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EVALUATION OF ELITE PADDY GENOTYPES ACROSS DIVERSE LOCATIONS USING MULTIVARIATE STABILITY PARAMETERS

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ABSTRACT

Genotype and environment interaction plays a crucial role in plant breeding since the performance of crop varieties often varies considerably with changes in sowing date, season and location. Therefore, identifying stable genotypes that perform consistently across diverse environments is essential for the development of improved varieties. A study was conducted with nine elite genotypes at four rice growing ecologies of Telangana. Grain yield stability performance was assessed by using multivariate statistics. The data were subjected to multivariate statistics such as Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE biplot analysis. The AMMI analysis revealed highly significant differences ($p < 0.01$) for genotype and G × E interaction and significant variation for environment. The first two principal components (PC1 and PC2) of the interaction accounted for 91.40% of the total variability in grain yield. The GGE biplot results revealed that G2 (RNR25842) was best performing genotype in E2, (Warangal) whereas genotype G1 (RNR25783) was the best-performing genotype tested across the environments E1 (Jagtial) and E3 (Kunaram). The genotypes G5 (BV166), G6 (SVIN301) and G9 (RNR 15048) are poorly performing genotypes. The pattern of genotypes ranking for GGE biplot for grain yield is G1 (RNR25843) > G3 (RNR25843) > G2 (RNR25842) > G8 (CR 4351-14398-68-1) >G4 (MGC276).

Keywords: Additive Main Effect and Multiplicative Interaction (AMMI), Rice, Stability, GGE biplot, G×E interaction

Rice thrives well in tropical climates with a majority of its annual production originating from tropical regions such as India, Bangladesh and various Southeast Asian countries (Aswidinnoor *et al*., 2023). In the state of Telangana, rice cultivation represents a major component of the agricultural sector, the *rabi* temperature in Telangana is characterized by extreme heat, low humidity, occasional heat waves and significant impacts on agriculture. It is, therefore, challenging to increase the production per hectare.

Rice serves as the primary staple food for more than half of the global population. While substantial advancements have been made recently in enhancing yields through the adoption of high-yielding varieties, there remains a pressing need to boost production to meet the demands of a growing population (Chandra Mohan *et al*., 2021). Rice grain yield has been reported to decline by 6% and head rice recovery by 9-14% for every 1°C increase in temperature (Peng *et al*., 2004; Welch *et al*., 2010; Lyman *et al*., 2013). This wasted food could have been made available to help the global food requirement given that rice feeds roughly half of the world's population. In order to meet the challenges of the ever-increasing world population and climate change, rice production must be increased through breeding programs that have major goals to achieve high yielding cultivars (Aswidinnoor *et al*., 2023).

Yield is an example of quantitative traits whose expressions are strongly influenced by environments (Wang *et al*., 2008; Li *et al*., 2019). For that reason, multi-environment trials (METs) are needed to identify a superior genotype with stable and high yield potential and as part of the final stages to release a variety. Genotype-by-environment interaction is inevitable in plant breeding and crop production (Yan, 2016). The presence of G×E refers to the differential response of genotypes among a range of environments (Kang, 1997). Considering G×E through stability analysis models could facilitate the accurate cultivar recommendation for the target environment (Huang *et al*., 2021). Stable high-yielding paddy varieties play a pivotal role in mitigating

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the adverse effects of climate change on agriculture in India. Their resilience to climate variability, contribution to food security, economic benefits for farmers and sustainability make them indispensable in ensuring the future of paddy cultivation amidst changing climatic conditions.

Examining stability and adaptability in rice genetics and breeding is essential for identifying varieties that consistently excel across diverse environments. This is particularly critical because rice cultivation spans various agro-ecological zones and climates. The AMMI model is especially effective in analyzing multilocation yield trials (MLYTs) (Krishnamurthy *et al*., 2021) which assess rice germplasm across multiple environments where genotype-environment interaction significantly influences outcomes. In the AMMI model, additive components capture the primary effects of genotypes and environments, while multiplicative components describe their interactions which enables the estimation of genetic variance from additive contributions. Another widely utilized approach is the Genotype plus Genotype-by-Environment Interaction (GGE) biplot analysis, which visually depicts GEI patterns and identifies genotypes performing well across varied environments (Kebede *et al*., 2023). The present study aims to identify rice genotypes with stable higher yields and broad adaptability in rice-growing areas of Telangana.

