



Identifying Mega-environments and Evaluating Grain Yield Stability in Bio-fortified Rice Using AMMI and GGE Approaches

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ABSTRACT

The experiment was conducted during July–November, 2022 in Raipur, Bilaspur, Kawardha, Mahasamund, and Jagdalpur districts of Chhattisgarh, India to identify promising rice genotypes under diverse environmental conditions. Thirty micronutrient-rich rice varieties, along with yield and micronutrient checks, were evaluated using RCBD with two replications per location. None of the candidate genotypes outperformed the standard check, Swarna, in combined mean yield performance. AMMI analysis revealed significant genotype, environment, and genotype-by-environment interactions ($p < 0.05$). Environment 5 recorded the highest mean grain yield ($6560.75 \text{ kg ha}^{-1}$), followed by E_4 ($5783.33 \text{ kg ha}^{-1}$) and E_2 ($5123.67 \text{ kg ha}^{-1}$). PCA1 and PCA2 captured 57.49% and 18.61% of genotype-environment interaction, respectively, explaining 76.10% cumulatively. Genotypes G_{28} and G_{29} demonstrated high mean yields and stability, suitable for commercial cultivation, while G_{19} showed high yield but lower stability, indicating potential for specific environments. Genotypes G_2 , G_4 , and G_{18} , though low-yielding, exhibited greater stability, making them valuable for stability-focused breeding. “Which-won-where” analysis revealed G_{19} excelling in E_5 , G_{11} performing well in E_1 , E_2 , and E_3 and G_{28} succeeding in E_4 . AMMI bi-plot showed E_1 as the most informative environment for selecting widely adapted genotypes, while E_3 was highly representative but less discriminative. E_4 and E_5 were discriminative but less representative. These findings highlight promising genotypes for the release of nutrient-rich rice varieties well-adapted to Chhattisgarh’s growing areas.

KEYWORDS: AMMI analysis, GGE biplot, stability, discriminative and representative

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Rice serves as a staple food for 4 billion people globally, contributing 27% of daily calorie intake in low- and middle-income regions. Asia produces over 90% of the world's rice and is home to 60% of the global population (Peng et al., 2005). India, the second-largest rice producer, cultivates 45.07 mha, yielding 122.27 mt with a productivity of 2713 kg ha⁻¹ (Anonymous, 2021). Despite its self-sufficiency, challenges such as population growth and climate change demand improvements in productivity.

India has released over 900 rice varieties, yet many are discontinued due to inconsistent performance across environments, leaving only a few stable varieties widely cultivated after 15–20 years (Nitiprasad et al., 2015). Yield is a complex trait influenced by genetic and environmental factors, complicating the identification of superior genotypes through genotype-environment interactions (GEI) (Mohan et al., 2021). Genetic improvement in yield potential is vital to meet growing demands and mitigate climate change impacts on rice production (Saito et al., 2021). Rice breeders must accelerate yield enhancements (Cobb et al., 2019) by understanding GEI to ensure adaptability and stability (Dewi et al., 2014).

Rice breeding aims to develop high-yielding, nutritionally rich, pest-resistant, and climate-smart cultivars (Hickey et al., 2019). Addressing GEI is critical for identifying stable, adaptable genotypes (Bocianowski et al., 2020; Annicchiarico, 2002; Karimizadeh et al., 2013; Yan et al., 2007). Multi-environment trials (MET) evaluate genotype performance and stability across diverse conditions. However, the complexity of GEI poses challenges, as genotype performance often varies significantly across locations and seasons. METs simulate future growing environments (Crespo-Herrera et al., 2021; Cooper et al., 2023). To minimize yield gaps between potential and on-farm yields, selecting testing locations and understanding their relationship to target production environments (TPE) are essential. Enviromics or envirotyping leverages environmental covariates to analyze MET groupings, aligning with TPE to model genotype reaction norms (Cooper and Messina, 2021; Costa-Neto et al., 2023; Callister et al., 2024).

To address these complexities, statistical methods such as AMMI (Additive main effects and multiplicative interaction) and GGE (Genotype and genotype×environment interaction) biplot analyses are employed. AMMI combines ANOVA for main effects with principal component analysis to capture interaction effects, aiding in the identification of stable genotypes across environments (Yan et al., 2022). Studies confirm its effectiveness using multi-location data (Yan and Hunt, 2001; Mohan et al., 2021).

