



Evaluation of G×E Interaction and Stability Parameters for Yield and Yield-related Traits in Rice Hybrids (*Oryza sativa* L.)

Srikanth Thippani^{1*}, S. Sudheer Kumar¹, P. Senguttuvel², M. Sheshu Madhav³ and S. Narender Reddy⁴

¹Dep. of Genetics and Plant Breeding, Professor Jayashankar Telangana Agricultural University, Hyderabad, Telangana (500 030), India

²Dept. of Plant Breeding, Hybrid Rice, Indian Institute of Rice Research, Hyderabad, Telangana (500 030), India

³Dept. of Biotechnology, Indian Institute of Rice Research, Hyderabad, Telangana (500 030), India

⁴Dept. of Crop Physiology, Professor Jayashankar Telangana Agricultural University, Hyderabad, Telangana (500 030), India

Corresponding Author

Srikanth Thippani

e-mail: gpbr111agcjl@gmail.com

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Abstract

The present study was undertaken during the *rabi* (January–May, 2016) at three diverse locations of Telangana i.e., College of Agriculture, Rajendranagar, Agricultural Research Station (ARS), Kampasagar, and Regional Sugarcane and Rice Research Station (RSRRS), Rudrur to evaluate the adaptability and stability of rice hybrids. Stability analysis is essential for identifying genotypes with consistent performance across varying environmental conditions, particularly for yield and its contributing traits. A total of 20 rice hybrids and their parental lines were evaluated using analysis of variance (ANOVA) and the stability model, which involves regression coefficient (b_i) and deviation from regression (S^2_{di}). The results revealed significant differences among genotypes, environments, and genotype×environment (G×E) interactions, indicating differential responses of genotypes across environments. Based on mean performance, b_i values close to unity, and non-significant S^2_{di} values, stable parents such as IR-68897A and PUSA-5A and hybrids including PUSA-5A×AR-7-75 and IR-68897A×TCP-657 were identified. These hybrids not only exhibited stable performance across locations but also recorded higher grain yields compared to the standard hybrid check KRH-2, demonstrating wide adaptability and superior yield potential. The study highlights the importance of multi-environment testing and stability analysis in identifying promising rice genotypes. These findings can contribute to the development of high-yielding, stable rice hybrids suitable for cultivation under diverse agro-climatic conditions, thereby supporting food security and sustainable rice production.

Keywords: Rice hybrids, genotype×environment interaction, stability, eberhart and russell

1. Introduction

Rice (*Oryza sativa* L.) is one of the most widely cultivated cereal crops globally, feeding more than half of the world's population. It plays a crucial role in ensuring food and nutritional security, particularly in the Indian subcontinent, as it is rich in carbohydrates along with essential nutrients such as vitamins, antioxidants, and minerals (Sen et al., 2020). The global population is projected to peak at around 10.4 billion by the 2080s, with approximately 9.7 billion expected by 2050 (Norrman, 2023). This poses a formidable challenge to feeding the world within the ecological limits of the planet (Rockstrom et al., 2020, Saito et al., 2021, Prado et al., 2024).

One of the primary objectives of rice breeding programs is

the development and release of cultivars with improved yield, enhanced nutritional quality, resistance to pests and diseases, and adaptability to climate change (Beres et al., 2020, Hickey et al., 2019). Considering increasing population pressure, decreasing arable land, and climate variability, enhancing rice productivity has become imperative (Saito et al., 2021). Hybrid rice technology, which exploits heterosis or hybrid vigor, has shown considerable potential, offering a yield advantage of 15–20% over conventional inbred varieties (Virmani, 1996; Senguttuvel, 2021).

Despite its promise, one of the major challenges in hybrid rice breeding is the genotype×environment (G×E) interaction (GEI), wherein the relative performance of genotypes varies across different environments (Cooper et al., 2023, Kumar et



al., 2023). GEI is influenced by the interplay of a genotype's genetic constitution with environmental variables such as temperature, rainfall, soil fertility, and agronomic practices (Sharma et al., 2024; Lee et al., 2023). These interactions can obscure the expression of key traits, reducing the efficiency of selection. Thus, understanding and dissecting GEI is critical for developing hybrids with broad adaptability and stable performance (Chandra Mohan et al., 2021, Cooper and Messina, 2021, Singh et al., 2022).

