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Genotype × environment interaction, phenotypic stability and multivariate divergence of rice (*Oryza sativa* L.) genotypes

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Abstract

Stable performance across heterogeneous environments is a critical consideration in rice improvement and varietal advancement. The present investigation evaluated genotype × environment (G×E) interaction and phenotypic stability for eleven agronomic traits in 24 rice genotypes tested across three contrasting environments during Kharif 2019 at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India. Stability parameters were estimated using the Eberhart-Russell (1966) joint regression model, and multivariate trait variation was further examined using hierarchical cluster analysis and principal component analysis (PCA). Pooled analysis of variance revealed effects of genotype, environments and G×E interaction for the traits evaluated, demonstrating substantial environmental heterogeneity and differential genotypic responses. For grain yield per plant, CSR 43 recorded an above-average mean yield (32.07 g plant⁻¹) and a low regression coefficient ($b_i = 0.239$), together with a small adjusted deviation estimate ($S^2d_i = -7.36$), indicating relatively stable performance with limited responsiveness to improving environmental conditions. CSR-C27 SM-117 ($b_i = 0.936$) and RP 5706-120-7-2-2 ($b_i \approx 1$) showed responses closer to the average environmental trend, whereas CSR 2711-103, CR 3890-35-1-3-4 and CSRRIL-01-IR 165 exhibited strong responsiveness to favourable environments. CSR 2016-IR-18-12 recorded the highest mean grain yield (40.28 g plant⁻¹) but a large deviation estimate ($S^2d_i = 152.66$), indicating substantial environmental unpredictability. Cluster analysis grouped the 24 genotypes into five phenotypically divergent clusters, with the largest reported inter-cluster distance occurring between Clusters II and V ($D^2 = 5.526$). PCA of cluster means accounted for 79.8% of the total variation in the first two components, with harvest index, grain yield and plant height contributing substantially to multivariate differentiation. Collectively, the results provide a quantitative basis for prioritising genotypes for further multi-environment testing and parental selection in rice improvement programmes.

Keywords: Genotype × environment interaction; Eberhart–Russell model; phenotypic stability; *Oryza sativa*; regression coefficient; multivariate divergence; principal component analysis.

Introduction

Rice (*Oryza sativa* L.) is a major staple crop and a cornerstone of food security in Asia. Its productivity is strongly influenced by environmental heterogeneity, while grain yield itself is a complex, quantitatively inherited trait that integrates the effects of multiple yield components and environmental factors. In India, substantial variation in productivity among rice-growing regions underscores the importance of developing genotypes that combine desirable mean performance with predictable responses across target environments. (FAO, 2023) A central challenge in rice improvement is that grain yield is a complex, polygenically controlled trait that responds differentially to environmental variation. This differential response, expressed as genotype × environment (G×E) interaction, can cause genotypes selected under one set of conditions to perform inconsistently when exposed to different agro-ecological conditions (Comstock and Moll, 1963; Lin *et al.*, 1986; Becker and Leon, 1988; Crossa, 1990) [3, 8, 9]. Consequently, identifying genotypes that combine high mean performance with predictable responses across environments remains a key objective of multi-environment testing. Phenotypic stability analysis provides a quantitative framework for characterising differential genotypic responses to environmental

Variation. The joint regression model of Eberhart and Russell (1966) describes stability using the regression coefficient (b_i), which reflects the responsiveness of a genotype to environmental quality, and the deviation from regression (S^2_{di}), which represents the extent of non-linear or unpredictable response. A genotype with high mean performance, b_i close to unity and a small, non-significant S^2_{di} is generally considered broadly adapted, whereas $b_i > 1$ indicates greater responsiveness to favourable environments and $b_i < 1$ indicates relatively greater performance under less favourable environments when the deviation from regression is small. (Eberhart and Russell, 1966). Stability statistics used in multi-environment trials include parametric approaches such as the Eberhart–Russell regression parameters, Wricke's ecovalence and Shukla's stability variance, as well as non-parametric ranking procedures. Multivariate methods, including the Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype plus Genotype-by-Environment (GGE) biplot, provide complementary approaches for describing complex $G \times E$ patterns and visualising genotype–environment relationships (Yan and Tinker, 2006; Somanagoudra and Manonmani, 2020)^[34, 36]. The Eberhart–Russell model was selected here because its parameters provide readily interpretable measures of environmental responsiveness and predictability, while cluster analysis and PCA were used to characterise multivariate phenotypic differentiation among the genotypes. Despite extensive research on $G \times E$ interaction and stability in rice (Arumugam *et al.*, 2007; Biswas *et al.*, 2012; Bhatt *et al.*, 2015; Lee *et al.*, 2023; Rahim Soroush *et al.*, 2024; Ghazy *et al.*, 2024; Mamidi *et al.*, 2026)^[2, 5, 6, 13, 20, 24, 31], comparatively limited information is available on the stability behaviour and multivariate phenotypic diversity of newly developed rice germplasm under contrasting environments of the Indo-Gangetic Plain. Such information is particularly relevant for eastern Uttar Pradesh, where spatial and temporal environmental heterogeneity can complicate the identification of consistently performing genotypes. Integrating stability analysis with multivariate characterisation can therefore help distinguish genotypes with desirable mean performance from those exhibiting environment-specific responses. The objectives of the present study were therefore to: (i) quantify the nature and magnitude of $G \times E$ interaction across three contrasting environments; (ii) estimate Eberhart–Russell stability parameters for eleven yield and yield-related traits; (iii) characterise multivariate phenotypic divergence among the 24 genotypes and identify potentially divergent parental combinations; and (iv) identify genotypes warranting further multi-environment evaluation for stable and superior performance in the target region.

2. Materials and methods

2.1 Plant Material and Experimental Design

Twenty-four rice genotypes predominantly newly developed salt-tolerant lines, together with two check varieties (PUSA 44 and CSR 43) were evaluated during Kharif 2019. The experiment was conducted simultaneously across three environments representing contrasting agronomic conditions at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya: (i) the Genetics and Plant Breeding Research Farm, (ii) the Student Instructional Farm, and (iii) the MES Farm. Each environment was treated as an independent experimental location. At each location, the experiment followed a Randomised Complete Block Design (RCBD) with three replications. Each genotype was grown in a plot of 2.4 m $\times$ 2.0 m, with a spacing of 20 cm $\times$ 15 cm (row $\times$ plant). Recommended agronomic practices for the Kharif season were followed uniformly across all three

environments.

2.2 Traits Assessed

Data were recorded for eleven quantitative traits: days to 50% flowering, plant height (cm), productive tillers per plant, panicle length (cm), leaf area index, number of fertile spikelets per panicle, spikelet fertility (%), biological yield per plant (g), harvest index (%), grain length-to-breadth (L/B) ratio of grain, and grain yield per plant (g). Measurements followed the Standard Evaluation System for Rice (IRRI, 2013).

2.3 Statistical Methods

All data were subjected to pooled analysis of variance (ANOVA) under the RCBD framework after assessment of homogeneity of error variances across environments using Bartlett's test. Statistical significance was evaluated at the 5% and 1% probability levels ($p \leq 0.05$ and $p \leq 0.01$, respectively).

Phenotypic stability was assessed using the joint linear regression model of Eberhart and Russell (1966)^[11]. For each genotype, mean performance, the regression coefficient (b_i), and the mean squared deviation from regression (S^2_{di}) were estimated. The regression coefficient quantified responsiveness to environmental quality, with $b_i \approx 1$ denoting average responsiveness, $b_i > 1$ denoting greater responsiveness to favourable environments, and $b_i < 1$ denoting relatively greater performance under less favourable environments. A small, non-significant S^2_{di} was interpreted as greater predictability of response. The environmental index (I_j) was calculated as the deviation of each environmental mean from the grand mean. Multivariate phenotypic divergence among the 24 genotypes was assessed using hierarchical cluster analysis based on standardised values of the eleven traits and Ward's minimum-variance linkage method. The reported intra- and inter-cluster distance measures were used to identify divergent groups and potential parental combinations for subsequent breeding programmes. Because the analysis was based on phenotypic traits rather than molecular markers, the resulting groups are interpreted as phenotypically divergent clusters rather than genetically distinct populations.

