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Relative Discriminatory Ability of AMMI and GGE Biplot in Analysis of G×E Interaction for Yield and Seed Index in Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Background: The research focused on investigating the impact of genotype-environment interaction on the yield stability and performance of eight chickpea genotypes across three different locations (Bhatapara, Kawardha and Raipur).

Method: The study employed a randomized block design with two replications in each environment in *Rabi* season during 2021-22. Analysis of variance (ANOVA) revealed significant variations between environments and genotype-environment interaction (G × E) based on AMMI and GGE biplot.

Results: To visualize the genotype-environment relationship, a two-dimensional GGE biplot was created using the first two principal components, which accounted for 87.8% and 11.5% of the interaction's variation. The GGE biplot indicated that genotype g4 (ICCX 161100-B-B-B-B) in environment e2 (Kawardha) and g8 (JG-24) in environment e1 (Bhatapara) exhibited high yield. Genotype g3 (ICCV 201112) in environment e3 (Raipur) also showed high yield, while genotype g5 (JG 2020-10) demonstrated stability across all three environments. Furthermore, the AMMI analysis identified genotype g2 (ICCV 201103) as a superior performer in terms of yield stability across environments. By employing the GGE biplot and AMMI analysis, the study categorized the genotypes into three groups, facilitating simplified visual evaluations. The GGE biplot highlighted that genotype g8 (JG-24) exhibited better seed index in environment e3 (Raipur), while genotype g1 (ICCV 201210) performed well in environment e1 (Bhatapara). Genotype g2 (ICCV 201103) demonstrated a good seed index in all three environments. The AMMI analysis indicated that genotype g3 (ICCV 201112) had a slightly lower seed index but maintained stability across all environments. Overall, the findings of this investigation, as represented by the GGE and AMMI biplots, visually illustrated the relationship between genotypes and environments. The identified genotypes hold potential for improving yield production and further research and breeding efforts can be based on these findings.

Key words: AMMI, Chickpea, GGE, MET.

INTRODUCTION

The adaptability of promising genotypes of main crops to diverse climatic and soil conditions is studied in various agro-ecological locations. Multi-location variety adaptability trials "MVATs" (Abeysiriwardena *et al.*, 1991) or Multi-environment trials "MET" are two terms used to describe these studies (Crossa, 1990). G × E interaction refers to yield fluctuation caused by changes in the environment (Kempton, 1984). The presence of G × E interaction makes selecting a genotype with higher adaptability to various environments more difficult. In comparing genotype performance across contexts, the genotype × environment interaction (GEI) is a crucial issue. In their crop-growing recommendations, researchers frequently overlook GEI. Genotypes are developed in diverse locations and over a period of time to determine the impact of G × E interaction and performance stability. To study genotype adaptability, a variety of statistical approaches have been presented. METs are used to accurately estimate and predict yield based on limited experimental data, establish yield stability and genotype response patterns across environments and provide dependable aid in selecting the best genotypes for planting in future years and at new sites (Crossa, 1990). GGE bi-plot analysis has grown in importance as a statistical method, with recent advances in its application to data from multi-environment studies. Gabriel (1971) used bi-plots for

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the first time in agriculture. Kempton (1984), Gauch and Zobel (1997) and Kroonenberg (1995) were among pioneers to use bi-plot. GGE bi-plot is an advanced version of bi-plots which considers the genotype (G) and genotypes × environment (GE) as two different sources of variations and must be considered simultaneously to evaluate genotypes and environment interaction. GGE bi-plot analysis has been used by researchers for different crops: Yan *et al*., (2000) for winter wheat; Fan *et al*. (2007) for maize; Samonte *et al*., (2005) for rice, Farshadfar *et al*., (2011) for chickpea, Yan and Tinker, 2005 for barley and Rezene *et al*., (2014) for fieldpea. In this study, we will use the AMMI model to assess yield. The Additive Main Impacts and Multiplicative Interaction (AMMI) examination is one of the most generally used variable approaches for the GEI. The AMMI model combines multivariate analysis of genotype and their major effects with chief parts analysis to investigate the leftover growing collaboration across genotypes and environments in order to calculate the sum of squares of GEI with the fewest possible degrees of freedom. This technique captures a large portion of the GEI aggregate of squares; it identifies important and interaction effects and gives a deliberate interpretation of knowledge on a regular basis. Seed yield is a complex character and largely depends upon other independent component characters, with an interaction with the environment resulting into the ultimate product, *i.e*., seed yield. To breed a stable variety, it is necessary to get the information on the extent of genotype × environment interaction for yield and its component characters (Jayalaxmi *et al*., 2023). In this study, AMMI and GGE bi-plot are applied to evaluate the superior high yielding genotype of chickpea along with seed index or hundred seed weight across the locations of Chhattisgarh with the objective, to determine the interaction of different genotype of chickpea with different environment and, to evaluate superior and stable genotype across the environments based on yield and seed index.

