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GENOTYPE × ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY IN ADVANCED RICE BREEDING LINES EVALUATED USING AMMI AND GGE BIPLOTS

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ABSTRACT

Grain yield stability is important in rice breeding, as genotypes may perform differently under varying environmental conditions. The present study evaluated 40 rice genotypes along with three checks across three environments (*Kharif* 2022, *Rabi* 2022-23, *Kharif* 2023) to identify high-yielding and stable entries using additive main effects and multiplicative interaction (AMMI) and genotype plus genotype × environment (GGE) biplot analyses. AMMI-I identified RP6469-139 (G14) as a promising genotype, combining a high mean grain yield of 22.69 g plant^{-1} with relatively stable performance. The first two principal components of the GGE biplot explained 81.71% of total variation and it identified RP6469-56 (G21) recorded the highest mean grain yield (23.35 g plant^{-1}), whereas RP6469-139 (G14) showed a favourable combination of yield and stability. Genotypes were subsequently ranked based on their Yield Stability Index (YSI) values, with lower ranks (rYSI) indicating a more favourable combination of yield and stability and based on this a total of six promising genotypes were nominated for the All India Coordinated Research Project on Rice (AICRPR) trials during *Kharif* 2025 targeting various biotic and abiotic stresses. Based on the AICRPR screening results, RP 6469-173 (G29) exhibited moderate resistance to leaf blast (Susceptibility index (SI)- 4.0) and resistance to rice tungro disease (SI- 3.0), highlighting its potential for multiple disease resistance. RP 6469-143 (G28) exhibited tolerance to salinity and osmotic stress, with a low SES score of 3 under saline conditions, indicating its potential for improving tolerance to multiple abiotic stresses.

***Key words*:** Rice, AMMI, GGE biplot, genotype × environment interaction, grain yield, stability analysis

Introduction

Rice (*Oryza sativa* L.) is a major staple food crop worldwide and plays a vital role in food security. During 2024–25, rice cultivation in India covered 51.02 million hectares, yielding 150.18 million tonnes at an average productivity of 2.92 tonnes ha^{-1} (DA & FW, 2026). Enhancing grain yield while maintaining stability across environments remains a major objective of rice breeding, as yield is a complex trait influenced by several yield-attributing traits and environmental factors (Cooper *et al*., 1996; Yan and Kang, 2003; Gauch *et al*., 2008). Hybrid rice offers a 15–25% yield advantage over inbred varieties, however, its success depends on superior parental lines with desirable agronomic traits and strong combining ability (Bandela *et al*., 2026). Therefore, parental line improvement is essential for developing high-yielding and heterotic hybrids.

Genotype × environment interaction (G×E) can alter the relative performance of genotypes across environments, making selection based solely on mean yield unreliable. Multi-environment evaluation is therefore essential for identifying genotypes with broad or specific adaptation (Crossa, 1990; Yan *et al*., 2007). In particular, evaluating advanced breeding lines across diverse

environments enables the assessment of yield stability and the identification of promising lines for further testing and varietal development (Gauch *et al*., 2008; Chandra *et al*., 2022; Vikram *et al*., 2025).

Several statistical approaches are available for analysing genotype × environment interaction (G×E) and yield stability. The additive main effects and multiplicative interaction (AMMI) model combines analysis of variance with principal component analysis to quantify and visualize G×E patterns (Zobel *et al*., 1988; Gauch, 1992; Gauch *et al*., 2008). The genotype plus genotype × environment (GGE) biplot focuses on genotype and G×E effects, enabling the assessment of yield performance and stability, identification of environment-specific winners, and evaluation of test environments based on their discriminating ability and representativeness (Yan *et al*., 2000; Yan *et al*., 2007) Thus, both approaches provide complementary insights into genotype performance and adaptability.

The application of AMMI and GGE biplots in rice has been demonstrated across diverse genetic backgrounds and environments. Previous studies have highlighted their usefulness in identifying stable and environment-responsive genotypes, evaluating test environments, and emphasizing the need to consider yield and stability together for effective selection (Vanave *et al*., 2014; Koli *et al*., 2016; Ponnusamy *et al*., 2018; Chandra *et al*., 2022; Reshma *et al*., 2024; Vikram *et al*., 2025). Integrating mean yield with G×E analysis therefore facilitates the identification of genotypes with broad or specific adaptation and supports effective selection in rice breeding programmes.

Despite the extensive application of stability analysis in rice, the evaluation of advanced breeding lines for grain yield, stability and adaptability remains important because they represent potential candidates for further testing and varietal development. The All India Coordinated Rice Improvement Project (AICRIP), initiated by ICAR in 1965, facilitates the multidisciplinary evaluation of rice varieties, hybrids and production technologies across diverse agro-ecological conditions in India (Babu, 2015). Such multi-environment testing helps identify high-yielding, stable and widely adapted genotypes with resistance to major biotic and abiotic stresses for future rice improvement programmes.Therefore, in the present study ANOVA, AMMI and GGE biplot analyses were used to evaluate 40 advanced rice breeding lines and three released check varieties across three environments, with particular emphasis on identifying genotypes with stable grain yield performance.

Table 2: ANOVA for G × E interaction.