MATERIALS AND METHODS

Genetic materials and experimental sites

The present study investigated the adaptability mechanisms of these nine experimental genotypes including check RNR 15048 (Table 1), across four locations in Telangana comprising different agro-climatic zones (Fig. 1) during *rabi* 2022-23.

Agronomic and cultural practices

Crop was raised by sowing the nursery during first fortnight of December and 25-30 days age seedlings were transplanted in the main field under irrigated farming system at all the four locations. The spacing was 15 × 15 cm between rows and hills with plot size of 10-15 m^2 replicated thrice in randomized complete block design (RCBD). A recommended dose of nutrients (120:60:40 kg of NPK ha^{-1}) was applied through urea, single superphosphate and murate of potash, respectively. The crop was kept weed-free and hand weedings were carried out during the crop growth

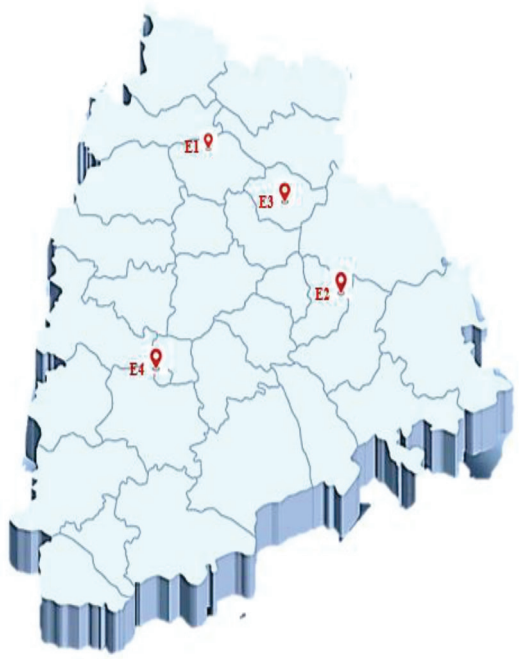


Fig. 1. Map of experimental sites across Telangana indicating the locations of the institutes

E1: Northern Telangana RARS, Jagtial, 18.49° N, 78.56° E, 243.40 m amsl
E2: Central Telangana RARS, Warangal, 15.50° N, 79.28° E, 268.50 m amsl
E3: Northern Telangana ARS, Kunaram, 18.49° N, 78.56° E, 243.40 m amsl
E4: Southern Telangana, RRU, ARI, Hyderabad, 17.33° N, 78.40° E, 586.60 m amsl

Table 1. Details of experimental material

Sr. No.	Genotype	Code	Source
1	RNR25783	G1	RRU-PJTAU, Hyderabad
2	RNR25842	G2	RRU-PJTAU, Hyderabad
3	RNR25843	G3	RRU-PJTAU, Hyderabad
4	MGC276	G4	IRRI, Philippines
5	BV166	G5	IIRR, Hyderabad
6	SVIN301	G6	IRRI, Philippines
7	CRR DHAN 201	G7	NRRI, Cuttack
8	CR 4351-14398-68-1	G8	NRRI, Cuttack
9	RNR 15048	G9	RRU-PJTAU, Hyderabad

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period. Proper soil moisture was maintained throughout the crop growth period. Data were taken for grain yield.

Statistical Tools

Multi variate stability analysis

Multivariate stability analysis through AMMI (Zobel *et al*., 1988) and GGE biplot (Yan *et al*., 2001) were conducted to evaluate the best genotypes respective to testing environments comprising the high stability and yield performance, thereby better understanding of the G×E.

AMMI model

In the present study, multivariate stability was evaluated using the Additive Main Effect and Multiplicative Interaction (AMMI) model to assess genotype vs. environment interaction and predict the stability of genotypes. The AMMI model combines pooled ANOVA to assess additive main effects followed by employing singular value decomposition (SVD) on the total error matrix to compute the interaction principal components (IPCs). The AMMI model was determined in R by utilizing the metan library (Olivoto and Lúcio, 2020). The following equation was used to compute the AMMI model (Zobel *et al*., 1988):

$$Y = \mu + \alpha_i + \beta_j + \sum_{k=1}^{n} \lambda_k \delta_{jk} \gamma_{ik} + \varepsilon_{ij}$$

Here, Y_{ij} denotes the mean values of performance of the i^{th} genotype in the respective j^{th} environmental conditions, α_i represents the fixed effect of the respective genotype, β_j shows the environmental effect, n is the total number of IPCA hold in AMMI model, λ_k is individual value for IPC axis k, γ_{ik} represents the i^{th} genotype value of eigenvector for IPC axis k, δ_{jk} shows the eigenvector value for j^{th} environment for IPC axis k and ε_{ij} denotes the mean residual.