GEI significantly affects genotype performance and adaptability across agro-ecological zones (Mahmood et al., 2022, Singh et al., 2023; Bomma et al., 2024). A thorough understanding of the magnitude and nature of GEI is essential for breeding high-yielding, stable rice hybrids with either broad or specific adaptation to target environments (Kumar et al., 2023, Ahmed et al., 2024). In this regard, multi-environment trials and stability analysis are central to modern plant breeding, aiding in the identification of consistently performing genotypes (Sharma et al., 2022). Evaluating genotypes across multiple, contrasting environments provides critical insights into genotypic responses and improves selection accuracy by integrating GEI complexity into breeding decisions (Jat, 2020; Verma et al., 2023).

Various statistical models have been developed to analyze GEI, from classical analysis of variance (ANOVA) to advanced multivariate techniques like the Additive Main Effects and Multiplicative Interaction (AMMI) model, Genotype and Genotype×Environment (GGE) biplot, and factor analytic models (Yan and Kang, 2003; Abdelrahman et al., 2022, Dwivedi et al., 2024, Xu et al., 2024). However, widely used approach for stability evaluation is the Eberhart and Russell (1966) regression model, which assesses stability through regression coefficients. A stable genotype in this model is characterized by a unit regression coefficient ($b_i \approx 1.0$), low deviation from regression ($S^2d_i \approx 0$), and a high mean yield (Kumar et al., 2023). These parameters help identify genotypes suitable for diverse environments while maintaining consistent yields (Mishra et al., 2024). Moreover, such studies are essential for recommending genotypes for release, ensuring their adaptability and reliability across environmental gradients (Singh and Verma, 2022).

Therefore, the main objective of this study is to identify rice hybrids with stable and superior yield performance across diverse environments of Telangana, utilizing the Eberhart and Russell (1966) model of stability analysis.

2. Materials and Methods

The present study was undertaken during the *kharif* (July to December, 2015–16) and *rabi* (January–May 2016). During *kharif* (July to December, 2015–16) four CMS lines and ten restorer lines were crossed in a line x tester mating design to obtain 40 F_1 hybrids. Forty hybrids along with 10 restorers, 4 maintainer lines of corresponding male sterile lines and

2 checks were evaluated during the Rabi (January–May, 2016) at three diverse locations of Telangana i.e., College of Agriculture, Rajendranagar,; Agricultural Research Station (ARS), Kampasagar; and Regional Sugarcane and Rice Research Station (RSRRS), Rudrur. Nurseries were raised and twenty-one days old seedlings were transplanted in the field. The list of the 56 treatments including 40 hybrids, 10 restorers, 4 maintainers and two checks used in the study.

2.1. Experimental design

This study used a randomized block design, with two replications and three locations. The row to row and plant-to-plant spacing of $20 \times 15 \text{ cm}^2$ was maintained with net plot size of $3 \times 1.5 \text{ m}^2$.

2.2. Statistical analysis

Data on eleven quantitative traits were subjected to combining ANOVA across three environments to assess the main and interaction effects of genotypes and environments, considering genotypes, environments, replication, and block as random effects. The stability model proposed by Eberhart and Russell (1966) was implemented to analyze the data over six conditions (environment). The model includes the assessment of stability parameters like mean, regression coefficient (b_i) and deviation from regression (S^2d_i). Analysis was done by using SPAR 2.0 software. Stability parameters and their estimation was carried out by subjecting the data to the condition that G×E interaction is significant when tested against pooled error the stability parameter are figured.

The two stability parameters, regression coefficient (b_i) and deviation from regression (S^2d_i) were estimated as follows:

a) Regression coefficient

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij} I_j$ = The sum of products of environmental index (I_j) with corresponding mean of that genotype at each environment (Y_{ij})

$\sum_j I_j^2$ = The sum of squares of the environmental index I_j

(b) Mean square deviations (S^2d_i) from linear regression

$$S^2d_i = \left[\sum_j d_{ij}^2 / (e-2) \right] - S_e^2 / r$$

Where, $\sum_j d_{ij}^2 = \left[\sum_j Y_{ij}^2 - (Y_i^2 / g) \right] - \left[(\sum_j Y_{ij} I_j)^2 / (\sum_j I_j^2) \right]$ = Variance due to deviation from regression for a genotype

$\sum_j Y_{ij}^2 - (Y_i^2 / g)$ = Variance due to dependent variable and

$\left[(\sum_j Y_{ij} I_j)^2 / (\sum_j I_j^2) \right]$ = Variance due to regression