Source	Degrees of freedom	Sum of squares	Mean sum of squares
Genotype	42	563.33	13.41**
Environment	2	296.42	148.21**
G × E	84	1111.32	13.23**
Heterogeneity	42	339.10	8.07
Residual	42	772.23	18.39
Pooled error	252	1580.86	6.27
Total	386	3594.31	
** Significant at $P < 0.01$			

Materials and Methods

Experimental site and environments

The experiment was conducted at the Research Farm, Indian Institute of Rice Research (ICAR-IIRR), Hyderabad, India, located at 17°19' N latitude and 78°29' E longitude, at an altitude of 549 m above mean sea level. The experimental material was evaluated across three growing seasons, *viz*., *Kharif* 2022 (E1), *Rabi* 2022–23 (E2) and *Kharif* 2023 (E3), with each season considered as a distinct environment for the multi-environment analysis**.**

Plant material and experimental design

The experimental material comprised of 40 advanced breeding lines (G1–G40) and three released check varieties, BPT-5204 (C1), DRR Dhan 50 (C2) and RNR 15048 (C3), (Table 1). The RP lines included in the study were developed through the improvement of hybrid rice parental lines at ICAR-IIRR, with the objective of enhancing their genetic potential for multiple stress tolerance. The genotypes were evaluated in a randomized block design (RBD) with three replicates in each environment. Grain yield (GY) was recorded on a single-plant basis for each genotype in each replication and environment. The environment-wise grain yield data were subsequently subjected to multi-environment analysis to assess genotype × environment interaction, stability and adaptability of the genotypes.

Statistical analysis and stability assessment

Grain yield data was initially subjected to environment-wise analysis of variance (ANOVA), followed by combined ANOVA across environments to determine the effects of genotype (G), environment (E), and genotype × environment interaction (G×E). All statistical analyses were performed using R software (v4.6.1; R Core Team, 2026). The significant G×E interaction was further investigated using the additive main effects and multiplicative interaction (AMMI) model, which integrates

ANOVA for the additive effects of G and E with principal component analysis (PCA) to characterise the multiplicative G×E interaction. The AMMI model is:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^{N} \lambda_k \gamma_{ik} \delta_{jk} + \epsilon_{ij}$$

Where,

Y_{ij} is the mean grain yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; α_i and β_j are the genotype and environment deviations from the grand mean, respectively; λ_k is the singular value of the k^{th} interaction principal component axis (IPCA); γ_{ik} and δ_{jk} are the corresponding genotype and environment eigen vector scores; and ϵ_{ij} is the residual error (Dessie *et al.*, 2018).

The G×E interaction was decomposed into IPCAs using singular value decomposition (SVD), and the first two significant IPCAs were considered for AMMI biplot interpretation.

AMMI Stability Value (ASV)

The AMMI Stability Value (ASV) was calculated using the scores of IPCA1 and IPCA2 to quantify the stability of genotypes across environments. This index combines the contributions of the two interaction axes into a single measure, facilitating the comparative assessment of genotype stability. ASV was calculated using the following formula:

$$ASV = \sqrt{\frac{ss(IPCA1)}{ss(IPCA2)}} \times (IPCA\ 1)^2 + (IPCA\ 2)^2$$

A lower ASV indicates greater stability, reflecting a smaller contribution of G×E interaction to genotype performance, whereas a higher ASV indicates greater interaction effects and comparatively lower stability.

GGE biplot analysis

GGE biplot analysis was performed to assess genotype performance, stability, and environmental adaptability by examining the combined effects of genotype (G) and genotype × environment interaction (GE). The genotype × environment mean matrix was environment-centred by subtracting the grand mean and the respective environmental effects, thereby retaining the G+GE components. The resulting matrix was subjected to singular value decomposition (SVD), and the first two principal components (PC1 and PC2) were used to construct the GGE biplot (Yan *et al.*, 2000; Yan *et al.*, 2001). The model was expressed as:

$$Y_{ij} - \mu - \beta_j = \sum_{k=1}^{n} \lambda_k \gamma_{ik} \delta_{jk} + \epsilon_{ij}$$

Where,

Y_{ij} is the mean grain yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; β_j is the main effect of the j^{th} environment; λ_k is the singular value of the k^{th} principal component; γ_{ik} and δ_{jk} are the corresponding genotype and environment eigen vector scores; and ϵ_{ij} is the residual error.

Symmetric singular-value partitioning was used to obtain genotype and environment scores for the biplot. The resulting GGE biplots were used to evaluate genotype performance and stability, assess the discriminating ability and representativeness of test environments, and perform the which-won-where biplot to identify mega-environments and their respective winning genotypes (Yan *et al.*, 2000).

Results

The analysis of variance revealed significant effects of genotype, environment and genotype × environment interaction for grain yield (Table 2), indicating significant variation among genotypes and differential genotypic responses across environments. The significant G × E interaction justified further evaluation of genotype stability using AMMI and GGE biplot analyses. This confirms that both the genotypes and the test environments differed significantly for grain yield, and further, that the genotypes did not maintain a consistent rank across the three environments.