To complement the cluster analysis, Principal Component Analysis (PCA) was performed on standardised cluster-mean values for five key traits (days to 50% flowering, plant height, grain yield per plant, harvest index, and spikelet fertility) using the correlation matrix. The first two principal components were visualised as a biplot to identify major trait contributions to multivariate differentiation among clusters.

3. RESULTS

3.1 Pooled Analysis of Variance

Pooled analysis of variance across the three environments revealed highly significant ($p \leq 0.01$) mean squares for genotype for all eleven characters examined, indicating substantial phenotypic variation among the test genotypes (Table 1). Environments were also highly significant for all characters, reflecting pronounced differences among the three test environments. Most importantly for stability assessment, genotype $\times$ environment ($G \times E$) interaction mean squares were significant ($p \leq 0.05$ or $p \leq 0.01$) for all traits, demonstrating differential genotypic responses to environmental variation.

The linear component of the $G \times E$ interaction was significant or highly significant for the majority of traits, indicating that a substantial proportion of the interaction was associated with differential genotypic regression on the environmental index. This supports the use of the Eberhart–Russell (1966)^[11] framework for characterising environmental responsiveness.

However, significant pooled deviations for several traits, particularly days to 50% flowering and spikelet fertility, also indicate that a component of the response remained non-linear and environment-specific. Partitioning of the pooled sum of squares for grain yield per plant showed that environment accounted for the largest share of the variation (approximately 46%), followed by G×E interaction (approximately 39%) and

genotype (approximately 15%). Thus, within the present trial, environmental heterogeneity was the dominant contributor to variation in grain yield per plant. This result reinforces the importance of multi-environment evaluation when assessing the consistency of genotype performance (Arumugam *et al.*, 2007; Biswas *et al.*, 2012)^[2, 6].

Table 1: Pooled analysis of variance (mean squares) for grain yield and selected yield-related traits in 24 rice genotypes across three environments (Kharif 2019)

Source of Variation	df	Days to 50% Flowering	Plant Height (cm)	Productive Tillers/Plant	Panicle Length (cm)	Spikelet Fertility (%)	Biological Yield/Plant (g)	Grain Yield/Plant (g)
Replication	2	14.00	194.07	23.14	53.10	22.88	3.977	5.77
Genotype	23	92.93**	694.41**	13.54**	43.75**	37.16**	142.80**	8.95**
Environment	2	7.68**	1274.86**	47.44**	55.98**	98.16**	92.64**	327.96**
Rep × Environment	4	0.99	22.55**	1.88**	0.63**	1.80**	1.73**	1.89**
Genotype × Environment	46	19.78*	75.10**	4.37**	11.21**	7.68**	15.94**	12.21**
Pooled Error	138	14.81	95.23	5.61	16.35	8.29	18.88	6.20

*Significant at $p \leq 0.05$; **Significant at $p \leq 0.01$.

3.2 Phenotypic stability for grain yield per plant

Grain yield per plant ranged from 27.96 g (CSR 2711-103) to 40.28 g (CSR 2016-IR-18-12), with an overall mean of 29.50 g across the three environments (Table 2). Eleven genotypes recorded mean grain yield above the general mean. The Eberhart–Russell analysis revealed substantial variation among genotypes in both environmental responsiveness and predictability. Genotypes combining above-average yield with relatively small deviation estimates included CSR 43 (32.07 g; $b_i = 0.239$; $S^2d_i = -7.36$), CSR-C27 SM-117 (31.79 g; $b_i = 0.936$; $S^2d_i = -15.78$), CSR-2748-4441-193 (29.76 g; $b_i = 0.578$; $S^2d_i = -16.07$), CSR-27 (30.96 g; $b_i = 1.255$; $S^2d_i = -15.26$), and RP 5706-120-7-2-2 (29.26 g; $b_i \approx 1$; $S^2d_i \approx 0$). Their regression coefficients, however, indicate different degrees of environmental responsiveness rather than a uniform pattern of broad adaptation. CSR-C27 SM-117 and RP 5706-120-7-2-2 were closest to average responsiveness, whereas CSR 43 and CSR-2748-4441-193 showed relatively lower responsiveness. Genotypes CSR 2711-103 (27.96 g; $b_i = 3.880$), CR 3890-35-1-3-4 (29.29 g; $b_i = 2.700$), and CSRIL-01-IR 165 (29.10 g; $b_i = 2.351$) exhibited regression coefficients well above unity. Their high b_i values indicate strong responsiveness

to improvements in environmental quality and suggest potential utility under favourable or high-input conditions, subject to confirmation across additional environments (Ramalingam *et al.*, 1990; Panwar, 2008; Manjunatha *et al.*, 2018; Prajapati and Kathiria, 2018; Pandey *et al.*, 2020)^[25, 27, 28, 29, 32]. CR 2851-S-B-1-2B-1 (30.69 g; $b_i = 0.917$), CSR-2748-4441-193 (29.76 g; $b_i = 0.578$), and CR3437-1-5-200-83-1 (30.36 g; $b_i = 0.134$) exhibited regression coefficients below unity. When associated with small deviation from regression, such responses indicate relatively greater performance under less favourable environments. These genotypes therefore merit consideration for further evaluation under resource-limited or stress-prone conditions (Subudhi *et al.*, 2008; Kesh *et al.*, 2023)^[18, 35]. CSR 2016-IR-18-12 recorded the highest mean grain yield (40.28 g plant⁻¹) but an exceptionally large positive S^2d_i value (152.66), indicating substantial environmental unpredictability. Despite its superior mean performance, the large deviation estimates limits confidence in its consistency across environments and supports its prioritisation for further targeted evaluation rather than immediate recommendation for broad adaptation (Bhakta and Das, 2008; Subudhi *et al.*, 2008; Kumar *et al.*, 2020)^[4, 10, 19, 35].

Table 2: Eberhart-Russell stability parameters (mean yield, regression coefficient b_i and deviation from regression S^2d_i) for grain yield per plant (g) of 24 rice genotypes evaluated across three environments.

Genotype	Mean Yield (g/plant)	b_i	S^2d_i	Adaptability Class
CR 2851-S-B-1-2B-1	30.69	0.917	-7.80	Unfavourable
CR 3890-35-1-3-4	29.29	2.700	-14.43	Favourable
CR3437-1-5-200-83-1	30.36	0.134	-16.06	Average/Wide
CR3878-245-2-4-1	29.61	0.460	-13.44	Unfavourable
CR3903-161-1-3-2	29.51	1.118	-14.34	Average/Wide
CSAR 1610	29.00	0.590	-16.07	Average/Wide
CSR-27	30.96	1.255	-15.26	Average/Wide
CSR-2748-4441-193	29.76	0.578	-16.07	Unfavourable
CSR-C27 SM-117	31.79	0.936	-15.78	Average/Wide
CSR 2016-IR-18-12	40.28	-8.920	152.66	Unstable
CSR 2016-IR 18-10*	30.38	-0.247	-15.97	Unfavourable
CSR 2711-103	27.96	3.880	-6.98	Favourable
CSR 36	29.81	1.744	-10.61	Average/Wide
CSR 43†	32.07	0.239	-7.36	Average/Wide
CSRIL-01-IR 165	29.10	2.351	-8.40	Favourable
CST 7-1	28.97	2.506	-15.88	Favourable
IR LON-GSR 29	29.16	2.365	-8.76	Favourable
KR15075	28.17	0.872	-14.27	Average/Wide
NARENDRA USAR 3	29.83	0.199	-15.66	Unfavourable
NSICRC 222	28.41	2.369	-9.33	Favourable
PAU 5563-23-1-2	29.82	1.980	-10.70	Average/Wide
PUSA 44 (Check)	29.60	1.262	-14.06	Average/Wide
RAU-1525-1-2	29.70	2.791	-1.17	Favourable
RP 5706-120-7-2-2	29.26	1.922	-12.14	Average/Wide

*Highest mean-yielding genotype with a large deviation from regression; †Check variety. Adaptability classes are interpreted using the Eberhart–Russell framework, with $b_i \approx 1$ indicating average responsiveness, $b_i > 1$ indicating greater responsiveness to favourable environments, $b_i < 1$ indicating relatively greater performance under less favourable environments, and a small/non-significant S^2_{di} indicating greater predictability.