S_e^2 = the estimate of pooled error

e = number of environments

r = number of replications

3. Results and Discussion

The analysis of variance (ANOVA) for the eleven traits evaluated across fifty-six genotypes, including forty hybrids, fourteen



parents, and two checks, showed significant differences for the genotypes and environments for all characters except for 1000-grain weight (Table 1). The significant genotype-by-environment (GxE) interaction observed for all traits except 1000-grain weight indicates a wide differential behavior of genotypes under different environmental conditions. This is consistent with previous studies that report significant GxE interactions for various agronomic traits, suggesting the importance of genotype adaptability to varying environmental conditions (Bremner et al., 2011; Ali et al., 2017).

Partitioning the sum of squares further highlighted the significant contribution of genotypes, with highly significant mean squares observed for all characters. This indicates the presence of considerable genetic variability in experimental material, essential for breeding programs aimed at improving these traits. The environmental effects, along with the GxE interaction, were significant for most traits, except for plant height, panicle length, and 1000-grain weight. This underlines the importance of environmental variability in influencing the expression of these traits (Ludlow and Muchow, 2017).

Table 1: Analysis of variance for yield and yield components for stability in rice

Source	df	Days to 50% flowering	Days to maturity	Plant height	Total tillers plant ⁻¹	Productive tillers plant ⁻¹	Panicle length
Replication within environment	3	0.426	1.61	2.216	1.084	0.09	1.427
Genotypes	55	86.79**	86.31**	266.71**	17.71**	14.02**	11.55**
Env.+(Var.×Env.)	112	6.62**	6.97**	15.43	3.79*	2.86**	3.19
Environments	2	28.90**	36.90**	204.78**	79.20**	87.24**	65.51**
Genotype×environment	110	6.21**	6.43**	14.98**	2.42*	1.323*	2.06*
Environment (linear)	1	57.81**	73.80**	409.56**	158.39**	174.47**	131.02**
Genotype×environment (linear)	55	9.64**	10.11**	16.58**	6.25*	1.798**	5.72*
Pooled deviation	56	2.74**	2.70**	12.16**	1.52*	0.83	1.35**
Pooled Error	165	1.09	1.07	1.24	0.80	0.70	0.87

Tale 1: Continue...

Source	No. filled grains panicle-1	Spikelet fertility	Biomass	Harvest Index)	1000-seed weight	Single plant yield
Replication within environment	23.006	2.06	0.07	0	0.024	0.199
Genotypes	3101.87**	37.93**	51.59**	0.003**	28.10**	74.96**
Env.+(Var.×Env.)	183.17**	7.106*	3.63**	0.001**	0.42	7.156**
Environments	3241.57**	142.67**	40.42**	0.012**	5.75**	239.73**
Genotype×Environment	127.56**	4.84**	2.96*	0.001**	0.32	2.93*
Environment (linear)	6483.14**	285.34**	80.84**	0.025**	11.49**	479.46**
Genotype×Environment (linear)	201.96**	5.02*	4.16**	0.002**	0.21	3.90**
Pooled Deviation	52.21**	4.18**	1.73**	0.001**	0.42	1.92**
Pooled Error	4.74	0.92	0.86	0	0.36	0.99

*: Significant at ($p=0.05$) level; **: Significant at ($p=0.01$) level

Partitioning of the sum of squares indicated highly significant mean squares due to genotypes for all twelve characters, reinforcing the presence of substantial genetic variability within the experimental material. This finding is consistent with recent research by Kesh (2023), who reported significant genotypic differences in Basmati rice genotypes across multiple environments.

The mean squares due to environments+(genotypes×environments) were significant for all characters except plant height, panicle length, and 1000-grain weight, aligning

with findings by Islam et al. (2024), who observed significant environmental effects on grain yield in Boro rice genotypes. Further partitioning revealed significant variation due to the environment (linear) for all studied characters, indicating substantial linear contributions of environmental effects on these traits. This result corroborates the findings of Kesh (2023), who noted significant environmental effects on various rice quality parameters.

The linear component of the genotype×environment interaction was significant for all characters except 1000-grain



weight, indicating that the genotypes differed significantly in their linear response to environmental changes. Importantly, the mean sum of squares for pooled deviation was significant for all characters except 1000-grain weight, suggesting a significant non-linear and unpredictable component in the genotype-environment interaction for these traits. This underscores the importance of both linear and non-linear components in determining the interaction of genotypes with environments, consistent with reports by Islam et al. (2024) who highlighted the significant contribution of G×E interaction to grain yield stability in Boro rice.