GGE biplot analysis

The biplot graphs designed in this study represent the variables which impact the genotype, where the ordinate is the IPCA1. The average of collected data was analyzed graphically (Yan and Tinker, 2006 through R 4.1.3 software). The study utilized polygon biplot graphs to analyze response of individual genotypes to specific environments across different experimental sites revealing the GGE (Genotype plus Genotype-by-Environment interaction) pattern. Additionally, the research aimed to identify the most appropriate genotypes by considering both average performance and stability. Furthermore, concentric circle diagrams with vectors of entries were employed to elucidate relationships between various environmental factors and genotypes placing particular emphasis on identifying stable genotypes.

RESULTS AND DISCUSSION

Additive main effect and multiplicative interaction (AMMI) analysis

The additive main effects and multiplicative interaction (AMMI) model was employed to evaluate the genotype × environment interaction (G × E) of nine genotypes across four locations for grain yield. The analysis revealed highly significant differences ($p < 0.01$) for genotype and G × E interaction and significant variation for environment (Table 2). The first two principal components (PC1 and PC2) of the interaction accounted for 91.40% of the total variability in grain yield.

Pooled mean performance of genotypes for grain yield

The pooled mean performance of eight genotypes: RNR 25783, RNR 25842, RNR 25843, MGC 276 and BV-166, CR 4351-14398-68-1, CRR DHAN 201 and SVIN

Table 2. AMMI analysis of variance for grain yield and head rice recovery of rice genotypes over locations

Source of variation	Degree of freedom	Grain yield (kg/ha)			
		MSS	*F* value	Pr(>F)	Proportion
Environment	3	23600261.00	1558.71	2.09E-11	
Replication	8	15141.00	0.46	0.882	
Genotype	8	26495024.00	798.49	4.91E-61	
Genotype×Environment	24	4282730.00	129.07	2.92E-45	
PC1	10	6975542.00	210.22	0	67.90
PC2	8	3017536.00	90.94	0	23.50
PC3	6	1481636.00	44.65	0	8.60
Residual	64	33182.00			
Total	131	3744861.00			

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Table 3. Pooled mean performance of genotypes for grain yield and per cent increase or decrease over local check RNR 15048

Genotype code	Genotype	Pooled grain yield (kg/ha)	Per cent increase/ decrease in grain yield over check
G1	RNR 25783	9279	30.45
G2	RNR 25842	9101	27.94
G3	RNR 25843	8700	22.31
G4	MGC 276	6975	-1.94
G5	BV-166	5873	-17.44
G6	CR 4351-14398-68-1	7934	11.54
G7	CRR DHAN 201	6437	-9.51
G8	SVIN 301	4965	-30.19
G9	RNR 15048 (Check)	7113	0.00
Mean		7375	
Min		4965	
Max		9279	

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301 were evaluated in comparison with the local check RNR 15048 for grain yield. The results are presented in tables 3 and figure 2. Among the genotypes evaluated, RNR 25783 exhibited the highest grain yield of 9279 kg/ha, which was 30.45% higher than the check variety RNR 15048 (7113 kg/ha). RNR 25842 also performed exceptionally, producing 9100 kg/ha, representing a 27.94% increase over the check. RNR 25843 recorded a grain yield of 8700 kg/ha, which was 22.31% higher than the check. CR 4351-14398-68-1 yielded 7934 kg/ha showing a 11.54% improvement compared to RNR 15048, while MGC 276 produced 6975 kg/ha 1.94% lower than the check.

In contrast, CRR DHAN 201 recorded a lower yield of 6437 kg/ha (9.51% less than the check), whereas BV-166 yielded 5873 kg/ha, 17.44% below the check. The lowest grain yield was observed in SVIN 301 which produced 4965 kg/ha corresponding to a 30.51% reduction compared to RNR 15048.

