Plant Archives Vol. 25, No. 1, 2025 pp. 261-268 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.040

DELINEATION OF GENOTYPE × ENVIRONMENT INTERACTION FOR IDENTIFICATION OF STABLE RICE HYBRIDS FOR TELANGANA STATE, INDIA

Y. Chandra Mohan[1]*, L. Krishna[1], S. Sridhar[2], B. Satish Chandra[3], P. Madhukar[4], V. Sridhar[5], K. Sai Kylash[1], T.V.J. Singh[1], E. Sudhishna[1], E. Santosh Kumar[1] and P. Raghu Rami Reddy[1]

[1]Institute of Rice Research, ARI, PJTAU, Rajendranagar, Hyderabad - 500 030, Telangana, India.
[2]Agricultural Research Station, PJTAU, Kunaram, Pedapally Dist. - 505 174, Telangana, India.
[3]Regional Research Station, PJTAU, Warangal - 506 007, Telangana, India.
[4]Regional Agricultural Research Station, Polasa, Jagtial district - 505 529, Telangana, India
[5]Agricultural Research Station, Kampasagar, Nalgonda Dist. - 508 287, Telangana, India.
*Corresponding author E-mail : drycmohan@gmail.com; ORCID: https://orcid.org/0000-0002-8480-7148

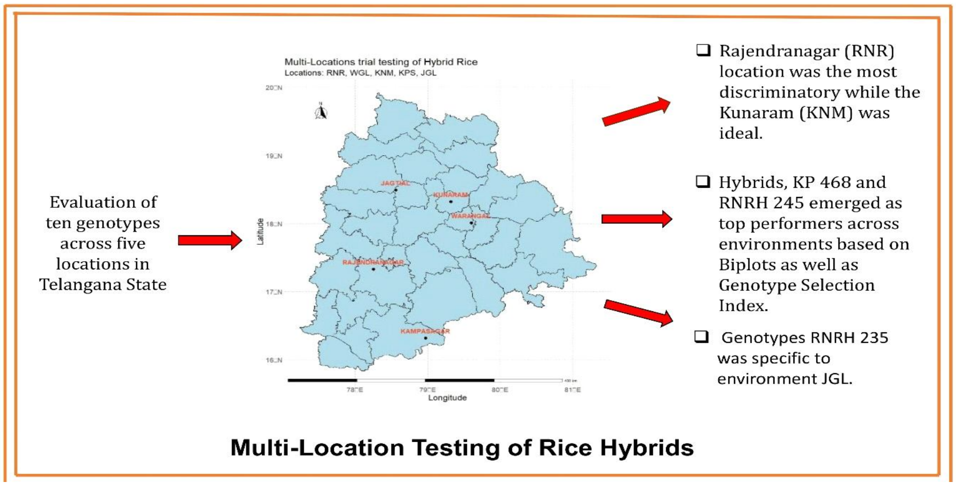
(Date of Receiving-21-11-2024; Date of Acceptance-31-01-2025)

ABSTRACT

The study conducted an in-depth analysis of grain yield data of rice hybrids from multiple environments, employing AMMI and GGE bi-plots to assess the significance of genotypic, environmental, and genotype-environment interaction (GEI) effects on grain yield and identification of promising stable hybrids.

Stability of the rice hybrids was assessed through multi-location testing at different agroclimatic zones of Telangana and assessing its yield performance.The analysis revealed that environmental effects (61.33%) accounted for the major proportion of the total variance. Grain yield varied considerably across the environments, with the hybrid KP 468 emerging as the top performer, followed closely by RNRH 245 and RNRH 235. The genotypes KP 468, RNRH 245, RNRH 197, and RNRH 98 exhibited high grain yield and positive IPCA scores, suggesting their stability across environments.

Key words : AMMI, Bi-plots, GGE, Multi-environment trials, Rice hybrids.



Evaluation of ten genotypes across five locations in Telangana State

- ☐ Rajendranagar (RNR) location was the most discriminatory while the Kunaram (KNM) was ideal.
- ☐ Hybrids, KP 468 and RNRH 245 emerged as top performers across environments based on Biplots as well as Genotype Selection Index.
- ☐ Genotypes RNRH 235 was specific to environment JGL.

Multi-Location Testing of Rice Hybrids

Introduction

Rice is cultivated under different climates, including temperate, sub-tropical, and tropical regions and is the major staple food for Asians and it is eaten in significant quantities on a daily basis. Yield in rice depends on genotype, environment, management practices and their interaction with each other (Messina *et al.*, 2009). Climate change and abiotic stresses are causing shifts in agricultural landscapes (Kylash *et al.,* 2023). On the other hand, the environment comprises the diverse set of ecological factors, such as soil type, temperature, precipitation, and other agro-climatic variables, which significantly influence rice growth and yield. To meet the challenges of population growth, climate change and limited arable land, rice production must be expanded through increase in yield potential. Phenotypes are the mixture of Genotype (G), Environment (E) components and their interactions (G × E) between them (Darai *et al*., 2017). The key to significantly increasing agricultural production, is to increase productivity per hectare and per dollar, which includes understanding and exploiting GEI (Genotype × Environment Interaction) (Kang, 2002). A strong G×E interaction slows down selection and identification of genotypes, and makes recommendations difficult.

