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AMMI and GGE Stability Analysis of Drought Tolerant Chickpea (*Cicer arietinum* L) Genotypes for Target Environments

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ABSTRACT

Background: Chickpea is an important nutrient rich food legume cultivated mainly as rainfed crop in arid and semiarid regions of India. Due to changed climatic conditions incidence of frequent drought stress events are causing significant yield losses.

Methods: In order to identify superior and locally adaptable genotypes under rainfed conditions multi-environment chickpea evaluation trial was conducted in five environments with 50 genotypes during *Rabi,* 2021-2022 stability analysis for grain yield was performed by deploying the AMMI (Additive Main Effects and Multiplicative Interaction) model and GGE (Genotype and Genotype by Environment) biplot method with an aim to identify the high yielding stable chickpea genotypes.

Result: The AMMI analysis of variance for grain yield (kg ha^{-1}) of 50 chickpea genotypes revealed significant genotype, environment and G×E interaction indicating the presence of variability among the genotypes and environments. The mean grain yield of 50 genotypes over environments ranged from 1296 kg/ha (G39) to 2222 kg/ha (G8). The genotype G24 exhibited high grain yield than mean yield with specific adaptability for the environment E2 (Palem). The results indicated that, environment E5 (Warangal) was identified as the best suited for potential expression of grain yield. Results of stability analysis revealed that genotype G17 exhibited high grain yield along with high stability across the locations with desirable mean performance.

Key words: AMMI, Chickpea, Genotype × Environment interaction, GGE biplot, Stability.

INTRODUCTION

Chickpea (*Cicer arietinum* L.; 2n = 2× = 16) is the second most important food legume next to dry bean grown under residual soil moisture conditions. Globally chickpea cultivated in an area of 15 M ha with a total production of 15.8 Mt (FAOSTAT, 2021). India alone contributes >75% of global chickpea area as well as production. India imports chickpea grain to meet the local demand from Australia (83.5%), USA (3.8%), Myanmar (3.5%), Tanzania (3.3%) and Sudan (2.1%) (http://agricoop.nic. 2021). Within India, central (Madhya Pradesh, Maharashtra, Gujarat) and southern states (Karnataka, Telangana and Andhra Pradesh) are the major chickpea producing regions in terms of area, production and productivity (http://dpd.gov.in, 2021).

In Telangana, chickpea cultivated during winter as a single crop with 1 or 2 supplementary irrigations or planted under residual soil moisture conditions after harvesting the preceding *kharif* crops like rice, maize, cotton and soybean. Hence it is important to identify suitable chickpea genotypes adaptable to local growing conditions of Telangana state with market preferred seed traits.

Early flowering or early maturity and suitability to machine harvesting are the two important traits should be embedded in the newly developed drought tolerant varieties along with basic resistance to fusarium wilt disease (Gaur *et al.,* 2019). In India, the traditional chickpea varieties are short and bushy types where farmers use human labour for harvesting and threshing operations. The recently developed varieties NBeG 47, RVG 204, Phule Vikram and BG 3062

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(Divya Madhuri and Jayalakshmi, 2020; Jayalakshmi *et al*., 2017; Mannur *et al*., 2013; https://www.icrisat.org/two-new-machine-harvestable-chickpea-varieties-released-in-india) are tall (>55 cm height) types with erect to semi-erect growth habit which are amicable for machine harvesting. Such varieties can be harvested using combine harvesters with <5% threshing losses and farmers save time and money.

The majority of chickpea was grown under receding soil moisture conditions under rainfed conditions. Thus, soil moisture deficit during the reproductive stages of the crop growth period called terminal drought became the most frequent abiotic stress that affected over two thirds of the global chickpea area (Gaur *et al*., 2019; Rani *et al*., 2020). As a result, drought stress conditions have resulted in significant yield losses in chickpea (Devasirvatham and Tan, 2018; Rani *et al*., 2020). The differential response of chickpea cultivars under diverse environmental conditions decreases yield stability (Funga *et al*., 2017).

Yield is a complex trait controlled by several quantitative loci and the direct selection of genotypes with high yield under stress conditions is highly influenced by G×E interactions (Kushwah *et al*., 2021). Hence, estimation of G×E is a critical component in identifying superior and stable genotypes as well as their adaptation to diverse environments (Kanouni *et al*., 2015). Genotype environment interaction (GEI) is associated with the performance and stability of cultivars across different environments (Yan and Hunt, 2002; Mwiinga *et al*., 2020). It is important to analyse the yield and stability of chickpea genotypes through multi-environment trials. The GGE biplot analysis is a modification of best linear unbiased prediction (BLUP) and is superior as it displays both genotypes and GEI which are the sources of variation. GGE biplot analysis is widely used for identifying and selecting the best performing lines in specific and across environments (Khan *et al*., 2021).

MATERIALS AND METHODS

A set of 50 desi genotypes of chickpea collected from ICRISAT, Hyderabad which includes 47 advanced breeding lines bred exclusively for drought tolerance and 3 commercial lines as check varieties were evaluated for their yield performance (kg/ha) at different locations in the state of Telangana, India during *rabi* 2021-2022. The experiment was conducted at five research cum instructional farms *viz.,* Adilabad (19°39′ N, 78°32′E), Palem (16°35′ N, 78°10′E), Rudrur(18°58′N, 77°88E), Tandur (17°15′N, 77°35′E), Warangal (18°03′N, 79°22′E) of Professor Jayashankar Telangana State Agricultural University during crop season of 2021-2022 (Table 1). Each trial was conducted in randomized block design with three replications. The seeds were planted at a spacing of 30×10 cm on a 4 m row plot. Experiments were conducted on vertisols and 5 cm flood or sprinkler irrigation was given to establish uniform germination across the locations. Standard agronomic practices were followed for successful crop establishment in each environment. A single manual weeding and two intercultural operations were conducted within 35 days after sowing and grain yield (GY) were recorded in each plot.