Based on the pooled per se mean performance across the three environments, the grand mean grain yield was 20.44 g plant^{-1}, with genotype means ranging from 18.63

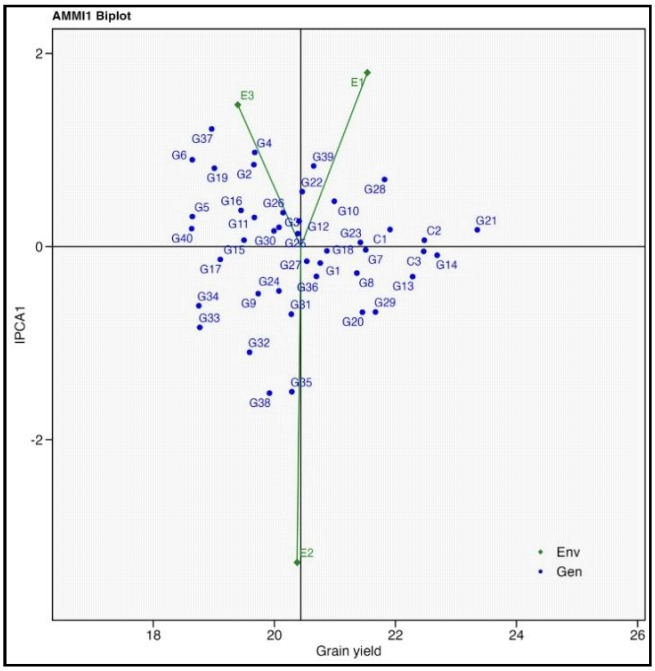


Fig. 1: AMMI1 biplot for grain yield (GY).

Table 1: List of genotypes used in the present study.

Code	Genotype	Pedigree/Source
G1	IND116	From IRRI
G2	IR17A1416	From IRRI
G3	IR17A1929	From IRRI
G4	IR17A2297	From IRRI
G5	IR17A2490	From IRRI
G6	IR17A2755	From IRRI
G7	RP6469-171	IR 36 GMSRPIDL
G8	RP6469-105	IR 36 GMSRPIDL
G9	RP6469-109	IR 36 GMSRPIDL
G10	RP6469-118	IR 36 GMSRPIDL
G11	RP6469-119	IR 36 GMSRPIDL
G12	RP6469-122	IR 36 GMSRPIDL
G13	RP6469-131	IR 36 GMSRPIDL
G14	RP6469-139	IR 36 GMSRPIDL
G15	RP6469-138	IR 36 GMSRPIDL
G16	RP6469-134	IR 36 GMSRPIDL
G17	RP6469-144	IR 36 GMSRPIDL
G18	RP6469-152	IR 36 GMSRPIDL
G19	RP6469-179	IR 36 GMSRPIDL
G20	RP6469-259	IR 36 GMSRPIDL
G21	RP6469-56	IR 36 GMSRPIDL
G22	RP6469-52	IR 36 GMSRPIDL
G23	RP6469-68	IR 36 GMSRPIDL
G24	RP6469-74	IR 36 GMSRPIDL
G25	RP6469-85	IR 36 GMSRPIDL
G26	RP6469-89	IR 36 GMSRPIDL
G27	RP6469-91	IR 36 GMSRPIDL
G28	RP6469-143	IR 36 GMSRPIDL
G29	RP6469-173	IR 36 GMSRPIDL
G30	WIL-4	Wild Introgression lines
G31	WIL-12	Wild Introgression lines
G32	WIL-15-12-38	Wild Introgression lines
G33	WIL-15-12-41	Wild Introgression lines
G34	WIL-24	Wild Introgression lines
G35	WIL-35	Wild Introgression lines
G36	WIL-44	Wild Introgression lines
G37	WIL-45-2	Wild Introgression lines
G38	WIL-54	Wild Introgression lines
G39	WIL-76	Wild Introgression lines
G40	WIL-143	Wild Introgression lines
C1	BPT-5204	Released variety
C2	DRR Dhan 50	Released variety
C3	RNR 15048	Released variety

GMSRPIDL: Genetic male sterile restorer population improvement derived line

g plant^{-1} in WIL-143 (G40) to 23.35 g plant^{-1} in RP6469-56 (G21). Nineteen genotypes recorded grain yields above the grand mean (Table 3). RP6469-56 (G21) recorded the highest pooled mean yield (23.35 g plant^{-1}), followed by RP6469-139 (G14, 22.69 g plant^{-1}), DRR Dhan 50 (C2, 22.48 g plant^{-1}), RNR 15048 (C3, 22.47 g plant^{-1}). Among the three checks, DRR Dhan 50 recorded the highest pooled mean yield, followed by RNR 15048 and BPT-5204 (21.91 g plant^{-1}). Notably, RP6469-56 (G21), RP6469-139 (G14) and RP6469-131 (G13) outperformed BPT-5204, while RP6469-56 (G21) and RP6469-139 (G14) also exceeded both DRR Dhan 50 and RNR 15048. These genotypes may therefore be considered promising for further multi-environment evaluation.

Stability analysis using AMMI biplots

The AMMI1 biplot (Fig. 1) revealed considerable variation in the interaction patterns of the genotypes, with those positioned closer to the horizontal axis exhibited relatively lower interaction with the environments. Among the evaluated entries, RP6469-139 (G14) recorded a favourable combination of high mean grain yield (22.69 g plant^{-1}) and a near-zero IPCA1 score, indicating relatively stable performance across environments. Similarly, RP6469-171 (G7) and RP6469-68 (G23) exhibited comparatively low IPCA1 scores, accompanied by mean grain yields of 21.51 and 21.42 g plant^{-1}, respectively. The check varieties DRR Dhan 50 (C2) and RNR 15048 (C3) also demonstrated relatively stable performance, with mean grain yields of 22.48 and 22.47 g plant^{-1}, respectively. In contrast, genotypes such as WIL-35 (G35), WIL-54 (G38) and WIL-45-2 (G37) exhibited larger IPCA1 scores, indicating greater interaction with the environments. Although RP6469-56 (G21) recorded the highest mean grain yield (23.35 g plant^{-1}), its IPCA1 score (-0.17) and ASV (0.725) indicated some degree of interaction with the environments.