MATERIALS AND METHODS

The present investigation was carried out at three different locations of Chhattisgarh in Rabi season during 2021-22 (Table 1). The experimental material was comprised of 8 chickpea genotypes including 2 checks *viz*. Chhattisgarh Chana-2 and JG-24 (Table 2). The trial was conducted in a Randomized block design with three replications in Rabi season 2021-22 over 3 locations. The plot size area of each genotype was 4.8 m^2. For yield, the data was recorded in g/plot which was later converted to Kg/hectare (Kg ha^{-1}), likewise, the weight of 100 seeds (g) were taken to record the seed index or hundred seed weight (Table 3). For successful rising of crop recommended agronomical practices were followed. The mean values of each genotype and replications were used in the statistical analysis. The replication wise mean values of five randomly selected plants were used for the statistical analysis PB Tools.

Bi-plot interpretation for multivariate analysis

The prefix ‘Bi’ in the term bi-plot indicates dual (genotype and environment) factors on the same graph. A bi-plot is made up of an asymmetrical polygon with stripes or lines running vertically at a right angle from the bi-plot’s centre to the polygon. All genotypes that are not adjacent to the bi-plot centre are linked to the polygon, which covers all genotypes in the polygon marker. The environment marker (vertical stripe) running perpendicular to the polygon from the bi-plot’s centre represents an expected environment in which the two genotypes on opposite sides of the polygon should behave similarly. It also divides the bi-plot into distinct sections, each with its own enticing or winning genotypes.

Additive main effects and multiplicative interaction (AMMI)

The additive main effect and multiplicative interaction (AMMI) method combines variance analysis and principal component analysis into a single methodology. It may be used to analyze multi-site trials, according to Zobel *et al*. (1988) and Crossa *et al*. (1990). Analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and environment main effects and linear regression models account for only a small portion of the interaction sum of squares. The AMMI technique serves three primary functions. The first is model diagnostics; AMMI is better suited in the initial statistical analysis of yield trials because it gives an analytical tool for diagnosing alternative models as sub cases when these are better for certain data sets. Second, AMMI defines the GEI. AMMI describes genotype and environment patterns and connections. The third application is to increase the precision of yield estimations. Gains in yield estimate accuracy have been obtained that are comparable to

Table 1: Weather and meteorological data during Rabi cropping season in year 2021-22.

Parameter/location	Bhatapara (e1)	Kawardha (e2)	Raipur (e3)
Altitude (m)	261 m	353 m	298m
Latitude	21.73°N	22.01°N	21.25°N
Longitude	81.94°E	81.23°E	81.62°E
Avg. Rainfall (mm)	178.4 mm	175.2 mm	184.3 mm
Avg. Temp °C	21° - 33°	23° - 35°	22° - 33°
Relative humidity	75%	78%	76%
Wind velocity	1.8 kmph	1.5 kmph	1.6 kmph

increasing the number of replicates by a factor of two to five. Such advantages might be utilized to lower testing costs by lowering the number of replications, include additional treatments in studies, or enhance efficiency in picking the best genotypes. The AMMI model combines analysis of variance for the main effects of genotype and environment with principal component analysis for the genotype-environment interaction. It has shown to be effective in comprehending sophisticated GEI. The data may be graphed in an informative bi-plot that displays both main and interaction effects for both genotypes and environments. AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters. The AMMI model is a combination of analysis of variance and principal components analysis, as well as prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates. The interaction is depicted in the form of a bi-plot display, in which PCA scores are plotted against each other and visual inspection and interpretation of the GEI components is provided. By combining bi-plot display and genotypic stability statistics, genotypes can be grouped based on performance similarity across diverse environments.

