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STABILITY ANALYSIS IN RICE (*ORYZA SATIVA* L.) GENOTYPES ACROSS CONVENTIONAL, ORGANIC, AND NO-INPUT MANAGEMENT SYSTEMS

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SUMMARY

Rice is a staple crop for over half of the global population, necessitating improved yield stability to meet the increasing demand for food. As it is grown under different input management systems depending on resource availability, farmers' capacity, and production objectives, genotype × environment interactions greatly affect yield, underscoring the need for breeding programs that improve stability and adaptability across varied management systems. The effects of G × E under conventional (CM), organic (OM), and no-input (NM) management remain poorly understood. With this objective, an evaluation of 46 rice genotypes across three systems used the additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment (GGE) biplot models to assess yield stability. A multivariate analysis of variance (MANOVA) showed that genotype (G), management (M), and their interaction (G × M) significantly influence yield. GGE biplot analysis identified Kattuyanam, ASD19, Sennar20, Navera, Kalanamak, and Pokkali as highly stable genotypes, while KR09003 and CR1009 showed limited adaptability. AMMI analysis confirmed the results, with PC1 explaining 69.83% of variation, highlighting management as the main factor. Genotypes CO(R)50, PY7, and ADT38 exhibited broad adaptability, whereas KR10019 and Mappillai Samba were suitable under organic systems. Under conventional management, KKL(R)-1, Mappillai Samba, CO(R)50, Kattuyanam, and KR10023 performed well. In organic management, Karudan Samba, Poongar, and Mappillai Samba excelled, while in no-input systems, Mappillai Samba, Kattuyanam, Karuppu Kavuni, and Kitchilli Samba showed a stable performance.

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Keywords: rice stability, organic management, conventional management, no-input management, GGE biplot, AMMI, MANOVA

Key findings: Results revealed that Kattuyanam, ASD19, Sennar 20, Navera, Kalanamak, and Pokkali are highly stable genotypes across all management systems. Meanwhile, KR10019 and Mappillai Samba were suitable for OM, KKL(R)-1, Mappillai Samba, CO(R)50, Kattuyanam, and KR10023 performed well in CM. In NM, Mappillai Samba, Kattuyanam, Karuppu Kavuni, and Kitchilli Samba showed a stable performance.

INTRODUCTION

As rice is a staple food for over half of the global population, enhancing its productivity is imperative to meet future demands. According to the Food and Agriculture Organization (FAO, 2023), global agricultural demand projections will increase by 60% in 2050, requiring advancements in farming practices, crop genetics, and resource management. Indian rice cultivation faces climate stress, water scarcity, soil degradation, and socioeconomic limitations, necessitating sustainable practices. In this context, organic farming promotes ecological balance, safeguards human health by limiting chemical exposure, and provides farmers with higher returns through premium markets (Srivastava and Kumar, 2022). Breeding crop varieties specifically adapted to low-input and organic conditions is essential to achieve high productivity and resilience without dependence on synthetic inputs (Molitorisová *et al.,* 2025). Rice landraces, naturally suited to local conditions and low-input farming, offer valuable traits for enhancing nutrient use efficiency and stress tolerance. The yield gap between controlled trials and on-farm conditions highlights the need for multi-environment testing to identify stable, high-yielding genotypes suited for organic farming (Khah *et al.*, 2019). This approach helps target key traits, such as nutrient efficiency, disease resistance, and weed competitiveness, which are crucial under low-input conditions. Utilizing diverse donor germplasm and appropriate breeding methods like recurrent and participatory selection further supports the development of resilient varieties adapted to organic systems, ensuring practical benefits for farmers and sustainable production (Esan *et al.*, 2023).

Stability analysis in crop breeding focuses on identifying genotypes that exhibit consistent performance across diverse environmental conditions and different management conditions. GGE (genotype and genotype × environment) biplot analysis is a key tool that visualizes genotypic performance across environments and identification of stable, high-yielding varieties. It provides insights into "which-won-where" patterns, genotype ranking, and environment discriminativeness, supporting effective selection in multi-environment trials (Hudson *et al.*, 2022). The AMMI (additive main effects and multiplicative interaction) model, used alongside the GGE biplot, offers complementary insights into yield stability by effectively dissecting genotype-by-environment interactions. These models facilitate the prediction of genotypic performance in untested environments, characterization of the test environments, and evaluation of per se genotype performance under specific environmental conditions. This comprehensive understanding supports targeted, sustainable breeding strategies by identifying stable and high-performing genotypes tailored to specific agroecological zones (Wodebo and Labuschagne, 2023). In this backdrop, the following study sought to identify stable and adaptable rice genotypes to different management systems, specifically for organic and no-input management systems.

MATERIALS AND METHODS

Evaluation of rice accessions

The trial crop, laid out at the institutional farm of the Pandit Jawaharlal Nehru College of

Agriculture and Research Institute (PAJANCOA&RI), Karaikal, commenced during the *Samba* season (July-August). It is a tropical, humid coastal zone with moderate rainfall and clayey soil with moderate water-holding capacity suitable for lowland cultivation. Rice accessions totalling 46 included landraces, modern varieties, and pre-release cultures (Table 1), which were evaluated under three distinct management systems: conventional (CM), organic (OM), and no-input (NM). Each system's assignment to a separate location reflected its typical agronomic practices: location 1 (CM), location 2 (OM), and location 3 (NM). Trials at each site had a randomized complete block design (RCBD) layout with three replications for spatial variability. Crop establishment through transplanting with 25-day-old seedlings followed a spacing of 20 cm × 15 cm. Each experimental plot measured 5 m × 4 m, with standard agronomic practices followed according to the respective management systems.