Construction of GGE biplots

GGE biplots were constructed using the site regression (SREG) model, which incorporates both the genotype main effects and the genotype × environment interaction while excluding random error. The analysis revealed that for grain yield the first two principal components (PCs) together explained 92.78% of the total variation with PC1 contributing 74.72% and PC2 18.06%. Genotypic stability and the relationships among test environments were assessed through

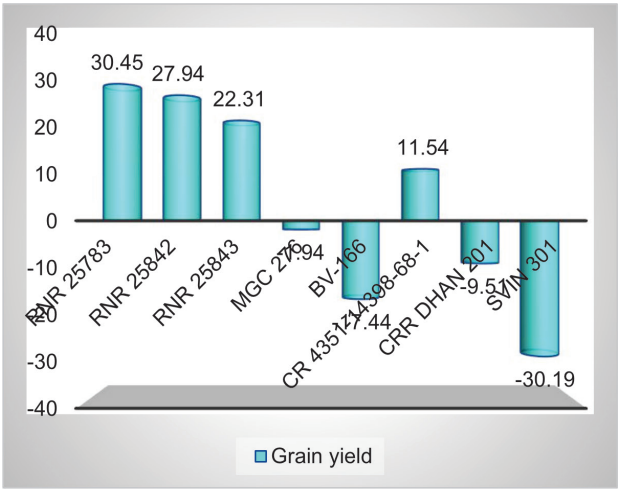


Fig. 2. Per cent increase/ decrease in grain yield over check RNR 15048 in different genotypes

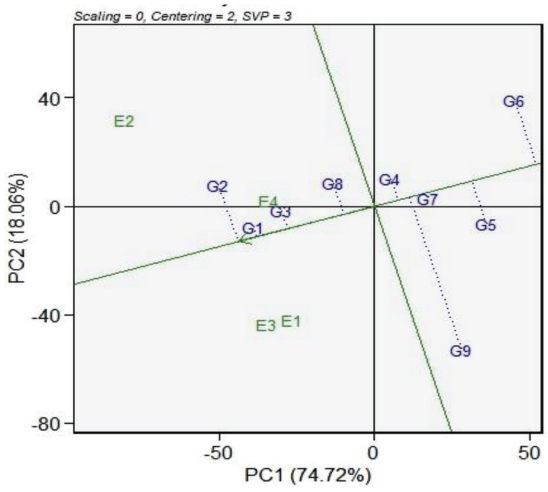


Fig. 3. Mean versus stability GGE biplot for grain yield

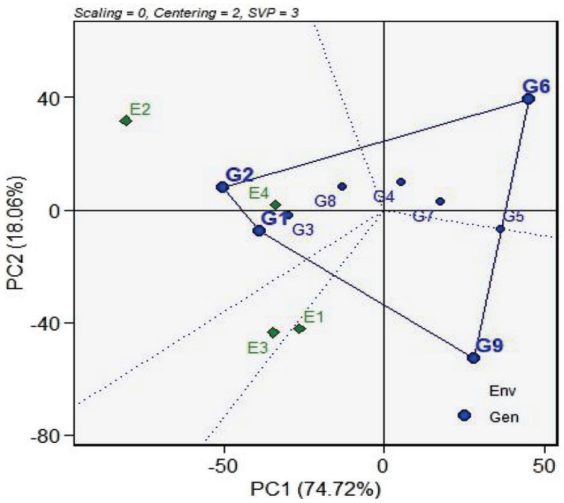


Fig. 4. Which-won-where view of GGE biplot for grain yield

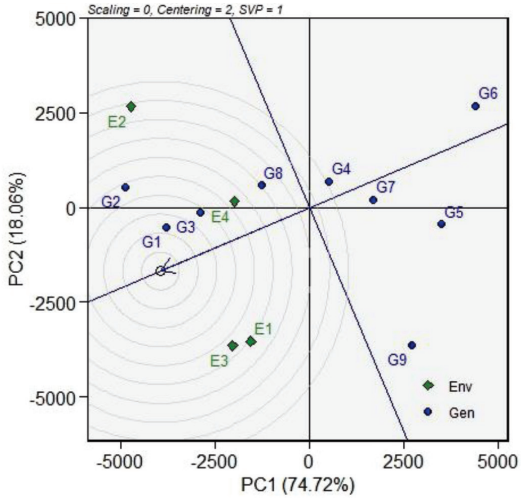


Fig. 5. GGE biplot 'Ranking genotypes' profile to rank for the ideal genotypes for grain yield

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different biplot visualizations such as 'which-won-where', 'mean vs. stability' and 'ranking genotypes and environments'. All biplots were generated using environment-centered data (centering = 2) without scaling (scale = 0) and applying the genotype-focused singular value partitioning method.