GGE bi-plot analysis (Genotype + Genotype by environment)

Yan *et al*. (2000) used the ”GGE bi-plot” in for the first time. It’s a bi-plot that shows the G and GE of genotype-by-environment data. The main feature of a GGE bi-plot is that it is based on Tester centered data, which means that the environment main effects (E) are removed while the genotype main effect (G) and interaction (GE) are retained and combined. As a result, a bi-plot based on tester-centered data contains only G+GE, abbreviated GGE. The test location is evaluated graphically in GGE Bi-plot analysis (Yan, 2001). The ability to discriminate between genotypes (discrimination ability), the ability to represent the target region (representativeness) and the bi-plot distance from an ideal location are used to evaluate test locations (desirability index). The ability to discriminate is affected by a variety of factors that are either static or dynamic. A representative location implies that varieties chosen in that location are likely to perform well in other locations of the same region. Finally, test locations are evaluated based on their “distance” from an ideal location, which is designed to be on the average test-location axis and with the longest vector of all test-locations on the GGE bi-plot. As a result, a test location’s discrimination ability is measured by the length of its vector on the bi-plot; representativeness is measured by the cosine of the angle between the test location and the “average” location; and “distance” from an ideal location is the product of discrimination ability and representativeness (Yan and Holland, 2010). Gabriel (1971) invented the bi-plot method, which was later popularized by Kempton (1984) and Zobel *et al.* (1988). The GGE bi-plot, where G = Genotype + G × E = Genotype by environment effect, was described by (Yan, 2001). GGE bi-plot analysis is also used to generate graphs that show the following: comparison of environments to ideal environments (Yan and Kang, 2003); “which-won-where” pattern; and environment vectors. Correlations (similarities/dissimilarities) between pairs of environments were judged using the angles between environment vectors. These features combine to make the GGE bi-plot the most comprehensive tool for quantitative genetics and varietal stability.

RESULTS AND DISCUSSION

Combined analysis of variance

A combined analysis of variance was performed to describe the main effect and quantify the interactions among and within the sources of variation (Table 4). The mean square of environment (location) and genotype by environment

Table 2: Genotype name and their code.

Genotype code	Genotype name
g1	ICCV 201210
g2	ICCV 201103
g3	ICCV 201112
g4	ICCX 161100-B-B-B-B
g5	JG 2020-10
g6	JG 2020-01
g7	Chhattisgarh chana-2 (C)
g8	JG - 24 (C)

Table 3: Mean data over the locations for yield (Kg/ha) and seed index (g).

Genotypes	Bhatapara		Kawardha		Raipur	
	Yield	Seed index	Yield	Seed index	Yield	Seed index
ICCV 201210	1947.61	36.15	3456.00	25.63	656.00	20.05
ICCV 201103	2197.57	20.45	2241.00	20.43	1114.00	26.85
ICCV 201112	1895.53	26.32	2063.00	25.02	1625.00	27.75
ICCX 161100-B-B-B-B	1801.80	25.12	3267.00	27.25	1057.00	28.00
JG 2020-10	2332.96	15.38	1721.00	21.23	698.00	22.15
JG 2020-01	2374.62	26.00	1673.00	19.35	1187.00	28.40
Chhattisgarh Chana-2	2228.81	21.17	2606.00	25.53	833.00	25.60
JG - 24	2447.53	25.03	996.00	24.81	1323.00	30.30
Mean	1914.04	21.73	2002.55	21.02	943.66	23.23

