Original Research Article

GGE Biplot Model based Yield Stability Analysis in Chickpea (*Cicer arietinum* L.)

ABSTRACT

The present study evaluates the yield stability of eight chickpea genotypes across three locations in two seasons to identify high-yielding, stable genotypes suitable for Odisha. The Analysis of variance (ANOVA) revealed significant differences~~among genotypes, environments, and their interactions (G×E).~~The Pooled ANOVA across environments indicated highly significant differences ~~for~~ key agronomic traits such as days to 50% flowering, plant height, number of pods per plant, and 100-seed weight, while seed yield exhibited significant variation. The GGE biplot analysis was ~~employed~~ used to assess genotype stability and adaptability. Mean vs. stability analysis showed that ICCV 14102 had the highest mean grain yield, whereas ICCV 15114 was the most stable genotype. The 'which-won-where' biplot demonstrated three distinct mega-environments: the first, containing E6, was dominated by ICCV 15118 and JAKI 9218; the second, comprising E4 and E5, was led by ICCV 14108; and the third, covering E1, E2, and E3, identified ICCV 14102 as the best performer. ~~Ranking genotypes in relation~~When ranking genotypes relative to an ideal genotype indicated ICCV 14108 as the most preferred, followed by ICCV 14102, ICCV 15115, and JAKI 9218. Similarly, environments were ranked based on their discriminating power(ability to distinguish genotype differences) and representativeness (ability to reflect overall performance trends), with E4 emerging as the most ideal environment, followed by E5, E2, and others. The results highlight the effectiveness of GGE biplot analysis in genotype selection by providing insights into adaptability, stability, and performance across diverse environments. ~~These findings contribute valuableinformation for chickpea breeding programs, aiding in the identification of genotypes with superior yield potential and stability, thereby enhancing productivity in Odisha.~~These findings provide valuable insights for the development of high-yielding and stable chickpea varieties in Odisha, with potential applications in other regions facing similar environmental challenges.

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Comment [a2]: Instead of just saying "revealed significant differences," it would be more precise to state : TheAnalysis of variance (ANOVA)*indicated significant effects of genotypes, environments, and their interactions (G×E) on the traits measured."* This emphasizes the statistical testing and the sources of variation.

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Keywords: Chickpea, GGE biplot, Genotype × environment interaction, Stability analysis

1. INTRODUCTION

Chickpea, the world's third-most cultivated legume, holds a position of immense significance in global agriculture and diets. Widely recognized as an essential source of dietary protein, especially in the Global South, chickpea is a staple food for many populations, particularly in South Asia, the Middle East, and North Africa (Pareeketal., 2022 and Ali et al., 2011).During 2021-22 (fourth estimate), chickpea production of India was 13.75 million tonnes from an acreage of 10.91 million ha with a productivity of 12.6 q/ha (Anon, 2023a). Chickpea solely contributes nearly 50% of the Indian pulse production. States like Maharashtra (25.97% contribution to national production), Madhya Pradesh (18.59%), Rajasthan (20.65%), Gujarat (10.10%) and Uttar Pradesh (5.64%) are major chickpea producing states of India. Chickpea has a diverse consumption pattern in the Indian market. With the increasing trend of the market of products based on plant protein (protein isolates etc.), importance of chickpea to the processing sector has enhanced further (Anon., 2023b).With its cultivation spanning over 40 countries, chickpea has become an integral part of food security strategies, ensuring access to affordable and nutritious food. Beyond its importance in human nutrition, chickpea cultivation brings significant benefits to agricultural systems. It helps break disease and pest cycles, enhances soil fertility, and promotes crop rotation, reducing dependence on monoculture practices (Richards et al., 2022). By contributing to more resilient and productive farming

Comment [a4]: Chickpea is cultivated in over 40 countries and plays a key role in food security by ensuring access to affordable and nutritious food systems, chickpea plays a vital role in sustainable agriculture, supporting both environmental health and economic prosperity. With its adaptability, nutritional value, and economic significance, chickpea remains a key player in global food systems, fostering human well-being and agricultural sustainability. As we embrace the importance of diverse and resilient crops, chickpea stands as an exemplary model for nourishing communities and fostering a sustainable future for all (Anon., 2024). Being such an important crop, it has long been the concern for agricultural research owing to its increase of yield as well as yield stability over varied environments of India, not to mention, it's high nutrition value owing to the fact that it contains carbohydrate, protein, dietary fibres, amino acids, alpha-tocopherol, minerals like Fe, Zn, Mg, Ca, and vitamins like folic acid, B_2, B_5 and B_6(Jukanti*et al*., 2012). Stability can be generally defined in simple terms as the consistency of a genotype to yield approximately equal over different environments. The yield stability is a function of the genotype × environment interaction and not just the genotype and environments individually. Usually, it is observed that the higher the yield, the lesser the stability(Funga et al., 2017). The identification of comparatively stable and better yielding genotypes can be done by multi environment trials. Genotypes that are put to experiment in varied environments might have significant variations in several parameters including those of yield owing to their response to the specific environments in concern. These interactions are universally referred to as the Genotype × Environment Interactions with the acronym GEI.