The GGE biplot method, developed to analyze GEI data, builds on the AMMI approach by focusing on G+GE components, which account for most MET data variability (Kaplan et al., 2017). It visualizes patterns like “which-won-where,” identifies mega-environments, and selects genotypes for specific or broad adaptability (Maksimovic et al., 2021; Behera et al., 2022). Applications of GGE biplots have been validated in various crops, including durum wheat (Kendal and Sener, 2015), maize (Oyekunle et al., 2017), barley (Solonechnyi et al., 2018), sorghum (Gasura et al., 2016), lentils (Karimizadeh et al., 2013), sweet potato (Mustamu et al., 2018), and Bambara groundnut (Tena et al., 2019; Olanrewaju et al., 2021).

Combined AMMI and GGE analyses provide comprehensive insights into GEI (Rad et al. (2013), Haider et al. (2017), Kesh et al. (2021). AMMI identifies stable genotypes, while GGE biplots visually depict genotype-environment relationships, aiding selection of promising breeding materials (Kilic et al., 2020). These methods deliver comparable results and help identify locations with minimal crossover interactions relative to top-performing genotypes (Rubio et al., 2004; Chandrashekhara et al., 2020). Recent studies highlight their effectiveness in evaluating rice yield stability and adaptability across multiple environments (Singh et al., 2023).

This research was aimed to assess rice genotype performance in Multi-environment trials (METs), offering critical insights for developing high-yielding, stable, and adaptable rice varieties. We write about the methods as AMMI and GGE biplot analyses.

2. MATERIALS AND METHODS

2.1. Description of experimental area

The experiment was carried out under five locations (Table 1) i.e. Raipur (E₁), Bilaspur (E₂), Kawardha (E₃), Mahasamund (E₄) and Jagdalpur (E₅) of Chhattisgarh, India with 30 micronutrient rich rice varieties (Table 2) along with yield and micronutrient check (Swarna, Zinco Rice MS, MTU-1172 and MTU-1140) during *kharif* (July–November, 2022) (under Multi location trial conducted by department of PMBB, IGKV Raipur, Chhattisgarh).

Table 1: List of environment and their respective location

Sl. No.	Environment	Location
1.	E ₁	Raipur
2.	E ₂	Bilaspur
3.	E ₃	Kawardha
4.	E ₄	Mahasamund
5.	E ₅	Jagdalpur

Table 2: Mean performances of 30 nutri rich rice genotypes evaluated across five testing environments

