



RESEARCH ARTICLE

Stability and adaptability analysis of rice (*Oryza sativa* L.) genotypes across contrasting seasonal environments using AMMI, WAASB and multi-trait stability indices

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Abstract

Evaluation across contrasting crop seasons is important for identifying rice (*Oryza sativa* L.) genotypes with stable performance under variable field conditions. In the present study, 16 rice genotypes were evaluated across three seasonal environments at Rudrur to assess grain yield stability, adaptability and genotype $\times$ environment interaction. The experiment was conducted under recommended agronomic practices and grain yield data were subjected to stability analysis using the additive main effects and multiplicative interaction (AMMI) model and the best linear unbiased prediction (BLUP) approach. Stability was further assessed using the weighted average of absolute scores from the BLUP (WAASB) index and the AMMI stability value (ASV). Significant differences were observed among genotypes, environments and genotype $\times$ environment interactions, indicating that the performance of genotypes varied considerably across seasonal conditions. The AMMI analysis effectively partitioned the interaction effects, with the first two interaction principal component axes explaining most of the genotype $\times$ environment interaction variation. Based on WAASB and ASV, the genotypes RDR5289, KNM1638 and JGL24423 exhibited high stability and consistent grain yield across the tested environments. Multi-trait stability analysis further identified KNM1638 as the most balanced genotype, combining stable grain yield with desirable expression of important agronomic traits. Among the test environments, kharif 2022 provided the most stable conditions for evaluating genotype performance. The identified stable genotypes can be utilised for multilocation testing, varietal recommendation and as valuable parental lines in rice breeding programmes aimed at developing high-yielding cultivars with broad adaptation and stable performance under diverse seasonal environments.

Keywords: additive main effects and multiplicative interaction analysis; genetic variability; genotype $\times$ environment interaction; multi-trait stability index; rice; yield stability

Introduction

Rice remains the principal food crop supporting the livelihood and nutritional security of a large section of the population in India (1). Despite its wide cultivation, yield levels are often inconsistent across regions and seasons, particularly under the agro-climatic conditions of Telangana where fluctuations in rainfall, temperature and humidity are common between kharif and rabi seasons (2–4). Such variability frequently results in differential genotype responses across seasons, making the identification of superior and stable

genotypes more challenging.

One of the major reasons for this inconsistency is genotype $\times$ environment (G $\times$ E) interaction, which influences the relative performance of genotypes under different environmental conditions (5). In practical breeding programmes, this interaction complicates selection, as genotypes performing well in one season may not maintain the same level of performance in another. Therefore, selection based only on mean yield may not be reliable and evaluation of stability across environments becomes essential (6).

To address this issue, multi-environment trials are conducted to assess genotype adaptability under diverse conditions (6–8). Among the available analytical approaches, the additive main effects and multiplicative interaction (AMMI) model have been widely used to partition and interpret interaction effects effectively. More recently, stability indices such as weighted average of absolute scores from best linear unbiased prediction (BLUPWAASB) and multi-trait stability index (MTSI) have gained importance, as they allow simultaneous evaluation of yield along with associated agronomic traits (9). These approaches are particularly useful in crops like rice, where multiple traits collectively influence productivity and adaptability under varying environments (10).

Several earlier studies have successfully applied AMMI and genotype and genotype $\times$ environment interaction (GGE) biplot approaches for evaluating genotype stability and adaptability in rice under contrasting environments (11–17). Recent studies have also highlighted the usefulness of integrated stability indices, environmental characterisation and multivariate approaches for identifying stable rice genotypes across varying environments (18–22).

Although these methods are increasingly applied, studies integrating seasonal environmental variation with multi-trait stability analysis under Indian conditions remain limited. In particular, understanding how variations in temperature, rainfall and humidity during critical growth stages influence genotype performance is essential for improving selection efficiency.

Given these considerations, the present study was undertaken to evaluate rice (*Oryza sativa* L.) genotypes across contrasting seasonal environments at Rudrur. Unlike conventional studies that focus primarily on mean yield, this work integrates seasonal variation (kharif and rabi) with AMMI-based interaction analysis and multi-trait stability indices. Special emphasis was given to relating genotype performance with key weather variables during the reproductive stage. This combined approach provides a more comprehensive framework for identifying rice genotypes with stable seasonal performance under variable environmental conditions.

Materials and Methods

Plant material and experimental environments

Sixteen rice (*O. sativa*) genotypes obtained from the biotic breeding programme of the Rice Section at Regional Sugarcane and Rice Research Station (RS and RRS), Rudrur, were used in the present study. The experimental material consisted of advanced breeding lines and released varieties representing diverse genetic backgrounds.

Field evaluation was carried out across three contrasting seasonal environments at RS and RRS, Rudrur, Nizamabad, Telangana. The trials were conducted during kharif 2022 (Environment 1), rabi 2022–23 (Environment 2) and kharif 2023 (Environment 3). These seasons differ in temperature regime, rainfall pattern and relative humidity, thereby providing suitable conditions to assess genotype performance under varying environments.

The experimental site was located at Rudrur, Nizamabad, Telangana (18.68° N latitude and 77.90° E longitude) at an altitude of approximately 404 m above mean sea level. The experimental soil was clay loam in texture with slightly alkaline reaction (pH 7.6), medium organic carbon content (0.58 %) and medium fertility status. The soil contained available nitrogen 248 kg ha⁻¹, available phosphorus 32 kg ha⁻¹ and available potassium 410 kg ha⁻¹, which are considered suitable for rice cultivation.