Although, Genotype by environmental interaction are treated as noise or confounding factorby the biometricians and quantitative geneticists, breeders focus more on matching genotypes with environment to understand the G × E interaction.If G×E exists, it is necessary to determine whether there are important crossovers, *i.e*., rank changes of the genotypes in different environments, such that different winners are picked up in different environments. If not, Superior genotypes can be identified in any of the environments but there exists an ideal test environment in which the best genotypes can be most easily identified (Crossa, 2012). If crossover interactions exist, it is necessary to determine whether the crossover G×E patterns are repeatable across years. Data from multiple years are necessary to address this question. If there are repeatable interactions then the target environments should be divided into different mega-environments and genotype evaluation should be conducted separately for each mega-environment. Dividing target environments intomeaningful mega-environments is the only way that G×E can be exploited (Yan and Tinker, 2005a). If there is no recognizable pattern of G×E, then the target environment is a single mega environment with unpredictable G×E, and models addressing random sources of variation may be appropriate(Yan and Kang, 2003).This can be achieved by advent of biplot analysis, where biplot is a scatter plot that approximates and graphically displays a two-way table by both its row and column factors such that relationships among therow factors, relationships among the column factors, and the underlying interactions between the row and column factors can be visualized simultaneously (Yan and Kang, 2003). More recently, the term "GGE biplot" was proposed and various biplot visualization methods developed to address specific questions relative to genotype byenvironment data (Yan et al., 2000). The main target of Genotype by Environment data evaluation by Biplot analysis is to out four major objectives: (i) Multi-years data to divide the target environment into meaningfulmega-environments so that some of the GE can be exploited;(ii) The data of Genetic andenvironmental covariates are required to address to identify the causes of GE;(iii) Identification of the best test environments(representative and discriminating) and(iv) Identifying the superior genotypes (both high and stableperformance within a mega-environment).

Comment [a5]: While some biometricians and quantitative geneticists treat genotype-environment interactions (G×E) as noise or confounding factors, breeders focus on matching genotypes with specific environments to better understand G×E interactions.

As the yields of different genotypes is almost always the function of the main effect of the environment, the main effect of the genotypes as well as the GEI, this GEI needs to be evaluated so as to assess the stability of the variety in question. The GEI can be evaluated in to different approaches such as the graphical approach and the non-graphical approach. The graphical approach encompasses GGE and performance biplots while the non-graphical approach is again sub divided into parameric and non-parameric types. The parameric type includes univariate and multivariate analyses. Yan *et al.*(2000) took into consideration both G and G×E at a time which later came to be referred as biplots. The G×E generates a huge number of MET (Multi Environment variety Trial) data which can be reduced down for easier consideration by plotting them into biplots. Therefore, GGE biplot has evolved as a competent MET data analysis tool.

2. MATERIALS AND METHODS

2.1. Study Site and Experimental Materials

The present investigation was conducted during the cropping season*rabi*(2016-17) and *rabi* (2017-18)across three locations (R.R.T.T.S., Bhawanipatna; R.R.T.T.S., Keonjhar and K.V.K., Shyamakhunta) under Odisha University of Agriculture and Technology, Odisha, India. The details of testing environment and its climatic condition during the crop growth are mentioned in Table-1. The present study was consisted of the materials provided by ICRISAT, Hyderabad for stability analysis and thesixtest genotypes are; (G1-ICCV 14106, G2- ICCV 15114, G3- ICCV 15115, G4- ICCV 15118, G5- ICCV14102; and G6- ICCV14108)along with two standard checks (G7-JAKI 9218 and G8- JG-14).

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2.2. Experimental Design and Data Collection

The experiment was laid in a randomized complete block design (RCBD) with three replications. Each unit in the experimental was consists of 6 rows of 4 m length with 10cm plant to plant spacing and 30cm row-row spacing. All the crop management practices were followed dung the cropping season to raise a good crop. The following observations *viz*.,days to 50% flowering, plant height (cm), no. of pods per plant, 100 seed weight (g) and grain yield (kg/ha)were recorded for statistical analysis of the experiment. The pods from individual plots were harvested first andgrain yield per plot was estimated and later ~~it~~ converted to grain yield per hectare (kg/ha).

Comment [a8]: was laid out

Comment [a9]: Each experimental unit consisted of

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Comment [a11]: The following observations were recorded

2.3. Statistical Data Analysis

The data collected on grain yield and other yield attributesof chickpea varieties across six environments were subjected to combined analysis of variance (ANOVA). All the statistical analysis was done by using the software R-studio 4.1.0with the help of package Metan 1.15.0 (Olivoto and Lucio, 2019 and 2020). The genotype-by-environment interaction effects were identified by using GGE-biplot model.The model for a GGE biplot (Yan et al., 2007) based on singular value decomposition (SVD) of t principal components is:

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Comment [a13]: were performed using RStudio 4.1.0

Comment [a14]: with the Metan 1.15.0 package

$$Y_{ij} – \mu_i – \beta_j = \sum_{k=1}^{t} \gamma_k \alpha_{ik}\ \gamma_{jk} + \epsilon_{ij}$$

Where; Y_{ij} is the performance of genotype i in environment j, μ is the grand mean, β_j is the main effect of environment j, k is the number of principal components (PC); λ_k is singular value of the k^{th} PC; and α_{ik} and γ_{jk} are the scores of i^{th} genotype and j^{th} environment, respectively for PC_k; ϵ_{ij} is the residual associated with genotype i in environment j.