The AMMI2 biplot (Fig. 2), constructed using the

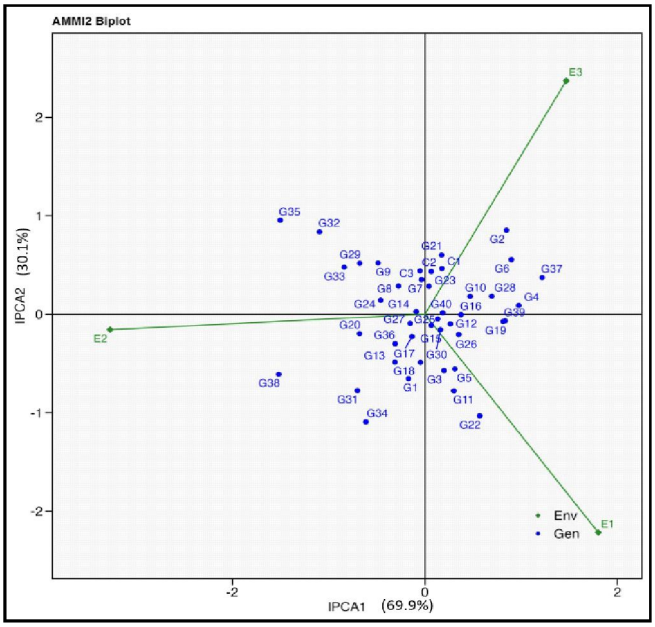


Fig. 2: AMMI2 biplot for grain yield (GY).

first two interaction principal component axes (IPCA1 and IPCA2), further explained the stability patterns of the evaluated genotypes. RP6469-139 (G14), RP6469-138 (G15), RP6469-85 (G25), RP6469-68 (G23) and RP6469-171 (G7) were positioned relatively close to the origin, indicating their lower genotype × environment interaction (GEI). This visual interpretation was supported by the AMMI stability value (ASV), which identified RP6469-138 (G15), RP6469-139 (G14), RP6469-68 (G23), RP6469-85 (G25) and RP6469-171 (G7) as the genotypes with the lowest ASV values (Table 3), further supporting their relatively high stability across the test environments. Considering both mean grain yield and stability, RP6469-139 (G14) was identified as a promising entry with a low ASV (0.21). RP6469-171 (G7) and RP6469-68 (G23) also demonstrated favourable combinations of yield and stability. The check varieties DRR Dhan 50 (C2) and RNR 15048 (C3) also exhibited favourable yield performance, recording 22.48 and 22.47 g plant^{-1}, respectively, with relatively low ASV values. In contrast, WIL-35 (G35), WIL-54 (G38), WIL-15-12-38 (G32) and WIL-24 (G34) were located farther from the origin, indicating greater interaction with the environments. These findings highlight the importance of considering mean grain yield along with stability parameters for identifying superior genotypes suitable for evaluation in subsequent breeding trials.

Stability analysis using GGE biplots

From the GGE biplot (Fig. 3), the first two principal components, PC1 and PC2, explained 47.58% and 34.13% of the total G + GE variation, respectively, accounting for 81.71% of the variation represented in the biplot. The GGE biplot also revealed that genotypes positioned closer to the origin exhibited comparatively lower interaction with the environments. Among the evaluated entries, RP6469-139 (G14), RP6469-138 (G15), RP6469-85 (G25), RP6469-91 (G27) and RP6469-68 (G23) had comparatively stable performance.

The discriminativeness versus representativeness biplot revealed that E2 exhibited the longest environmental vector, indicating the greatest discriminating ability among the three test environments. The environmental vectors differed in their orientations, suggesting contrasting patterns of genotype response. The which-won-where GGE biplot (Fig. 4) showed the specific association of genotypes with the three test environments. The polygon formed by the genotypes located farthest from the origin, and the environments fell into different sectors, indicating differences in genotype performance across environments. E3 was located in the sector associated with RP6469-56 (G21), indicating that G21 had the highest estimated performance in E3. E1 was positioned in the sector associated with WIL-45-2 (G37), suggesting that WIL-45-2 (G37) performed best in E1. Similarly, E2 fell in the sector associated with G35 (WIL-35), indicating that G35 (WIL-35) was the winning genotype for E2. Thus, the biplot indicated different winning genotypes for the three environments, showing the presence of specific adaptation among the genotypes.

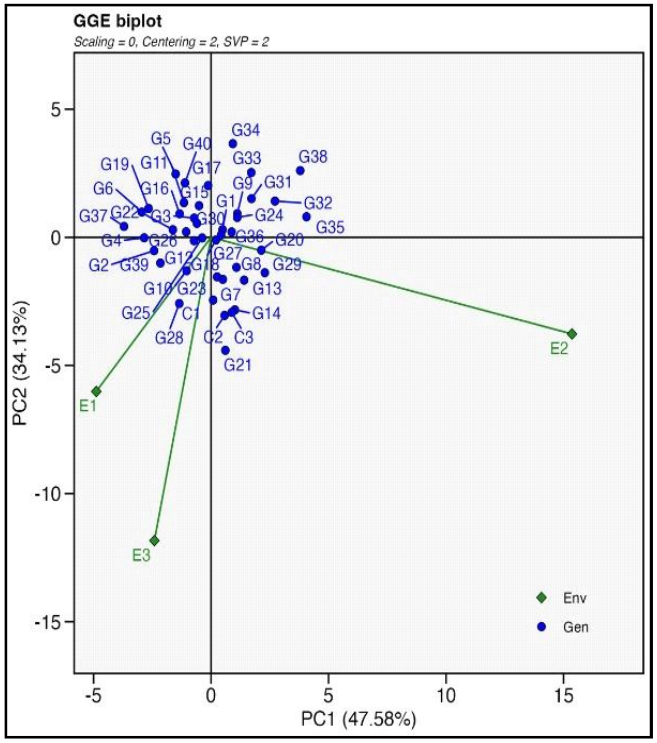


Fig. 3: GGE biplot grain yield (GY).