Experimental design and crop management

The experiments were laid out in a randomised block design (RBD) with 3 replications in each environment. Each genotype was grown in plots of 12 m² with a spacing of 20 cm between rows and 15 cm between plants. In kharif (June 2nd week to October last week), 27 days old seedlings and in rabi (December 1st week to May last week), 35-days old seedlings were transplanted. Recommended agronomic practices were followed uniformly across all environments to minimise non-experimental variation. A basal dose of fertilisers was applied as per regional recommendations, followed by split application of nitrogen at critical growth stages. Irrigation was provided as required depending on seasonal conditions. Standard plant protection measures were adopted to control pests and diseases.

Trait measurement

Observations were recorded on grain yield and important agronomic traits. Data were collected from ten randomly selected plants from the central rows of each plot to avoid border effects. The traits measured included grain yield (kg ha⁻¹), days to 50 % flowering, plant height (cm), panicle length (cm), number of panicles m⁻², number of filled grains panicle⁻¹ and test weight (g). Grain yield was recorded on a plot basis and grain yield values were adjusted to 13 % moisture content before conversion to kg ha⁻¹.

Statistical analysis

Pooled analysis of variance was conducted to evaluate the effects of genotype, environment and G $\times$ E interaction. Normality and homogeneity of variance assumptions were examined prior to pooled analysis of variance (ANOVA) analysis. The AMMI model was used to further analyse the interaction component. Genotypic performance and variance components were estimated using restricted maximum likelihood. Stability parameters were calculated using WAASB, AMMI stability value (ASV) and MTSI. Statistical analyses were carried out using R software version 4.5.0. The AMMI-based stability indices were calculated using the metan R package (23).

The AMMI model was fitted according to the following equation:

$$Y_{ge} = \mu + G_g + E_e + \sum \lambda_n \gamma_{gn} \delta_{en} + p_{ge} + \epsilon_{ger}$$

where μ is the grand mean, G_g is the genotype effect, E_e is the environment effect, λ_n is the singular value for the n th interaction principal component axis (IPCA), γ_{gn} and δ_{en} are genotype and environment eigenvectors respectively, p_{ge} represents the residual interaction effect and ϵ_{ger} is the residual error. Interaction principal components with significant contribution and higher explained variation were retained for interpretation. Genotype effects were treated as fixed, whereas environmental effects were considered random. The BLUP-based stability analysis and MTSI computation were performed using the metan package in R software version 4.5.0. The AMMI and GGE interpretation procedures followed standard statistical approaches described previously (24).

Weekly meteorological observations recorded during critical crop growth stages were used to characterise environmental variation across seasons. Detailed weekly weather parameters across environments are presented in Supplementary Table 1. Weather data including rainfall (mm), maximum temperature (°C) and relative humidity (%) were recorded during the flowering to grain filling stage for each environment. Pearson's correlation analysis was used to examine relationships between grain yield, IPCA1 scores and weather variables. Seasonal averages and correlation matrices were computed using Microsoft Excel. Regression analysis was

used to visualise the relationship between IPCA1 scores and environmental parameters. However, interpretation of this relationship should be made cautiously because the analysis was based on only three environments.

Results

Effect of genotype, environment and genotype $\times$ environment interaction on grain yield

The combined analysis of variance showed that grain yield was significantly affected by environment, genotype and their interaction (Table 1). The environmental effect was highly significant, indicating clear differences among the test seasons. Genotypic effects were also significant, confirming the presence of genetic variability among the sixteen rice genotypes evaluated. The $G \times E$ interaction was large and highly significant, indicating that genotype performance varied across environments. The observed environmental and interaction effects indicated differential genotype responses under varying seasonal conditions.

Additive main effects and multiplicative interaction, analysis of variance and partitioning of genotype $\times$ environment interaction

The AMMI analysis showed that environment accounted for the largest share of variation in grain yield, followed by genotype and $G \times E$ interaction (Table 1). The relatively high F -values for environment reflected clear seasonal differences, whereas significant genotypic effects indicated the presence of variability among the tested lines. The significant $G \times E$ interaction indicated that genotype performance changed across environments, making selection based solely on mean yield less reliable.

Further partitioning of the interaction revealed that the first two interaction principal component axes explained most of the $G \times E$ variation. This indicated that the interaction followed a structured pattern that could be effectively interpreted through the AMMI model. Replication effects within environments were non-significant, indicating uniform experimental conditions and good precision of the data.

Table 1. Additive main effects and multiplicative interaction analysis of variance for grain yield of rice genotypes across three environments

Source	DF	Sum of squares	Mean square	F-value
Environment (ENV)	2	8178921.38	4089460.69	3478.98***
Replications within environments	6	7052.87	1175.48	1.14 ns
Genotype (GEN)	15	54905003.34	3660333.56	3551.39***
Genotype $\times$ Environment ($G \times E$)	30	56209597.18	1873653.24	1817.89***
Interaction principal component axis 1 (IPCA1)	16	43023219.02	2688951.19	2608.92***
Interaction principal component axis 2 (IPCA2)	14	13186378.16	941884.15	913.85***
Residuals	90	92760.87	1030.68	—

*** $p < 0.001$; ns: non-significant; DF: degrees of freedom.

Table 2. Combined analysis of variance for agronomic traits of rice genotypes across three environments

Source	DF	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Number of panicles m^{-2}	Number of filled grains panicle ⁻¹	Test weight (g)	Grain yield ($kg\ ha^{-1}$)
Environment	2	6774.68***	1394.16***	0.75ns	509.12***	228.26***	424.57***	205.44***
Genotype (GEN)	15	4.90***	6.26***	5.09***	1.72ns	2.37*	3.35**	2.12*
Replications within environments	6	29.91***	12.41***	28.58***	10.45***	38.44***	37.09***	1.20ns
Environment $\times$ Genotype ($G \times E$)	30	38.35***	11.12***	3.73***	393.25***	1303.22***	72.46***	1773.53***

*** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$; ns: non-significant; DF: degrees of freedom.

Combined analysis of variance for agronomic traits

The combined analysis across environments indicated that most of the agronomic traits were significantly influenced by environmental conditions (Table 2). However, panicle length did not show significant variation across environments ($F = 0.75$; $p = 0.48$), suggesting relative stability of this trait. Traits such as days to 50 % flowering, plant height, number of panicles m^{-2} , number of filled grains panicle⁻¹, test weight and grain yield were strongly affected by environmental variation ($p < 0.001$). Significant genotypic differences were also observed for most traits, confirming the availability of genetic variability for selection. In contrast, the number of panicles m^{-2} showed comparatively less variation among genotypes ($p = 0.10$). The $G \times E$ interaction was significant for all traits ($p < 0.001$), indicating that trait expression varied across environments. Replications within environments were consistent for most traits, supporting the reliability of the experimental layout.