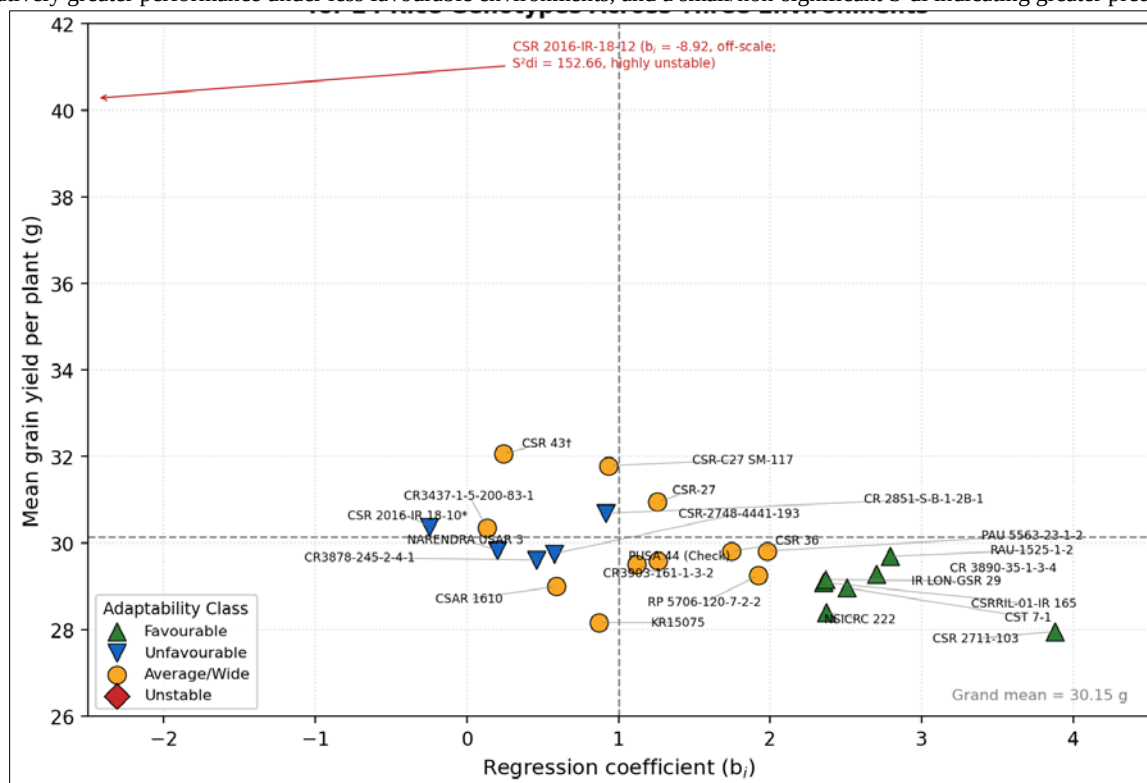


Fig 1: Stability biplot of mean grain yield per plant (g) against the regression coefficient (b_i) for 24 rice genotypes evaluated across three environments, derived from Table 2. Vertical and horizontal dashed lines mark $b_i = 1$ and the grand mean yield (30.15 g), respectively, delineating quadrants corresponding to the Eberhart and Russell (1966)^[11] adaptability classes. CSR 2016-IR-18-12 ($b_i = -8.92$) lies outside the plotted range and is indicated separately owing to its markedly high S^2_{di} (152.66), reflecting unpredictable performance.

3.3 Stability Analysis for Other Yield Components

Stability analysis of the remaining ten traits revealed substantial variation in the magnitude and direction of environmental responsiveness. For several traits, the linear component of $G \times E$ interaction predominated, whereas significant deviations from regression for selected traits indicated additional non-linear, environment-specific responses. The trait-wise stability estimates are presented in Supplementary Tables S1–S10. Days to 50% flowering: CR3903-161-1-3-2 recorded the maximum mean (90.89 days) with $b_i > 1$ and a small deviation estimate, indicating greater responsiveness to favourable environments. In contrast, IR LON-GSR 29 recorded the lowest mean (79.00 days) with $b_i < 1$ and a small deviation estimate, indicating relatively lower environmental responsiveness and potential suitability for environments where shorter duration is desirable. Plant height ranged from 111.2 cm (CR3903-161-1-3-2) to 143.02 cm (CSR-C27 SM-117). The stability estimates indicate genotype-specific responses of plant height to environmental quality. The observed lower plant height of CR3903-161-1-3-2 should not, however, be interpreted as direct evidence of lodging resistance because lodging was not independently measured in the present study. Panicle length: PUSA 44 recorded the maximum panicle length (31.62 cm) with $b_i < 1$, indicating relatively lower responsiveness to environmental improvement, whereas IR LON-GSR 29 ($b_i > 1$, with a small deviation estimate) showed greater responsiveness of panicle length under favourable environments. Spikelet fertility: CSAR 1610 recorded the highest spikelet fertility (85.44%) with $b_i > 1$ and a small deviation estimate, indicating greater responsiveness of this trait to favourable environments. CR 2851-S-B-1-2B-1, with the lowest fertility mean (76.55%)

and $b_i < 1$, showed relatively lower environmental responsiveness in spikelet fertility. Harvest index: CR3437-1-5-200-83-1 recorded the highest harvest index (38.56%) with $b_i > 1$ and a small deviation estimate, indicating greater responsiveness to favourable environments, whereas IR LON-GSR 29 maintained comparatively lower responsiveness ($b_i < 1$) in harvest-index expression.

3.4 Multivariate Phenotypic Divergence Analysis

Hierarchical cluster analysis using standardised values of the eleven traits and Ward's minimum-variance linkage method partitioned the 24 rice genotypes into five phenotypically divergent clusters (Table 3). Cluster I was the most populous (nine genotypes), followed by Cluster II (seven genotypes) and Clusters III and IV (three genotypes each), while Cluster V comprised two genotypes (CR 2851-S-B-1-2B-1 and CSR 2016-IR-18-12). Because the clustering was based on agronomic and phenotypic traits, these groups represent multivariate phenotypic differentiation rather than molecularly defined genetic structure. Intra-cluster distances were modest (range: 0.227–1.746), whereas the maximum reported inter-cluster distance occurred between Clusters II and V ($D^2 = 5.526$), followed by Clusters I and V ($D^2 = 5.273$) and Clusters II and III ($D^2 = 4.709$) (Figure 1). These differences indicate phenotypically divergent groups that may be considered when selecting parents for subsequent crossing and recombination. The exact interpretation of D^2 should follow the distance metric and clustering procedure used in the original statistical analysis. Cluster V recorded the highest mean values for grain yield per plant (30.20 g), harvest index (37.00%), biological yield per plant (58.50 g), and panicle length (33.85 cm),

whereas Cluster I was characterised by the lowest plant height (122.01 cm) and highest spikelet fertility (84.78%). These contrasting trait profiles indicate potentially complementary phenotypes that could be exploited in subsequent breeding cycles, subject to validation of their combining ability and performance in progeny.

Table 3: Cluster means for selected traits across five phenotypically divergent clusters of 24 rice genotypes

Cluster	No. of Genotypes	Days to 50% Flowering	Plant Height (cm)	Grain Yield/Plant (g)	Harvest Index (%)	Spikelet Fertility (%)
I	9	80.22	122.01†	29.98	32.22	84.78‡
II	7	81.29	126.57	26.59	30.00	83.29
III	3	79.33†	124.97	23.40†	28.67†	82.33
IV	3	81.67‡	128.77	27.27	30.67	81.33†
V	2	79.50	130.75‡	30.20‡	37.00‡	84.50

†Lowest value in the cluster row; ‡Highest value in the cluster row.