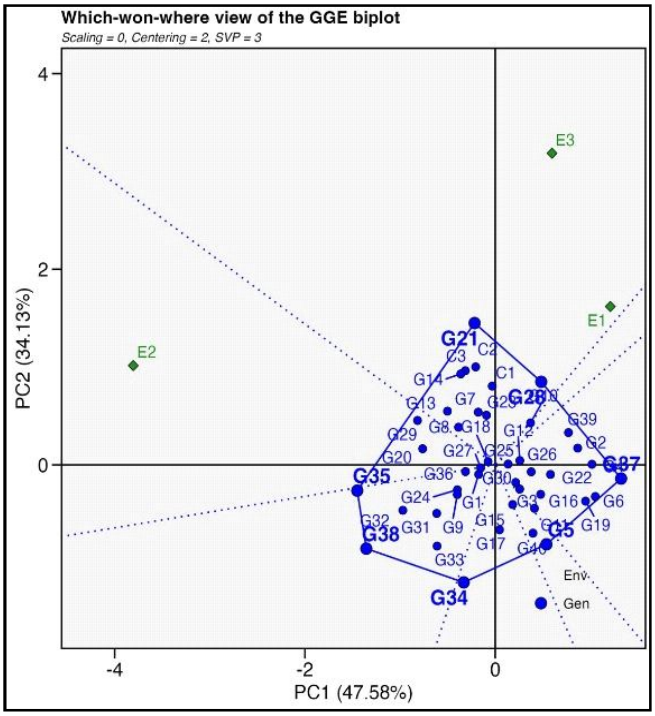


Fig. 4: Which-won-where biplot for grain yield (GY).

Table 3: AMMI (IPCA1, IPCA2, ASV, YSI, rASV, rYSI) and GGE (PC1, PC2) stability scores of genotypes for grain yield (GY).

Code	Genotype	Mean GY (g)	AMMI IPCA1	AMMI IPCA2	ASV	YSI	rASV	rYSI	GGE PC1	GGE PC2
G1	IND116	20.76	-0.17	-0.65	0.76	33	18	15	-0.70	-0.36
G2	IR17A1416	19.66	0.85	0.85	2.15	69	37	32	3.50	0.64
G3	IR17A1929	20.08	0.20	-0.57	0.74	42	17	25	1.04	-0.92
G4	IR17A2297	19.68	0.97	0.09	2.27	69	39	30	4.10	0.02
G5	IR17A2490	18.64	0.31	-0.55	0.91	64	23	41	2.17	-3.02
G6	IR17A2755	18.64	0.90	0.56	2.16	80	38	42	4.25	-1.20
G7	RP6469-171	21.51	-0.03	0.35	0.36	14	5	9	-0.72	2.00
G8	RP6469-105	21.36	-0.27	0.29	0.70	27	15	12	-1.56	1.43
G9	RP6469-109	19.73	-0.49	0.52	1.25	56	27	29	-1.61	-1.13
G10	RP6469-118	20.99	0.47	0.18	1.11	39	26	13	1.50	1.59
G11	RP6469-119	19.67	0.30	-0.78	1.05	55	24	31	1.67	-1.65
G12	RP6469-122	20.41	0.26	-0.10	0.62	34	14	20	1.04	0.16
G13	RP6469-131	22.28	-0.31	-0.49	0.87	26	21	5	-2.03	2.04
G14	RP6469-139	22.69	-0.09	0.03	0.21	4	2	2	-1.46	3.46
G15	RP6469-138	19.50	0.07	-0.11	0.19	35	1	34	0.74	-1.51
G16	RP6469-134	19.45	0.37	0.00	0.87	57	22	35	1.93	-1.12
G17	RP6469-144	19.11	-0.13	-0.23	0.38	43	7	36	0.18	-2.47
G18	RP6469-152	20.87	-0.04	-0.49	0.50	26	12	14	-0.30	0.13
G19	RP6469-179	19.01	0.81	-0.07	1.89	71	34	37	3.83	-1.38
G20	RP6469-259	21.45	-0.68	-0.20	1.59	38	28	10	-3.08	0.61
G21	RP6469-56	23.35	0.17	0.60	0.73	17	16	1	-0.88	5.39
G22	RP6469-52	20.46	0.57	-1.03	1.68	50	31	19	2.34	-0.36
G23	RP6469-68	21.42	0.04	0.29	0.30	14	3	11	-0.37	1.89
G24	RP6469-74	20.08	-0.46	0.14	1.08	51	25	26	-1.61	-0.95
G25	RP6469-85	20.39	0.13	-0.05	0.32	25	4	21	0.55	0.03
G26	RP6469-89	20.14	0.35	-0.21	0.84	44	20	24	1.53	-0.26
G27	RP6469-91	20.54	-0.15	-0.09	0.37	24	6	18	-0.62	-0.11
G28	RP6469-143	21.82	0.69	0.18	1.63	36	29	7	1.95	3.16
G29	RP6469-173	21.67	-0.68	0.52	1.66	38	30	8	-3.30	1.69
G30	WIL-4	19.99	0.16	-0.16	0.41	35	8	27	0.87	-0.67
G31	WIL-12	20.28	-0.70	-0.77	1.80	56	33	23	-2.48	-1.84
G32	WIL-15-12-38	19.59	-1.09	0.84	2.68	73	40	33	-3.92	-1.73
G33	WIL-15-12-41	18.77	-0.84	0.48	2.01	75	36	39	-2.47	-3.09
G34	WIL-24	18.75	-0.61	-1.09	1.79	72	32	40	-1.34	-4.46
G35	WIL-35	20.29	-1.50	0.96	3.62	65	43	22	-5.85	-0.98
G36	WIL-44	20.69	-0.31	-0.30	0.78	35	19	16	-1.26	-0.26
G37	WIL-45-2	18.96	1.22	0.37	2.86	79	41	38	5.34	-0.52
G38	WIL-54	19.92	-1.52	-0.61	3.58	70	42	28	-5.47	-3.18
G39	WIL-76	20.65	0.83	-0.07	1.94	52	35	17	3.11	1.23
G40	WIL-143	18.63	0.19	0.02	0.43	52	9	43	1.60	-2.59
C1	BPT-5204	21.91	0.18	0.47	0.62	19	13	6	-0.13	2.99
C2	DRR Dhan 50	22.48	0.07	0.44	0.46	14	11	3	-0.83	3.72
C3	RNR 15048	22.47	-0.05	0.44	0.46	14	10	4	-1.27	3.58