Environmental characterisation based on weather variables and interaction principal component axis 1

To examine the role of environmental factors in influencing $G \times E$ interaction, key weather variables during the flowering to grain filling stage were analysed in relation to grain yield and AMMI interaction scores (Table 3). Detailed weekly meteorological observations recorded during crop growth stages across environments are presented in Supplementary Table 1. Grain yield showed a moderate positive relationship with rainfall, emphasising the importance of sufficient moisture during the reproductive stage. A slight positive association was observed with maximum temperature, whereas relative humidity showed a weak negative association with grain yield.

The IPCA1 scores exhibited comparatively stronger associations with environmental variables (Fig. 1). The IPCA1 showed descriptive negative trends with rainfall and temperature, whereas it was positively associated with relative humidity. These trends indicate that seasonal fluctuations in temperature and moisture conditions contributed to the observed interaction effects.

Table 3. Weather variables, grain yield and interaction principal component axis 1 scores during the flowering to grain filling stage across environments

Season	Grain yield (kg ha ⁻¹)	IPCA1	Rainfall (mm)	Tmax (°C)	Mean relative humidity (%)
Kharif 2022	7835.71	12.01	151.3	31.9	77.4
Rabi 2022–23	7620.20	−48.26	122.0	36.6	55.8
Kharif 2023	7258.10	36.25	130.9	30.9	78.8

	Yield	IPCA1	Rainfall	Tmax	RH
Yield	1.00	-1.00	0.57	0.31	-0.20
IPCA1	-1.00	1.00	-1.00	-1.00	1.00
Rainfall	0.57	-1.00	1.00	-0.61	0.70
Tmax	0.31	-1.00	-0.61	1.00	-0.99
RH	-0.20	1.00	-0.20	0.70	1.00

Fig. 1. Correlogram showing associations among grain yield, interaction principal component axis 1 scores, rainfall, maximum temperature and relative humidity during the flowering to grain filling stage.

Seasonal trends further clarified environmental differences. Kharif 2022 recorded the highest mean yield, coinciding with moderate temperature, better rainfall distribution and favourable humidity. This environment also showed a relatively low IPCA1 score, indicating greater environmental stability. In contrast, rabi 2022–23 experienced higher temperature and reduced rainfall, resulting in a large negative IPCA1 score and increased genotype differentiation. Kharif 2023 was characterised by higher humidity and moderate rainfall; however, yield levels were comparatively lower, with a positive IPCA1 score indicating altered genotype responses under humid conditions.

Regression analysis suggested a negative association between IPCA1 scores and maximum temperature across the evaluated environments (Fig. 2). However, interpretation of this relationship should be made cautiously because the analysis was based on only three environments.

Mean grain yield and stability of rice genotypes

Grain yield and stability of the tested rice genotypes were evaluated across three environments using WAASB and AMMI-based stability parameters. The WAASB represents the weighted average of absolute scores obtained from the BLUP-based AMMI model. Among the environments, Environment 1 recorded higher mean grain yield and lower WAASB values, indicating greater environmental stability. Environment 2 showed higher WAASB values, suggesting greater environmental variability, whereas Environment 3 displayed intermediate stability. These results indicate differences in $G \times E$ interaction among the test environments.

Grain yield varied considerably among the evaluated genotypes (Table 4). Mean yield ranged from 5878.67 kg ha⁻¹ in

RDR5305 to 8492.67 kg ha⁻¹ in RDR5288, indicating substantial genetic variability among the tested rice genotypes.

Stability analysis using WAASB and ASV revealed clear differences among genotypes (Table 4). RDR5289 recorded the lowest WAASB (1.89) and ASV (5.75), indicating high yield stability across environments. The genotypes KNM1638 and JGL24423 also showed relatively low WAASB values with moderate ASV. These genotypes combined good yield potential with stable performance across environments. In contrast, genotypes such as RDR5287, RDR5302 and RDR5307 showed higher WAASB and ASV values, indicating greater yield fluctuation under changing environmental conditions.

Overall, genotypes RDR5289, KNM1638 and JGL24423 showed both high yield and stable performance across the evaluated seasonal environments. These genotypes may therefore be considered promising candidates for further evaluation under similar agro-climatic conditions, whereas less stable genotypes may perform better under specific environments.

The heatmap derived from the WAASB / GY ratio provided a clear visual representation of the relationship between yield and stability (Fig. 3). The transition in colour from dark purple to bright yellow reflects increasing WAASB / GY values across genotypes. Genotypes such as RDR5305 and RDR5302 recorded higher ratios, suggesting greater fluctuation in yield across environments. In contrast, RDR5289 and RDR5290 showed lower values, indicating more stable performance with a better balance between yield and stability. Overall, the heatmap clearly differentiated relatively stable and unstable genotypes and aided in identifying lines with consistent performance across seasons.