The combined analysis of variance was preceded to study the genotype × environment interaction of the genotypes across all environments. The AMMI model which combines standard analysis of variance with PC analysis was used to study the interactions (Zobel *et al.,* 1988).

The AMMI model for G genotypes and E environments can be written as:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\lambda_n\alpha_{in}\lambda_{ijn} + \theta_{ij}$$

Where,

Y_{ij} = Mean yield of i^{th} genotype in the j^{th} environment.

μ = General mean.

g_i = i^{th} genotypic effect.

e_j = j^{th} location effect.

λ_n = Eigen value of the principal component axis n.

α_{in} and λ_{jn} = i^{th} genotype.

j^{th}= Environment principle component analysis (PCA) scores for the PCA axis n.

θ_{ij} = Residual.

n= Number of PCA axis retained in the model.

A windows based software GEA-R9 genotype × environment analysis with R for (Windows) version 4.1 developed by CIMMYT, Mexico was used for AMMI and GGE biplot analysis (Pacheco *et al.,* 2015). The number of PCA axis to be retained is determined by testing the mean square of each axis with the estimate of residual through F-statistic (Gollob, 1968; Gauch, 1988). GGE biplot analysis was carried out using the AMMI model R-packages 1.5 PBTools 1.4 version IRRI (PBTools 2014). The AMMI biplot is generated by placing both genotype of environment mean value on X-axis and the respective IPCA axis eigen vector on the Y-axis (Zobel *et al*., 1988).

Table 1: Meteorological data recorded during cropping season of 2021-22.

Locations	Code	Soil type	Total rainfall (mm)	Average min. temp. (°C)	Average max. temp. (°C)	Mean R.H (%)	Mean bright sunshine (hrs)	Date of sowing
Adilabad	ENV 1	Black	110.60	16.61	31.83	74.10	8.90	13.11.2021
Palem	ENV 2	Light red sandy	64.30	18.68	31.58	72.18	5.63	26.11.2021
Rudrur	ENV 3	Black	60.20	18.72	30.01	75.33	6.22	14.11.2021
Tandur	ENV 4	Black	61.00	18.00	33.33	80.00	6.38	26.11.2021
Warangal	ENV 5	Black	71.80	19.70	31.00	70.50	7.20	18.11.2021

RESULTS AND DISCUSSION

The pooled analysis of variance for grain yield (Table 3) revealed significant differences among genotypes, environments and significant genotype × environment interaction. The genotype × environment interaction effect was significant emphasizing the influence of environment on grain yield of chickpea genotypes under study. In the current study, as depicted by the mean grain yield of 50 genotypes ranged 1296 kg/ha (G39) to 2222 kg/ha (G8) with mean yield of 1870 kg/ha (Table 2). Among the five environments tested, highest and lowest mean grain yields were obtained from environments E5 (Warangal; 2080 kg/ha) and E2 (Palem;1526 kg/ha) respectively. Genotypic performance of pigeonpea and other crops in relation to different environments has been estimated by worker like Xing *et al.* (2021); Amiri *et al.* (2015).

The AMMI analysis of variance for grain yield (kg ha^{-1}) of 50 chickpea genotypes evaluated across the five environments revealed that the main effects of genotypes (G) and environments (E) accounted for 22.71% and 17.86%

Table 2: Mean grain yield of fifty chickpea genotypes.

Genotype and environment names	Genotype and environment code	Grain yield (kg/ha)
ICCX-060157-F3 (Early)-BP-P24-BP-BP-P4-BP	G1	1777
ICCX-060157-F3 (Early)-BP-P24-BP-BP-P5-BP	G2	1598
ICCX-060157-F3 (Early)-BP-P24-BP-BP-P9-BP	G3	1635
ICCX-060157-F3 (Early)-BP-P24-BP-BP-P11-BP	G4	1562
ICCX-060157-F3 (Early)-BP-P24-BP-BP-P13-BP	G5	1880
ICCX-060156-F3-BP-P22-BP-BP-P1-BP	G6	1930
ICCX-060156-F3-BP-P22-BP-BP-P63-BP	G7	1463
ICCX-100105-F4-P16-BP-BP	G8	2222
ICCX-100105-F4-P23-BP-BP	G9	1925
ICCX-100106-F4-P11-BP-BP	G10	2172
ICCX-110055-F3-P35-P2-BP	G11	1733
ICCX-100098-F4-P37-BP-BP	G12	1619
ICCX-100102-F4-P7-BP-BP	G13	1967
ICCX-100102-F4-P25-BP-BP	G14	2037
ICCX-100103-F4-P9-BP-BP	G15	1789
ICCX-100106-F4-P9-BP-BP	G16	1983
ICCX-100107-F4-P1-BP-BP	G17	2059
ICCX-110049-F3-BP-P23-BP	G18	1737
ICCX-110051-F3-BP-P6-BP	G19	1962
ICCX-110051-F3-BP-P7-BP	G20	2111
ICCX-110051-F3-BP-P22-BP	G21	1566
ICCX-110053-F3-BP-P8-BP	G22	2069
ICCX-110053-F3-BP-P36-BP	G23	2133
ICCX-110054-F3-BP-P9-BP	G24	1912
ICCX-110054-F3-BP-P27-BP	G25	1901
ICCX-110054-F3-BP-P33-BP	G26	2157
ICCX-110055-F3-BP-P21-BP	G27	1840
ICCX 120041-B-B-B-B-50-B	G28	2102
ICCX 120041-B-B-B-B-54-B	G29	1575
ICCX 120041-B-B-B-B-57-B	G30	1950
ICCX 120041-B-B-B-B-63-B	G31	2063
ICCX 120041-B-B-B-B-67-B	G32	1864
ICCX 120041-B-B-B-B-75-B	G33	1631
ICCX 120041-B-B-B-B-85-B	G34	1737
ICCX 120041-B-B-B-B-94-B	G35	2204
ICCX 120043-B-B-B-B-20-B	G36	2042
ICCX 120044-B-B-B-B-8-B	G37	1757
ICCX 120044-B-B-B-B-28-B	G38	1518
ICCX 120044-B-B-B-B-31-B	G39	1296