IPCA1: First Interaction Principal Component Axis, IPCA2: Second Interaction Principal Component Axis; ASV: AMMI Stability Value; YSI: Yield Stability Index; rASV: Rank of AMMI Stability Value; rYSI: Rank of Yield Stability Index; PC1: First Principal Component; PC2: Second Principal Component.

Table 4: Performance of the entries and checks for rice blast.

Genotype /check	Role	SI	Locations with score ≤ 3 (PI)	Locations with score ≤ 5 (PI)
RP 6469-139	Test entry	3.9	7/15 (47%)	14/15 (93%)
RP 6469-173	Test entry	4.0	5/15 (33%)	14/15 (93%)
HR-12	Susceptible check	6.5	1/15 (7%)	4/15 (27%)
Tetep	Resistant check	3.9	5/15 (33%)	14/15 (93%)

(**Source**: ICAR-IIRR, Progress Report, AICRPR 2025, Volume II, DSN leaf-blast screening); SI, susceptibility index; PI, Promising index of locations.

Identification of stable, high-yielding genotypes

The combined assessment of mean grain yield plant^{-1} and stability using the ranks of yield stability index (rYSI) identified RP6469-56 (G21) as the most promising entry based on its highest mean grain yield (23.35 g plant^{-1}) and lowest YSI rank (1). RP6469-139 (G14) also exhibited a favourable combination of high yield (22.69 g plant^{-1}) and stability (ASV = 0.210; YSI rank = 2). Among the check varieties, DRR Dhan 50 and RNR 15048 exhibited superior overall performance, combining desirable grain yield with greater stability across environments. Although RP6469-138 recorded the lowest ASV (0.192), its comparatively lower yield resulted in a less favourable YSI rank. Overall, the combined interpretation based on grain yield plant^{-1} and YSI ranks highlighted RP6469-56, RP6469-139, RP6469-131, RP6469-143, RP6469-171 and RP6469-173 as promising genotypes for further evaluation (Table 3). Based on their promising performance in previous screenings conducted at ICAR-IIRR, these six genotypes were nominated for - screening at multiple locations under the All India Coordinated Research Project on Rice (AICRPR) trials during *Kharif*, 2025, targeting various biotic and abiotic stresses (ICAR-IIRR, Progress Report, AICRPR 2025, Volume II and III). The results of these evaluations are presented in Tables 4–8.

Performance of the entries and checks under biotic and abiotic stress conditions (AICRPR, *Kharif* 2025)

Screening for rice blast: The Donor Screening Nursery (DSN) was evaluated for rice blast during *Kharif* 2025 across 18 locations. Of these, 15 locations were considered for selection after excluding those with inadequate disease pressure. Screening was conducted under both natural and artificial infection conditions, and the results are presented in Table 4. RP 6469-139 exhibited a susceptibility index (SI) of 3.9, comparable to that of the resistant check Tetep (3.9), highlighting its potential for leaf blast resistance. Similarly, RP 6469-173, with a SI of 4.0, was classified as moderately resistant to leaf blast.

Table 5: Performance of the entries and checks for rice tungro disease.

Genotype/ check	Role	CB	HB	SI	PI ≤ 3	PI ≤ 5
RP 6469-173	Test entry	3	3	3.0	100%	100%
RP 6469-171	Test entry	-	-	4.0*	-	-
TN1	Susceptible check	7	7	7.0	0%	0%
Vikramarya	Resistant check	5	3	4.0	50%	100%

CB: Coimbatore; HB: IIRR, Hyderabad
(**Source**: ICAR-IIRR, Progress Report, AICRPR 2025, Volume II, rice tungro disease screening). SI, susceptibility index; PI, Promising index of locations. *The score of 4.0 for RP 6469-171 is reported in the multiple-disease reaction record and is not presented as a location-based SI. "–" indicate data not reported in the corresponding RTD screening table.

Screening for rice tungro disease: Rice tungro disease screening was conducted in the Donor Screening Nursery (DSN) during *Kharif* 2025 under artificial infection conditions at Coimbatore and ICAR-IIRR, Hyderabad. The results are presented in Table 5. From the screening, RP 6469-173 was identified as resistant, recording a susceptibility index (SI) of 3.0, whereas RP 6469-171 was classified as moderately resistant, with a SI of 4.0.