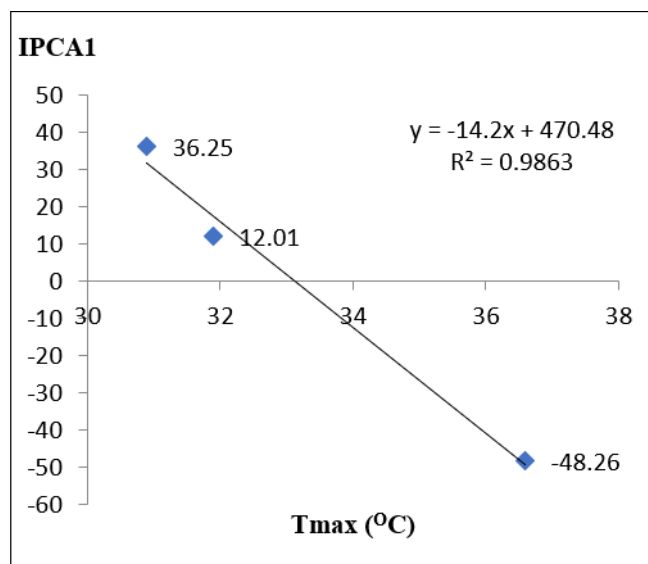


Fig. 2. Scatter plot showing the relationship between interaction principal component axis 1 scores and mean temperature during the flowering to grain filling stage across environments. Interpretation should be made cautiously because the analysis was based on a limited number of environments.

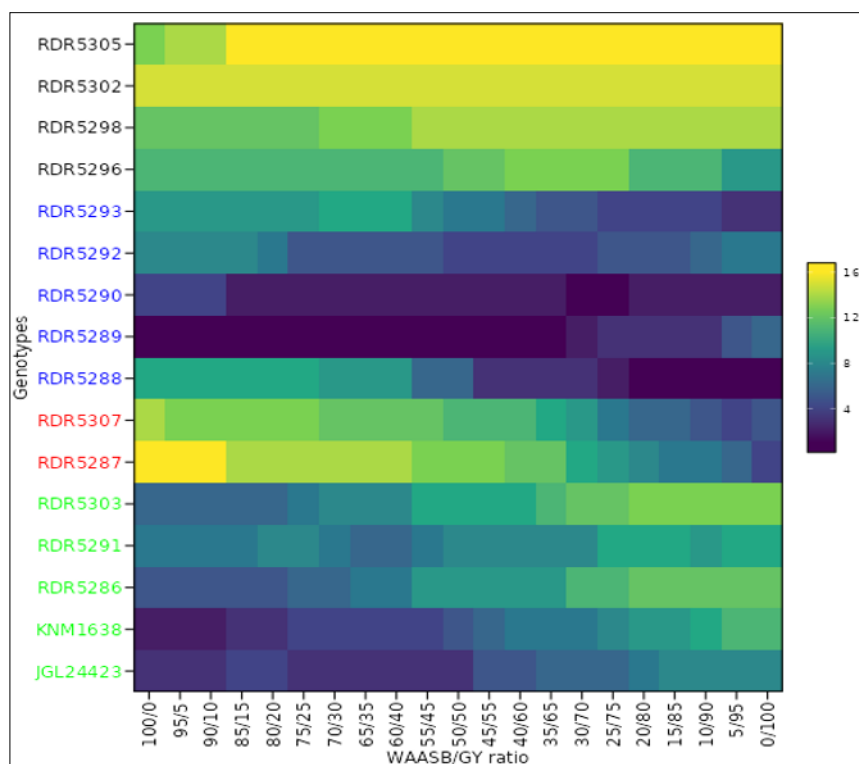


Fig. 3. Heatmap representing the weighted average of absolute scores from the best linear unbiased prediction (WAASB) / grain yield (GY) ratio across genotypes, where colour intensity from purple to yellow reflects increasing stability-yield balance.

Additive main effects and multiplicative interaction stability parameters and mean grain yield of rice genotypes

The AMMI model was used to analyse $G \times E$ interaction and identify stable rice genotypes across environments. Mean grain yield of the evaluated genotypes ranged from 5878.67 kg ha⁻¹ in RDR5305 to 8492.67 kg ha⁻¹ in RDR5288 (Table 4). This variation indicates substantial genetic variability and differential adaptability among the tested genotypes.

However, mean yield alone is not sufficient for genotype selection. Stability across environments is equally important for identifying stable seasonal performance genotypes. The ASV was therefore used to evaluate yield stability. Among the genotypes, RDR5289 recorded the lowest ASV value (5.75), indicating superior stability across environments. The genotypes KNM1638 (17.33) and

JGL24423 (18.49) also showed relatively low ASV values, suggesting consistent yield performance under different environmental conditions.