To enhance the selection method, it is important to take advantage of the possibility of finding genotypes that are less influenced by G × E interaction (GEI). Information of genotype × environment interaction leads to successful evaluation of stable genotypes, which could be used for general cultivation (Akter *et al*., 2015). Hybrid rice typically has a genetic advantage known as heterosis or hybrid vigor, which leads to significantly higher yields compared to traditional varieties. Although, some hybrids may have wide adaptability across environments, some are highly influenced by the change in the environment which performs inconsistently in other locations (Akter *et al.,* 2019).

Multivariate stability methods are the most recently used analysis in exploring and discovering patterns of G × E interactions. Among these, AMMI analysis is the most recent and widely exploited in different crops for the identification of stable genotypes over locations. The additive main effects and multiplicative interaction (AMMI) and genotype main effect (G) and GE, also known as GGE biplot, are the most commonly used multivariate approaches for the analysis of GE interactions. AMMI is especially effective tool where the assumption of linearity of the response of genotype to a change in the environment is not fulfilled and which usually separates the interaction part of the multiplicative components into the additive main effects by principal component analysis. Both methods provide a graphical representation of the interaction patterns and describe the interrelationships between genotypes, environments, and GE interactions to identify stable genotypes suitable for an environment, as well as of genotypes with a general behaviour that are suitable across several environments (Annichiarico and Perenzin, 1996). The AMMI result is gaining popularity and has been widely preferred in recent years for breeding programs, judgments such as definite and extensive alterations, as well as for the assortment of the environments (Gruneberg *et al*., 2005).

Proposed by Gauch (1992), the AMMI model uses analysis of variance and principal component analysis to achieve a better understanding of GEI, its causes and consequences. Yan *et al.* (2000) proposed the GGE Biplot analysis, which considers both genotype main effects and GEI effects as important for the analysis Miranda *et al.* (2009). The only difference between these models is in the initial steps of the analysis, where GGE analyzes G plus GE (or GEI) while AMMI separates G from GE; and at the final steps where the biplots for the interpretation are built. Despite the possibility of their complementing each other due to their equivalent features, there has been discussion among authors about the effectiveness of AMMI and GGE in depicting the adaptive responses of genotypes over environments (Yan and Tinker, 2005; Gauch, 2006; Yan and Tinker, 2006; Gauch *et al.*, 2008). However, such differences do not imply the superiority of either of the methods. AMMI Biplot's graphic analysis provides relatively simple analysis for breeding researchers. Based on the data, it allows conclusions to be drawn concerning phenotypic stability, genotype behavior, genetic divergence between genotypes, and environments with optimal performance. As for GGE Biplot, it complements AMMI Biplot's environmental stratification, making it possible to delineate mega-environments and genotypes with optimal performance in such groups (Miranda *et al*., 2009).

Stability analysis in rice involves assessing the impact of genotype and environment on the crop's performance across different growing conditions. By conducting stability analysis, researchers aim to identify rice genotypes that consistently perform well and exhibit minimal variations in yield under different environmental conditions. This understanding is crucial for developing climate-resilient and high-yielding rice cultivars, ultimately contributing to global food security and sustainable agriculture. As there is no dearth in the creation of new cultivars more focus should be based on providing rice growers, the most diverse stable cultivars that could generate high yielding stable rice for diverse conditions. The main objective of the present study is to identify high yielding stable promising hybrids. Information on GE interactions and stability factors for Telangana state environments can help to identify stable and high-yielding hybrids for cultivation across local rice granary areas, increasing rice production and farmer income level.

Materials and Methods

The experiment was conducted with materials (Table 1) at five locations in the state of Telangana comprising different agro-climatic zones as detailed in Table 2 during *kharif*, 2022. Crop was raised by sowing the nursery during first fortnight of July and 25-30 days age seedlings were transplanted in the main field under irrigated farming system at all the five locations. The spacing adopted was 15 × 15 cm between rows and hills with plot size of 10-15 m^2 replicated thrice in Randomized Complete Block Design. Crop was well managed by adopting recommended agronomic package and suitable plant protection measures to realize potential yields. Data was taken on various quantitative traits such as days to 50% flowering, plant height, panicle length, number of filled grains per panicle, test weight, head rice recovery %, and grain yield. Grain yield was recorded in each plot and expressed in kg/ha. Statistical analysis for grain yield were subjected to combined ANOVA and AMMI analysis to understand the genotype performance across the five locations.

ANOVA was used to partition genotypic, environmental and G × E deviations from the total variation. To compute G × E interaction, AMMI methods were used. The combined variance analysis was done and the means served as a basis for the AMMI analysis. The AMMI model used in the stability analysis is as follows:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\lambda_k \, a_{ik} \, \gamma_{jk} + \varepsilon_{ij}$$

Where,

Y_{ij} = mean of a trait of i^{th} genotype in j^{th} environment;

μ = the grand mean; g_i = genotypic effect;

e_j = environmental effect;

λ_k = eigen value of Interaction Principal Components Axes (IPCA) k;

a_{ik} = eigen vector of genotype i for PC k;

γ_{jk} = eigen vector for environment j for PC k;

ε_{ij} = error associated with genotype *i* in environment *j* (Gauch, 1992).