Table 2: Continue....

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ICCX 120046-B-B-B-B-2-B	G40	1996
ICCX 120046-B-B-B-B-27-B	G41	2039
ICCX 120046-B-B-B-B-43-B	G42	1973
ICCX 120046-B-B-B-B-49-B	G43	2123
ICCX 120046-B-B-B-B-52-B	G44	1903
ICCX 120046-B-B-B-B-54-B	G45	1714
ICCX 120046-B-B-B-B-55-B	G46	1449
ICCX 120046-B-B-B-B-59-B	G47	1828
NBeG 47	G48	1726
NBeG 3	G49	2090
ICCV 93952	G50	2089
Adilabad	ENV1	1849
Palem	ENV2	1526
Rudrur	ENV3	1838
Tandur	ENV4	2057
Warangal	ENV5	2080

Table 3: AMMI analysis of variance for G × E interaction.

Source	d. f	SS	MS	F	% Explained SS
Genotypes (G)	49	37878789	773036	12.41	22.71
Environment (E)	4	29804324	7451081	119.63	17.86
Genotypes × Environment (G × E)	56	99101239	505618	8.12	59.41
ICPCA 1	52	10707871	629874	14.15	46.33
ICPCA 2	50	5038998	335993	9.09	28.63
ICPCA 3	48	2440765	187751	5.77	17.46
ICPCA 4	46	1495952	135995	2.62	7.60
Error	500	31141655	62283		-

of the total sum of squares respectively (Table 3). The G × E interaction also accounted for 59.41% of the total sum of squares clearly depicting the diversity among the genotypes and their differential reaction to environmental conditions, which facilitates selection of genotype suitable for particular environment or multiple environments.Similar findings found in the studies by Dehghani *et al.* (2006); Tolessa *et al.* (2013) and Singamsetti *et al.* (2021) and Sriwichai *et al*. (2021) where GEI accounted maximum among the genotypes of field pea, wheat, maize and winged bean respectively indicating that the differences in the response of the genotypes across the environment were substantial and the presence of G × E interaction. AMMI revealed major part of the variation in yield is due to environment indicating the diversity of the environment in the present study when the interaction was partitioned among the first four interaction principal component axis (IPCA) as they were significant in predictive assessment. All the interaction PCA were highly significant capturing 46.33%, 28.63%, 17.46% and 7.6% of the total variation in the G × E interaction sum of squares, respectively. The first two interaction PCA axes combinedly accounted for 80.0% of the G × E interaction sum of squares, endorsing that the model's use of GGE biplot to explain variation caused by G+E+GEI across environments was effective. Similarly, Zewdu *et al.* (2020); Das *et al*. (2010) and Umma *et al.* (2013) earlier reported that first two PCAs explained the maximum GEI. Thus, the GEI of the 50 chickpea genotypes tested in five diverse environments was mostly explained by the first two principal components of genotypes and environments. AMMI revealed major part of the variation in yield is due to environment indicating the diversity of the environment in the present study. Previous reports confirmed that in most of the cases the maximum GEI could be explained through using the first two PCAs (Fikere *et al*., 2014; Biswas *et al.,* 2019). Hence, IPCA1 and IPCA2 were used for generation of AMMI1 and AMMI2 biplots.

Biplot analysis

The results of AMMI analysis further elucidated the relative contribution of first two IPCA axes to the interaction effects by plotting with genotype and environment means as depicted in Fig 1 and 2. The mean performances along with PCA1 scores for both varieties as well as environments used to construct the biplots are presented in Table 2 and 3. In the biplot, environments are designated by the letter 'ENV' followed by numbers 1 to 5 as suffix (Table 1, Fig 1), while genotypes represented by numbers from 1 to 50 (Table 2,

Fig 1). The quadrants in the graph represent: (QI and QII) higher mean, (QIII and QIV) lower mean, (QI and QIV) +ve IPCA1 and (QII and QIII) –ve IPCA1 scores (Fig 1). When a variety and the environment have similar sign on PCA1 axis, their interaction is meant positive and if opposite, their interaction is considered negative. Therefore, a variety with near to zero PCA1 score mean that it had small interaction effect and hence was considered as stable over wide