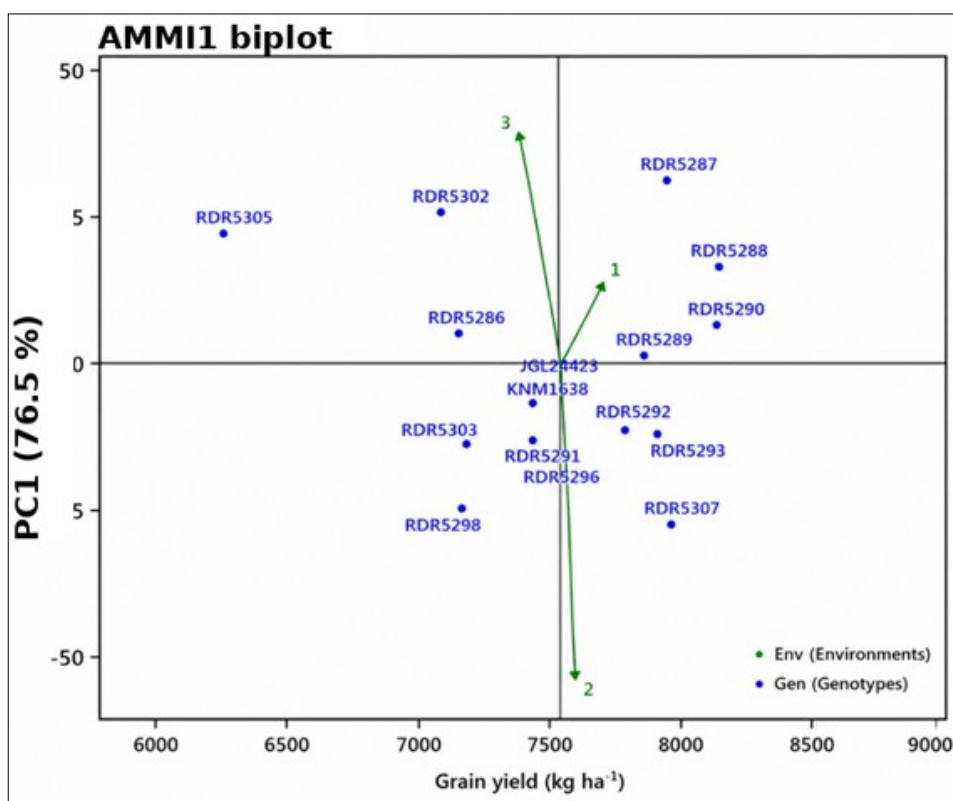
In contrast, genotypes such as RDR5287, RDR5302 and RDR5305 recorded very high ASV values (> 70), indicating greater sensitivity to environmental variation and lower stability. Other AMMI-derived parameters including ASTAB, AVAMGE and SIPC also supported these results. Genotypes with lower values for these parameters generally exhibited better stability and productivity. Detailed values of these parameters are provided in Supplementary Table 2.

The AMMI1 biplot illustrated the relative performance of genotypes along with their interaction across environments (Fig. 4). Genotypes such as RDR5287, RDR5288, RDR5290 and RDR5289 were

Table 4. Genotype-wise mean grain yield, weighted average of absolute scores from best linear unbiased prediction and additive main effects and multiplicative interaction-based stability parameters across seasonal environments

Genotype	Mean grain yield (kg ha ⁻¹)	WAASB	WAASB rank	ASV	PC1	PC2	Pct. WAASB (%)	Pct. Resp (%)	SIPC	AMGE
JGL24423	7592.8	5.5	3	18.5	-1.77	-17.56	82.9	65.6	19.3	-5.68×10^{-13}
KNM1638	7375.9	5.0	2	17.3	-5.14	4.32	85.5	57.3	9.5	1.99×10^{-13}
RDR5286	7182.3	6.7	5	23.8	7.11	-5.45	77.1	49.9	12.6	-2.56×10^{-13}
RDR5287	8089.3	22.9	16	91.0	27.79	-7.11	0.0	84.6	34.9	-3.98×10^{-13}
RDR5288	8492.7	14.0	10	57.1	17.49	-2.75	42.3	100.0	20.2	-1.42×10^{-13}
RDR5289	7960.3	1.9	1	5.8	1.08	-4.53	100.0	79.6	5.6	-1.42×10^{-13}
RDR5290	8238.7	6.1	4	19.4	5.37	-8.32	80.2	90.3	13.7	-2.84×10^{-13}
RDR5291	7430.3	7.7	7	32.6	-9.98	0.18	72.5	59.4	10.2	9.95×10^{-14}
RDR5292	7899.3	8.5	8	29.2	-8.63	-7.93	68.8	77.3	16.6	-2.56×10^{-13}
RDR5293	8093.0	12.7	9	39.2	-10.13	-21.06	48.7	84.7	31.2	-6.25×10^{-13}
RDR5296	7504.3	16.1	11	56.3	-16.68	14.40	32.3	62.2	31.1	5.68×10^{-13}
RDR5298	7131.7	17.6	12	74.9	-22.96	0.33	25.2	47.9	23.3	-5.68×10^{-14}
RDR5302	7022.7	21.7	15	79.2	23.85	14.54	6.0	43.8	38.4	6.25×10^{-13}
RDR5303	7162.3	6.8	6	24.4	-7.31	5.16	76.7	49.1	12.5	1.85×10^{-13}
RDR5305	5878.7	20.3	13	71.0	21.09	17.55	12.7	0.0	38.6	6.25×10^{-13}
RDR5307	8087.0	20.5	14	71.5	-21.20	18.22	11.6	84.5	39.4	8.53×10^{-13}

WAASB: weighted average of absolute scores from BLUP; ASV: AMMI stability value; PC1 and PC2: first two interaction principal components derived from the AMMI model; Pct. WAASB and Pct. Resp: percentage contribution of WAASB and response respectively; SIPC: sum of interaction principal component scores; AMGE: average marginal effect of genotype. Lower WAASB and ASV values indicate greater yield stability across environments.

**Fig. 4.** Additive main effects and multiplicative interaction 1 biplot showing the first principal component (PC1) explaining 76.5 % of the variation versus grain yield. Genotypes (blue dots) and environments (green vectors) are displayed to illustrate genotype performance and genotype-by-environment interactions.

positioned on the positive side of the biplot and exhibited higher grain yield levels (≥ 8000 kg ha⁻¹). In contrast, RDR5305, RDR5302 and RDR5286 were located on the opposite side, with comparatively lower yields ranging between 6000 and 7000 kg ha⁻¹. The direction and spread of environmental vectors further indicate that the test environments exerted differing influences on genotype performance.

The AMMI2 biplot described the interaction pattern using the first two principal components (Fig. 5). PC1 accounted for 76.5 % of the total interaction variation, while PC2 accounted for 23.5 %. Genotypes such as RDR5305, RDR5302 and RDR5287 were grouped on the positive side of PC1, whereas RDR5293 and RDR5292 were positioned on the negative side. The placement of environments in the biplot indicates that each environment imposed a different level of influence on genotype performance.