Table 1 : Details of experimental material under study along with parentage.

S. no.	Genotype	Parentage	Source	Grain Type
1	RNRH 245	CMS 67A x SN 1666	IRR, Rajendranagar, PJTAU	LS
2	KP 468	Hybrid Check	Kaveri Seeds Pvt. Ltd	LS
3	RNRH 98	CMS 64 A x SN 232	IRR, Rajendranagar, PJTAU	LS
4	US 312	Hybrid Check	US Agriseeds Pvt. Ltd.	MS
5	RNRH 186	CMS 59 A x SN 1407	IRR, Rajendranagar, PJTAU	MS
6	JGL 24423	Variety Check	RARS, Jagtial, PJTAU	LB
7	RNRH 197	CMS 67 A x SN 232	IRR, Rajendranagar, PJTAU	LS
8	JGLH 440	JMS 19A x JGL 36147	RARS, Jagtial, PJTAU	MS
9	RNRH 235	RMS 2A x SN 1606	IRR, Rajendranagar, PJTAU	MS
10	JGLH 442	JMS 19A x JGL 36172	RARS, Jagtial, PJTAU	MS

Table 2 : Details of the five environments in Telangana State used for evaluation of genotypes.

Location name	Code	District	Agro-climatic Zone	Latitude (N)	Longitude (E)	Altitude (m)
Regional Agricultural Research Station, Jagtial	JGL	Jagtial	Northern Telangana	18.49°	78.56°	243.4
Agricultural Research Station, Kunaram	KNM	Peddapally	Northern Telangana	18.32°	79.32°	231.0
Agricultural Research Station, Kampasagar	KPS	Nalgonda	Southern Telangana	16.59°	79.28°	152.0
Institute of Rice Research, ARI, Rajendranagar	RNR	Ranga reddy	Southern Telangana	17.33°	78.40°	586.6
Regional Agricultural Research Station, Warangal	WGL	Warangal	Central Telangana	15.50°	79.28°	268.5

DFF: Days to flowering; PH: Plant Height (cm); PL: Panicle Length (cm); NFG: Number of Filled Grains per panicle; NPT: No. of Productive Tillers/plant TW: 1000 Grain Weight (g); HRR: Head Rice Recovery (%); GY: Grain Yield (kg/ha)

The AMMI stability value (ASV) was calculated by the method formulated by Purchase *et al.* (2000)

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(ICPA_1)\right]^2 + (ICPA_2)^2}$$

Where, SS represents the sum of squares of first (IPCA1) and second (IPCA$_2$) interaction principal component axes; and IPCA$_1$ and IPCA$_2$ are the genotypic scores obtained from the AMMI model. Genotype selection index (GSI) was obtained by following the method devised by Farshadfar and Sutka (2003).

$$GSI_i = RY_i + RASV_i$$

Where, GSI$_i$ denotes the genotype selection index for ith genotype,

RY$_i$ is rank of mean grain yield for ith genotype,

RASV$_i$ represents rank for the AMMI stability value for the ith genotype.

GGE analysis was performed with the model equation:

$$Y_{ij} = \mu + G_i + E_j + \Sigma\lambda_k\alpha_{ik}\gamma_{jk} + e_{ij}$$

Where, Y_{ij} is the yield of ith genotype in the jth environment;

G_i and E_j represent the genotype and environment deviations from the grand mean, respectively;

μ denotes the grand mean;

λ_k is the eigenvalue of the PCA axis k;

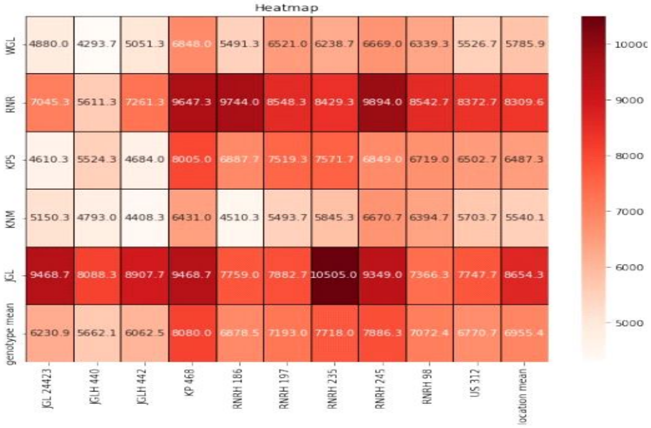
α_{ik} and γ_{jk} indicate the genotype and environment PC scores, respectively, for the axis k and

e_{ij} denotes the error term.