3. RESULTS AND DISCUSSION

3.1. Analysis of Variance (ANOVA)

Multiple genes control grain yield, and the substantial influence of the G×E interaction makes genotype evaluation hard (Elbasyoni 2018). ~~Accordingly, plant breeders may be able to choose a genotype that is appropriate for a certain environment and explore its greater stability and adaptability across different places by using GGE biplot and G×E interaction analysis using AMMI~~Accordingly, plant breeders can identify genotypes suitable for specific environments while assessing their stability and adaptability across locations using GGE biplot and G×E interaction analysis through the AMMI model(Yan et al., 2000, Yan and Tinker, 2006). The analysis of variance (ANOVA) for key yield-attributing traits of desi chickpea revealed significant effects of environment (E), genotype (G), and genotype-by-environment interactions (G×E), ~~highlighting the complexity of yield determination in chickpea~~emphasizing the intricate nature of yield determination in chickpea. (Table-2). The environment had a highly significant effect (p < 0.001) on all the studied traits, including days to 50% flowering, plant height, number of pods per plant, 100-seed weight, and seed yield. The highest F-value was observed for seed yield (F = 299.80), indicating that environmental factors strongly influence productivity. Similarly, the significant impact of environment on plant height (F = 9.45), number of pods per plant (F = 171.32), and 100-seed weight (F = 15.90) suggests that these traits are

Comment [a15]: challenging

highly sensitive to varying environmental conditions. Genotypic differences were also highly significant ($p < 0.001$) across all traits, confirming the presence of genetic variability.

Table 1: Description of the test environment along with geographical position and the climatic condition during the cropping season

Location	Environment Code	Cropping Season	Longitude	Latitude	Total Rainfall (mm)	Average Temperature (^{0} C)	Type of Soil
R.R.T.T.S., Bhawanipatna	E1	*Rabi* (2016-17)	82^0 61' to 83^0 79' E	19^0 17' to 20 45' N	82.96	24.50	Black soil
R.R.T.T.S., Keonjhar	E2	Rabi (2016-17)	85°11' E and 86°22' E	21^0 01' N and 22°10' N	80.05	24.00	Red lateritic soil
K.V.K., Shamakhunta	E3	Rabi (2016-17)	80^0 40' E to 87^0 11' E	21^0 16' N to 22^0 34' N	90.26	24.75	Sandy loam soil
R.R.T.T.S., Bhawanipatna	E4	Rabi (2017-18)	82^0 61' to 83^0 79' E	19^0 17' to 20 45' N	111.32	25.25	Black soil
R.R.T.T.S., Keonjhar	E5	Rabi (2017-18)	85°11'E and 86°22' E	21^0 01' N and 22°10' N	133.36	24.25	Red lateritic soil
K.V.K, Shamakhunta	E6	Rabi (2017-18)	80^0 40' E to 87^0 to 11' E	21^0 16' N to 22^0 34' N	125.00	24.75	Sandy loam soil

Comment [a16]: Italic all rabi word in whole manuscript

Table 2: Analysis of variance (ANOVA) for various yield attributing traits of desi Chickpea

Source	Df	Days to 50% flowering			Plant Height (cm)			No. of pods per plant			100 Seed weight (g)			Seed yield (kg/ha)		
		Mean Sq	F-value	Pr (>F)	Mean Sq	F-value	Pr (>F)	Mean Sq	F-value	Pr (>F)	Mean Sq	F-value	Pr (>F)	Mean Sq	F-value	Pr (>F)
Env	5	701.61	173.89	0.00	346.84	9.45	0.00	1540.21	171.32	0.00	20.86	15.90	0.00	1804888	299.80	3.64E-12
Rep (Env)	12	4.03	2.20	0.02	36.71	2.77	0.00	8.99	0.32	0.98	1.31	1.78	0.06	6020.22	0.48	0.916693
Gen	7	41.41	22.55	0.00	118.23	8.92	0.00	282.38	9.92	0.00	159.34	216.77	0.00	152953.	12.39	8.56E-11
Gen: Env	35	19.53	10.64	0.00	43.12	3.25	0.00	114.33	4.02	0.00	5.77	7.84	0.00	77669.58	6.29	2.84E-12
PC1	11	51.89	28.26	0.00	100.53	7.58	0.00	225.37	7.92	0.00	18.19	24.75	0.00	192879.9	15.62	0
PC2	9	10.58	5.76	0.00	38.40	2.90	0.00	95.72	3.36	0.00	0.10	0.14	1.00	36831.94	2.98	0.004
PC3	7	2.35	1.28	0.27	6.53	0.49	0.84	54.59	1.92	0.08	0.09	0.12	1.00	33779.18	2.74	0.013
PC4	5	0.16	0.09	0.99	1.68	0.13	0.99	48.67	1.71	0.14	0.02	0.03	1.00	5641.931	0.46	0.8049
PC5	3	0.11	0.06	0.98	1.19	0.09	0.97	11.83	0.42	0.74	0.00	0.00	1.00	201.65	0.02	0.9961
Residual	84	1.84			13.26			28.47			0.74			12344.37		
Total	178	30.16			40.08			113.37			9.55			93489.64		