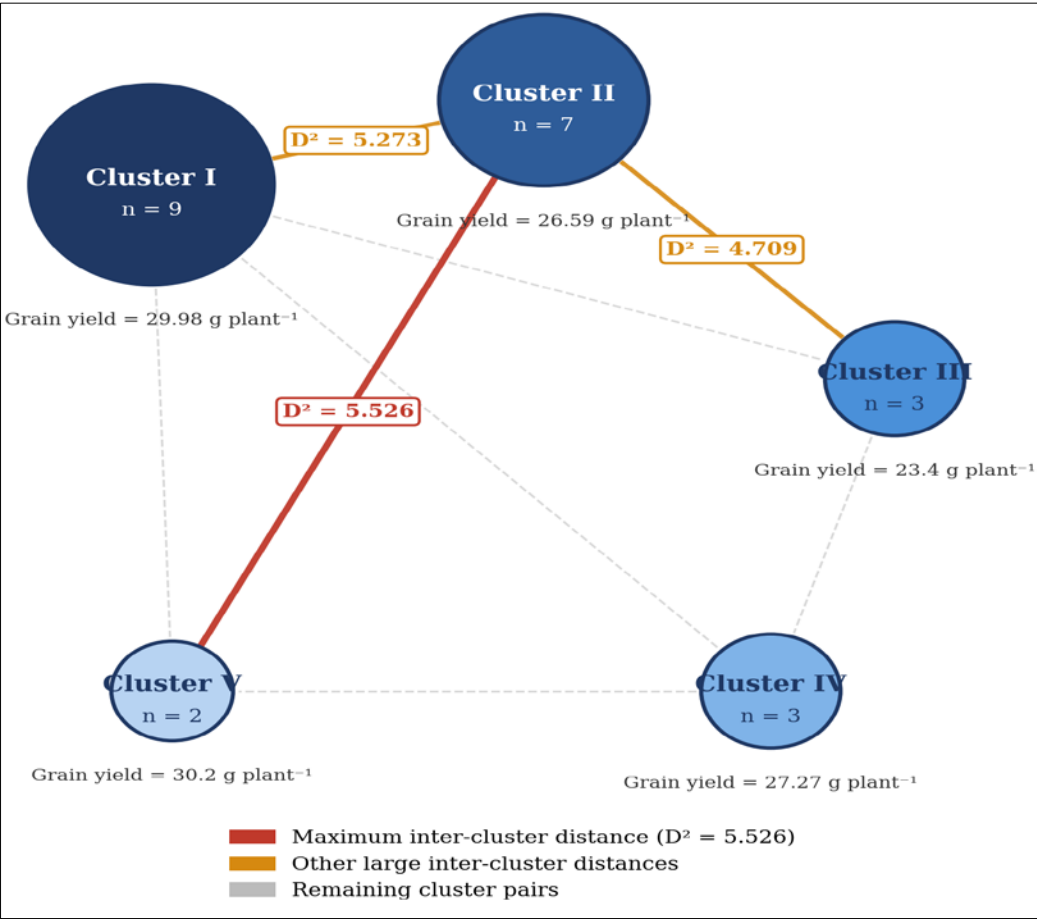


Fig 2: Hierarchical cluster diagram of 24 rice genotypes based on standardised phenotypic traits and Ward's minimum-variance linkage. Cluster sizes reflect the number of genotypes; reported inter-cluster D² values are shown where applicable.

3.5 Principal Component Analysis

Principal Component Analysis of the five cluster-mean traits reduced the original trait space to two dominant axes: PC1 accounted for 52.2% of total variance and PC2 accounted for a further 27.7%, together explaining 79.8% of the variation among clusters (Figure 2). PC1 was most strongly and positively associated with harvest index, grain yield per plant and spikelet fertility, and negatively associated with days to 50% flowering, broadly representing a productivity–earliness gradient. PC2 was dominated by plant height and, to a lesser extent, days to 50% flowering, representing a plant-stature dimension that was

comparatively independent of the principal productivity gradient. Cluster V occupied the positive end of PC1, consistent with its higher mean grain yield, harvest index and spikelet fertility, whereas Cluster III occupied the opposite region. Cluster IV separated primarily along PC2, reflecting differences in plant stature and flowering time, while Clusters I and II were relatively close along PC2 but differed along PC1. The agreement between the cluster structure and PCA ordination provides complementary evidence of multivariate phenotypic differentiation; however, it should not be interpreted as molecular evidence of genetic divergence.

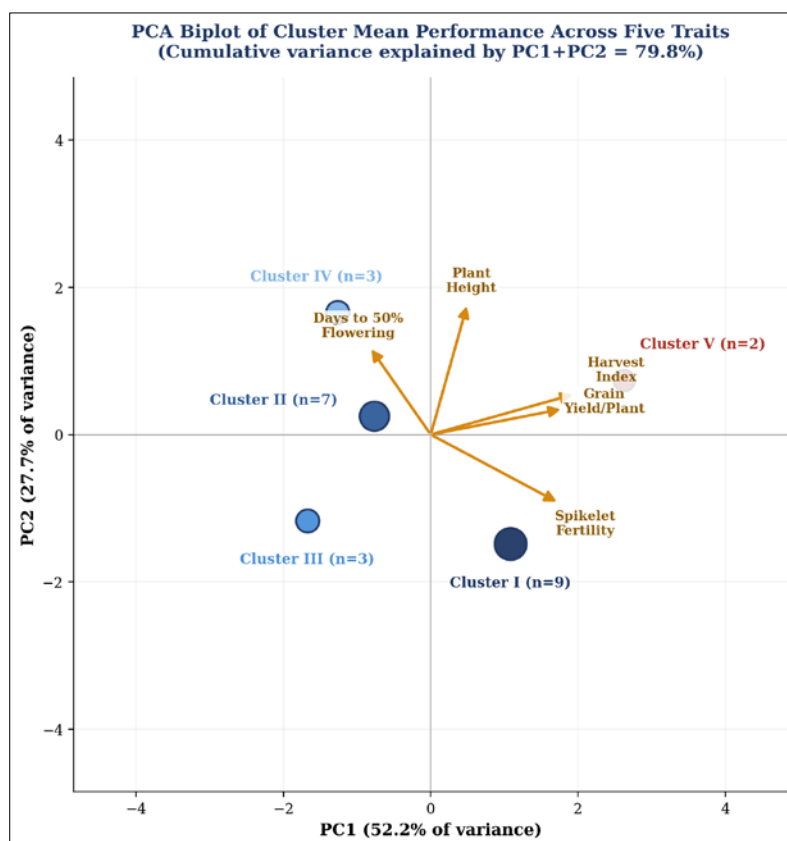


Fig 3: Principal Component Analysis biplot of cluster-mean performance for five key traits. Points represent the five phenotypic clusters; arrows represent trait loading vectors, with their direction and magnitude indicating the contribution of each trait to the principal components.