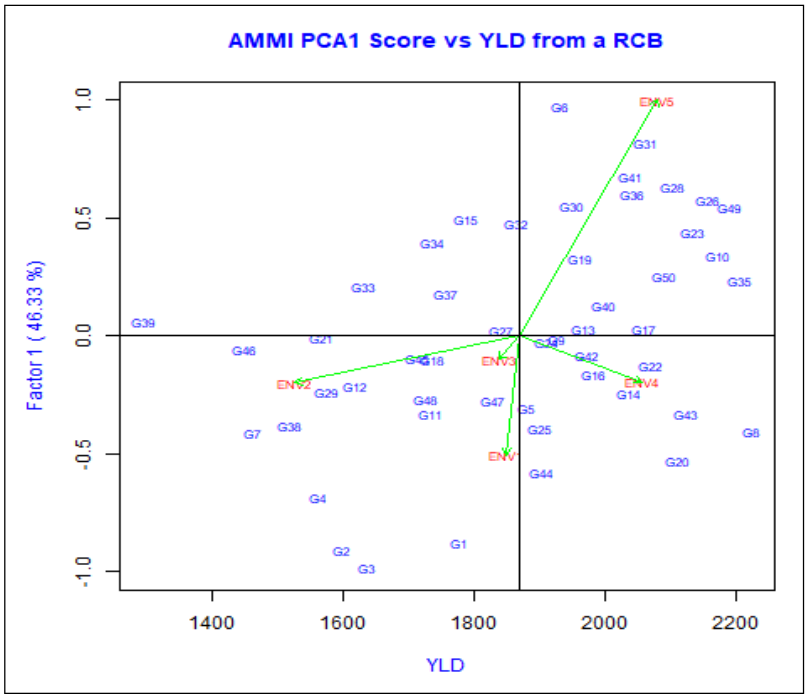


Fig 1: The AMMI biplot of the first interaction principal component axis (PCA 1) versus mean yields of fifty chickpea genotypes across five environments.

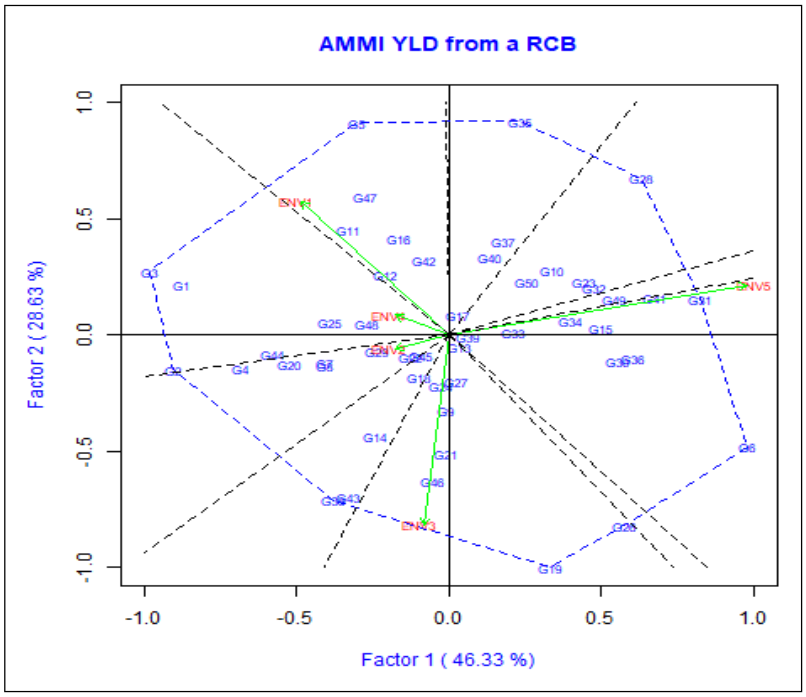


Fig 2: The AMMI 2 biplot of the first interaction principal component axis (PCA 1) versus the second interaction principal component axis (PCA 2) for chickpea genotypes.

environments. On the contrary, varieties with high mean yield and large PCA scores were regarded as clearly adapted to specific environments (Abdi and Williams, 2010; Askari *et al*., 2017; Mustapha and Bakari, 2014).

Accordingly, in the present study, the chickpea genotypes, G35, G10 and G49 exhibited high yield positive IPCA 1 score and among all genotypes, G35 is being the overall best genotype. On the other hand, G8, G43 and G20 were high yielding genotypes with negative IPCA 1 scores, While IPCA 1 for G9, G24, G7 and G13 were near to zero score and hence have less interaction with the environments out of which G9 and G13 had above average yield performance.

AMMI-2 relationships among genotypes and environments

In AMMI 2 biplot (Fig 2), The biplot 2 provides on the G×E interaction only and not like AMMI 1as the AMMI biplot 1 included main effect also. It was observed from the AMMI 2 biplot analysis (Fig 2) that genotypes showing less interaction in both axes are positioned near to the origin and vice versa. So, the genotypes placed near the origin were regarded as stable compared to others. Likewise, genotypes lying away from the origin and having long spokes were considered as highly interacting types. Hence, environments E5, E1 and E3 exerted strong interaction forces while, the rest two E2 and E4 did less. In the present study, G6, G19, G20, G21, G28, G35, G5 and G3 had more responsive since they were located far from the origin,while the genotypes G39, G17, G13 and G33 were nearer to origin and hence they were less sensitive to environmental forces. In overall, G17 (2059 kg/ha) showed very less genotype × environmental interaction and high stability with high yield.

GGE Bi-plot analysis

GGE Biplot of Environment-view for yield

Environment centered GGE biplot used to estimate the pattern of environments (Fig 3). Lines connecting the test environments to biplot origin as environment vectors were drawn to compare the association between environments. The angle cosine between two environments is used to explain the extent of correlation among them (Dehghani *et al.,* 2010).