Mentioned full form all source, here

Comment [a17]:

The F-values for genotypic effects were highest for 100-seed weight (F = 216.77) and seed yield (F = 12.39), indicating that these traits are strongly controlled by genetic factors. The observed genetic variation ~~suggeststhat~~highlights the potential ofselective breeding can improve these traits, particularly for yield stability and adaptability.Significant G×E interactions were detected for all traits ($p < 0.001$), implying differential performance of genotypes across environments. The highest F-value for G×E was observed for seed yield (F = 6.29), suggesting that yield expression varies significantly across different testing environments (Table-2). This reinforces the importance of multi-location testing for identifying stable and high-yielding genotypes. The first principal component (PC1) accounted for a major portion of the variation in all traits, showing significant effects ($p < 0.001$) with the highest F-value for seed yield (F = 15.62). PC2 also contributed significantly ($p = 0.004$) but to a lesser extent. However, PC3, PC4, and PC5 showed non-significant effects for most traits, suggesting that the first two principal components explain the majority of variability in genotype performance. The significant environmental and G×E effects on all traitssuggest that genotype selection should be environment-specific. The strong genetic influence on 100-seed weight and seed yield indicates the potential for direct selection to improve these traits. The PCA results also emphasize that a few key factors dominate variability, supporting the use of stability analysis methods like GGE biplots to identify superior genotypes for targeted environments. Overall, the study confirms that chickpea yield and its component traits are significantly influenced by both genetic and environmental factors. Breeders should focus on selecting genotypes with high adaptability and stability to ensure consistent yield across diverse environments.

Comment [a18]: highly significantly

3.2. Mean performance

The evaluation of eight desi chickpea genotypes for key yield-contributing traits reveals notable variations in their performance.ICCV 14102 exhibited the earliest flowering with an average of 41.67 days to 50% flowering, while ICCV 14106 and JAKI 9218 were the latest, both at 44.61 days. In terms of plant height, ICCV 15118 and ICCV 14106 were the tallest, measuring 44.46 cm and 44.57 cm respectively, whereas JAKI 9218 was the shortest at 37.96 cm. The number of pods per plant varied, with ICCV 14102 producing the highest average of 56.24 pods, and ICCV 15114 the fewest at 44.24 pods. Regarding 100-seed weight, ICCV 15118 had the heaviest seeds at 30.00 g, contrasting with ICCV 14108, which had the lightest at 20.91 g. Yield per hectare ranged from 940.09 kg/ha in ICCV 15118 to 1220.57 kg/ha in ICCV 14102 (Table-3). These findings underscore the genetic diversity among the genotypes, particularly in traits such as days to flowering, plant height, and seed weight. Such variability is crucial for breeding programs aiming to enhance yield and adaptability. The significant differences observed in days to 50% flowering and plant height align with previous research highlighting the importance of these traits in chickpea adaptation and yield potential (Maleki et al., 2024).

Comment [a19]: This sentence is generally fine, but it would benefit from some statistical context. For example, a mention of whether the differences observed are statistically significant (through p-values or F-values) would add robustness to the findings. If possible….**Statistical significance** should be consistently mentioned when comparing genotypes

Comment [a20]: specifying whether these differences are statistically significant.

The variation in the number of pods per plant and 100-seed weight among the genotypes suggests potential for selecting high-yielding lines. For instance, ICCV 14102 not only had the highest number of pods per plant but also achieved the highest yield per hectare, indicating its promise as a high-yielding genotype. Conversely, ICCV 15118, despite having the heaviest seeds, recorded the lowest yield, suggesting that seed weight alone may not directly correlate with overall yield(Table-3). This observation is consistent with studies that emphasize the complex interplay between yield components in chickpea (Shimray et al., 2022). The observed variability in yield and its components among the genotypes highlights the importance of multi-trait selection in chickpea breeding programs. By considering traits such as flowering time, plant height, pod number, and seed weight, breeders can develop genotypes with enhanced yield potential and adaptability to diverse environments. This approach is supported by recent studies advocating for comprehensive trait evaluation to improve chickpea productivity (Deb et al., 2024). In conclusion, the significant differences in yield-contributing traits among the evaluated desi chickpea genotypes provide valuable insights for breeding strategies. Genotypes like ICCV 14102, with early flowering, moderate plant height, high pod number, and competitive yield, emerge as promising candidates for further development. These findings contribute to the ongoing efforts to enhance chickpea yield and stability across various growing conditions.

Comment [a21]: The variation in the number of pods per plant and 100-seed weight among the genotypes suggests that these traits, along with others, should be considered when selecting high-yielding lines.

Comment [a22]: It would be beneficial to provide a brief explanation of how your study builds on or contrasts with the cited literature to emphasize the contribution of your findings.