showed a significant difference ($p \leq 0.01$) for yield. Environment and genotype by environment have highly significant differences that may be attributed to changes in environment and genetic makeup which differ from one environment to next. The partitioning of the G × E interaction percentage computed from total sum of the square which describes the percentage of variation for all factors. The environment (46.97%) contributed highest followed by genotype by environment (36.94%) whereas replication within environment (1.34%) and genotype (4.26%) attributed least contribution towards total sum of square. Likewise for seed index, genotype by environment (57.74%) contributed highest followed by genotype (34.29%) for total sum of squares. The analysis of various components does not provide a true overview of genotype by environment interaction. As a matter of fact, other statistical techniques, such as multivariate analysis, are required for a clearer appreciation of the GEI. Based on these findings, we predict that environment has a significant impact on yield as compared to seed index and the G × E also reported greater influence on both yield and seed index.

GGE bi-plot (What-won-where pattern)

The eight genotype tested in three locations generates a bi-plot which is divided into 5 clockwise fan-shaped sections (Fig 1) for yield. The genotype g4 showed the high yield in environment (e2), followed by genotype g5 in environment (e1). Genotype g1, g3 performed well in environment e2 and e3, respectively. The results were visualized using a bi-plot divided into 3 clockwise fan-shaped sections (Fig 1) for seed index. The genotype, g8 displayed higher seed index in e3, followed by g1 in e1. Genotype g2 showed better performance in e3. If all the environment markers (vertical stripes) are positioned in one section of the biplot, then this indicates that there is a unique genotype which performs best under all tested environments. And different genotypes are gained if the environment marker got paced in different sections of the biplot. If a genotype is placed in a sector where no environment marker falls then this genotype is considered as poorly performing in all the environments. The genotype which falls on the vertex of the polygon where an environment marker drops such genotype is suggested to provide better yield and perform better in that particular environment. On the other hand, the genotype linked to the polygon vertex where no environment marker drops in the sector indicates that such genotype performs poorly across the environments. The genotypes falling within the polygon are less stable in the environment then the corner genotypes.

Relationship among environments

Based on the bi-plot graph (Fig 2) for yield, the three environments were divided into two groups the environments having shorter vector length (e1, e3) and environments having longer vector length (e2). The vector view of the GGE bi-plot summarized the inter-relationships between the locations. Environment vectors are the lines that connect the test environments to the bi-plot origin. The correlation between two environments is approximated by the cosine

Table 4: Pooled ANOVA for yield and sees index over the three locations.

Source	DF	SS		MS		F value		Pr (>F)		TSS %	
		Yield	Seed index	Yield	Seed index	Yield	Seed index	Yield	Seed index	Yield	Seed index
Env	2	13977325.44	51.39	6988662.74	25.69	52.00	13.11	0.0047	0.03	46.97	6.01
Rep within Env	3	401368.75	5.88	133789.58	1.96	0.83	3.83	0.4915	0.02	1.34	0.68
Gen	7	1269265.36	293.17	181323.62	41.88	1.13	81.80	0.3838	0.00	4.26	34.29
Env × Gen	14	10725540.79	493.54	10725540.79	35.25	4.76	68.86	0.0007	0.00	36.04	57.74
Pooled Error	21	3378949.92	10.75	160902.37	0.51						
Total	47	29752450.33	854.74								

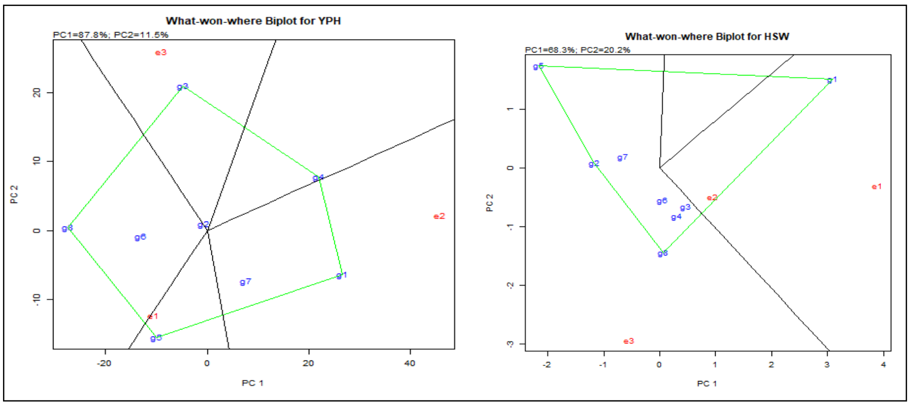

Fig 1: What-Won-Where view of GGE bi-plot for yield and seed index.