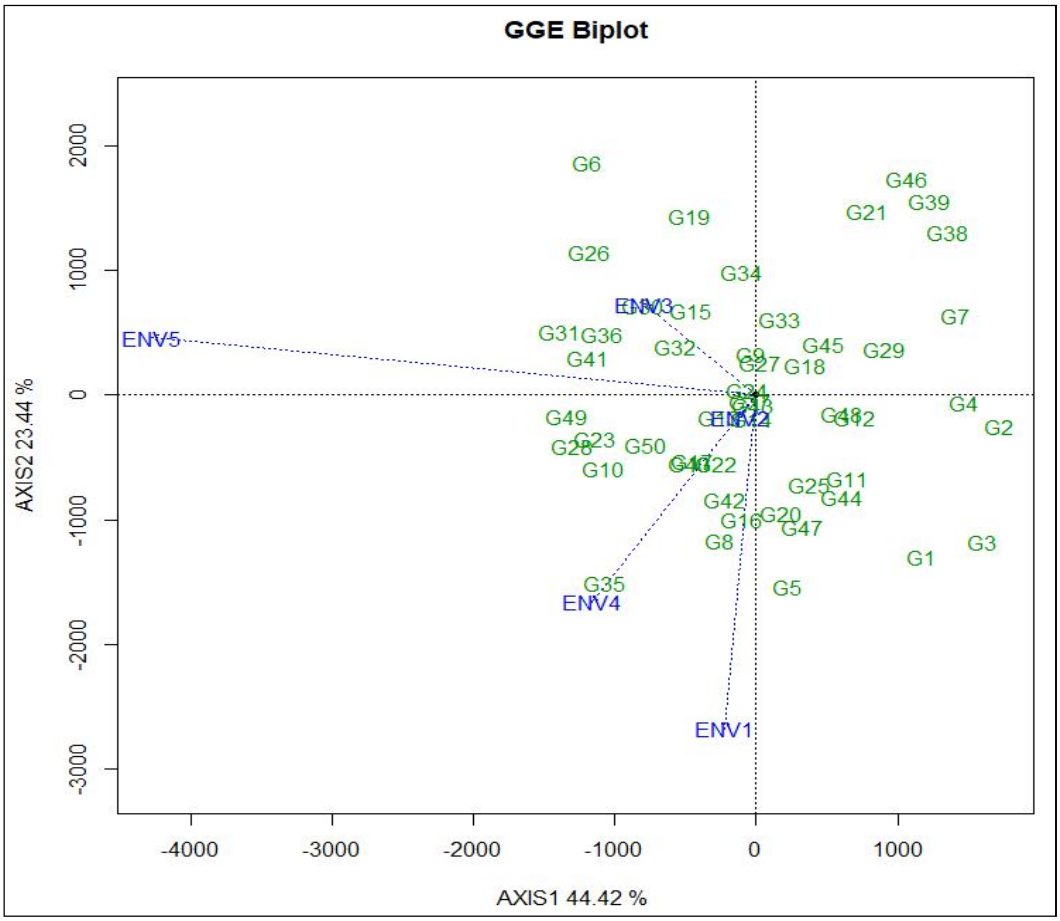


Fig 3: Environment vector view of the GGE-biplot showing the relationship among five environments.

Environments E2 and E4 are positively correlated (an acute angle). The presence of wide obtuse angle among environments is an indication of high cross over genotype × environment interaction (Yan and Tinker, 2006). In the present study, the environments E3 and E1 are negatively correlated (an obtuse angle).

GGE Biplot on environment for comparing environments with ideal environment

An ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Differentiating capability and precise representation of testing environments are two pivotal roles of GGE biplot. The concentric circles depicted in Fig 4 and 5 aid in visualizing the length of environment vectors, which are the indicators of the discriminating ability of environments and also standard deviation within the respective environments. (Kang-Bo-Shim *et al.,* 2015). The environments E1 and E5 are most discriminating. Accordingly, the environments E2 is the most representative whereas the environments E1 and E5 are least representative. Test environments possessing discriminating ability as well as representativeness are highly suitable for selecting adaptable genotypes. Discriminating but non representative test environment like E1 and E5 are useful for selecting adaptable genotypes.

Biplot of stability and mean performance of genotypes across average environments

The line passing through biplot origin and the average environment depicted with a single arrow constitutes the average environment axis (AEA). Projections of genotypic markers to AEA represent the mean genotype yield (Fig 6). Genotypes are ranked along the ordinate. The results revealed that the line perpendicular to the average environment axis (AEA) separated the genotypes into two groups (those above average and those below average).