Table 3: Mean performance of genotypes for yield contributing traits in desi Chickpea

Environment	Days to 50% Flowering	Plant Height (cm)	No. of Pods/Plant	100 SW (g)	Yield (kg/ha)
ICCV 15115	42.61	39.51	53.33	23.55	1125.40
ICCV14102	41.67	39.27	56.24	22.31	1220.57
ICCV 15118	43.72	44.46	47.23	30.00	940.09
ICCV14108	40.94	41.42	50.99	20.91	1110.01
ICCV 15114	41.56	44.01	44.24	21.88	1034.37
ICCV 14106	44.61	44.57	54.89	21.34	1006.67
JG-14	41.17	41.63	51.46	21.21	1030.43
JAKI 9218	44.61	37.96	49.72	23.93	968.29

This biplot illustrates the principal component analysis (PCA) results, explaining 70.77% (PC1) and 22.41% (PC2) of the total variation (Figure-1A). The distribution of genotypes and environments indicates their performance and interaction. Genotypes positioned farther from the origin exhibit a stronger interaction with specific environments, while those near the center show stable performance across multiple environments. ICCV 15118, ICCV 14108, and JAKI 9218 were placed farthest, indicating their responsiveness to specific environments, whereas ICCV 14102 and ICCV 15116 were relatively closer to the origin, suggesting their broad adaptability.This biplot evaluates how well the environments differentiate genotypes (discriminativeness) and how well they represent the overall environment (representativeness). Environments with longer vectors (such as E4 and E5) are more discriminative, meaning they provide valuable insights into genotype performance (Figure-1B). The proximity of genotypes to the average environment axis indicates their adaptability. ICCV 15118 and ICCV 15114 appear to be the highest-yielding genotypes, while ICCV 14102 and ICCV 15116 display more stable performance. This plot ranks environments based on their ability to differentiate genotypes. E4 and E5 are positioned at a greater distance from the origin, indicating they are ideal for testing due to their strong discriminative power. Conversely, environments E1 and E2 are closer to the origin, suggesting they are less effective in differentiating genotypic performance (Figure-1C). Selecting environments with high discriminativeness can improve the reliability of genotype selection in breeding programs. This plot displays the similarity among environments in assessing genotype performance. Environments positioned close to each other (E5 and E6) exhibit strong correlations, meaning they provide similar information about genotype performance (Figure-1D). In contrast, environments like E4 and E2 are distantly placed, indicating distinct environmental influences. This information is critical for multi-environment trials, where selecting non-redundant testing environments enhances breeding efficiency. The GGE biplots indicate that E4 and E5 are the most discriminative environments, making them ideal for identifying superior genotypes. ICCV 15118 and ICCV 14108 appear to be high-yielding but environment-specific, while ICCV 14102 and ICCV 15116 demonstrate stable performance. Future breeding strategies should focus on selecting genotypes with both high performance and stability across multiple environments.

Comment [a23]: Mentioning the eigenvalues or variance explained by each component in a more detailed manner could enhance the transparency of the analysis.

Comment [a24]: The proximity of genotypes to the average environment axis, representing the mean performance across all environments, indicates their adaptability.

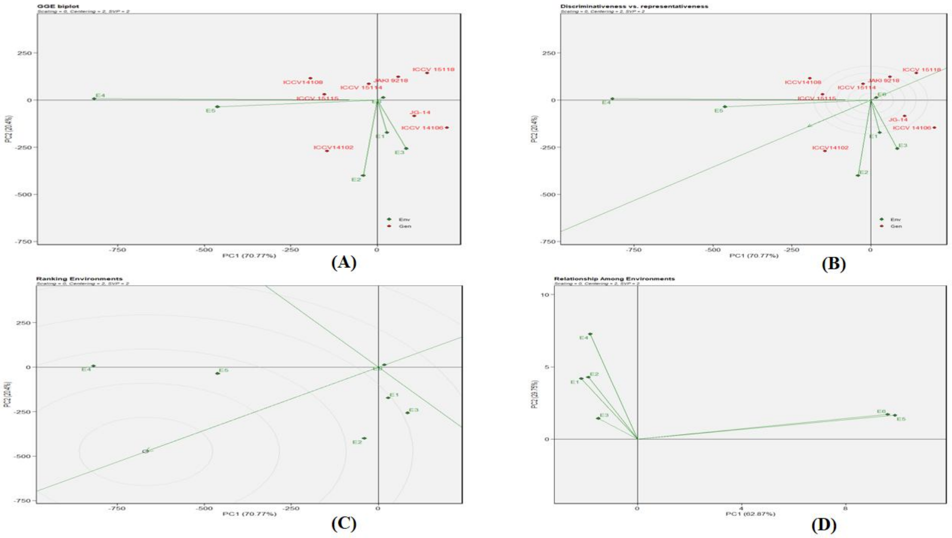

Figure-1: GGE Biplot analysis (A) GGE biplot; (B) Discriminativeness Vs representativeness; (C) Ranking environment; and (D) Relationship among environment