of the angle between their vectors (Kroonenberg, 1995; Yan, 2002). The environment having shorter vector length provides very less or little information on genotype on the other hand environment having longer vector length are appropriate for selection of promising genotype. The e1 and e3 sharing acute angle between environment vectors, it represents the weak crossover GE, whereas e2 had obtuse angle with both e1 and e3 environment, implying that GE is moderately large. The presence of close association among environment suggested the same information about genotypes could be obtained from any of environment which will potentially reduce the testing cost. If two environments consistently correlated across year then one environment may drop down. The three environments were classified into two categories based on the bi-plot graph (Fig 2) for seed index. The environment having shorter vector length (e2) and environments having longer vector length (e1, e3). The GGE bi-plot's vector view described the relationship between the locations. The environment vectors with an acute angle between them are more associated with each other than the environment vectors with an obtuse angle. As a result of the shorter angle between them, environments e1 and e2 have some similarities.

Mean performance and stability of genotype

The mean performance and stability of the genotype should be evaluated across environments. Ideal genotypes should have the highest mean performance and be absolutely stable across environments (Yan and Kang 2003). For this purpose, Average environmental co-ordinate (AEC) view (Fig 3) for yield of the GGE bi-plot is used. The double-arrowed line is the Average Environment Co-ordinate (ACE) and shows grater variability (less stability) moving in both the directions. An ideal genotype is a genotype which lies on the AEA line, genotype located closer to the ideal genotype are more stable than others. Thus, genotype g2 is highly stable performing across all environments consistently followed by genotype g5 for yield. Genotype g3 consistently performed well in all the environments, followed by genotype g4 for seed index. This meant that "stable" genotypes were only desirable if they had high mean performance. The relative contributions of stability and high seed yield and seed index to the identification of desirable genotypes in this study were similar to those found in other crop stability studies using the ideal genotypes procedure of the GGE biplot (Samonte *et al.,* 2005).

Discriminative and representative environments

The environment e1 and e3 had the shortest vector which showed that environment e1 and e3 have least discriminating for genotypes while, environment e2 have a longer vector showing that e2 has the ability to discriminate between the genotypes on the basis of yield (Fig 4) for yield. An ideal environment is one which is both discriminative and

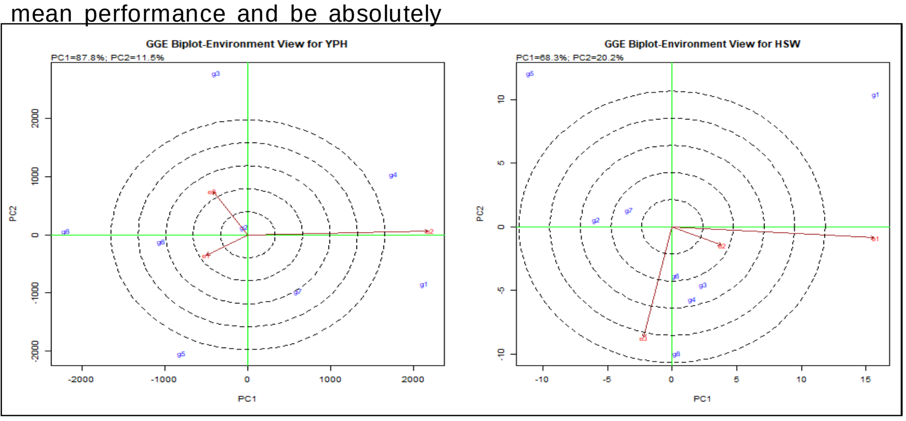

Fig 2: Relationship among environments for yield and seed index.