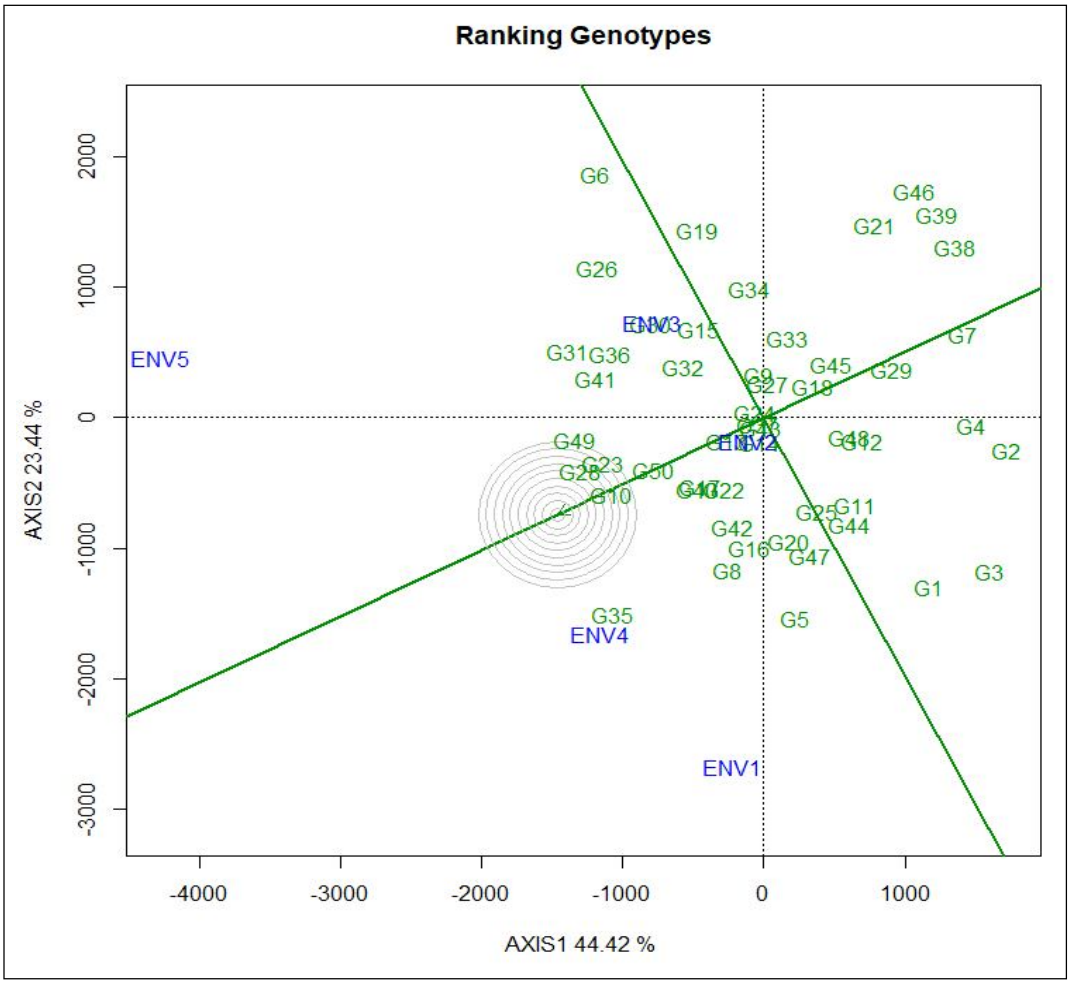


Fig 4: Vector view of GGE biplot of genotype-focused scaling.

The genotypes with above average yield are G35, G28, G17, G49, G23, G30, G8, G36, G40, G32, G15, G20, G47. The genotypes with below average yield are G44, G11,G29, G34, G33, G18, G45, G1, G48, G12, G45, G29,G46, G39 and G38. Of all the genotypes G8 and G35 were high yielders, while G39 was the poorest yielder. The AEA ordinate is the double arrowed line that passes through the biplot origin and is perpendicular to the AEA abscissa. Greater projection onto AEA ordinate regardless of the direction means greater stability (Yan, 2001; Yan *et al*., 2007). The genotypes G10, G23, G28, G18, G12, G9, G27 and G24 with shorter projections are stable over environments. Among these, genotypes stable and high yielding are G10, G23, G28, G17, G9 and G24. Whereas the genotypes G18, G12 and G27 were considered stable but had low seed yield. Therefore genotypes G10, G23, G17 and G28 were identified as stable and high yielding genotypes. The genotype G17 recorded the shortest projection and lies closest to the AEA ordinate hence chosen as best genotype and is at par in yield with the best checks.An ideal genotype express its full genetic potential and perform consistently across the environments. (Kaya *et al*., 2006; Yan and Tinker, 2006). The environment (ENV2) has been located in the closest of the axis and is thought to be best environment for assessing the stability of the genotypes. This environment is the most representative of all. The ability of genotypes to withstand the aberrant weather conditions in the representative environment are the best ones for the selection. These results are in compliance with the findings of Akinyosoye, (2022) and Tiwari *et al*. (2022) that the environment closest to the axis/concentric point is ideal for selection of stable genotypes. Environment 5 (ENV5) recorded longest projectiles from the axis implying that this is the best environment for selecting high yielding genotypes but it does