Sl. No.	Genotype no.	Genotype name	E ₁	E ₂	E ₃	E ₄	E ₅	Mean
1.	G ₁	R-RHZ-MI-95	3826.30	3900.00	4106.00	4625.00	5227.27	4336.91
2.	G ₂	R-RHZ-CC-162	2100.80	3300.00	4144.00	3958.30	5227.27	3746.07
3.	G ₃	R-RHZ-CC-164	3988.80	3950.00	5232.00	6250.00	6044.03	5092.97
4.	G ₄	R-RHZ-CB-184	2053.20	3330.00	4670.00	3916.70	6676.14	4129.21
5.	G ₅	R-RGY-SM-128	3221.30	3900.00	5754.00	6750.00	7279.83	5381.03
6.	G ₆	R-RGM-AS-45	5042.00	6100.00	4942.00	6583.30	7698.86	6073.23
7.	G ₇	R-RHZ-RH-126	3781.50	4950.00	4164.00	5583.30	6775.57	5050.87
8.	G ₈	R-RHZ-SH-187	5462.20	5500.00	4254.00	5291.70	5901.99	5281.98
9.	G ₉	R-RHP-IC-151	4902.00	6600.00	5432.00	6875.00	7265.63	6214.93
10.	G ₁₀	R-RGY-SA-189	6582.60	5300.00	4722.00	6250.00	7805.40	6132.00
11.	G ₁₁	R-RGY-SI-190	6162.50	6570.00	5268.00	6916.70	8948.86	6773.21
12.	G ₁₂	R-RGY-SM-112	5602.20	5100.00	5070.00	6500.00	6974.43	5849.33
13.	G ₁₃	RK-211-X Chandrahasni-4	2661.00	5750.00	4696.00	6791.70	7694.60	5518.66
14.	G ₁₄	RK-211-X Chandrahasini-155	3803.90	4150.00	5442.00	5166.70	7826.70	5277.86
15.	G ₁₅	RK-211 X Chandrahasini 208	2381.00	3700.00	4752.00	6333.30	5696.02	4572.46
16.	G ₁₆	RK-211 X Chandrahasini-210	4271.70	4950.00	4590.00	4666.70	7990.06	5293.69
17.	G ₁₇	R-RHZ-IR-201	5367.00	5300.00	4942.00	5125.00	7393.47	5625.49
18.	G ₁₈	R-RHZ-SK-129	2501.40	3700.00	3930.00	4250.00	5447.44	3965.77
19.	G ₁₉	R-RKY-IS-191	6677.90	6370.00	5234.00	4000.00	7720.17	6000.41
20.	G ₂₀	R-RHZ-KH-127	4481.80	6230.00	4956.00	4541.70	3645.00	4770.90
21.	G ₂₁	R-RHZ-SH-195	4131.70	5670.00	5038.00	4666.70	7393.47	5379.97
22.	G ₂₂	R-RHZ-AS-40	4972.00	5700.00	5094.00	6083.30	7578.13	5885.49
23.	G ₂₃	R-RGY-SD-194	4902.00	6430.00	4845.00	6458.30	6264.20	5779.90
24.	G ₂₄	R-RHY-SH-193	4201.70	5780.00	4616.00	6416.70	5234.38	5249.76
25.	G ₂₅	R-RHZ-SD-94	3781.50	6060.00	4284.00	7333.30	7017.05	5695.17
26.	G ₂₆	R-RHP-IR-142	2100.80	4900.00	4386.00	5750.00	3416.19	4110.60
27.	G ₂₇	ZINCO RICE -MS	4481.80	4500.00	4092.00	5250.00	5994.32	4863.62
28.	G ₂₈	SWARNA	6162.50	6100.00	5888.00	7250.00	6761.36	6432.37
29.	G ₂₉	MTU-1172	6911.80	5200.00	5376.00	7083.30	7137.78	6341.78
30.	G ₃₀	MTU -1140	3910.40	4720.00	4432.00	6833.30	4786.93	4936.53
Mean			4347.58	5123.67	4811.70	5783.33	6560.75	5325.41

The experiment was conducted in Randomized Block Design (RBD) with Two replications having a plot size of 5 m² in each replication each environment. All the experiments of five different locations were carried out at irrigated ecosystem with transplanted nursery establishment. Standard agronomic practices and appropriate control measures for weeds, insect pests and diseases were followed. Fertilizer was applied at the recommended dose of 100:60:40 (N: P: K) at each experimental location. Yield data was

recorded at physiological maturity and plot data harvested was converted to kg ha⁻¹ using the plot size as factor.

2.1. Statistical analysis

Multivariate analysis was carried out in using R (4.0.5) software packages and R studio (R Core Team 2019) . Multi-trait multi-environment analysis including GGE bi-plot analysis for grain yield plant⁻¹ (GYP) was analyzed using METAN packages (Olivoto and Lúcio, 2020). The

ggplot 2 packages were used to create the GGE bi-plot display (Wickham et al., 2016).

We used statistical analysis (ANOVA) to study differences in yield among genotypes and locations. We also examined combinations like genotype by location, genotype by season (genotype by environment). This analysis was performed using the R-package for multivariate analysis. To understand the interaction between genotype and environment (G×E), we conducted a visual multivariate stability analysis using GGE biplot and AMMI in R studio, which is a simplified version of R statistical software developed by the R Core Team. For GGE biplots, we utilized the GUI package in R studio, and for AMMI, we employed the Agricolae package, which incorporates two important concepts the biplot concepts (Gabriel et al. (1971), (Yan et al. (2007) as well as the GGE concept (Yan et al. (2000).

2.2. AMMI model

AMMI model analyzes how genotypes and environments interact in agriculture. It has additive parts for direct effects and a multiplicative component showing how genotypes behave in different environments. AMMI model, an advanced form of mean regression, effectively understands how genotypes and environments interact. Developed by (Gollob (1968) (Mandel (1971) and (Gabriel (1978). It includes ANOVA, PCA, and regression. This equation evaluates crop impacts, aiming for a simple grasp of combined effects on yield and productivity in different situations.