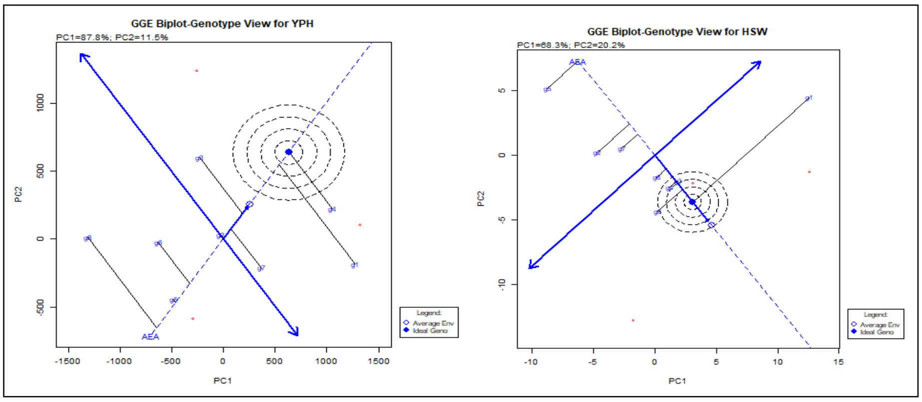

Fig 3: Mean performance and stability of genotype for yield and seed index.

representative and we may conclude that environment e2 has the longest vector and had smallest acute angle with the AEA line making it the best representative environment for discriminating the genotypes. On the other hand the environment e1 and e3 have a short vector length and a greater angle with the AEA line and thus, are not suitable for discriminating the genotypes but can be used for calling the unstable genotypes. The bi-plot analysis reveals important characteristics of the three environments (e1, e2 and e3) based on their vector lengths and angles with the AEA line (Fig 4) for seed index. The e2 has shortest vector length, indicating its limited ability to discriminate among genotypes based on seed index. On the other hand, environments e1 and e3 have longer vectors, suggesting a higher discriminatory capacity. Based on the analysis, environment e1 exhibits the longest vector length and the smallest angle with the AEA line, making it the best representative environment for genotype discrimination. In contrast, environment e2, with its small vector length and environment e3, with its larger angle with the AEA line, are less suitable for genotype discrimination but can still be used to identify unstable genotypes. The cosine of the angle between the average environment coordinate (AEC), also known as the average environment axis (AEA) and the environment vector is approximately equal to the correlation coefficient between the genotype mean value over the environment and the genotype values in that environment. Smaller the angle between AEC abscissa and the vector of the test environment, better the environment in comparison to those that generate larger angles. The direction of the AEC abscissa line is indicated by an arrow, while the average value of the environment is indicated by a small concentric circle and the length of the test environment vector denotes the discriminating ability. The length of each environment vector indicates how good it is at distinguishing genotypes in the environment (discriminating ability).

Additive main and multiplicative interaction (AMMI) model

The additive main and multiplicative interaction model is a principal component (PC1 and PC2) based graphical presentation of information put in a nutshell. Fig 5 illustrated that the first principal component interaction PC1 accounts for 88.5% of the G + G × E interaction variation and the principal component PC2 accounts for 11.5% of the G + G × E interaction variation for yield. In this study, genotype g3 is found stable in environment e3, genotype g1 is stable in environment e2 and genotype g5 is stable in environment e1, whereas genotype g2 is less yielding but stable across environments. For seed index (Fig 5), the interaction of the first principal component PC1 accounts for 79.4 percent of the variation in the G + G × E interaction, while PC2 accounts