The GGE biplot provided additional insight into $G \times E$ interaction (Fig. 6), with the first two principal components explaining 91.93 % of the total variation. Most genotypes were located near the origin, suggesting relatively stable performance with moderate interaction effects. In contrast, genotypes such as RDR5305 and RDR5287 were positioned farther from the origin, indicating greater sensitivity to environmental variation. Among the test environments, environment 2 showed a stronger role in differentiating genotypes, while environment 3 displayed contrasting interaction patterns along PC2.

Multi-trait stability index of rice genotypes

The MTSI was used to assess genotype performance by considering multiple agronomic traits simultaneously. Unlike single-trait approaches, MTSI combines grain yield with traits such as days to flowering, plant height, panicle number, number of filled grains and test weight. This approach enables a more balanced evaluation of genotype adaptability across environments (Table 5).

The MTSI values varied considerably among the sixteen genotypes. The genotype KNM1638 recorded the lowest MTSI value (0.8081), indicating superior stability and balanced performance across the evaluated traits. The genotypes RDR5286 (0.8649) and JGL24423 (0.8763) also recorded relatively low MTSI values, reflecting stable performance across traits and good adaptability under different environments.

In contrast, genotypes such as RDR5307 (3.2151), RDR5305 (3.0446) and RDR5287 (3.4343) exhibited higher MTSI values, indicating greater variability in performance across environments. Such genotypes may perform well under specific environmental conditions but may not be suitable for wide adaptation.

The MTSI ranking showed good agreement with the WAASB and AMMI stability parameters. This consistency confirms the usefulness of MTSI as a reliable selection tool for multi-trait evaluation. Based on the combined analysis, KNM1638, RDR5286 and JGL24423 were identified as promising genotypes with stable performance across multiple traits and environments.

Principal component and factor analysis

Principal component analysis (PCA) was performed to identify the major sources of phenotypic variation among the rice genotypes (Supplementary Table 3). Six principal components with eigenvalues greater than one were retained for interpretation. Among these, PC1 accounted for 35.4 % of the total variation, followed by PC2 (21.8 %) and PC3 (18.8 %). Together, these three components explained 76.0 % of the overall phenotypic variability, indicating that most of the variation among the evaluated genotypes was captured within a limited number of components. The remaining components (PC4-PC6) contributed comparatively smaller proportions and together accounted for the remaining 24.0

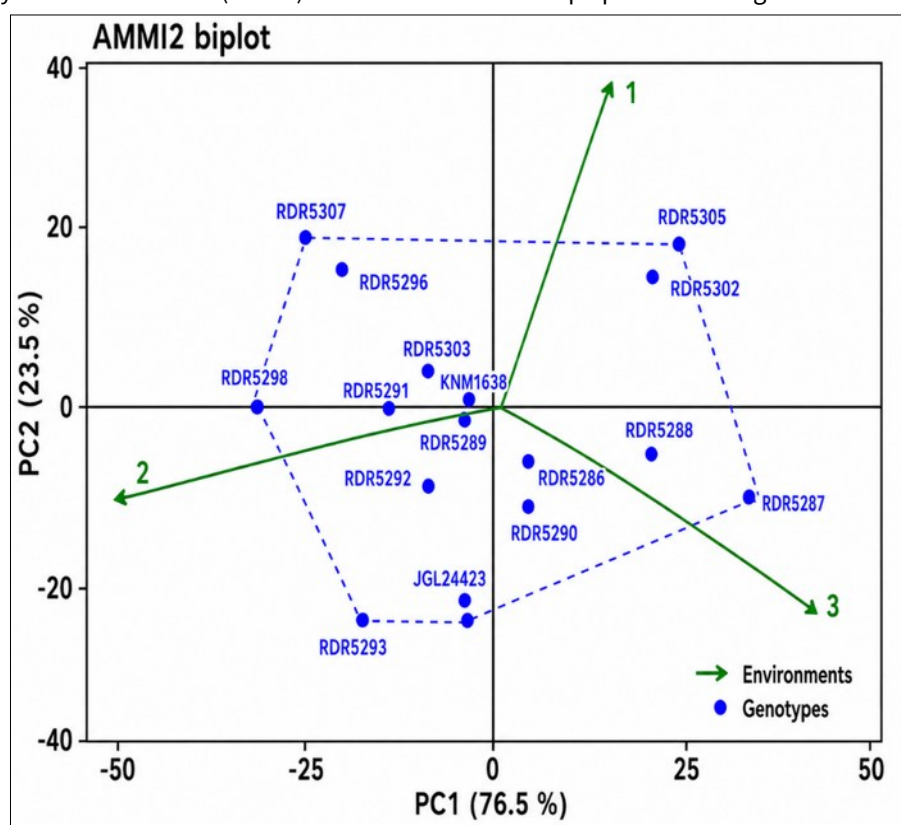


Fig. 5. Additive main effects and multiplicative interaction 2 biplot showing the interaction of genotypes and environments based on PC1 (76.5 %) and PC2 (23.5 %) variation. Genotypes (blue dots) and environments (green vectors) illustrate differential responses and adaptation patterns across environments.