Stability parameters, including mean performance (μ), regression coefficient (b_i), and mean square deviation from regression (S^2di), were estimated following Eberhart and Russell's (1966) model. In this study, S^2di was considered the primary measure of stability, while the regression coefficient (b_i) and mean performance were used to determine the type of stability. A genotype with a high mean, a regression coefficient close to unity ($b_i \approx 1$), and a non-significant S^2di was considered to possess good stability and consistent performance across environments. A regression coefficient greater than unity ($b_i > 1$) indicated below-average stability and adaptation to favorable environments, whereas a regression coefficient less than unity ($b_i < 1$) suggested above-average stability and wider adaptability, even in unfavorable conditions (Table 2 and Table 3).

3.1. Days to 50% flowering

Among the genotypes, IR-68897A and PUSA-5A, along with several hybrids, exhibited desirable stability characteristics, with regression coefficients (b_i) close to unity. These genotypes demonstrated high mean values for early flowering and were found to be adaptable across different environmental conditions. Hybrids like IR-68897A×AR-9-21 and IR-68897A×AR-7-75 exhibited stable flowering times and were considered ideal for diverse environments.

3.2. Days to maturity

The performance for days to maturity was also influenced by both linear and non-linear components of G×E interaction. Genotypes like IR-68897A and AR-19-18 with unit regression coefficients and non-significant deviations from regression showed stable maturity periods across environments. Hybrids such as IR-68897A×AR-19-18 and PUSA-5A×AR-19-18 showed stability, indicating their potential for consistent performance.

3.3. Plant height

The significant G×E interaction for plant height emphasized the variability in genotype responses. Genotypes with regression coefficients near unity, such as IR-68897A and AR-9-21, demonstrated stable plant heights across environments. However, some hybrids like APMS-6A×AR-19-42 exhibited higher plant heights and were suitable for favorable environments based on their stability parameters.

3.4. Total tillers plant⁻¹

The number of total tillers plant⁻¹ is a key determinant

Table 2: Mean performance and stability parameters for single plant yield in rice

Parent/ Cross	Single plant yield		
	Mean	b_i	S^2di
Parents			
Lines			
IR-68897A	26.44	0.08*	-0.96
IR-79156A	25.75	0.56	-0.71
APMS-6A	26.08	0.25	-0.06
PUSA-5A	20.33	0.18	-0.49
Testers			
AR-9-21	21.85	1.56	9.62**
AR-19-18	29.29	0.72	-0.32
AR-7-75	22.49	-0.02	-0.81
AR-19-42	28.25	1.66	7.14**
AR-7-65	18.72	-0.25	-0.77
TCP-650	33.36	0.16*	-0.98
TCP-657	29.77	0.12*	-0.95
TCP-661	27.44	0.38*	-0.97
TCP-585	21.03	0.78	-0.61
TCP-643	29.95	0.31	-0.90
Crosses			
IR-68897A×AR-9-21	26.87	-0.54	-0.22
IR-68897A×AR-19-18	21.15	1.68	0.17
IR-68897A×AR-7-75	24.07	1.08	-0.34
IR-68897A×AR-19-42	22.28	1.12	-0.84
IR-68897A×AR-7-65	28.15	1.22	3.44*
IR-68897A×TCP-650	29.20	1.12	-0.91
IR-68897A×TCP-657	31.67	0.58	-0.05
IR-68897A×TCP-661	17.61	1.64*	-0.98
IR-68897A×TCP-585	25.56	0.59	30.28**
IR-68897A×TCP-643	28.35	1.44	-0.14
IR-79156A×AR-9-21	27.51	1.34	-0.72
IR-79156A×AR-19-18	15.71	1.29	3.85*
IR-79156A×AR-7-75	25.15	1.91	-0.36
IR-79156A×AR-19-42	16.60	1.15	-0.45
IR-79156A×AR-7-65	25.69	2.09	0.87
IR-79156A×TCP-650	25.72	1.29	-0.78
IR-79156A×TCP-657	27.72	0.26	3.06*
IR-79156A×TCP-661	27.96	1.43	7.44**
IR-79156A×TCP-585	18.27	1.90	0.60
IR-79156A×TCP-643	23.63	1.51	3.94*
APMS-6A×AR-9-21	16.50	0.90	-0.33

Table 2: Continue...