3.3. Mega-environment and winning genotype

The analysis of environmental effects on key yield-contributing traits in desi chickpea revealed significant variations across six environments (E1–E6). ~~Days to 50% flowering ranged from 32.79 days (E6) to 48.58 days (E4), indicating a strong influence of environmental conditions on the phonological development of chickpea genotypes~~Days to 50% flowering varied across environments, from the shortest period of 32.79 days in E6 to the longest period of 48.58 days in E4, suggesting that environmental factors such as temperature and photoperiod influenced flowering time(Table-4). Similar trends have been reported in studies where temperature and photoperiod were identified as critical factors affecting flowering time in chickpea (Varshney et al., 2021). Plant height also varied significantly, with E5 exhibiting the tallest plants (45.63 cm), while E3 had the shortest plants (34.34 cm). The variation in plant height across environments can be attributed to differences in soil fertility, moisture availability, and climatic conditions. Similar findings have been observed in chickpea adaptation studies, where plant height was found to be highly sensitive to environmental variations (Singh et al., 2022). The number of pods per plant, a critical determinant of yield, was highest in E4 (66.28) and lowest in E1 (46.03). The superior pod production in E4 suggests that this environment provided optimal growing conditions for reproductive success. This aligns with previous studies indicating that pod development in chickpea is significantly influenced by environmental factors such as temperature fluctuations and soil moisture levels (Ahmad et al., 2023). Seed weight (100-seed weight) ranged from 22.05 g (E6) to 24.22 g (E1), demonstrating minor but noticeable environmental effects on seed development (Table-4). The highest 100-seed weight observed in E1 indicates favorable conditions for seed filling, possibly linked to adequate soil nutrients and moisture during the seed development phase. Prior studies have highlighted that variations in seed weight across environments result from differences in assimilate partitioning and stress tolerance (Kumar et al., 2023).

Comment [a25]: Try to incorporate more details from the studies being cited.

Comment [a26]: The plant height differences observed, with E5 showing the tallest plants (45.63 cm) and E3 the shortest (34.34 cm), were likely influenced by varying soil fertility, moisture levels, and climatic conditions, as well as genotype × environment interactions.

The seed yield per hectare varied significantly across environments, with the highest yield recorded in E4 (1570.13 kg/ha) and the lowest in E6 (836.23 kg/ha). The substantial yield difference among environments underscores the importance of genotype × environment interactions in chickpea productivity. Similar findings have been reported, emphasizing that yield stability depends on selecting genotypes with consistent performance across varying environmental conditions (Sharma et al., 2022). Table-5 identifies the best-performing genotypes within each environment, highlighting their adaptability to specific conditions. JAKI 9218 was the earliest flowering genotype across multiple

Comment [a27]: including statistical analysis to confirm the significance of the observed yield differences.

environments (E1–E4), reinforcing its potential as an early-maturing variety suitable for short-season environments. ICCV 15118 consistently exhibited high seed weight across all environments, emphasizing its genetic potential for seed size improvement. Furthermore, ICCV 14102 emerged as the highest-yielding genotype in E1 and E2, while ICCV 14108 outperformed others in E4, demonstrating its superior adaptability to high-yielding conditions (Table-5). These results indicate that genotype-by-environment interactions play a crucial role in determining chickpea performance. Breeding programs should focus on identifying genotypes with stable performance across diverse environments to enhance yield resilience. Studies suggest that multi-environment trials are essential for developing climate-resilient chickpea varieties with broad adaptability (Gaur et al., 2023).

Comment [a28]: Discuss how breeding strategies should adapt to climate change challenges.

Table 4: Mean performance of environment for yield contributing traits in desi Chickpea

Environment	Days to 50% Flowering	Plant Height (cm)	No. of Pods/Plant	100 SW (g)	Yield (kg/ha)
E1	45.04	41.90	46.03	24.22	914.78
E2	45.21	42.11	46.75	23.13	912.58
E3	42.63	34.34	47.28	22.14	940.03
E4	48.58	42.94	66.28	24.14	1570.13
E5	41.42	45.63	53.63	23.17	1153.13
E6	32.79	42.71	46.13	22.05	836.23

Table 5: Winners within each environment

Environment	Days to 50% Flowering	Plant Height (cm)	No. of Pods/Plant	100 SW (g)	Yield (kg/ha)
E1	JAKI 9218	ICCV 15118	ICCV 14106	ICCV 15118	ICCV14102
E2	JAKI 9218	ICCV 15114	ICCV14102	ICCV 15118	ICCV14102
E3	JAKI 9218	ICCV 15118	ICCV 14106	ICCV 15118	ICCV 14106
E4	JAKI 9218	ICCV 14106	ICCV14108	ICCV 15118	ICCV14108
E5	ICCV 14106	ICCV14108	ICCV 15115	ICCV 15118	ICCV 15115
E6	ICCV 14106	ICCV14108	JAKI 9218	ICCV 15118	JG-14