All the statistical analysis was done by using the software R-studio 4.1.0 with the help of package Metan 1.15.0 (Olivoto and Lucio, 2020)

Results and Discussion

The mean grain yield ranged from 4299 kg/ha (JGLH 440 in WGL) to 10,505 kg/ha (RNRH 235 in JGL) with an overall mean of 6960 kg/ha (Fig. 1, Table 3). Mean grain yield of the hybrids across five environments revealed that the hybrid KP 468 (8080 kg/ha) was the top-ranking hybrid followed by RNRH 245 (7886 kg/ha) and RNRH 235 (7718 kg/ha). However, among the locations Jagtial was found to be the best location with highest mean grain yield for all the hybrids under study with 8654 kg/ha followed by Rajendranagar with 8310 kg/ha, whereas Kunaram was the poorest location with the least mean grain yield of 5540 kg/ha. Five hybrids showed above average yield in Warangal, Kunaram and Jagtial, where as in case of Kampasagar and Rajendranagar six and seven genotypes outperformed the location's mean grain yield, respectively. Genotypes KP 468 and RNRH 245 not only exceed the mean grain yield of all environments but also demonstrate adaptability across multiple environments, indicating their potential as stable high-yielding hybrids.


Heatmap

	JGL 24423	JGLH 440	JGLH 442	KP 468	RNRH 186	RNRH 197	RNRH 235	RNRH 245	RNRH 98	US 312	location mean
WGL	4880.0	4293.7	5051.3	6848.0	5491.3	6521.0	6238.7	6669.0	6339.3	5526.7	5785.9
RNR	7045.3	5611.3	7261.3	9647.3	9744.0	8548.3	8429.3	9894.0	8542.7	8372.7	8309.6
KPS	4610.3	5524.3	4684.0	8005.0	6887.7	7519.3	7571.7	6849.0	6719.0	6502.7	6487.3
KNM	5150.3	4793.0	4408.3	6431.0	4510.3	5493.7	5845.3	6670.7	6394.7	5703.7	5540.1
JGL	9468.7	8088.3	8907.7	9468.7	7759.0	7882.7	10505.0	9349.0	7366.3	7747.7	8654.3
genotype mean	6230.9	5662.1	6062.5	8080.0	6878.5	7193.0	7718.0	7886.3	7072.4	6770.7	6955.4

Fig. 1 : Heat map of the mean grain yield of the test entries across different environments.

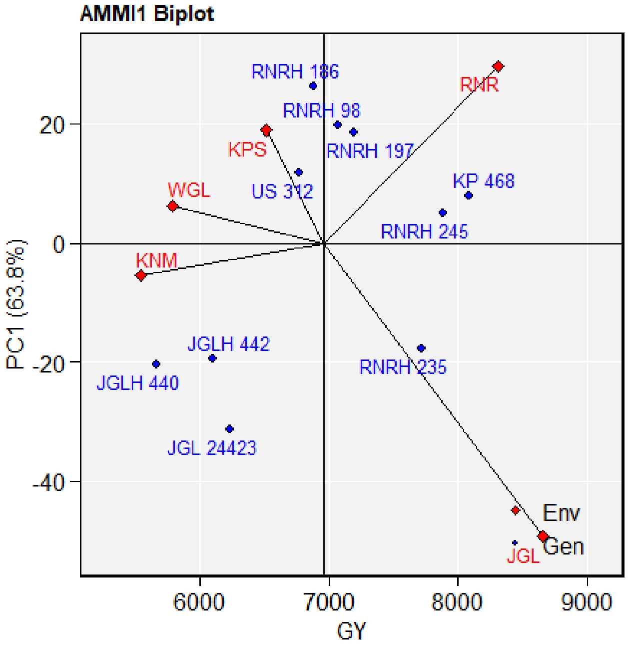


Fig. 2 : AMMI 1 Bi-plot for mean grain yield of hybrids and environments under study against their respective IPCA1 scores.

Analysis of Variance

AMMI analysis of variance for pooled mean grain yield (kg/ha) of the rice hybrids from five environments (JGL, KNM, KPS, RNR and WGL) explained that the major portion of the total sum of squares was contributed by environmental effects (61.3%) followed by genotypic effects (21.3%) and GEI effects (16.1%) (Table 4). AMMI ANOVA revealed significant differences among

Table 3 : Mean performance of the entries studied for stability analysis

Trait	Jagtial			Kunaram			Kampasagar			Rajendranagar			Warangal		
	Mean	**Max**	**Min**	**Mean**	**Max**	**Min**	**Mean**	**Max**	**Min**	**Mean**	**Max**	**Min**	**Mean**	**Max**	**Min**
DFF	102	112	98	89	104	82	96	104	87	99	106	91	95	107	89
PH	112.5	124.2	95.0	130.1	153.2	118.2	105.0	129.0	90.0	102	113	94	121	142	109
PL	27.0	31.0	25.2	27.0	31.0	24.8	25.8	30.4	23.1	25.8	30.0	23.0	26.9	30.2	24.2
NFG	227	355	136	281	474	138	222	296	130	161	220	101	222	328	140
NPT	354	387	299	365	457	264	355	440	264	525	676	382	398	484	343
TW	23.48	32.10	14.20	22.41	29.68	14.83	22.48	29.09	14.02	25.1	32.1	14.3	22.88	29.80	14.50
HRR	40.6	58.5	22.0	57.0	65.3	40.9	49.30	56.20	42.3	46.8	68.5	24.3	61.2	68.2	53.1
GY	8654	10763	7082	5540	6755	4243	6507	8653	3468	8310	10777	5256	5786	7346	3979

Table 4 : AMMI analysis of variance for mean grain yield of the test material under study.