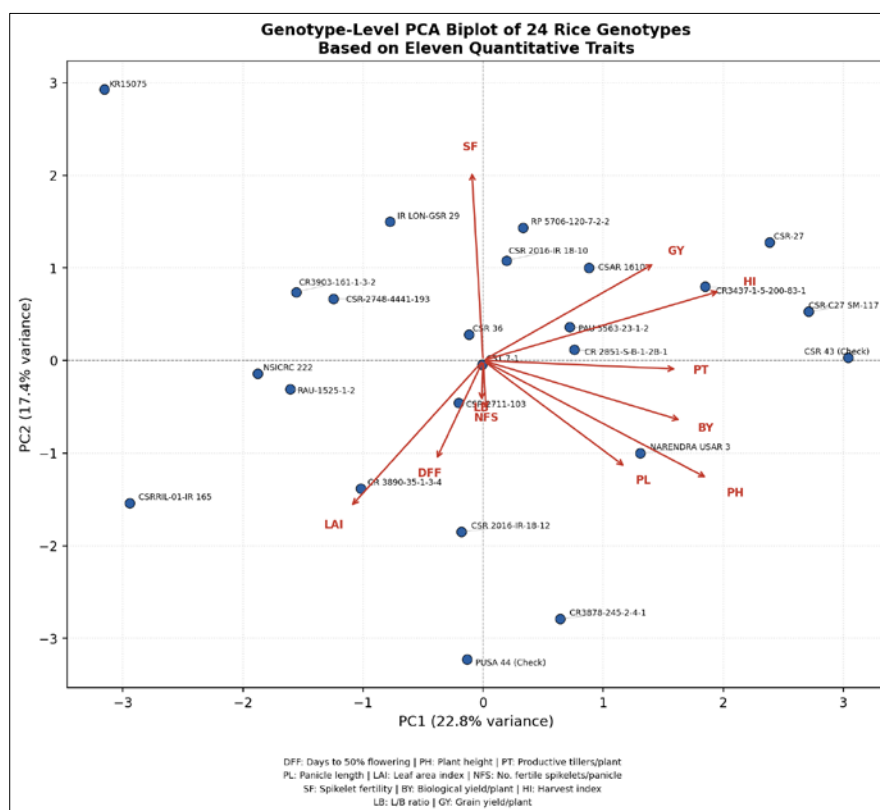


Fig 4: Genotype-level Principal Component Analysis biplot of the 24 individual rice genotypes based on eleven quantitative traits. PC1 and PC2 accounted for 22.8% and 17.4% of total variance, respectively (40.3% cumulative). Figure 4. Genotype-level Principal Component Analysis biplot of the 24 individual rice genotypes based on eleven quantitative traits. PC1 and PC2 accounted for 22.8% and 17.4% of total variance, respectively (40.3% cumulative). Trait loading vectors represent days to 50% flowering (DFF), plant height (PH), productive tillers per plant (PT), panicle length (PL), leaf area index (LAI), number of fertile spikelets per panicle (NFS), spikelet fertility (SF), biological yield per plant (BY), harvest index (HI), grain length-to-breadth ratio (LB), and grain yield per plant (GY). Unlike Figure 2, this biplot resolves the dispersion of individual genotypes and complements the cluster-based analysis by showing genotype-specific associations with the measured traits.

4. DISCUSSION

The significant genotype $\times$ environment (G $\times$ E) interaction observed in the present study demonstrates that the performance of the evaluated rice genotypes was not consistent across the three test environments. Such differential genotypic responses are a well-established phenomenon in rice and have been reported across diverse agro-ecological conditions (Mahapatra, 1993; Das and Choudhury, 1996; Arumugam *et al.*, 2007; Biswas *et al.*, 2012; Bhatt *et al.*, 2015; Lee *et al.*, 2023; Singh *et al.*, 2023; Habib *et al.*, 2024; Islam *et al.*, 2024) [2, 5, 6, 10, 14, 16, 20, 22, 33]. The predominance of the linear component of G $\times$ E interaction for most traits indicates that a substantial proportion of the observed interaction could be explained by differential genotypic responses to environmental quality. This finding supports the utility of the Eberhart–Russell (1966) [11] model for characterising environmental responsiveness and predictability. Nevertheless, the significant non-linear component observed for traits such as days to 50% flowering and spikelet fertility indicates that a proportion of the genotypic response remained environment-specific and could not be adequately explained by linear regression alone. Similar complexity in G $\times$ E interaction has been documented in rice stability studies (Arumugam *et al.*, 2007; Bhatt *et al.*, 2015; Lee *et al.*, 2023) [2, 5, 20].

Environmental variation accounted for the largest proportion of the variation in grain yield per plant, followed by G $\times$ E interaction and genotype effects. This indicates that environmental heterogeneity among the three test locations exerted a stronger influence on grain-yield expression than genotype effects alone during the study period. Comparable patterns, in which environmental effects contributed substantially to yield variation, have been reported in multi-environment rice trials (Habib *et al.*, 2024; Islam *et al.*, 2024) [14, 16]. From a breeding perspective, this finding emphasises the importance of evaluating candidate genotypes across multiple environments and seasons rather than relying on performance under a single test environment. Multi-environment testing provides a more reliable basis for distinguishing genotypes with consistent performance from those exhibiting strong environment-specific responses (Crossa, 1990) [9]. CSR 43 combined an above-average grain yield (32.07 g plant⁻¹) with a low regression coefficient ($b_i = 0.239$) and a small adjusted deviation estimate ($S^2d_i = -7.36$). According to the Eberhart–Russell framework, a regression coefficient substantially below unity indicates relatively low responsiveness to improvement in environmental quality, whereas a small deviation from regression indicates comparatively predictable performance (Eberhart and Russell, 1966) [11]. Therefore, the performance of CSR 43 should not be interpreted as evidence of average responsiveness or broad adaptation solely on the basis of its low b_i value. Rather, its response suggests relatively limited environmental responsiveness and potential suitability under less favourable conditions, provided that this pattern is confirmed across additional environments. The concept of stability as a combination of desirable mean performance and predictable response has also been emphasised by Becker and Leon (1988) and Purchase *et al.* (2000) [3, 30].

Several other genotypes displayed regression coefficients close to or moderately above unity. CSR-C27 SM-117 ($b_i = 0.936$) and RP 5706-120-7-2-2 ($b_i \approx 1$) exhibited responses close to the average environmental trend, suggesting comparatively broad environmental responsiveness when considered together with their relatively small deviation estimates. Similar interpretations of near-unity regression coefficients and small deviations have been used for identifying rice genotypes with relatively stable performance across environments (Ramalingam *et al.*, 1990;

Panwar, 2008; Manjunatha *et al.*, 2018; Prajapati and Kathiria, 2018; Pandey *et al.*, 2020; Makwana *et al.*, 2025) [23, 25, 27, 28, 29, 32]. However, because the present evaluation involved only three environments in a single season, these genotypes should be considered as candidates for further multi-environment evaluation rather than as immediately suitable for formal varietal release. In contrast, CSR 2711-103 ($b_i = 3.88$), CR 3890-35-1-3-4 ($b_i = 2.70$) and CSRRIL-01-IR 165 ($b_i = 2.351$) exhibited regression coefficients substantially greater than unity. Such high b_i values indicate strong responsiveness to improvements in environmental quality and suggest that these genotypes may express greater performance under favourable or high-input conditions. Similar genotype-specific responses to favourable environments have been reported in rice stability studies (Ramalingam *et al.*, 1990; Panwar, 2008; Manjunatha *et al.*, 2018; Prajapati and Kathiria, 2018; Pandey *et al.*, 2020) [25, 27, 28, 29, 32]. These genotypes may therefore be useful for production environments characterised by favourable resource availability, although their specific adaptation should be validated through targeted multi-environment testing. CSR 2016-IR-18-12 recorded the highest mean grain yield (40.28 g plant⁻¹) but also exhibited a markedly large deviation from regression ($S^2d_i = 152.66$). The combination of high mean yield and large deviation indicates substantial environmental sensitivity and reduced predictability. Similar situations, in which high-yielding rice genotypes exhibited considerable instability across environments, have been reported previously (Bhakta and Das, 2008; Subudhi *et al.*, 2008; Jain *et al.*, 2019; Kumar *et al.*, 2020) [4, 10, 17, 19, 35]. Therefore, although CSR 2016-IR-18-12 represents an important high-yielding genotype, its performance should be examined across a larger number of environments before considering it for broad adaptation. Its contrasting response may also make it useful as a breeding resource for investigating yield plasticity and identifying progeny capable of maintaining high productivity under variable environmental conditions. The multivariate analysis provided additional information on the phenotypic structure of the evaluated germplasm. Hierarchical cluster analysis grouped the 24 genotypes into five phenotypically divergent clusters, indicating substantial variation in the joint expression of the measured agronomic traits. The lack of a clear correspondence between geographic origin and cluster membership suggests that geographic origin alone may not adequately reflect phenotypic similarity among rice genotypes. Similar observations have been reported in multivariate analyses of rice germplasm, where clustering based on agronomic traits has revealed substantial divergence among genotypes irrespective of their geographic background (Chandra *et al.*, 2007) [7]. Therefore, the observed cluster structure may provide useful information for selecting parents with contrasting phenotypic attributes.