2.3. Model's equation

$$Y_{ij} = \mu + g_i + e_j + n\sum k = n\lambda k a_i k_j y_{jk} + \epsilon_{ij}$$

Where

Y_{ij} : Represents the mean yield of genotype (i) in Environment (j)

μ : Signifies the overall mean yield across all genotypes and environments

g_i : Denotes the effect of the (i) genotype

e_j : Represents the effect of the j environment

$n\sum k = n\lambda k a_i k_j y_{jk} + \epsilon_{ij}$: Capture the multiplicative interaction effect

λk : is a singular value αk is a singular value of the (i) genotype and y_{jk} is the singular value of the (j) environment and ϵ_{ij} Represents the experimental error

3. RESULTS AND DISCUSSION

Combined analysis of variance was performed to describe the main effect and quantify the interactions among and within the sources of variation (Table 3). The mean square of environment (location) and genotype by environment showed a significant difference ($p \geq 0.01$) for

Table 3: Additive main effect and multiplicative interaction (AMMI) analysis of variance for grain yield

Source	Df	Sum Sq	Mean Sq	p value
ENV	4	193044249	48261062.2**	0.0000311
REP(ENV)	5	1864662	372932.4**	0.7612785
GEN	29	167428763	5773405.6**	0.0000000
GEN:ENV	116	163627528	1410582.1**	0.0000605
PC1	32	69470306	2170947.1**	0.0000000
PC2	30	53106108	1770203.6**	0.0002000
Residuals	145	104108017	717986.3	-
Total	415	793700746	1912531.9	-

yield. Environment and genotype by environment had highly significant differences that might be attributed to changes in the environment and genetic makeup which differed from one environment to next. The partitioning of the GXE interaction percentage computed from total sum of the square which described the percentage of variation for all factors. ANOVA table presented an analysis of various sources contributing to the variation observed in the dataset. All factors including Environmental (E), Genotype (G) and Genotype: Environment (GXE) were statistically significant.

The presence of GXE Interaction (GEI) was clearly demonstrated by AMMI model and the interaction was portioned among the first two interaction principal component axis (IPCA), while the cumulative variance was 100% for PCA-I and PCA-V thereby, demonstrating that genotypes might be selected for adaptation to specific environments. These results were in harmony with the findings of Aina et al. (2009) and Xu Fei-fei et al. (2014) in G×E interactions effects. The environmental variance was also found to be significant which indicated that the environments under study were different from each other. The model was additive and the results of AMMI analysis were represented in the form of graphs called bi-plots (Gauch and Zobel (1996). Further Gauch (1988) recommended that the most accurate model for AMMI could be predicted by using first two principal component analysis. Admassu et al. (2008), in accordance with Zobel et al. (1988), proposed that two interaction principal component axes for the AMMI model were sufficient for a predictive model. Thus, the interaction of 30 Nutri rich rice lines with five environments was predicted by the first two components.

The cumulative variance explained by first two principal components was 76.1%, supporting the selection of genotypes for specific environments, consistent with the studies by Aina et al. (2009) and Xu Fei-fei et al. (2014). The significant environmental variance confirmed that the

environments under study were distinct. The AMMI model results were additive and visually represented through bi-plots (Gauch and Zobel, 1996). Gauch (1988) suggested that the most accurate AMMI model predictions could be achieved using the first two principal components. Admassu et al. (2008) and Zobel et al. (1988) concurred that two interaction principal component axes were sufficient for predictive modeling. Accordingly, the interaction of 30 rice genotypes across five environments was modeled using these first two components (Sivapalan et al. (2000).

Stable genotypes were identified using graphical representations (GGE bi-plots), which combined genotype and $G \times E$ components to show interaction patterns across environments, highlighting which variety performed best in which environment. Vijay Kumar et al. (2001) explained that these bi-plots aided in visualizing GE interaction patterns and helped to identify genotypes or environments with low, medium, or high interaction effects. By analyzing $G \times E$ interaction, breeders could identify stable genotypes across environments and develop more adaptable and high-yielding varieties.