Source	**Degrees of Freedom**	**Total Sum of squares**	**Mean sum of squares**	**F-value**	**Pr (>F)**	**Proportion variance**	**Accumulated variance**
ENV	4	248733590	62183398	118.85548	2.19E-08	61.3	
REP (ENV)	10	5231850	523185	1.918934	5.25E-02		
GEN	9	86187137	9576348.6	35.124055	9.43E-26	21.3	
GEN: ENV	36	65413007	1817028	6.664481	1.56E-13	16.1	
PC1	12	41711583	3475965.3	12.75	0.00E+00	63.8	63.8
PC2	10	13236934	1323693.4	4.86	0.00E+00	20.2	84.0
PC3	8	8999953	1124994.2	4.13	3.00E-04	13.8	97.8
PC4	6	1464537	244089.4	0.9	4.99E-01	2.2	100
Residuals	90	24537924	272643.6				
Total	**185**	**495516515**	**2678467.6**				

the rice hybrids across the five environments. It depicts that grain yield is influenced by genotype (G), environment (E) and also the interaction between genotype and environment (GEI). The presence of significant proportion of GEI necessitates the analysis of the stability of rice hybrids over environments.

AMMI analysis further portioned the GEI into four multiplicative terms namely IPCA1, IPCA2, IPCA3 and IPCA4 with a contribution of 63.8, 20.2, 13.8 and 2.2% of the GEI sum of squares. The first two PCAs accounted for 84% of the variance. Zewdu *et al.* (2020) also had two PCAs explaining the major portion of variance. The IPCA score of a genotype in the AMMI analysis is a signal of the adaptability over environments and relationship between genotypes and environments. (Gauch *et al.*, 1996 and Mahalingam *et al.*, 2006). The mean yield and PC1 components were plotted on x and y axes, respectively for the construction if AMMI 1 Bi-plot. A genotype with PC1 score near to zero is considered to be steadier across the environments (Rao *et al.*, 2020). The hybrids KP 468, RNRH 245, RNRH 197 and RNRH 98 were found to be having high grain yield with positive IPCA scores (Fig. 2). The hybrid, RNRH 245 is found near to zero values of the IPCA score implies that it was the most stable genotype across all the environments. The environments Kunaram, Warangal, Kampasagar were very close whereas Jagtial was highly divergent followed by Rajendranagar.

GGE Bi-plot analysis

GGE Bi-plot analysis offers effective assessment of the material under study and allow complete understanding of the target and test environments through various IPCAs. GGE analysis portioned the GEI into 5 IPCAs and 85.04% variance was explained by the first two IPCAs. There exists a positive correlation between all the test environments under study as the angle between the environments was less than 90° (Fig. 3). The concentric circles on the bi-plot help us to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environment and is a measure of the discriminativeness (Yan and Tinker, 2006). The present study revealed that the environment Rajendranagar followed by Jagtial were found with the longest vector having more discriminatory power compared to other environments. The Average Environment Axis (AEA) or Average-tester-axis (represented by the small circle at the end of the arrows) has the average coordinates of all the test environments

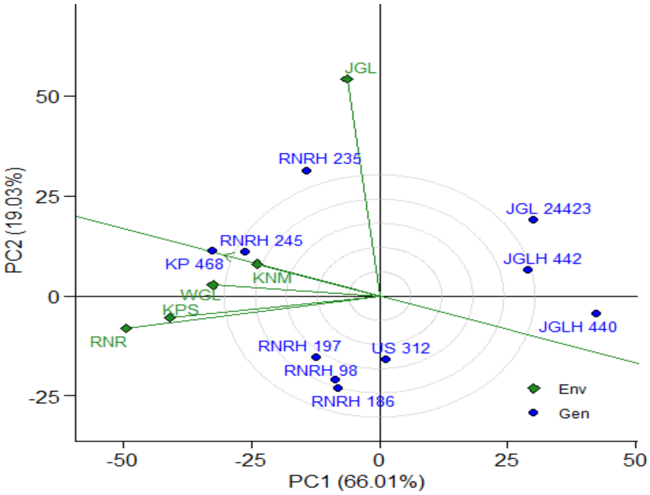


Fig. 3 : GGE Bi-plot of IPCA1 vs IPCA 2.

