hunt LA (2001). Two types of GGE biplot for analyzing multienvironment trial data. *Crop Sci.* 41: 656-663.

Yan W, Hunt LA, Sheng Q, Szlavnics Z (2000). Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Sci.* 40: 596-605.

Yan W, Manjit SK, Baoluo M, Sheila W, Paul LC (2006). GGE Biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* 47: 641-653.