3.1. Combined GGE biplot analysis: discriminativeness vs. Representativeness of test environments

The GGE biplot is a crucial tool for identifying ideal test environments, assessing their discriminativeness and representativeness, and selecting superior genotypes (Oladosu et al. (2017). In this analysis, the biplot explained 76% of the total variation in the environment-centered $G \times E$ interaction (Figure 1). The Average Environment Axis (AEA), a line that passed through the average environment and the biplot origin, represented the coordination of all test environments. The ideal test environment should be both highly informative and closely representative of the target environment. As shown in Figure 2, the “ideal test environment” was positioned at the center of the concentric circles. It represented the peak of the AEA in the positive direction, indicating the most representative point. Its distance from the biplot origin equaled the length of the longest vector among all environments, symbolizing the maximum level of informativeness. Environment E_3 formed the smallest angle with the AEA, followed by E_1 and E_2 , making E_3 the most representative environment, while E_4 and E_5 were the least representative.

The concentric circles in the biplot, proportional to the representativeness of the environments, indicated the discriminating ability of each environment. E_1 was both a representative and discriminative environment, making it ideal for selecting broadly adapted genotypes. On the other hand, E_4 and E_5 were discriminative but not representative, making them useful for selecting genotypes specifically adapted to certain conditions or for eliminating unstable

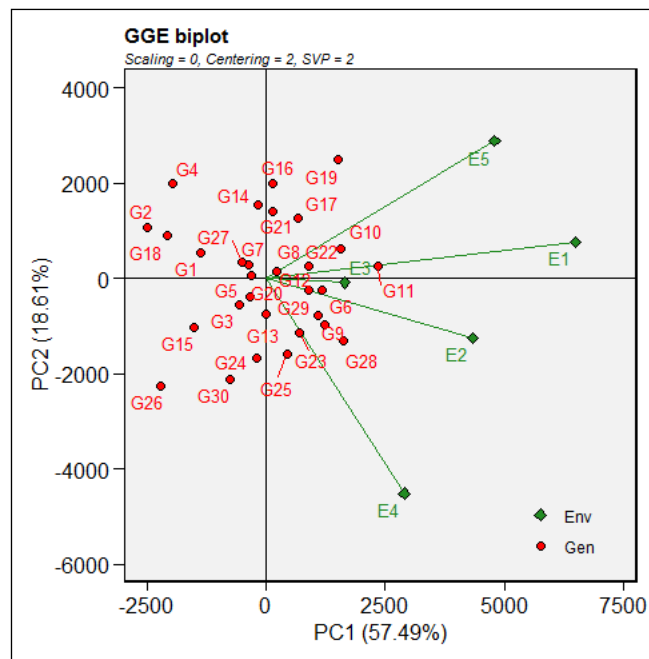


Figure 1: The GGE biplot ‘Discriminativiveness vs. representativeness’ for genotype comparison with ideal genotype showed the $G+G \times E$ interaction effect of 30 Nutri rich rice genotypes under five locations for plant yield

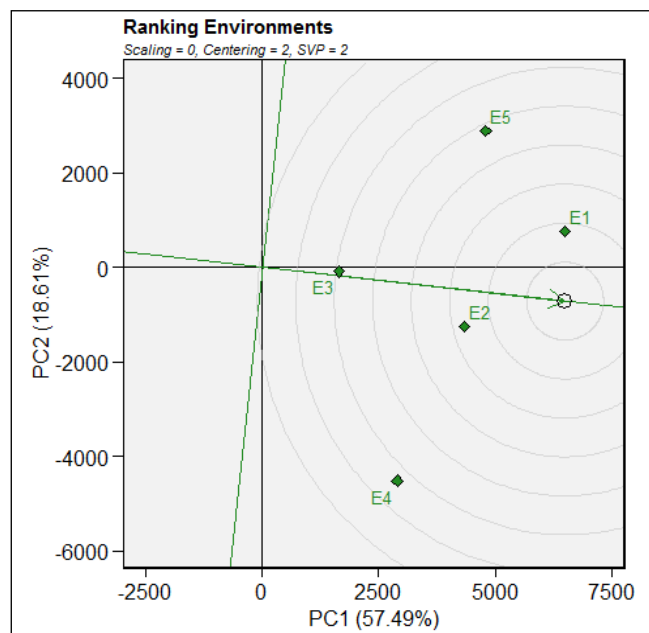


Figure 2: The GGE biplot ‘Environment ranking’ pattern for environment comparison with the ideal environment showed the $G+G \times E$ interaction effect of 30 Nutri rich rice genotypes under five locations for plant yield

genotypes. E_3 , with its short vector length, was non-discriminative and therefore less useful, as it provided little information for distinguishing genotypes.