Crosses	Single plant yield		
	Mean	bi	S ² di
APMS-6A×AR-19-18	32.66	1.36	-0.44
APMS-6A×AR-7-75	17.86	1.90	-0.81
APMS-6A×AR-19-42	29.78	-0.43	13.29**
APMS-6A×AR-7-65	24.56	1.44	-0.79
APMS-6A×TCP-650	20.52	1.19	-0.74
APMS-6A×TCP-657	21.46	1.68	-0.87
APMS-6A×TCP-661	16.73	1.55	-0.31
APMS-6A×TCP-585	18.78	1.86	0.48
APMS-6A×TCP-643	24.04	0.77	-0.94
PUSA-5A×AR-9-21	22.69	1.77	-0.07
PUSA-5A×AR-19-18	33.62	0.95	-0.65
PUSA-5A×AR-7-75	33.89	0.70	-0.43
PUSA-5A×AR-19-42	25.80	1.17	-0.59
PUSA-5A×AR-7-65	20.47	1.49	-0.50
PUSA-5A×TCP-650	34.08	1.39*	-0.98
PUSA-5A×TCP-657	20.97	0.13	-0.61
PUSA-5A×TCP-661	19.37	2.40	7.36**
PUSA-5A×TCP-585	15.95	0.97	-0.88
PUSA-5A×TCP-643	25.58	1.03	-0.31
Checks			
CSR-36	21.99	0.35	-0.83
KRH-2	24.93	0.87	-0.74
Population mean	24.49	-	-
SE of bi	-	0.4731	-
CD ($p=0.05$)	5.46	-	-

*: Significant at ($p=0.05$) level; **: Significant at ($p=0.01$) level

of rice yield potential, influenced by genetic factors and environmental conditions. In this study, a significant G×E interaction was observed, suggesting that the expression of this trait is influenced by both genetic makeup and the growing environment. Genotypes such as IR-68897A, APMS-6A, and PUSA-5A, along with testers AR-19-18, TCP-650, and TCP-661, exhibited high mean tiller numbers with regression coefficients near unity ($bi=1$), indicating stability across diverse environments.

Hybrids IR-68897A×TCP-657 and APMS-6A×AR-19-18 showed consistent tiller numbers across environments, thus exhibiting superior adaptability and the hybrid APMS-6A×AR-7-75, adapted to poor environments, showed less than average stability, underscoring its potential utility in environments with limited fertility.

3.5. Number of productive tillers plant⁻¹

The productive tiller count is another critical factor for

determining the grain yield in rice. Our results revealed that APMS-6A×AR-19-18 and PUSA-5A×AR-7-75 demonstrated significantly higher productive tillers than the best check, KRH-2, with stable performance across environments. These hybrids showed regression coefficients near unity ($bi\approx 1$), indicating stability.

The hybrid PUSA-5A×AR-19-18, demonstrating high mean productive tillers and significant superiority over the check. This suggests the importance of selecting hybrids that are stable in productive tiller count for improving yield across varying agro-climatic conditions.

3.6. Panicle length

Panicle length is another important determinant of rice yield, affecting the number of grains panicle⁻¹. Our analysis revealed that hybrids IR-68897A×TCP-657 and PUSA-5A×AR-7-75 exhibited significantly higher panicle lengths compared to the best check CSR-36. The stability of these hybrids, reflected by their non-significant deviations from regression (S^2di). These hybrids' high mean panicle length, coupled with stability, is promising for rice breeding programs targeting increased yield potential through improved panicle architecture. Further, hybrids like PUSA-5A×AR-7-75, identified as specifically adaptable to favorable environments, suggest that environmental specificity in panicle length expression could be leveraged for targeted breeding strategies.

3.7. Number of filled grains panicle⁻¹

Filled grains panicle⁻¹ directly contributes to the final grain yield, making this a crucial trait for evaluating rice performance. Hybrids such as IR-68897A×AR-7-75, APMS-6A×AR-19-18, and PUSA-5A×AR-7-75 recorded significantly higher numbers of filled grains compared to the best check, KRH-2. These hybrids, with regression coefficients near unity ($bi\approx 1$), demonstrate stability. The high stability and significant superiority of these hybrids suggest their suitability for environments with variable fertility and moisture regimes. This result aligns with Kumar et al. (2020), who noted that hybrids with higher filled grain numbers also tend to be more adaptable to varying climatic conditions.