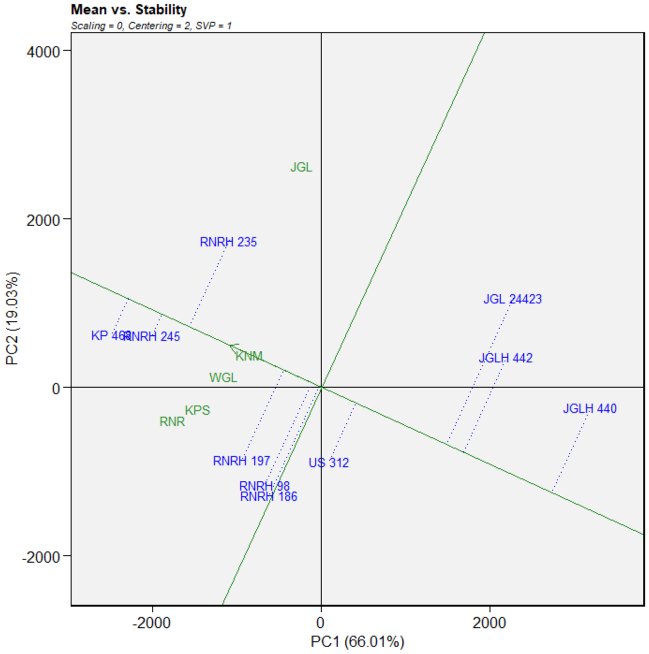


Fig. 4 : Mean vs Stability Bi-plot for Grain yield of hybrids.

and AEA is the line that passes through the average environment and the bi-plot origin. The environment Kunaram had the least angle with the AEA, hence Kunaram environment is highly representative or an ideal environment of all the test environments which could be drawn from the study as it had the least environmental mean grain yield.

The mean vs stability bi-plots depict the mean performance of the hybrids through environments. The lines passing through the origin in Fig. 4 represent the "Average Environment coordinate" (AEC) axis (x axis) and the second axis (y axis) denotes the stability. The single arrowed line or AEA line points to the higher mean yield across environments. Thus, hybrids KP 468, RNRH 235 and RNRH 245 had highest mean yields whereas the hybrid RNRH 186 (located at the center of the origin) had mean yield similar to the grand mean yield and JGLH 440 (located at the opposite side of the AEA arrow) had the lowest mean yield. The hybrid RNRH 245 was located very near to AEA axis followed by KP 468 and US 312 indicating that they were highly stable across environments whereas JGL 24423, RNRH 186 and RNRH 98 are highly unstable as they were located far from the AEA line. The varietal check, JGL 24423 had low mean yield than the average environmental mean yield for all the environments except in case of Jagtial location.

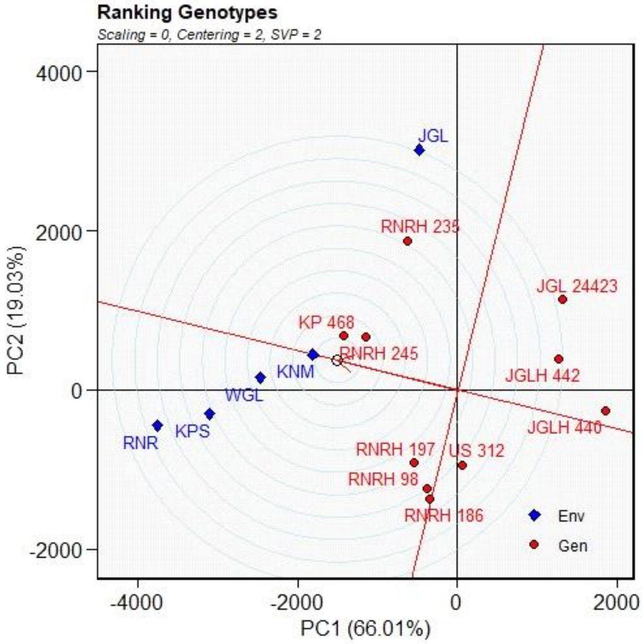


Fig. 5 : GGE Bi-plot ranking of genotypes based on grain yield and PC1.

An ideal genotype should have high mean performance and high stability across environments. An ideal genotype (located at the center of the concentric circle) to be a point on the AEA (Absolutely stable) in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive sides of AEA. Therefore, genotypes located closer to the "ideal genotype" are more desirable than the others. Thus, hybrids KP 468 was more desirable followed by RNRH 245 (Fig. 5). JGLH 440 was of course the poorest hybrid because it was consistently the poorest. According to the AMMI stability value (ASV), the hybrids having least ASV value are highly stable. According to the ASV value the genotypes with high stability were RNRH 245, KP 468 and US 312, whereas JGL 24423, RNRH 186 and JGLH 440 were highly unstable. Genotype Selection Index integrates both yield and stability across environments. Genotypes with low GSI value are highly desirable since