Screening for salinity stress: Seedling-stage salinity screening was conducted at a salinity level of 12 dS m^{-1} across eight locations. Data from Coimbatore (CBT) were excluded from the analysis because the tolerant check did not meet the prescribed threshold. Table 6 presents the mean physiological measurements of the three test entries along with the standard checks. Under saline conditions, RP 6469-143 exhibited the most promising response among the test entries, recording the highest root dry weight (0.081 g), shoot length (22.57 cm) and chlorophyll content (1.182 mg g^{-1} dry weight), along with a low SES score of 3, comparable to the tolerant checks FL478 and Rahaspanjar. RP 6469-131 also demonstrated favourable growth, with a shoot length of 19.70 cm and chlorophyll content of 1.030 mg g^{-1} dry weight, while RP 6469-56 recorded the highest root length (7.96 cm) and shoot dry weight (0.094 g) among the test entries. In contrast, the susceptible checks IR29 and Naveen recorded SES scores of 9 and 7, respectively, indicating greater sensitivity to salinity. These findings highlight RP 6469-143 as a promising source of salinity tolerance.

Table 6: Performance of the entries and checks for salinity stress.

Genotype/check	Role	RL	SL	RDW	SDW	CC	SES	SR
RP 6469-131	Test entry	7.12	19.70	0.057	0.083	1.030	NR	NR
RP 6469-56	Test entry	7.96	16.77	0.066	0.094	1.071	NR	NR
RP 6469-143	Test entry	7.76	22.57	0.081	0.090	1.182	3	NR
FL478	Tolerant check	NR	NR	NR	NR	NR	3	0.78
Rahaspanjar	Tolerant check	NR	NR	NR	NR	NR	3	0.82
IR29	Susceptible check	NR	NR	NR	NR	NR	9	2.32
Naveen	Susceptible check	NR	NR	NR	NR	NR	7	NR

RL: Root length (cm); SL: Shoot length (cm); RDW: Root dry weight (g); SDW: Shoot dry weight (g); CC: Chlorophyll content (mg g^{-1} dry weight); SES: SES score; SR: Shoot Naz /Kz ratio; **(Source**: ICAR-IIRR, Progress Report, AICRPR 2025, Volume III, salinity stress assessment). NR: Not reported; SES, Standard Evaluation System.

Screening for osmotic stress: Seedling-stage osmotic stress screening was conducted at nine research centres using 1% and 2% mannitol in hydroponic nutrient solution. The results are presented in Table 7. Under 2% mannitol-induced osmotic stress, RP 6469-143 recorded the highest tolerance score (6.75), followed by Vandana (6.44), indicating their promising potential for osmotic stress tolerance. RP 6469-131 exhibited the highest germination percentage (92.36%) and comparatively high total chlorophyll content (0.967 mg/100 g FW). RP 6469-143 also maintained a considerable chlorophyll content of 0.705 mg/100 g FW, further supporting its potential under osmotic stress. Collectively, these findings identified RP 6469-143 and RP 6469-131 as promising lines for osmotic stress tolerance and drought tolerance.

Screening for anaerobic germination: Anaerobic germination was evaluated across 10 locations. The anaerobic germination index (AGI) was calculated as the ratio of germination percentage under anaerobic conditions to that under aerobic conditions, expressed as percentage. The results are presented in Table 8. Under anaerobic germination conditions, RP 6469-56 exhibited the highest mean anaerobic germination index (AGI) of 51.22% among the test entries, followed by RP 6469-143 (45.98%) and RP 6469-131 (38.09%). RP 6469-56 exhibited favourable responses at Faizabad (95.71%), Karjat (89.04%) and Maruteru (64.00%), indicating its ability to germinate under waterlogged conditions across multiple locations. The performance of RP 6469-56 highlights its potential as a promising genetic resource for improving anaerobic germination tolerance. Collectively, these findings suggest that RP 6469-56 could be used in rice breeding programmes targeting improved crop establishment under flood-prone conditions.

Discussion

The increasing global demand for food highlights the importance of hybrid rice, which offers a 15–25% yield advantage over conventional inbred varieties. Developing high-yielding, stress-tolerant hybrids requires superior parental lines with desirable agronomic traits and strong combining ability (Ponnuswamy *et al.*, 2020). Since genotype performance varies across environments, AMMI and GGE biplot analyses provide valuable tools for assessing yield stability, environmental adaptability and G×E interactions (Yan *et al.*, 2000; Yan, 2001; Yan and Kang, 2003; Yan and Tinker, 2005; Gauch, 2006).

In the present study, the significant G × E interaction from ANOVA justified further evaluation of genotype stability using AMMI and GGE biplot analyses (Jain *et al.*, 2018; Parimala *et al.*, 2019). The AMMI2 biplot revealed that IPCA1 and IPCA2 accounted for 69.9% and 30.1% of the G×E interaction, respectively, together explaining the entire interaction variation. This indicates that the two principal interaction axes ftaken the differential responses of genotypes across environments, consistent with previous AMMI-based studies in rice (Jain *et al.*, 2018; Panda *et al.*, 2025; Vikram *et al.*, 2025). Genotypes positioned close to the origin exhibited relatively low G×E interaction and greater stability, whereas those farther from the origin showed stronger environmental interaction. Notably, RP6469-139 (G14), RP6469-138 (G15), RP6469-85 (G25), RP6469-68 (G23) and RP6469-171 (G7) showed low interaction effects, indicating their potential for stable performance across environments.