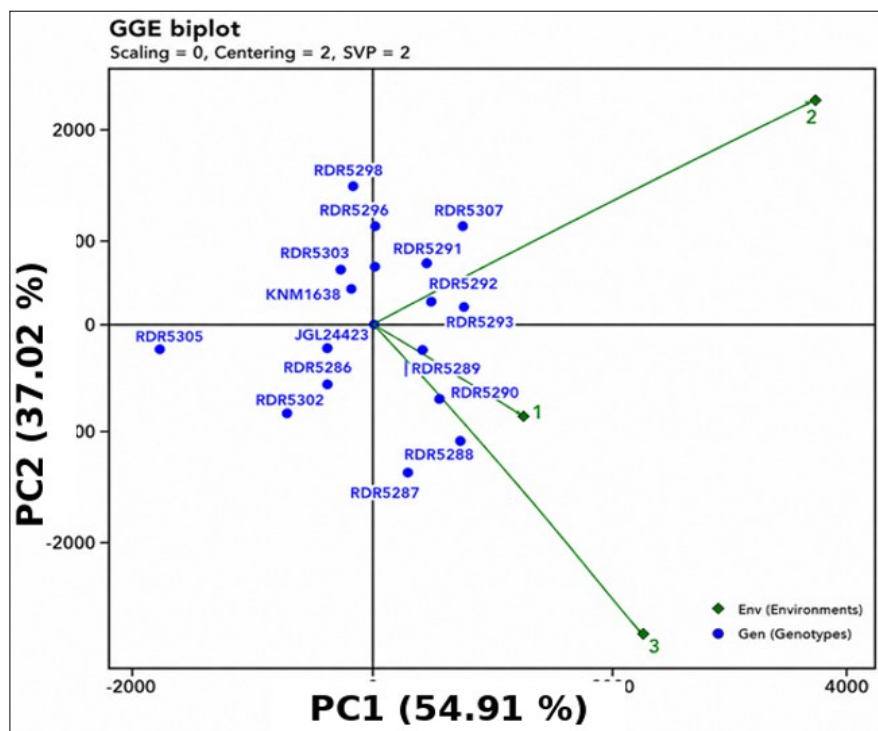


Fig. 6. Genotype and genotype $\times$ environment (GGE) biplot showing genotype-by-environment interaction based on PC1 (54.91 %) and PC2 (37.02 %). Genotypes near the origin indicate stability, while distant genotypes show greater environmental sensitivity.

Table 5. Multi-trait stability index and ranking of rice genotypes

Rank	Genotype	MTSI
1	KNM1638	0.8081
2	RDR5286	0.8649
3	JGL24423	0.8763
4	RDR5303	1.2477
5	RDR5289	1.3526
6	RDR5296	1.7994
7	RDR5293	2.0491
8	RDR5288	2.1101
9	RDR5291	2.2093
10	RDR5292	2.2691
11	RDR5298	2.3429
12	RDR5290	2.6254
13	RDR5302	2.7551
14	RDR5305	3.0446
15	RDR5307	3.2151
16	RDR5287	3.4343

% of the variation.

Factor analysis with varimax rotation further grouped the traits into three major factors (Supplementary Table 4). Grain yield and number of panicles m^{-2} showed strong loadings on Factor 1, indicating their major contribution to yield variation. Days to 50 % flowering and test weight showed higher loadings on Factor 2. Plant height and number of filled grains panicle $^{-1}$ were mainly associated with Factor 3. These groupings indicate that several traits contributed jointly to genotype performance across environments.

Selection differential and genetic gain under weighted average of absolute scores from best linear unbiased prediction-based selection

Selection differential (SD) analysis based on the WAASB index was used to examine changes in trait values between the original population and the selected genotypes (Supplementary Table 5). Grain yield under Factor 1 showed a reduction of 57.8 %. Days to 50 % flowering also declined, indicating selection toward earlier and more stable genotypes. Under Factor 2, moderate reductions were observed for plant height and number of panicles m^{-2} . In contrast,

Factor 3 showed a positive selection response for number of filled grains panicle $^{-1}$, which increased by 23.3 %.

Selection gain analysis showed a slight decline in overall grain yield, decreasing from 7571 to 7279 $kg\ ha^{-1}$ (-3.86 %). Grain yield exhibited moderate heritability ($h^2 = 0.488$), indicating scope for further improvement through continued selection (Supplementary Table 6). A reduction in plant height and flowering duration was also observed, which may be beneficial in terms of improved lodging resistance and earlier maturity. At the same time, a reduction in the number of filled grains panicle $^{-1}$ was observed under selection, indicating the influence of stability-based selection on yield component traits. Overall, selection based on the WAASB index resulted in genotypes with improved trait balance and more stable performance across environments.

Discussion

The present study confirmed that grain yield and associated agronomic traits in rice are influenced by genotype, environment and their interaction. The significant $G \times E$ interaction observed across seasons reflects the differential response of genotypes under varying field conditions. Similar trends have been reported in multi-environment trials of rice (11, 12). Such variability makes selection based solely on mean grain yield less dependable and emphasises the need to incorporate stability parameters in breeding programmes.

The AMMI approach enabled a clear separation of interaction effects into interpretable components. The first two interaction principal components accounted for most of the variation, indicating that the interaction followed a structured pattern rather than being random. This facilitated the identification of genotypes with stable performance across environments. Comparable observations have been reported in rice and other crops, where AMMI analysis proved useful in understanding interaction patterns and supporting genotype selection (13, 14). The

interaction pattern obtained through AMMI analysis also agrees with earlier reports where AMMI analysis effectively explained genotype adaptability in rice (13–16). The magnitude of interaction observed in the present study also suggests that the environments used were sufficiently contrasting to evaluate genotype adaptability.

Although the evaluated environments represented contrasting seasonal conditions, all trials were conducted at a single research location. Therefore, the present findings primarily reflect seasonal adaptability rather than broad multi-location adaptation across diverse agro-climatic zones. Further multilocation validation is necessary before recommending these genotypes for wider adaptation (25, 26).

Weather conditions during the flowering to grain filling stage played a decisive role in shaping yield performance and interaction effects. The association between IPCA1 scores and climatic variables indicates that both temperature and moisture influenced genotype behaviour across environments. Higher temperature and reduced moisture availability were associated with stronger interaction effects and greater differentiation among genotypes. Similar environmental influences have been documented in rice under contrasting seasonal conditions (21). The relationship between IPCA1 scores and climatic variables further confirms the importance of environmental factors in rice genotype performance (21). These findings underline the importance of considering environmental variability when interpreting $G \times E$ interaction.