The maximum reported inter-cluster distance occurred between Clusters II and V ($D^2 = 5.526$), indicating substantial multivariate divergence between these groups. In breeding programmes, crosses between phenotypically divergent parents may provide opportunities for generating segregating populations with complementary trait combinations. In the present study, Cluster V was characterised by comparatively high grain yield, harvest index, biological yield and panicle length, whereas Cluster I showed relatively lower plant height and higher spikelet fertility. Such contrasting trait profiles may provide useful parental combinations for subsequent breeding programmes. However, cluster distance alone does not guarantee superior combining ability or transgressive segregation; therefore, parental selection should subsequently be validated through crossing, progeny evaluation and combining-ability studies.

The PCA further complemented the cluster analysis by summarising the major sources of multivariate variation. The first two principal components of the cluster-mean dataset accounted for 79.8% of the total variation, with harvest index, grain yield and plant height contributing substantially to genotype differentiation. The identification of grain yield and harvest index among the major contributors is consistent with the importance of productivity-related traits in differentiating rice germplasm. PCA and biplot approaches have been widely used to identify major contributors to phenotypic variation and to visualise relationships among rice genotypes (Yan and Tinker, 2006; Yang *et al.*, 2025) [36, 37]. Importantly, the agreement between cluster analysis and PCA should be interpreted as complementary evidence of phenotypic structure rather than independent confirmation of molecular genetic divergence, because both analyses were derived from the same phenotypic dataset.

The integration of stability analysis with multivariate phenotypic characterisation provides a more comprehensive framework for genotype prioritisation than reliance on a single statistical criterion. Stability parameters describe how genotypes respond to environmental variation, whereas cluster analysis and PCA provide information on multivariate phenotypic relationships among genotypes. Such complementary approaches can assist breeders in identifying genotypes with desirable performance as well as potential parental contrasts for subsequent breeding cycles (Crossa, 1990; Nayak *et al.*, 2022; Kesh *et al.*, 2023; Abebe *et al.*, 2023; Yuriyah *et al.*, 2026) [1, 9, 18, 26, 38]. In the present study, CSR 43, CSR-C27 SM-117 and CSR-2748-4441-193 were particularly noteworthy because of their relatively favourable grain-yield performance and distinct environmental response patterns, while the divergent clusters provided additional opportunities for selecting contrasting parental material.

Overall, the findings indicate that genotype performance was strongly influenced by environmental heterogeneity and that substantial variation existed among genotypes in both environmental responsiveness and predictability. The results support the use of multi-environment stability analysis in combination with multivariate phenotypic characterisation for prioritising rice genotypes. However, the present conclusions are based on three environments evaluated during a single season; therefore, additional multi-season and multi-location testing is necessary to establish the repeatability of the observed stability patterns and to support subsequent varietal advancement or breeding decisions.

5. Conclusions

The present study demonstrated significant genotype $\times$ environment interaction for the eleven traits evaluated across three contrasting environments, with the linear component accounting for a substantial part of the interaction for most traits. Eberhart–Russell analysis revealed marked differences among genotypes in environmental responsiveness and predictability. CSR 43 recorded an above-average grain yield (32.07 g plant⁻¹) together with a low regression coefficient ($b_i = 0.239$) and a small adjusted deviation estimate ($S^2_{di} = -7.36$), indicating relatively limited responsiveness and comparatively stable performance under less favourable conditions. CSR-C27 SM-117 and RP 5706-120-7-2-2 showed responses closer to the average environmental trend, whereas CSR 2711-103, CR 3890-35-1-3-4 and CSRRIL-01-IR 165 exhibited strong responsiveness to favourable environments. CSR 2016-IR-18-12 recorded the highest mean yield but a large deviation estimate, indicating substantial environmental unpredictability. These genotypes should therefore be considered for further multi-environment and multi-season evaluation before varietal advancement decisions are made. Multivariate analysis grouped the 24 genotypes into five phenotypically divergent clusters, with the largest reported

inter-cluster distance between Clusters II and V ($D^2 = 5.526$). PCA of cluster means showed that the first two components accounted for 79.8% of the total variation, with harvest index, grain yield and plant height contributing strongly to multivariate differentiation. The combined use of stability parameters and multivariate phenotypic characterisation provides a useful framework for prioritising genotypes and potential parental contrasts. However, because the study was based on three environments in a single season, the identified stability patterns should be validated across additional environments and seasons before formal varietal recommendation. The findings therefore provide a quantitative foundation for continued breeding evaluation of rice germplasm under heterogeneous production conditions.

Declarations

Conflict of Interest: The authors declare no conflict of interest.

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SUPPLEMENTARY TABLES

Stability parameters (mean, regression coefficient b_i , and deviation from regression S^2d_i) for the ten yield-contributing traits summarised in Section 3.3 are presented in full below (Tables S1–S10), following the same Eberhart and Russell (1966) framework applied to grain yield per plant in Table 2.

Supplementary Table S1: Stability parameters (mean, b_i , S^2d_i) for days to 50% flowering across three environments.

Genotype	Mean (days)	b_i	S^2d_i	Adaptability Class
CR 2851-S-B-1-2B-1	81.11	4.687	-4.89	Favourable
CR 3890-35-1-3-4	80.11	4.470	-3.57	Favourable
CR3437-1-5-200-83-1	77.78	-1.519	-4.91	Unfavourable
CR3878-245-2-4-1	78.11	-8.723	5.79	Unfavourable
CR3903-161-1-3-2	90.89	10.090	-3.48	Favourable
CSAR 1610	81.11	6.705	16.65	Unstable
CSR-27	79.33	7.508	25.92	Unstable
CSR-2748-4441-193	87.89	-9.787	1.81	Unfavourable
CSR-C27 SM-117	84.22	-6.054	-1.57	Unfavourable
CSR 2016-IR-18-12	81.00	9.396	-2.22	Favourable
CSR 2016-IR 18-10	84.11	3.971	-4.67	Favourable
CSR 2711-103	79.56	-5.403	-3.98	Unfavourable
CSR 36	78.44	1.280	-4.77	Favourable

CSR 43	78.33	-3.624	-4.85	Unfavourable
CSRRIL-01-IR 165	81.56	9.374	-4.72	Favourable
CST 7-1	79.89	-2.213	-4.58	Unfavourable
IR LON-GSR 29	79.00	-5.989	-3.92	Unfavourable
KR15075	80.00	-3.732	-4.36	Unfavourable
NARENDRA USAR 3	81.22	-0.065	3.13	Unfavourable
NSICRC 222	78.67	1.758	-4.93	Favourable
PAU 5563-23-1-2	78.22	3.168	-4.78	Favourable
PUSA 44 (Check)	82.22	10.155	17.80	Unstable
RAU-1525-1-2	77.89	-4.253	-0.50	Unfavourable
RP 5706-120-7-2-2	79.00	2.799	-4.61	Favourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S2: Stability parameters (mean, bi , S^2di) for plant height (cm) across three environments.

Genotype	Mean (cm)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	130.29	1.550	-31.02	Favourable
CR 3890-35-1-3-4	132.29	0.281	-31.45	Unfavourable
CR3437-1-5-200-83-1	138.41	0.748	5.76	Unfavourable
CR3878-245-2-4-1	132.38	-0.027	10.65	Unstable
CR3903-161-1-3-2	111.20	0.600	-21.96	Unfavourable
CSAR 1610	125.11	0.003	-31.60	Unfavourable
CSR-27	131.09	0.199	-21.77	Favourable
CSR-2748-4441-193	112.29	1.387	-15.66	Favourable
CSR-C27 SM-117	143.02	0.678	-14.26	Unfavourable
CSR 2016-IR-18-12	133.28	0.954	28.04	Unstable
CSR 2016-IR 18-10	121.60	0.879	133.85	Unstable
CSR 2711-103	124.48	2.597	-5.98	Favourable
CSR 36	126.64	1.851	-29.42	Favourable
CSR 43	137.88	0.712	-27.91	Unfavourable
CSRRIL-01-IR 165	121.64	1.492	27.01	Unstable
CST 7-1	136.08	0.352	53.71	Unstable
IR LON-GSR 29	128.50	1.177	-11.82	Average/Wide
KR15075	108.99	2.037	-31.31	Favourable
NARENDRA USAR 3	133.79	0.499	-27.41	Unfavourable
NSICRC 222	132.22	0.868	-16.54	Average/Wide
PAU 5563-23-1-2	131.49	0.922	-14.93	Average/Wide
PUSA 44 (Check)	139.02	0.672	138.91	Unstable
RAU-1525-1-2	126.34	1.798	-24.70	Favourable
RP 5706-120-7-2-2	133.58	1.772	-30.94	Favourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S3: Stability parameters (mean, bi , S^2di) for productive tillers per plant across three environments.