The GGE biplot further explained genotype and G×E

Table 7: Performance of the entries and checks for osmotic stress.

Genotype	Role	TM	GN	TC
RP 6469-143	Test entry	6.75	NR	0.705
RP 6469-131	Test entry	NR	92.36	0.967
RP 6469-56	Test entry	NR	NR	NR
Vandana	Comparison entry	6.44	NR	NR

TM: Tolerance score under 2% mannitol; GN: Germination (%); TC: Total chlorophyll (mg/100 g FW) **(Source**: ICAR-IIRR, Progress Report, AICRPR 2025, Volume III, osmotic stress assessment). FW: Fresh weight.

Table 8: Performance of the entries and checks for anaerobic germination.

Genotype/check	Role	CBT	FZB	KRK	KJT	KAUL	PTB	MTU	PNR	TTB	CRRI	Mean AGI (%)
RP 6469-131	Test entry	33.33	58.72	66.67	43.32	13.64	10.00	20.20	59.09	50.94	25.00	38.09
RP 6469-56	Test entry	10.00	95.71	89.04	35.84	22.73	50.00	64.00	68.09	25.58	NR	51.22
RP 6469-143	Test entry	20.00	100.00	60.24	29.90	23.08	40.00	52.17	50.97	37.50	NR	45.98
Rahaspanjar	Tolerant check	82.70	49.41	47.16	57.14	50.00	50.63	53.85	88.07	59.87	NR	59.87
FL478	Susceptible check	37.30	45.50	43.62	13.64	16.67	21.05	45.45	27.84	NR	NR	31.38
IR29	Susceptible check	22.22	47.73	25.00	46.30	27.27	28.57	43.81	11.14	NR	NR	31.51

(Source: ICAR-IIRR, Progress Report, AICRPR 2025, Volume III, anaerobic germination assessment). AGI, anaerobic germination index; NR, not reported; FW, fresh weight; CBT, Coimbatore; IIRR, ICAR-Indian Institute of Rice Research; FZB, Faizabad; KRK, Karjat; KJT, Karnataka (as coded in the report); KAUL, Kaul; PTB, Pattambi; MTU, Maruteru; PNR, Ponnampet; TTB, Tirur; CRRI, Central Rice Research Institute.

variation, with PC1 and PC2 accounting for 47.58% and 34.13% of the total variation (81.71%), respectively. E1 and E3 showed similar patterns of genotype responses, whereas E2 exhibited a distinct response, suggesting differential environmental influences on genotype performance. The discriminativeness vs representativeness biplot revealed that E2 exhibited the longest environmental vector, indicating the greatest discriminating ability among the three test environments. The which-won-where analysis identified RP6469-56 (G21) as the vertex genotype for E3, WIL-45-2 (G37) for E1 and WIL-35 (G35) for E2, highlighting their specific adaptation to these environments. Similar applications of GGE biplot analysis for identifying discriminating environments and environment-specific genotypes have been reported in rice by Laxami *et al*., 2017; Chandra *et al*., 2022.

Considering both yield performance and stability, RP6469-56 recorded the highest mean grain yield (23.35 g plant^{-1}), with a low IPCA1 score, indicating a favourable combination of grain yield plant^{-1} and stability. RP6469-139 also exhibited high mean yield (22.69 g plant^{-1}) and low interaction effects, suggesting its potential for broad adaptation. Overall, the combined interpretation based on grain yield plant^{-1} and YSI ranks identified RP6469-56, RP6469-139, RP6469-131, RP6469-143, RP6469-171 and RP6469-173 as promising genotypes for further evaluation under AICRPR. These findings highlight the importance of integrating yield performance with stability analysis to identify superior rice genotypes.

The All India Coordinated Research Project on Rice (AICRPR) provided a valuable platform for evaluating promising entries across environments under diverse biotic and abiotic stresses. Among the entries evaluated, RP 6469-139 was identified as resistant to leaf blast, while RP 6469-171 exhibited a moderately resistant reaction to rice tungro disease (RTD), with a SI score of 4.0. RP 6469-173, was classified as moderately resistant to leaf blast and resistant to rice tungro disease (RTD), suggesting its utility as a potential donor for improving resistance to both diseases. Further evaluation of these genotypes across environments would facilitate their effective utilisation in future resistance breeding programmes.

The entries were evaluated across AICRIPR centres for tolerance to three major abiotic stresses: anaerobic germination (AG), salinity (12 dS m^{-1}) and osmotic stress induced by 1% and 2% mannitol. Under 2% mannitol-induced osmotic stress, RP 6469-143 recorded the highest tolerance score (6.75), followed by Vandana (6.44), whereas RP 6469-131 exhibited the highest germination percentage (92.36%), indicating its ability to maintain germination under severe osmotic stress. These promising responses highlight the potential of these genotypes as valuable genetic resources for developing drought-resilient rice varieties suited to water-deficient conditions. RP 6469-143 also demonstrated tolerance to salinity and osmotic stress, as evidenced by its low SES score and moderate shoot Naz /Kz ratio under saline conditions, highlighting its potential for improving tolerance to multiple abiotic stresses. Furthermore, RP 6469-56 was identified as tolerant to anaerobic germination, suggesting its utility in breeding rice cultivars adapted to flood-prone environments. The integration of these multi-stress evaluations with yield performance and stability assessments provides a comprehensive basis for identifying superior parental lines to develop high-yielding rice varieties or hybrids with enhanced resilience to diverse environmental stresses.

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