E_1 , having the longest environment vector, was the most

informative, while E_3 was the least (Figure 3). The cosine of the angle between environment vectors reflected the correlation between them; E_1 and E_3 , with the smallest angle, showed the closest association, followed by E_2 – E_3 and E_1 – E_2 , indicating similar results and low crossover $G \times E$ interactions. This close association suggested that the same information could be obtained from fewer test environments, potentially reducing testing costs by eliminating redundant locations. In contrast, E_4 and E_5 form a right angle, indicating no correlation between these environments. This insight could guide the optimal allocation of limited resources during multi-location trials

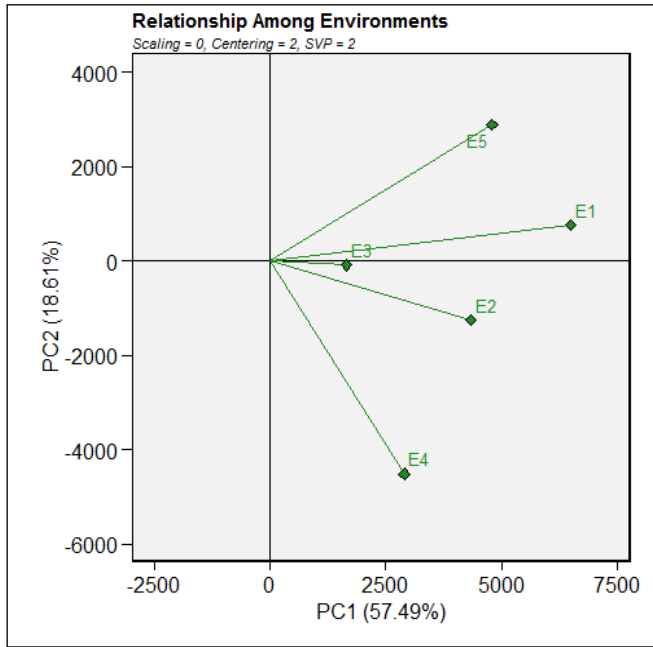


Figure 3: The environment-vector view of the GGE biplot showed similarities among test environments under five locations for plant yield

3.2. GGE biplot analysis: 'mean vs. stability' and ideal genotype evaluation

Biplot analysis is an essential statistical tool for assessing genotypic performance across various environments. The Average Environment Coordination (AEC) ranks genotypes based on their mean performance. The AEC was represented by a vertical line in the biplot, where genotypes positioned closer to this line and in the direction of the arrow indicated superior average performance across environments. The AEC Ordinate, a horizontal line, evaluated genotype stability, with those closer to it showing less variability in performance under different environmental conditions (Yan and Rajcan, 2002). Genotypes farther from the AEC exhibited greater variability and lower stability.

In this analysis, Figure 4 represented mean v/s stability pattern of GGE biplot, genotype G_{11} showed the highest

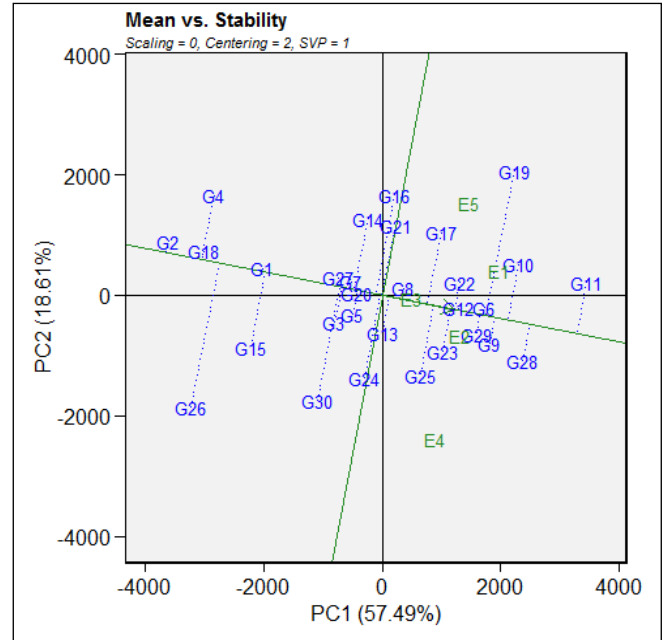


Figure 4: 'Mean vs. stability' pattern of GGE biplot illustrating interaction effect of 30 Nutri rich rice genotypes under five locations for plant yield