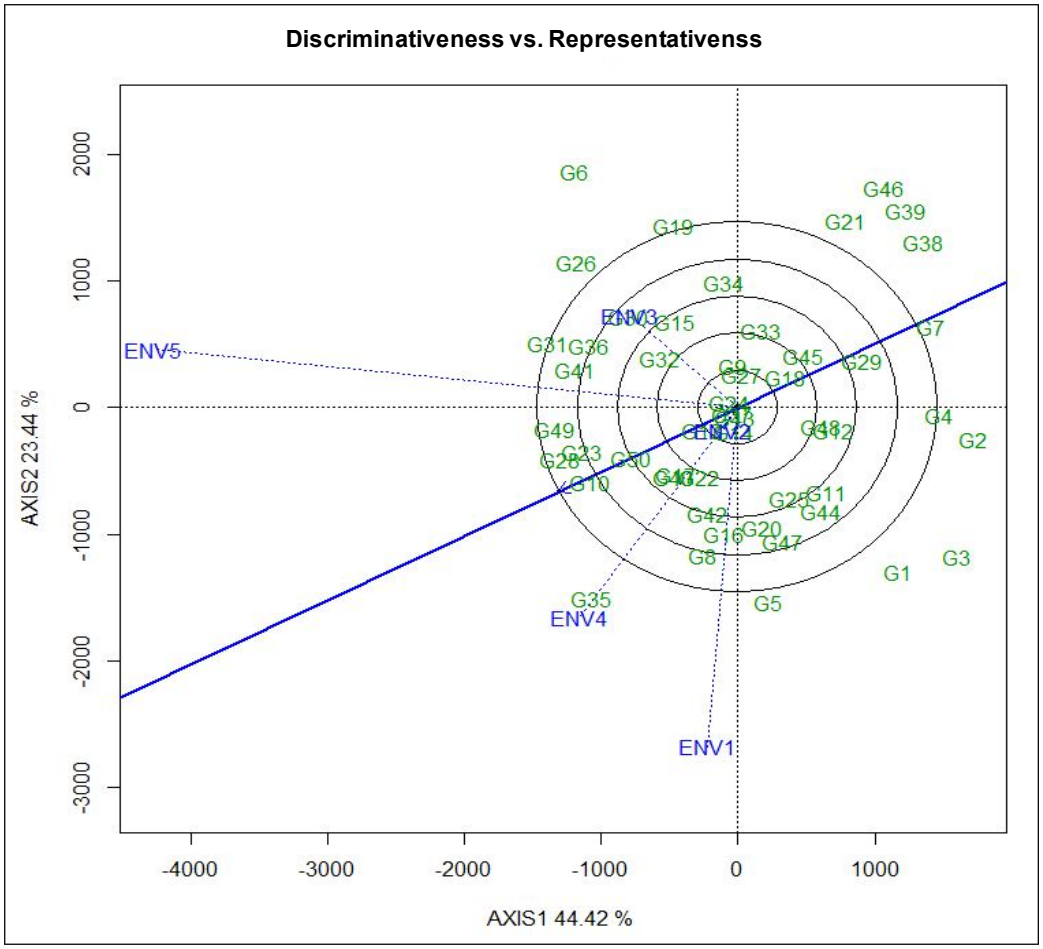


Fig 5: GGE biplot on environment focused for comparing environments with ideal environment.

not mean that genotypes chosen in these environment are stable, however genotypes selected for high yield in these environments can be utilized for breeding for high yielding varieties. Yan and Kang (2003) reported that the distances from the biplot origin were indicative of the amount of interaction exhibited by genotypes over environments or environments over genotypes.

"Which-Won-Where" pattern analysis

Genotypes having specific adaptative ability for specific environment or group of environments were identified using "Which-Won-Where pattern analysis" and "ranking of genotypes in individual environments" using GGE Biplot tools. In comparison to AMMI, GGE bi-plot precisely identifies the best G × E interaction and also clearly indicates as to which genotype performs best in what type of environment thereby aiding in identification of mega-environments (Yan and Kang, 2003). The studied environments were divided into three mega environments *i.e.,* E1, E3 and E5. In mega environment E5, the winning genotype is G31, while the genotype G6 is the winner in mega environment E1, whereas, E2 and E3 are closely related and fall under the mega environment E4 and the winning genotype is G35. The other promising genotypes in the mega environment are G10, G8, G28, G40 and G22. The polygon outlook of GGE bi-plot (Fig 7) gives inputs on the best genotype(s) in each environment. The vertex genotypes (G3, G2, G46, G6 and G35) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments (Fig 7). Vertex genotypes in every sector gave highest yields in the environments under that sector. The genotype with the high yield in E1, E2 and E4 is G35. The other vertex genotypes G46, G39, G38, G7 and G2 are the poorest in all environments because there is no environment in their sectors. Our findings are in agreement with those of Ebadi *et al.* (2010) and Akinyosoye (2022) who reported that genotype in each environment sector could be grown at each of the locations where they demonstrated comparative advantage