This GGE biplot ranks genotypes based on their overall performance across environments. The genotypes ICCV 15118, ICCV 14108, and JAKI 9218 are positioned at a greater distance from the origin, indicating their superior yield potential in specific environments (Figure-2A). Meanwhile, ICCV 14102 is placed in the opposite direction, suggesting lower adaptability across multiple environments. The ranking highlights genotypes with high yield performance, making them potential candidates for selection in breeding programs. This biplot evaluates the stability and mean yield performance of genotypes. Genotypes near the average environment coordinate (AEC) axis exhibit both high mean performance and stability, whereas those further from the axis indicate variability in response (Figure-2B). ICCV 15118 and JAKI 9218 show high yield potential but may lack stability, whereas ICCV 15116 and ICCV 14102 appear to be more stable but with relatively lower yields. This analysis suggests that breeders should consider a balance between high-yielding genotypes and those with stable performance across environments. This polygon view of the GGE biplot identifies the best-performing genotypes in specific environments. The genotypes at the vertices of the polygon (ICCV 15118, JAKI 9218, ICCV 14108, and ICCV 14106) performed best in certain environments, while others fell within the enclosed region, indicating a moderate response (Figure-2C). Environments are grouped based on the genotypic winners, emphasizing the importance of location-specific selection for maximizing chickpea yield.Based on the GGE biplot analysis, breeding programs should focus on selecting genotypes with high yield potential and stability across environments, while also considering location-specific performance for maximizing chickpea yield in diverse regions.

Comment [a29]: Expanding on the Polygon View, **like** This polygon view of the GGE biplot identifies the best-performing genotypes in specific environments. The genotypes at the vertices of the polygon (ICCV 15118, JAKI 9218, ICCV 14108, and ICCV 14106) performed best in certain environments, signifying their ability to adapt to specific conditions. Genotypes placed inside the polygon, such as ICCV 15116, performed moderately across the evaluated environments (Figure-2C). The positioning of genotypes within the polygon emphasizes the importance of location-specific selection for maximizing chickpea yield, as the environments are grouped based on the genotypic winners, highlighting the diverse performance of genotypes across regions.

The bar chart presents genotype yield performance across different environments, highlighting the variability in response. E4 consistently shows the highest yields across genotypes, suggesting favorable environmental conditions. ICCV 15118 and ICCV 15115 show notable yield differences across environments, reinforcing the need for targeted breeding strategies to develop broadly adapted cultivars (Figure-2D). The heatmap visually represents yield variations across genotypes and environments. Higher yields are indicated by lighter colors, while lower yields appear darker. Environments such as E4 show a distinct advantage, with genotypes ICCV 15118 and ICCV 14108 performing exceptionally well ((Figure-2E). Conversely, E1 and E2 show more uniform but lower yield performance, highlighting potential environmental limitations. The combined analyses emphasize the significant role of G×E interactions in chickpea yield performance. E4 emerges as the most favorable environment, while ICCV 15118 and ICCV 14108 show high potential for targeted breeding. Stability assessments suggest that ICCV 15116 and ICCV 14102 exhibit consistent performance, making them valuable for broad adaptation. Future breeding strategies should focus on selecting genotypes that balance both high yield and stability across diverse environments.

Comment [a30]: Focus on Stability and Broader Adaptation: Stability assessments suggest that genotypes like ICCV 15116 and ICCV 14102 exhibit consistent performance across environments, making them valuable candidates for breeding programs aimed at developing cultivars with broad adaptation and stability in varying conditions.

Comment [a31]: Future breeding strategies should focus on selecting genotypes that balance both high yield and stability across diverse environments. By integrating genotypes that perform well in both optimal and less favorable conditions, breeders can develop cultivars that maximize chickpea yield potential while ensuring consistent performance across a range of environments.

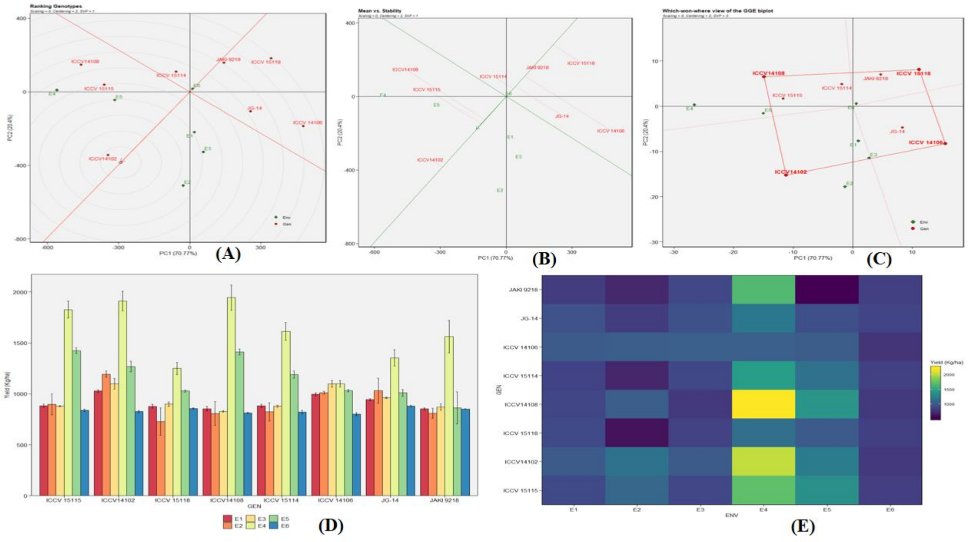

Figure-2: GGE Biplot analysis (A) Ranking genotypes; (B) which won where view of the GGE biplot; (C) Mean vs Stability; and (D) Bar graph view of yield stability of chickpea genotypes under different environment; and (E) Heat map view of yield variations across genotypes and environments