3.8. Spikelet fertility (%)

Spikelet fertility is a direct indicator of reproductive success and, consequently, yield potential. The hybrids IR-68897A×AR-7-75, PUSA-5A×AR-19-18, and PUSA-5A×AR-75 showed significantly higher spikelet fertility compared to the best check, KRH-2, and demonstrated stable performance across environments. The stability of these hybrids across environments suggests they can be reliably used in breeding programs aimed at improving spikelet fertility, particularly in regions with fluctuating environmental conditions.

3.9. Biomass plant⁻¹

Biomass accumulation is an important indicator of overall plant vigor and its potential for high grain yield. The hybrid IR-68897A×TCP-643, with a significantly higher biomass plant⁻¹



Table 3: Stable parents for grain yield and its component traits

Sl. No.	Characters	$X > X$, $b_i = 1$, $S^2 d_i = 0$	$b_i > 1$, $S^2 d_i = 0$	$b_i < 1$, $S^2 d_i = 0$
1.	Days to 50% flowering	IR-68897A, IR-79156A, PUSA-5A, AR-19-18, AR-7-75, AR-19-42, TCP-657, TCP-585	AR-7-65, TCP-661	-
2.	Days to maturity	IR-68897A, IR-79156A, PUSA-5A, AR-9-21, AR-19-18, AR-7-75, AR-19-42, TCP-657, TCP-661, TCP-585, TCP-643	-	-
3.	Plant height	IR-68897A, IR-79156A, PUSA-5A (88.88), AR-9-21, AR-19-18, AR-7-75, AR-7-65, TCP-657, TCP-661, TCP-643	-	-
4.	Number of total tillers plant ⁻¹	IR-68897A, APMS-6A, PUSA-5A, AR-19-18, TCP-650, TCP-661, TCP-643	IR-79156A	AR-19-42
5.	Number of productive tillers plant ⁻¹	IR-79156A, AR-19-18, TCP-650	-	PUSA-5A
6.	Panicle length	IR 68897A, APMS 6A, AR-9-21, AR-19-18, AR-7-75, TCP-661	-	-
7.	Number of filled grains panicle ⁻¹	PUSA-5A, AR-19-42, TCP-657	-	-
8.	Spikelet fertility (%)	IR-68897A, IR-79156A, APMS-6A, PUSA-5A, AR-7-75, AR-19-42, AR-7-65, TCP-650, TCP-585, TCP-643	-	AR-9-21
9.	Biomass plant ⁻¹	TCP-650, TCP-643	-	-
10.	Harvest index	AR-19-18, TCP-650	-	IR-68897A, AR-7-65
11.	Grain yield plant ⁻¹	IR-79156A, APMS 6A, AR-19-18, TCP-643	-	IR-68897A TCP-650, TCP-657, TCP-661

than the best check, CSR-36, was identified as highly adaptable across environments. Hybrids like PUSA-5A×AR-7-75, showing a high mean biomass but with regression coefficients less than unity, are particularly suited for poor environments.

3.10. Harvest index

The harvest index, defined as the ratio of grain yield to total biomass, is a critical trait for efficient grain production. The hybrids APMS-6A×TCP-585 and PUSA-5A×AR-19-18, with higher harvest indices and stable performance, were considered suitable for variable environments. Hybrids like APMS-6A×TCP-585 showed adaptability to favorable environments, suggesting that selection for high harvest index in specific environments can lead to more efficient breeding outcomes.

3.11. Grain yield plant⁻¹

Grain yield plant⁻¹ is the ultimate determinant of rice productivity. Hybrids PUSA-5A×AR-75, PUSA-5A×AR-19-18, and IR-68897A×TCP-657 exhibited significantly higher grain yields than the best check KRH-2, with unit regression coefficients ($b_i=1$) indicating stability. These hybrids' ability to maintain high grain yields across environments. Furthermore, the hybrid PUSA-5A×TCP-650, with a regression coefficient greater than unity, indicated better performance under favorable conditions.

4. Conclusion

The study identified promising lines, testers, and hybrids based on performance and stability across three locations. AR-19-18 was the best tester, while APMS-6A and IR-79156A were the most stable lines. Hybrids like PUSA-5A×AR-7-75 and APMS-6A×AR-19-18 showed superior yield stability. Significant genotype × environment interactions were observed. Grain yield per plant was stable in several genotypes. However, multi-season and multi-location trials are needed to confirm the consistency and suitability of these combinations for commercial release.

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