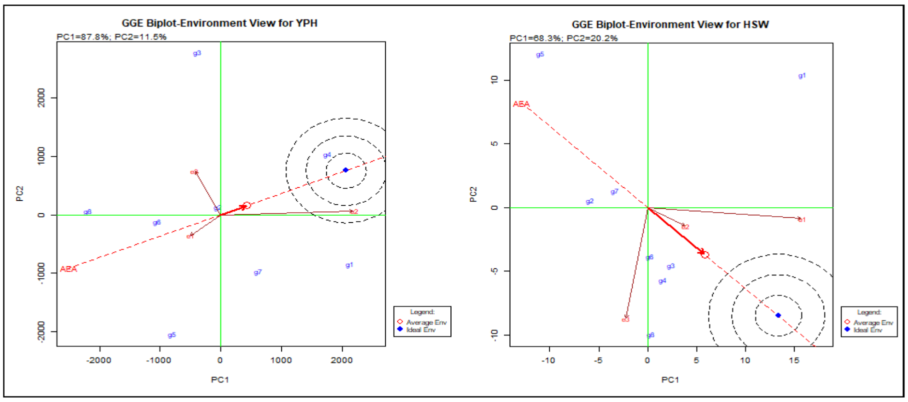

Fig 4: Discriminativeness and representativeness environments for yield and seed index.

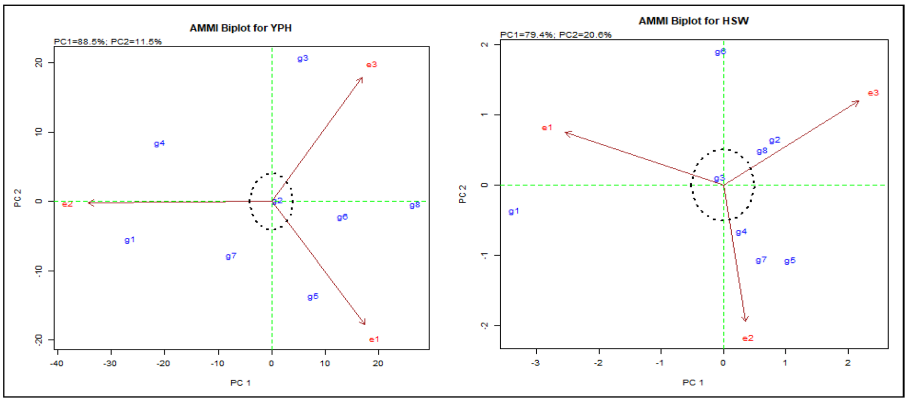

Fig 5: AMMI bi-plot for PC1 and PC2 for yield and seed index.

for 20.6 percent of the variation in the G + G × E interaction. In this study, genotype g3 is found to have less seed index but stable across environments, whereas, genotype g1 is stable in environment e1, genotype g7 is stable in environment e2 and genotype g2 is stable in environment e3. According to Gauch and Zobel, (1993) found that the first two PC's are sufficient for precisely projecting the AMMI model. The centre of the bi- plot is divided into four equal parts by the lines of PC1 and PC2 vertically and horizontally, respectively. The genotypes that are placed away from the bi-plot centre are treated as the winning genotype in that environment which falls in that sector. The genotype clustering together in the bi-plot origin tends to behave similarly or identical to all the environments, where as genotype far away from each other does not shows similarity. This statement is supported by report of Jayalaxmi *et al.* (2023) and Akter *et al.* (2014).

CONCLUSION

Based on the results of the multivariate AMMI and GGE bi-plot analysis, the genotypes can be classified into three distinct groups. The first group consists of genotypes that exhibit both high stability and high yield potential. Among these genotypes, g2 (ICCV 201103) stands out as a perfect fit, performing well across a wide range of environments. The second group comprises genotypes with lower stability but higher yielding capacity within specific environments. Genotype g4 (ICCX 161100-B-B-B-B) in environment e2 (Kawardha) and g8 (JG-24) in environment e1 (Bhatapara), along with genotype g3 (ICCV 201112) in environment e3 (Raipur), fall into this group. The third group consists of genotypes with lower overall yield but greater stability. Genotype g5 (JG 2020-10) is classified in this group. By categorizing the genotypes into these three groups based on their performance and stability, it provides valuable information for selecting suitable genotypes for specific environments and breeding purposes.

Conflict of interest

All authors declare that they have no conflict of interest.

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