Genotype	Mean (no.)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	9.78	2.700	-1.48	Favourable
CR 3890-35-1-3-4	10.56	0.352	-0.48	Unfavourable
CR3437-1-5-200-83-1	10.22	0.352	-0.48	Unfavourable
CR3878-245-2-4-1	10.33	0.787	-1.65	Unfavourable
CR3903-161-1-3-2	8.67	2.171	-1.71	Favourable
CSAR 1610	8.89	-0.041	-0.76	Unfavourable
CSR-27	10.00	3.161	-1.34	Favourable
CSR-2748-4441-193	8.56	1.153	-1.62	Average/Wide
CSR-C27 SM-117	10.89	1.736	-1.18	Favourable
CSR 2016-IR-18-12	9.67	0.204	-1.11	Unfavourable
CSR 2016-IR 18-10	9.22	0.272	-0.63	Unfavourable
CSR 2711-103	12.44	3.894	1.48	Favourable
CSR 36	11.00	2.849	0.25	Favourable
CSR 43	10.11	-0.068	-1.65	Unfavourable
CSRRIL-01-IR 165	9.67	1.981	-0.67	Favourable
CST 7-1	9.44	-0.258	-1.29	Unfavourable
IR LON-GSR 29	10.11	-0.651	-1.09	Unfavourable
KR15075	8.00	1.574	-1.43	Favourable
NARENDRA USAR 3	9.78	0.122	-0.33	Unfavourable
NSICRC 222	10.89	-0.231	-1.72	Unfavourable
PAU 5563-23-1-2	8.44	-0.258	-1.29	Unfavourable
PUSA 44 (Check)	8.89	1.641	-1.64	Favourable
RAU-1525-1-2	9.22	0.272	-0.63	Unfavourable
RP 5706-120-7-2-2	13.33	0.284	0.17	Unfavourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ =

Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S4: Stability parameters (mean, bi, S^2di) for panicle length (cm) across three environments.

Genotype	Mean (cm)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	23.88	-1.149	-5.43	Unfavourable
CR 3890-35-1-3-4	28.51	4.917	-4.32	Favourable
CR3437-1-5-200-83-1	24.98	1.504	-5.40	Favourable
CR3878-245-2-4-1	27.71	-1.086	-5.45	Unfavourable
CR3903-161-1-3-2	26.82	1.081	-3.16	Average/Wide
CSAR 1610	29.14	1.629	-4.84	Favourable
CSR-27	24.54	2.022	-5.44	Favourable
CSR-2748-4441-193	26.48	1.057	-5.44	Average/Wide
CSR-C27 SM-117	26.04	1.488	-4.44	Favourable
CSR 2016-IR-18-12	25.26	1.417	-4.52	Favourable
CSR 2016-IR 18-10	28.48	2.034	-0.21	Favourable
CSR 2711-103	26.57	0.709	-3.25	Unfavourable
CSR 36	27.99	1.370	-4.10	Favourable
CSR 43	28.70	2.010	10.47	Unstable
CSRRIL-01-IR 165	24.18	3.105	-5.20	Favourable
CST 7-1	28.59	1.198	-4.47	Average/Wide
IR LON-GSR 29	21.54	1.173	-5.18	Average/Wide
KR15075	23.71	-3.030	-5.43	Unfavourable
NARENDRA USAR 3	26.62	1.403	-3.25	Favourable
NSICRC 222	27.08	-0.922	-5.43	Unfavourable
PAU 5563-23-1-2	28.82	3.552	1.75	Favourable
PUSA 44 (Check)	31.62	-0.493	10.06	Unstable
RAU-1525-1-2	26.47	-1.894	-0.47	Unfavourable
RP 5706-120-7-2-2	27.08	0.903	-5.29	Average/Wide

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S5: Stability parameters (mean, bi, S^2di) for leaf area index (cm²) across three environments.

Genotype	Mean (cm ²)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	26.66	0.225	-745.46	Unfavourable
CR 3890-35-1-3-4	80.47	3.012	5085.30	Unstable
CR3437-1-5-200-83-1	30.92	-0.684	-737.02	Unfavourable
CR3878-245-2-4-1	32.60	-0.868	-591.04	Unfavourable
CR3903-161-1-3-2	28.02	0.359	-706.42	Unfavourable
CSAR 1610	28.67	0.329	-745.51	Unfavourable
CSR-27	45.70	2.452	-745.04	Favourable
CSR-2748-4441-193	60.97	5.551	1197.52	Unstable
CSR-C27 SM-117	32.63	0.940	-700.93	Average/Wide
CSR 2016-IR-18-12	29.84	0.657	-674.62	Unfavourable
CSR 2016-IR 18-10	27.78	0.018	-743.80	Unfavourable
CSR 2711-103	27.92	0.146	-745.94	Unfavourable
CSR 36	44.49	0.303	13.63	Unstable
CSR 43	23.89	0.001	-732.42	Unfavourable
CSRRIL-01-IR 165	25.67	-0.324	-743.55	Unfavourable
CST 7-1	46.00	2.988	-130.48	Favourable
IR LON-GSR 29	24.05	-0.207	-718.87	Unfavourable
KR15075	46.30	-0.356	947.41	Unstable
NARENDRA USAR 3	22.70	0.119	-723.98	Unfavourable
NSICRC 222	31.25	0.571	-736.73	Unfavourable
PAU 5563-23-1-2	24.86	-0.178	-745.72	Unfavourable
PUSA 44 (Check)	34.50	1.825	-515.60	Favourable
RAU-1525-1-2	67.85	6.825	1869.27	Unstable
RP 5706-120-7-2-2	25.64	0.296	-727.39	Unfavourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S6: Stability parameters (mean, bi, S^2di) for number of fertile spikelets per panicle across three environments.

Genotype	Mean (no.)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	177.56	0.867	-14.77	Average/Wide
CR 3890-35-1-3-4	173.44	1.662	7.50	Favourable
CR3437-1-5-200-83-1	183.89	0.572	-5.03	Unfavourable
CR3878-245-2-4-1	173.33	1.651	-6.28	Favourable
CR3903-161-1-3-2	176.22	0.652	-11.12	Unfavourable
CSAR 1610	175.11	0.557	-14.78	Unfavourable
CSR-27	166.67	0.733	-2.38	Unfavourable
CSR-2748-4441-193	176.33	0.525	-10.12	Unfavourable

CSR-C27 SM-117	171.56	1.114	-14.78	Average/Wide
CSR 2016-IR-18-12	175.11	1.420	-14.75	Favourable
CSR 2016-IR 18-10	185.56	1.336	-12.05	Favourable
CSR 2711-103	180.67	0.701	16.28	Unstable
CSR 36	179.11	1.340	-12.88	Favourable
CSR 43	176.67	1.050	3.84	Average/Wide
CSRRIL-01-IR 165	184.11	2.682	17.61	Unstable
CST 7-1	176.67	1.054	-14.75	Average/Wide
IR LON-GSR 29	177.67	1.393	-10.15	Favourable
KR15075	177.89	0.096	-9.51	Unfavourable
NARENDRA USAR 3	176.78	1.253	-13.59	Favourable
NSICRC 222	171.89	-0.990	2.58	Unfavourable
PAU 5563-23-1-2	176.00	1.277	-12.52	Favourable
PUSA 44 (Check)	177.56	0.831	-9.21	Average/Wide
RAU-1525-1-2	175.44	1.014	-8.35	Average/Wide
RP 5706-120-7-2-2	178.33	1.209	-11.18	Favourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S7: Stability parameters (mean, bi , S^2di) for spikelet fertility (%) across three environments.