Although several studies have reported the effectiveness of AMMI and GGE approaches in identifying stable rice genotypes, some investigations have observed stronger environmental influence leading to crossover interactions and reduced prediction consistency across seasons (14, 16). These differences may be associated with variation in environmental conditions, genetic background of experimental materials and seasonal climatic fluctuations during critical growth stages (21).

A notable aspect of the present study is the integration of seasonal environmental contrast with stability analysis. The comparison between kharif and rabi environments revealed clear differences in genotype response, largely influenced by temperature and moisture conditions during the reproductive stage. The association between IPCA1 scores and weather variables further highlights the role of environmental factors in shaping $G \times E$ interaction. In addition, the use of MTSI enabled identification of genotypes with balanced performance across traits, which may not be captured through yield-based evaluation alone (22). This combined analytical approach improves the reliability of selecting genotypes for diverse environments.

The WAASB-based analysis provided additional clarity on environmental stability. Environment 1 combined higher yield with lower WAASB values, suggesting relatively stable growing conditions. In contrast, environments with higher WAASB values showed greater variability and reduced predictability of genotype performance. Nevertheless, such environments are useful for identifying responsive genotypes and assessing tolerance to stress conditions (21). Therefore, including both stable and variable environments is important for effective evaluation of genotype adaptability.

Substantial variation among genotypes was observed for both yield and stability parameters. Genotypes such as RDR5289, KNM1638 and JGL24423 consistently recorded lower WAASB and

ASV, indicating reliable performance across environments. The agreement among different stability indices, including WAASB, ASV and related parameters, supports the robustness of these genotypes. Similar consistency among stability measures has been reported earlier (18, 22). The stable and unstable genotype responses observed in this investigation are also in agreement with previous reports in rice (15, 16). In contrast, genotypes with higher interaction scores appeared more sensitive to environmental changes and may be better suited for specific environments rather than broad seasonal adaptation.

The superior stability observed in genotypes such as RDR5289 and KNM1638 may be associated with their balanced phenological and yield component traits across environments. Stable performance under contrasting seasons could be attributed to efficient assimilate partitioning, better grain filling ability and reduced sensitivity to temperature fluctuations during the reproductive stage. Genotypes with lower interaction effects are generally considered less sensitive to environmental fluctuations, resulting in greater adaptability across seasons (17, 22). The substantial genetic variability and differential adaptability observed among genotypes in the present study further support the importance of stability analysis in rice improvement programmes (14, 17).

Genotypes positioned closer to the origin exhibited relatively stable responses because of lower interaction sensitivity, whereas genotypes located farther from the origin appeared more responsive to environmental fluctuations and may therefore possess specific adaptation rather than broad seasonal adaptability (14, 16, 24). The close agreement between graphical and numerical results strengthens the reliability of the analytical methods used.

The use of the MTSI allowed simultaneous evaluation of yield and related traits, providing a more balanced approach to genotype selection. Genotypes with lower MTSI values combined stable yield with favourable expression of key agronomic traits. The genotype KNM1638, in particular, emerged as a well-balanced genotype with consistent performance across environments. Multi-trait approaches are increasingly preferred in breeding programmes as they enable selection for both productivity and adaptability (22). The consistency between MTSI and other stability parameters further supports the usefulness of integrated stability indices in rice breeding programmes (18, 22).

Principal component and factor analysis revealed that a major proportion of phenotypic variability was explained by the first few principal components. These findings agree with earlier studies reporting that a few principal components explain most of the variability in rice germplasm (19, 20). The grouping of traits into distinct factors further indicated that several agronomic traits contributed jointly to genotype performance across environments.

Selection differential analysis indicated that stability-based selection resulted in moderate changes in important agronomic traits. Reductions in plant height and flowering duration may contribute to improved lodging resistance and earlier maturity. A reduction in filled grains per panicle was also observed, reflecting the trade-offs associated with simultaneous selection for stability and multiple agronomic traits. Moderate heritability estimates indicate that further improvement through selection remains feasible (25).

Conclusion

The present study demonstrated that grain yield and associated agronomic traits in rice were significantly influenced by genotype, environment and genotype $\times$ environment ($G \times E$) interaction. The significant interaction observed across seasons reflects differential genotype responses under varying environmental conditions. These findings indicate that selection based solely on mean yield may not be adequate, emphasising the importance of evaluating genotypes across multiple environments. The use of additive main effects and multiplicative interaction (AMMI), weighted average of absolute scores from best linear unbiased prediction (BLUP; WAASB), genotype and genotype $\times$ environment (GGE) biplot and multi-trait stability indices enabled effective interpretation of interaction effects and facilitated the identification of stable genotypes. Among the evaluated entries, KNM1638, RDR5289 and JGL24423 exhibited consistent performance across environments, with KNM1638 showing superior multi-trait stability and strong potential for utilisation in breeding programmes aimed at developing widely adapted rice varieties.

The integration of seasonal environmental analysis with AMMI and multi-trait stability indices provides a robust framework for identifying rice genotypes with high yield potential and stable performance. This approach can be effectively utilised in breeding programmes targeting the development of rice varieties with stable performance under seasonal environmental variation. Future research should focus on validating the identified stable genotypes across broader multi-location trials and diverse agro-climatic regions. Further studies integrating physiological, molecular and genomic approaches may help to better understand the mechanisms underlying genotype stability and environmental adaptability in rice.

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Authors' contributions

RR designed the experiment and conducted the field trials. KP, AD and BS assisted in data collection. RR, AD and SCM performed the statistical analysis. BBN supervised the study; RR and BBN revised the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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Declaration of Generative AI

During the preparation of this manuscript, the authors used generative AI tools for language editing and improving readability. The authors carefully reviewed and edited the content and take full responsibility for the content of the publication.

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