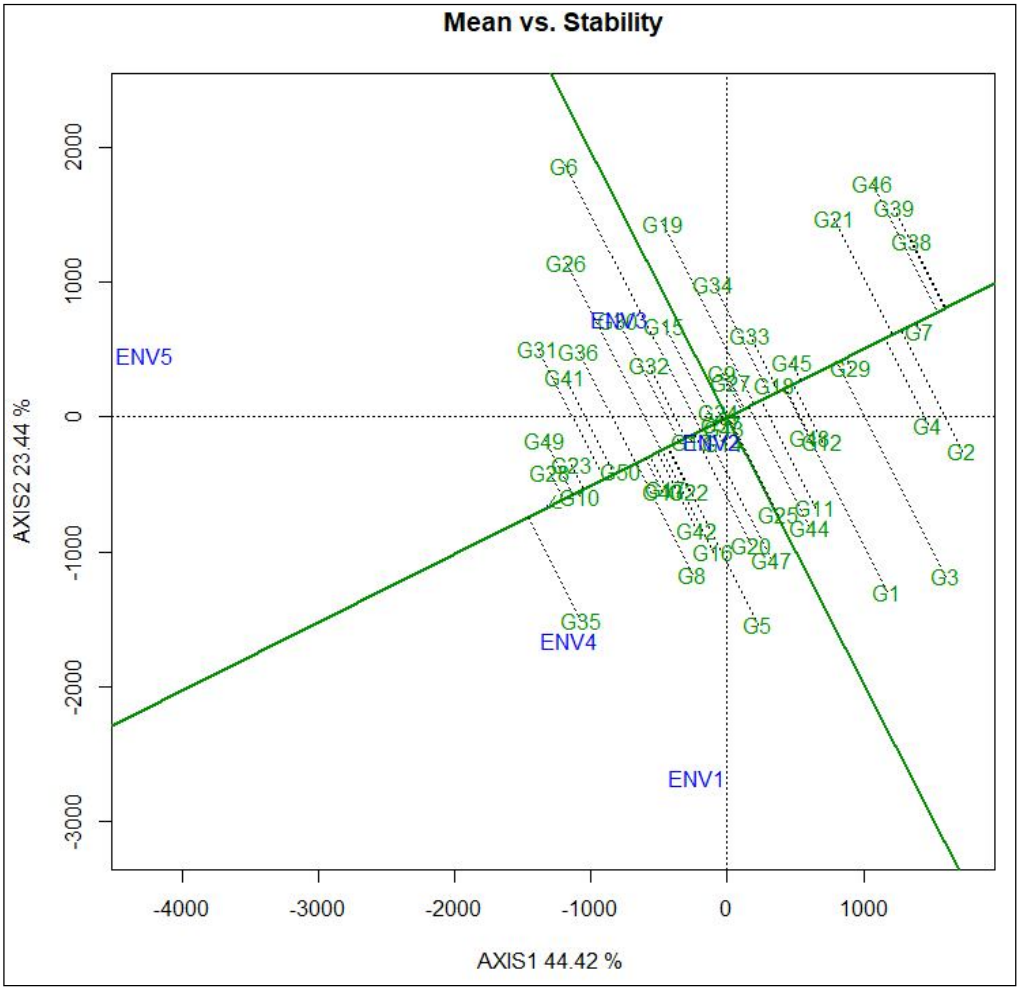


Fig 6: Biplot of stability and mean performance of genotypes across average environments.

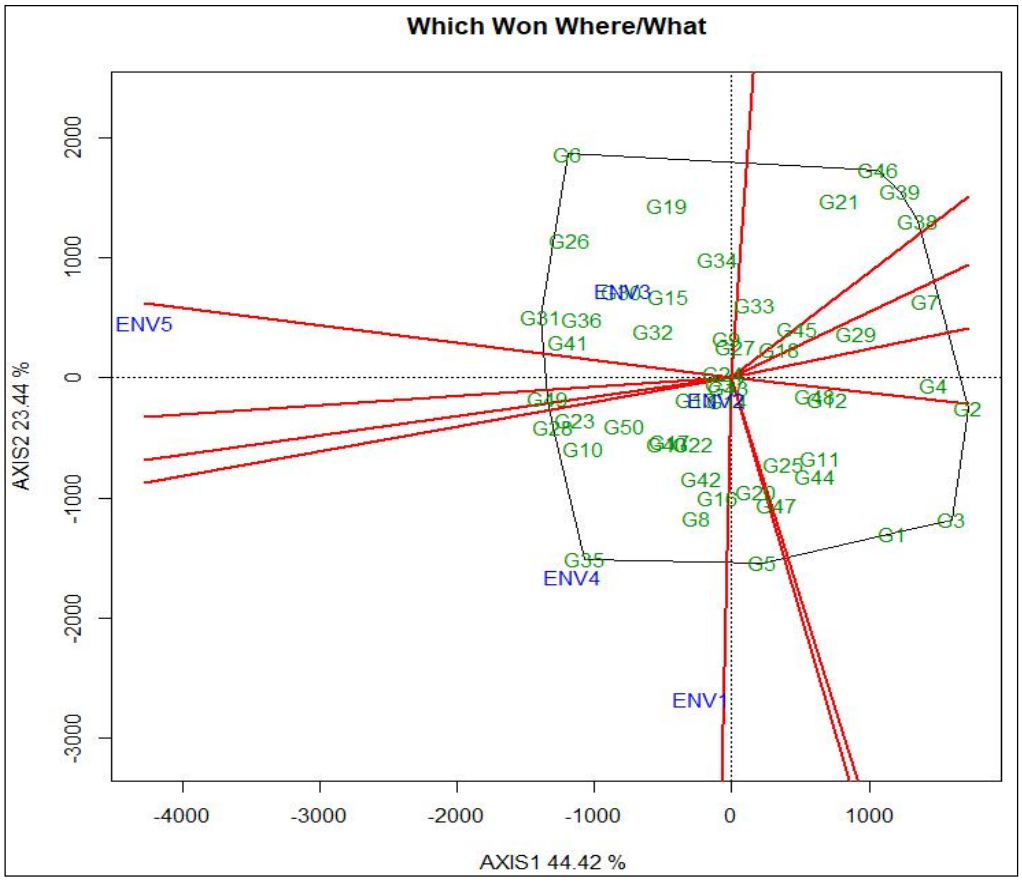


Fig 7: What-won-where GGE biplot of grain yields of fifty chickpea genotypes across five environments.

in seed production. Genotypes that did not fit into any of the environment sector are not appropriate for cultivation in any of the environments under study.

CONCLUSION

The study indicated that yield stability was significantly affected by genotype, environment and their interaction and major interaction effects were explained by the first two principal components as per the AMMI model. The genotypes G8 (2222 kg/ha), G35 (2204 kg/ha), G10 (2172 kg/ha), G26 (2157 kg/ha) G23 (2133 kg/ha) yielded above the overall genotypes average, whereas the genotype G39 (1296 kg/ha) was the poor yielder. The genotypes stable and high yielding are G10 (2172 kg/ha), G23 (2133 kg/ha), G28 (2102 kg/ha), G17 (2059 kg/ha), G9 (1915 kg/ha) and G24 (1912 kg/ha) respectively. The Genotype G24 exhibited high grain yield than mean yield with specific adaptability for the environment E2 (Palem), genotypes G6 is for the environment E3 (Rudrur) and genotype G34 for the environment E4 (Tandur). The environment E2 is the most representative whereas the environments E1 and E5 are least representative. The result indicated that Environment E5 (Warangal) has recorded highest mean grain yield (2080 kg/ha) and identified as best suited environment for potential expression of grain yield.

The genotype G17 presented high grain yield stability across the environments with desirable mean performance (2059 kg/ha) and this genotype can be given to farmers field for further evaluation before its release for general cultivation.

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