Genotype	Mean (%)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	76.56	0.645	5.95	Unfavourable
CR 3890-35-1-3-4	84.00	0.805	6.36	Average/Wide
CR3437-1-5-200-83-1	85.44	0.913	-2.74	Average/Wide
CR3878-245-2-4-1	81.78	1.321	-2.11	Favourable
CR3903-161-1-3-2	85.22	0.869	-2.75	Average/Wide
CSAR 1610	85.44	1.525	-1.47	Favourable
CSR-27	81.56	0.523	-2.55	Unfavourable
CSR-2748-4441-193	85.44	0.160	-2.76	Unfavourable
CSR-C27 SM-117	82.78	1.963	8.14	Favourable
CSR 2016-IR-18-12	82.22	1.002	-2.31	Average/Wide
CSR 2016-IR 18-10	84.22	0.727	-2.13	Unfavourable
CSR 2711-103	85.22	0.319	-2.75	Unfavourable
CSR 36	83.56	1.552	-2.59	Favourable
CSR 43	81.89	0.808	-0.92	Average/Wide
CSRRIL-01-IR 165	84.89	1.002	-2.31	Average/Wide
CST 7-1	82.67	1.233	-2.68	Favourable
IR LON-GSR 29	82.33	4.003	16.42	Unstable
KR15075	84.22	0.951	2.40	Average/Wide
NARENDRA USAR 3	80.78	-0.869	-2.75	Unfavourable
NSICRC 222	84.00	1.701	2.01	Favourable
PAU 5563-23-1-2	81.89	0.329	-0.32	Unfavourable
PUSA 44 (Check)	81.44	1.667	-2.71	Favourable
RAU-1525-1-2	83.56	0.044	-2.70	Unfavourable
RP 5706-120-7-2-2	84.56	0.808	-0.92	Average/Wide

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S8: Stability parameters (mean, bi , S^2di) for biological yield per plant (g) across three environments.

Genotype	Mean (g)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	52.89	-1.280	-3.43	Unfavourable
CR 3890-35-1-3-4	48.50	0.680	6.19	Unfavourable
CR3437-1-5-200-83-1	55.11	2.885	-4.99	Favourable
CR3878-245-2-4-1	56.67	0.210	-5.77	Unfavourable
CR3903-161-1-3-2	49.56	0.490	-3.32	Unfavourable
CSAR 1610	51.67	2.408	-1.32	Favourable
CSR-27	62.22	0.891	-5.66	Average/Wide
CSR-2748-4441-193	54.89	2.478	-2.36	Favourable
CSR-C27 SM-117	54.22	0.754	-3.96	Unfavourable
CSR 2016-IR-18-12	54.00	2.836	21.23	Unstable
CSR 2016-IR 18-10	51.56	2.241	-1.20	Favourable
CSR 2711-103	58.44	-0.572	-6.21	Unfavourable
CSR 36	54.11	1.280	-3.43	Favourable
CSR 43	54.00	-0.128	-1.69	Unfavourable
CSRRIL-01-IR 165	51.89	4.275	-0.44	Favourable
CST 7-1	55.11	-0.973	-1.39	Unfavourable
IR LON-GSR 29	48.56	0.964	-1.13	Average/Wide
KR15075	44.44	0.158	14.14	Unstable
NARENDRA USAR 3	56.22	0.362	-6.14	Unfavourable
NSICRC 222	52.67	-0.319	-5.03	Unfavourable

PAU 5563-23-1-2	54.44	0.806	-1.28	Average/Wide
PUSA 44 (Check)	56.11	2.521	-4.70	Favourable
RAU-1525-1-2	49.33	0.848	-3.98	Average/Wide
RP 5706-120-7-2-2	45.44	0.186	10.11	Unstable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S9: Stability parameters (mean, bi , S^2di) for harvest index (%) across three environments

Genotype	Mean (%)	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	32.00	0.368	-0.66	Unfavourable
CR 3890-35-1-3-4	30.56	0.549	-1.87	Unfavourable
CR3437-1-5-200-83-1	38.56	2.184	-0.25	Favourable
CR3878-245-2-4-1	32.22	1.748	-2.04	Favourable
CR3903-161-1-3-2	31.89	1.708	-0.57	Favourable
CSAR 1610	32.67	1.621	-1.90	Favourable
CSR-27	38.11	0.663	-2.01	Unfavourable
CSR-2748-4441-193	32.78	0.650	-1.55	Unfavourable
CSR-C27 SM-117	31.11	-0.563	-1.22	Unfavourable
CSR 2016-IR-18-12	30.44	1.835	0.08	Favourable
CSR 2016-IR 18-10	35.22	0.971	-0.75	Average/Wide
CSR 2711-103	32.56	2.157	-1.91	Favourable
CSR 36	33.67	2.057	0.45	Favourable
CSR 43	32.44	-0.073	2.44	Unfavourable
CSRRIL-01-IR 165	28.78	2.706	-1.33	Favourable
CST 7-1	31.67	-0.040	-0.08	Unfavourable
IR LON-GSR 29	29.89	-0.717	0.58	Unfavourable
KR15075	31.33	1.145	2.57	Average/Wide
NARENDRA USAR 3	32.89	1.012	4.50	Average/Wide
NSICRC 222	31.67	-0.885	5.78	Unfavourable
PAU 5563-23-1-2	32.78	1.153	5.74	Average/Wide
PUSA 44 (Check)	32.33	2.384	-1.05	Favourable
RAU-1525-1-2	31.44	0.730	2.34	Unfavourable
RP 5706-120-7-2-2	33.44	0.636	-0.64	Unfavourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.

Supplementary Table S10: Stability parameters (mean, bi , S^2di) for L/B ratio (%) across three environments

Genotype	Mean	bi	S^2di	Adaptability Class
CR 2851-S-B-1-2B-1	2.96	-1.109	0.03	Unfavourable
CR 3890-35-1-3-4	2.68	-1.373	-0.01	Unfavourable
CR3437-1-5-200-83-1	2.90	2.315	-0.03	Favourable
CR3878-245-2-4-1	3.00	0.318	-0.05	Unfavourable
CR3903-161-1-3-2	3.45	3.867	0.02	Favourable
CSAR 1610	2.78	3.003	-0.04	Favourable
CSR-27	3.04	-1.092	-0.04	Unfavourable
CSR-2748-4441-193	3.63	-1.921	-0.05	Unfavourable
CSR-C27 SM-117	2.75	5.483	0.01	Favourable
CSR 2016-IR-18-12	2.78	3.793	-0.03	Favourable
CSR 2016-IR 18-10	3.16	-0.366	0.06	Unfavourable
CSR 2711-103	3.44	-4.238	-0.04	Unfavourable
CSR 36	3.47	-2.948	-0.06	Unfavourable
CSR 43	2.89	0.017	-0.04	Unfavourable
CSRRIL-01-IR 165	3.50	1.642	0.26	Favourable
CST 7-1	3.33	4.908	-0.06	Favourable
IR LON-GSR 29	2.84	5.327	-0.05	Favourable
KR15075	2.44	1.914	-0.01	Favourable
NARENDRA USAR 3	3.17	0.552	0.02	Unfavourable
NSICRC 222	3.03	-1.327	0.02	Unfavourable
PAU 5563-23-1-2	3.01	-0.838	-0.00	Unfavourable
PUSA 44 (Check)	3.11	3.281	-0.04	Favourable
RAU-1525-1-2	2.59	0.679	-0.06	Unfavourable
RP 5706-120-7-2-2	2.47	2.113	0.11	Favourable

Adaptability class assigned as per Eberhart and Russell (1966): $bi \approx 1$ (0.8–1.2) = Average/Wide; $bi > 1.2$ = Favourable environments; $bi < 0.8$ = Unfavourable environments; $S^2di > 10$ = Unstable.