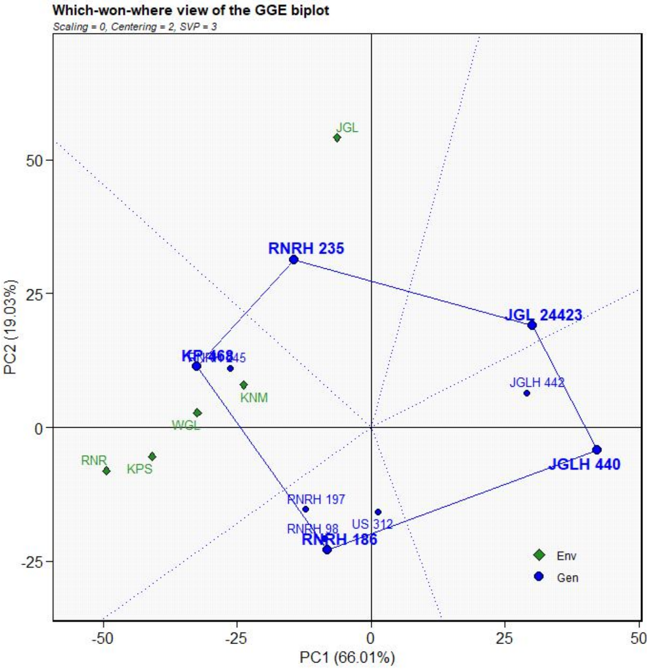


Fig. 6 : Which-won-where plot of rice hybrids and five environments.

Table 5 : AMMI stability value (ASV), Mean grain yield and Genotype selection index (GSI).

Genotype	ASV	rASV	Grain yield means	rYSI	GSI
KP 468	24.97	2	8080	1	3
RNRH 245	18.81	1	7886	2	3
RNRH 235	56.12	4	7718	3	7
RNRH 197	59.44	5	7193	4	9
RNRH 98	64.58	7	7072	5	12
RNRH 186	86.23	9	6878	6	15
US 312	37.66	3	6771	7	10
JGL 24423	99.13	10	6231	8	18
JGLH 442	62.75	6	6102	9	15
JGLH 440	68.39	8	5663	10	18

ASV- AMMI stability value; **YSI-**Yield selection index; **rASV-** rank of ASV; **rYSI-** rank of YSI; **GSI-** Genotype selection index.

they combine high yield and stability. The hybrid KP 468 followed by RNRH 245 were having low GSI value (Table 5).

Genotype Response to Specific Adaptation

Locating the most suitable hybrid for each location can be done by which-won-where pattern analysis. In this a polygon is created by joining the genotypes far away from origin consisting of all the genotypes inside the polygon (Fig. 6 which-won-where). The genotypes in a sector are similar in performance compared to genotypes in the other sectors. Many researchers found this biplot intriguing as it graphically addresses the important concepts such as crossover GE, mega environment differentiation, specific adaptation (Yan and Tinker, 2006; Mohan *et al.*, 2021). Based on the plot it was found out that the genotypes KP 468 and RNRH 245 are the best performing genotypes in the environments Rajendranagar, Kampasagar, Warangal, and Kunaram. Similarly, the hybrid RNRH 235 was found to be performing best in the environment Jagtial. The genotypes that were plotted at each vertex of the polygon were the best performing genotype to the environment near the vertex.

Conclusion

In conclusion, the comprehensive analysis of grain yield for rice hybrids across five diverse environments revealed significant contributions from environmental, genotypic and genotype-environment interaction effects. The genotypes KP 468, RNRH 245, RNRH 197 and RNRH 98 were found to be having high grain yield with positive IPCA scores. Notably, the genotypes, KP 468 and RNRH 245 emerged as top performers across multiple environments in yield capability, demonstrating their adaptability and consistently high yields. The stability analysis further underscored RNRH 245 as the most stable genotype, showcasing its reliability across diverse conditions. Among the environments, Kunaram stood out as an ideal and representative location, while Jagtial proved to be a discriminating environment. The which-won-where pattern analysis confirmed the suitability of KP 468 and RNRH 245 in various environments, reaffirming their potential for broader cultivation. These findings offer valuable insights for rice hybrid selection and cultivation strategies, emphasizing the significance of considering both genotypic and environmental factors in agricultural decision-making in the state of Telangana thus fully utilizing the maximum genotypic and environmental potential of the hybrids.

Acknowledgements

The work was conducted as a part of the Rice Crop Improvement of the Professor Jayashankar Telangana Agricultural University.

Authors contribution : All the authors have contributed equally.

Research content : The research content in this manuscript is original and has not been published or submitted elsewhere for publication.

Funding : The financial assistance for the said experiments was provided by Professor Jayashankar Telangana Agricultural University.

Ethical approval : Not applicable

Conflict of interest : Authors have no conflict of interest.

Data availability : Not applicable

References

Akter, A., Jamil Hasan M., Ummu Kulsum M., Lipi L.F., Begum H., Md Farhat Rahman N., Farhat T. and Ibne Baki M.Z. (2019). Stability and adaptability of promising hybrid rice genotypes in different locations of Bangladesh. *Adv. Plants Agricult. Res.*, **9(1)**, 35 – 39 (2019).

Akter, A., Jamil Hassan M., Umma Kulsum M.U., Rahaman M.H., Paul A.K., Lipi L.F. and Salma Akter (2015). Genotype x Environment interaction and yield stability analysis in hybrid rice (*Oryza sativa* L.) by AMMI Biplot. *Bangladesh Rice J.*, **19(2)**, 83-90 (2015).