Mean verses stability analysis of GGE (Genotype + Genotype × Environment) biplot

The stability pattern of genotypes was assessed based on their mean performance across various environments for grain yield and head rice recovery. The mean vs. stability graph is generated by the intersection of vertical and horizontal ordinate lines (Fig. **3**). Every genotype has a single arrow that has direction towards a mean performance for trait under study. The genotypes depicted less arrowhead lines considered as a best performing stable genotypes in almost all locations. The genotypes G2, G1 and G3 revealed higher grain yield. The genotypes G1, G3 and G4 performed as stable grain yielders across all environments.

Which-won-where GGE biplot

The GGE biplot is presented in polygon view in fig. 4. It has determined the best performing genotypes for grain yield in different locations. The GGE biplot was explained as described by Oladosu *et al*. (2017). The genotypes present near the vertex of polygon with no environment nearby are considered less stable and genotypes present on the vertex of polygon where one or more environments are prevalent are considered best performing genotypes in the respective environments. The genotypes present inside the polygon are less responsive to tested environment and are considered the best performing genotypes over a broad range of environments. For grain yield, the results revealed that G2 was best performing genotype in E2, (Warangal) whereas genotype G1 was the best-performing genotype in tested environments E1 (Jagtial) and E3 (Kunaram). The genotypes G5, G6 and G9 are poor performing genotypes because they are lying in an area with no representation of any environment. The genotypes *viz*. G3, G4, G7 and G8 that are less responsive to any environment and exhibited stable performance for yield in all the environments.

Ranking of genotypes

The GGE biplot for genotype ranking revealed the ideal genotype as compared to other genotypes under study (Fig. 5). The arrowhead indicates the ideotypes that performed well in all tested locations. The genotypes near to the concentric arrow are considered

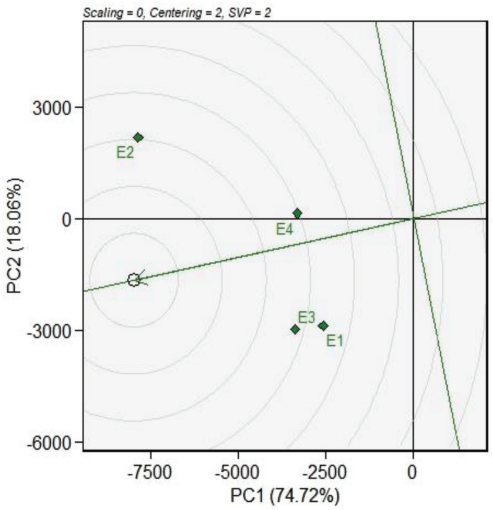


Fig. 6. GGE biplot 'Ranking Environments' profile for the ideal location for grain yield

the best performing genotypes. In this biplot analysis locations are considered as random samples of testing genotypes. The pattern of genotypes ranking for GGE biplot for grain yield is G1>G3>G2>G8>G4.

Ranking environments

The environment E2 (Warangal-Central Telangana) is the best environment for grain yield performance for all the genotypes tested (Fig. 6). The tested environment for grain yield was revealed based on nearness to the concentric centers. In this biplot analysis, genotypes are considered as random samples of testing environment. The pattern of environment ranking for GGE biplot for grain yield and head rice recovery is E2>E3>E4>E1.

Overall, G1 and G2 emerged as the most promising genotypes showing superior performance for both grain yield in multiple environments while G6, G7 and G8 were the least desirable due to their consistently poor performance.

CONCLUSION

Grain yield in rice is a complex polygenic trait governed by several factors. Environmental interaction of genotypes for the expression of genes related to yield is an important phenomenon. Testing of genotypes in a wide range of environmental conditions is a prerequisite before the commercial release of cultivar by plant breeders. To identify the most stable genotypes in a multi-environment, we evaluated nine genotypes including check using multivariate statistical approaches. Based on GGE biplot analyses, the genotypes namely G1 (RNR25843) and G3 (RNR25843) were observed better yield performing and stable. It is concluded from our study that these genotypes could be recommended for commercial cultivation in Telangana.

Conflict of interests

Authors declare that there is no conflict of interests.

Authors' contribution

Planning of experiment and manuscript writing (YCM, JAK, CNN, CAK) Execution, data recording, stability analysis and manuscript writing (ES).

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