3.4. Ranking genotypes in relation to the ideal genotypes

An ideal genotype is the one which is preferable in all conditions, *i.e*., has high mean yield as well as high stability. Theoretically, an ideal genotype can be defined as the one with the projection to mean environment axis which is equal to the vectors of genotypes longest in nature, having yield of more than average and also by a zero projection onto the perpendicular line (this signifies that the genotype expresses zero variability over varied environments). An ideal genotype may be only for reference rather than have any substantial existence but makes it easier to choose a better genotype based on the proximity of genotypes to it. The units of PC1, PC2, AEC abscissa, ordinate, and distance between genotype and ideal genotype are all the same as the unit of yield in a scaling focused on the genotypes solely. Ranking is also based on mean performance and stability as much as on genotype focused scaling. The experiment gave the results as below pertaining to the ranking of genotypes in the light of above explanation; ICCV 14108 > ICCV 14102 > ICCV 15115 = JAKI 9218 (Table-5).Genotypic differences have also been emphasized in recent research. A study by Joshi and Vandemark(2024) utilized AMMI and GGE biplot analyses to assess chickpea cultivars and breeding lines, providing valuable insights into how seed protein concentration, yield, and hundred-seed weight are influenced by genetic, environmental, and GEI effects. Furthermore, the application of GGE biplot analysis has been instrumental in understanding genotype performance across environments. A study by Srivastava et al. (2024) demonstrated the utility of this method in selecting stable chickpea genotypes under rainfed cultivation, providing a clear visualization of genotype performance and stability.

3.5. Ranking environment in relation to an ideal environment

An ideal genotype can be defined in simple words such as it is an average of all the test environments and is the most efficient in discriminating the experimented genotypes while bearing resemblance to all the test environments. From the experiment, it can thus be concluded that E4 > E5 > E2 > E1=E6=E3. The angles between environment vectors can be utilized to deduce the correlation existing between them such as an acute angle denotes positive correlation while a right angle corresponds to no correlation and obtuse angle means negative correlation.Recent studies have reinforced the significant influence of environmental factors on chickpea yield and its attributing traits. For instance, a study by Khan et al. (2024) highlighted the critical role of genotype × environment interactions in developing chickpea cultivars with improved and stable yield performance. The importance of multi-environment testing has been underscored in studies focusing on genotype stability. For example, a study by Gebeyaw et al. (2024) evaluated the stability and yield performance of desi and kabuli chickpea varieties across different agroecological regions, highlighting the necessity of such testing for identifying stable and high-yielding genotypes. These recent findings align with the current study's results, emphasizing the complex interplay between genetic and environmental factors in chickpea yield and the critical importance of selecting genotypes with high adaptability and stability across diverse environments.

4. CONCLUSION

The yield stability of eight genotypes of chickpea was evaluated across three locations in two seasons to select the suitable high yield stable genotype for Odisha. It can thus be concluded from the obtained results of the above experiment that GGE biplot can be undertaken to analyze stability of yield of chickpea varieties over environments. It lays down a good indication of the adapting ability of chickpea varieties to a varied range of environments in Odisha. From mean vs. stability analysis of the GGE biplot it was concluded that ICCV 14102 had the highest mean grain yield. ICCV 15114 is the most stable genotype. Efficient estimations of interactions of individual genotypes to each environment and the ones suited to an environment has been delineated from the polygon view of GGE biplot showing that the first mega environment contains environment E6 and the genotypes JAKI 9218 and ICCV 15118 with the latter being the winner, the second mega environment contains environments E4 and E5 with the genotype ICCV 14108 being the winner here and that the environments E1, E2 and E3 make up the third and last mega environment where ICCV 14102 is the best performer.The discriminating power of an environment vs representativeness of an environment has also been studied in the experiment along with the stability of genotypes and both have been subjecting to ranking giving the results of E4 > E5 > E2 > E1=E6=E3 and ICCV 14108 > ICCV 14102 > ICCV 15115 = JAKI 9218.The findings underscore the potential of **ICCV 14102** for high yield, **ICCV 15114** for stability, and **ICCV 14108** for adaptability in specific environments.

Comment [a32]: The polygon view of the GGE biplot provided further clarity on genotype-environment interactions, helping to delineate which genotypes are best suited to specific environments. The analysis identified three distinct mega-environments:

1. **Mega-environment 1**: Comprising **E6**, with **JAKI 9218** and **ICCV 15118** as the genotypes, with **ICCV 15118** emerging as the winner in this environment.
2. **Mega-environment 2**: Comprising **E4** and **E5**, with **ICCV 14108** being the best-performing genotype.
3. **Mega-environment 3**: Comprising **E1, E2, and E3**, where **ICCV 14102** was the highest-yielding genotype.

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