Annicchiarico, P. and Perenzin M. (1996). Adaptation patterns and definition of macro environment for selection and recommendation of common wheat. Italy. *J. Plant Breed.*, **113**, 197-205 (1996).

Darai, R., Sarker A., Sah R.P., Pokhrel K. and Chaudhary R. (2017). AMMI Biplot Analysis for Genotype × Environment Interaction on Yield Trait of High Fe content Lentil Genotypes in Terai and Mid-Hill Environment of Nepal. *Annals Agricult. Crop Sci.*, **2(1)**, 1026-1030.

Farshadfar, E. and Sutka J. (2003). Locating QTLs controlling adaptation in wheat using AMMI model. *Cereal Research Communications*, **31**, 249–254.

Gauch, H.G. (1992) Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs. Amsterdam, Netherlands: Elsevier Science Publishers.

Gauch, H.G. and Zobel R.W. (1996). AMMI analysis of yield trials. In: Kang, M.S. and Gauch H.G. (Eds.), *Genotype-by environment interaction*. Boca Raton, FL, CRC Press, 85–122.

Gauch, H.G. (2006). Statistical analysis of yield trials by AMMI and GGE. *Crop Science*, **46**, 1488-1500.

Gauch, H.G., Piepho H.P. and Annicchiarico P. (2008). Statistical Analysis of Yield Trials by AMMI and GGE: Further Considerations. *Crop Science*, **48**, 866- 889.

Gruneberg, W.J., Manrique K., Zhang D. and Hermann M. (2005). Genotype × environment interactions for a diverse set of sweet potato clones evaluated across varying eco geographic conditions in peru. *Crop Science*, **45**, 2160-2171.

Kang, M.S. (2002). Genotype-environment Interaction: Progress and Prospects. In: "*Quantitative Genetics, Genomics and Plant Breeding*". CAB International, Wallingford, England: 221-243, (2002).

Kylash, K.S., Shiva Prasad G., Vanisri S. and Saida Naik D. (2023). Phenotypic screening and Single marker analysis for salinity resistance in rice (*Oryza sativa* L.). *Biological Forum – An Int. J.*, **15(10)**, 860-865.

Mahalingam, L., Mahendran S., Chandra-Babu R. and Atlim G. (2006). AMMI Analysis for Stability of Grain Yield in Rice (*Oryza sativa* L). *Int. J. Botany*, **2(2)**, 104–106.

Messina, C., Hammer G., Dong Z., Podlich D. and Cooper M. (2009). Modeling crop improvement in a G× E ×M framework via gene-trait-phenotype relationships. In: Sardas, V.O. and Calderini D. (Eds). Crop physiology. *Applications for genetic improvement and Agronomy*, 235-265.

Miranda, G.V., Souza L.V., Guimarães L.J.M., Namorato H., Oliveira L.R. and Soares M.O. (2009) Multivariate analyses of genotype x environment interaction of popcorn. *Pesq. agropec. Bras*, **44(1)**, 45-50.

Mohan, Y.C., Krishna L., Sreedhar S., Chandra B.S., Raju Ch. D., Madhukar P. and Ramana M.V. (2021). Stability analysis of rice hybrids for grain yield in Telangana through ammi and GGE Bi-plot model. *Int. J. Bio-Resource Stress Manage.*, **12(6)**, 687–695, (2021).

Olivoto, T. and Lúcio A.D. (2020). Metan: An R package for multi environment trial analysis. *Methods in Ecology and Evolution*, **11(6)**, 783–789.

Purchase, J.L., Hatting H. and Vandeventer C.S. (2000). Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. stability analysis of yield performance. *South Afr. J. Plant Soil*, **17**, 101–107.

Rao, P.J.M., Kishore N.S., Sandeep S., Neelima G., Rao P.M., Das D.M and Saritha A. (2020). Evaluation of performance and yield stability analysis based on AMMI and GGE-biplot in promising Pigeonpea [*Cajanus cajan* (L.) Millspaugh] genotypes. *Legume Res.*, 1-7.

RStudio: Integrated development environment for R (Computer software v0.98.1074). RStudio. http://www.rstudio.org/.

Yan, W., Hunt L.A., Sheng Q. and Szlavnics Z. (2000). Cultivar evaluation and mega environment investigation based on the GGE biplot. *Crop Science*, **40(3)**, 597-605.

Yan, W. and Tinker N.A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian J. Plant Sci.*, **86(3)**, 623-645.

Yan, W. and Tinker N.A. (2005). An Integrated Biplot Analysis System for Displaying, Interpreting, and Exploring Genotype × Environment Interaction. *Crop Science*, **45**, 1004-1016.

Zewdu, Z., Abebe T., Mitiku T., Worede F., Dessie A., Berie A. and Atnaf M. (2020). Performance evaluation and yield stability of upland rice (*Oryza sativa* L.) varieties in Ethiopia. *Cogent Food and Agriculture*, **6**, 1–13.