mean yield (MY), followed by G_{28} , G_{10} and G_{29} . In contrast, G_2 had the lowest MY, followed by G_4 and G_{18} . Genotypes G_{19} and G_{26} , positioned furthest from the AEC, were the most unstable, exhibiting the greatest variation, while G_{28} , G_{29} , and G_{18} were the most stable genotypes. These findings were consistent with previous studies (Oladosu et al. (2017), Hashim et al. (2021), Sabri et al. (2020), Mahant et al. (2024).

3.3. Genotype ranking: identification of ideal genotypes

The genotype ranking biplot (Figure 5) is a valuable tool for identifying the best-performing genotypes. Genotypes positioned close to the ideal genotype were considered promising. In this analysis, G_{29} , G_{11} and G_{28} were identified as top performers due to their proximity to the arrowhead in the circle representing plant yield (Figure 3). Ideal genotypes were typically located within the innermost circle, near the arrowhead at the center of the circular ring. If no genotype fell within this inner circle, those closest to it were deemed ideal (Oladosu et al. (2017) and Mahant et al. (2024).

An ideal genotype should exhibit both high mean performance and stability (Yan and Tinker (2006). This was often represented by a point at the arrow's head on the AEC abscissa (horizontal axis). (Oladosu et al. (2017) reported that none of the genotype falls inside the inner circle. Therefore genotype markers next to the ideal inner circle are considered to identify promising genotype. Mahant et al. (2024) also finds that Genotypes close to the ideal genotype are promising.

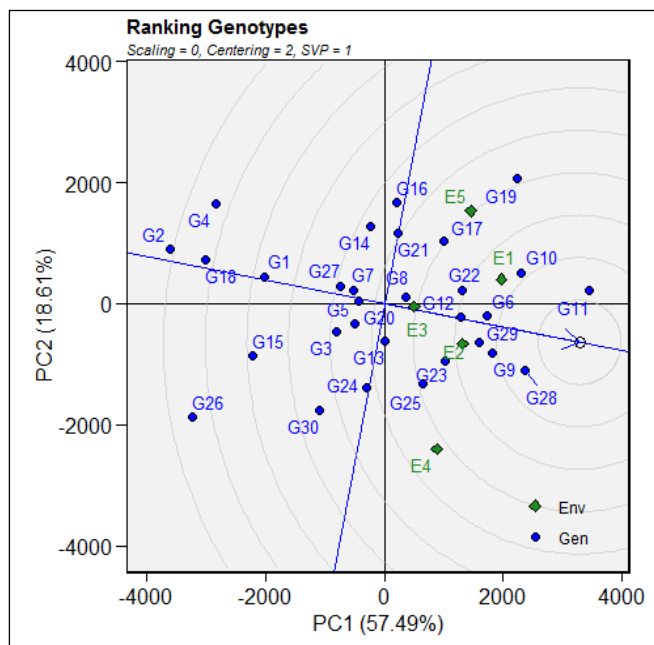


Figure 5: The GGE biplot 'genotypes ranking' pattern for genotype comparison with ideal genotype showing $G+G \times E$ interaction effect of 30 Nutri rich rice genotypes, under five locations for plant yield

3.4. Biplot analysis for interpreting multivariate data in multi-environment trials

In this study, thirty rice genotypes tested across five locations produced a biplot divided into heptagon sections (Figure 6) for yield. Genotypes G_4 , G_2 , G_{26} , G_{30} , G_{28} , G_{11} , and G_{19} were located at the vertices of the polygon, indicating that these genotypes performed either best or worst in one or more environments. Multi-environment trials (MET) are used to examine genotype-environment ($G \times E$) interactions in crop production (Oladosu et al. (2017). In MET, the main sources of variation are Genotype (G) and $G \times E$ interactions (Yan et al. (2000). The biplot technique plays a key role in interpreting MET data by revealing the "which-won-where" pattern of $G \times E$ interactions, assessing genotype stability and overall performance across different environments, and evaluating the representativeness and discriminating ability of test environments. A biplot graphically displays genotypes and environments on a two-dimensional scale based on their PC1 and PC2 scores, with high PC1 values indicating better yield potential and low PC2 values suggesting greater stability. Genotypes associated with the vertices of the encompassing polygon in the biplot, located far from the center, represented those best suited for specific environments, highlighting promising genotypes for future cultivation. The "which-won-where" analysis addresses genotype-by-environment interaction (GEI), mega-environment differentiation, and specific genotype adaptation graphically.

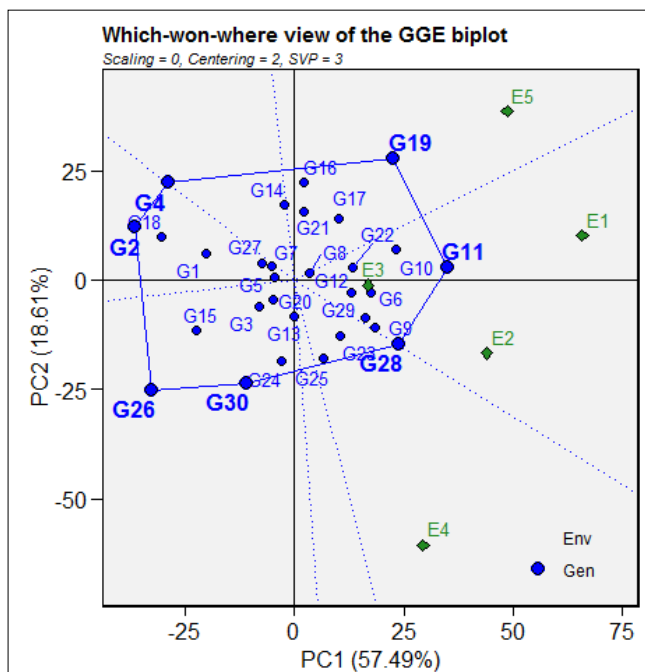


Figure 6: 'Which-Won-Where' polygon view of the GGE scatter biplot for yield in 2022 showing Nutri rich rice genotypes with best performance in each environment

The testing environments were partitioned into mega-environments (ME), with five testing environments distributed across three sectors in the biplot for yield. E_1 , E_2 , and E_3 fell within the same sector, while E_4 and E_5 occupied separate sectors. Sectors without any environment markers did not represent distinct mega-environments and could be merged with the nearest MEs. Genotype G_{19} was the top performer in E_5 , G_{11} was the winner across E_1 , E_2 , and E_3 , while G_{28} excelled in E_4 . This analysis demonstrated the usefulness of GGE biplot analysis for identifying stable and superior genotypes. Genotypes placed in sectors without environment markers were considered to perform poorly across all environments.

A genotype positioned at the vertex of a polygon section without an environment marker indicates poor performance across environments. Equality lines between G_{19} and G_{11} showed that G_{19} was superior in E_5 , while G_{11} excelled in other environments. Similarly, equality lines between G_{11} and G_{28} indicated that G_{28} performed better in E_4 , while G_{11} outperformed in the remaining environments. Genotypes situated within the polygon were less stable than those at the vertices (Yan and Tinker (2006). Similar results had been reported by Islam et al. (2014), Krishnamurthy et al. (2021) and Mahant et al. (2024).

Several authors had employed AMMI to analyze multi-environment trials, distinguishing the effects of genotype and environment and assessing GEI in a reduced dimensional space with minimal error. Comparable findings

were previously reported by Oikeh et al. (2004), Velu et al. (2012), Bishaw and Van Gastel (2009), and Suwanto and Nasrullah (2011), Bishwas et al. (2021), Dang et al. (2024). GGE biplots had proven valuable for selecting lines suitable for target environments and had been applied in multi-location trials and coordinated variety testing programs. Dwivedi et al. (2020) also identified suitable location for grain yield plant⁻¹.

4. CONCLUSION

Rice genotypes across environments to identify top-performing varieties. Multi-environment trials (MET) assessed the adaptability and stability, grouping genotypes into stable, high-yielding (G_{28} , G_{29}), high-yield but low-stability (G_{19}), and high-stability but low-yield (G_{27} , G_{47} , G_{18}) categories. MET and multi-location trials provided the insights into genotype performance, aiding the development of adaptable, high-yielding varieties. Notably, G_{28} , G_{29} , and G_{11} demonstrated consistent performance, making them promising candidates for commercial cultivation in Chhattisgarh.

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