In the CM system, the application of chemical fertilizers (150:60:60 kg/ha) took place, with pest and weed control achieved through threshold-based pesticides and herbicide-assisted manual weeding. OM in rice cultivation involved the application of farmyard manure, vermicompost, azolla, 'panchagavya,' and oil cakes. It included supplementation with biocontrol sprays and manual weeding, following a comprehensive package of practices designed to maintain ecological balance and promote sustainability (ICAR-NRRI, 2024). In contrast, NM relied solely on the inherent fertility of the soil and manual weeding. In the absence of a pre-experimental soil test, the field had been under continuous paddy cultivation with recommended fertilization practices, indicating a medium level of baseline soil fertility suitable for paddy cultivation. Under such conditions, residual nutrients and inherent soil fertility seemed adequate to support crop growth during the experimental period. Maintaining irrigation was uniform across all management systems.

Handling of plant materials

The collection, handling, and evaluation of plant materials followed established scientific guidelines and protocols to ensure data reliability, accuracy, and reproducibility (Gawdiya *et al.,* 2023). The traditional rice varieties used in this study entailed sourcing from local farmers and selecting based on the morphological characteristics and farmer-identified traits.

Phenotypic data collection

Data on growth and yield attributes measured included days to 50% flowering (days), plant height (cm), the number of tillers per square meter at three growth stages (numbers), root length (cm), root volume (ml/hill), and chlorophyll content (SPAD value). Moreover, the recording of yield-related traits included panicle length (cm), panicle weight (g), 1000-grain weight (g), single plant yield (g), and grain yield (t/ha). The study followed phenotyping protocols based on the methods outlined by the International Rice Research Institute (IRRI, 2013) in the Standard Evaluation System for Rice, with the collected data used for statistical analysis.

Statistical analysis

The performance of all analyses was run in R (Version 4.3.1; R Core Team, 2024). Combined ANOVA assessed G × E across management systems treated as environments for AMMI and GGE. For AMMI in R, assessment used "agricolae" and "ammistability" (Ajay *et al.,* 2019), while GGE biplots' generation was via a GUI (graphical user interface) tool. The conduct of MANOVA used "car" (De-Mendiburu, 2023), and ANOVA via the "agricolae" package (Porter and O'Reilly, 2017) enabled a comprehensive evaluation of genotype performance, stability, and adaptability across environments.

Table 1. Details of rice accessions/genotypes used in the study.

Accessions	Parentage	Origin / Breeding Station
Released Variety		
ADT38	IR1529-680-3-2 / IR4432-52-6-4 // IR7963-30-2	TRRI, Aduthurai, TN, India
ADT39	IR8 / IR20	
ADT43	IR50 / IW Ponni	
ADT46	ADT38 / CO45	
ADT49	CR 1009 / Jeeragasamba	
ASD19	Lalnaganda / IR 30	TNAU, Coimbatore, TN, India
BPT5204	GEB-24 / T(N)1 / Mahsuri	ICAR-IIRR, Hyderabad, India
CO(R)50	CO43 / ADT38	TNAU, Coimbatore, TN, India
CO(R)52	BPT5204 / CO(R)50	
CR1009	Pankaj / Jagannath	ICAR-NRRI, Cuttack, Odisha, India
HUR1	HBR92 / Pusa Basmati / Kasturi	BHU, Varanasi, India
HUR2	IR36 / HR137	
IR36	IR1561-228/1 IR24*4 / *O. nivara* / CR94-13	IRRI, Philippines
IR50	IR2113-14-1-6-2 / IR28 // IR36	
IW Ponni	Tg.65 / 2*ME80	TRRI, Aduthurai, TN, India
KKL(R)-1	CR1009 / ADT39	PAJANCOA&RI, Karaikal, India
PY7	IR-8 / Red Ponni	PKKVK, Puducherry, India
Swarna Sub1	Swarna / IR64-Sub1 // Swarna	IRRI, Philippines
Advanced Breeding Lines		
KR09003	Mutant of IW Ponni	PAJANCOA&RI, Karaikal, India
KR09008		
KR09009		
KR09011		
KR10019		
KR10022	Mutant of Pokkali	
KR10023	Mutant of IW Ponni	
Landraces		
Kalannamak	Landrace and Local Cultivar	Uttar Pradesh, India
Karudan Samba		Tamil Nadu, India
Karun Kuruvai		
Karuppu Kavuni		
Kattuyanam		
Kitchilli Samba		
Kuzhiadichan		
Mappillai Samba		
Maudamani		Odisha, India
Navara		Kerala, India
Norungan		Tamil Nadu, India
Nutripathu		
Pokkali		Kerala, India
Poongar		Tamil Nadu, India
Seeraga Samba		
SelamSanna		
Sennar 20		
Thanga Samba		
Thengapoo Seeraga Samba		
Thulasi Vasanai Seeraga Samba		
Thuyamalli		

Table 2. Analysis of variance (ANOVA) for AMMI model showing the effects of genotype, management, and their Interaction.

Source of variation	d.f.	Sum Sq	Mean Sq	*F* value	Pr(>*F*)
Genotype	45	21.3	0.473	6.107	$< 2e^{-16}$ ***
Management	2	7.73	3.865	49.861	
Genotype × Management	90	11.61	0.129	1.663	0.000941 ***
Residuals	276	21.39	0.078		

†***significance at the 0.1% level.

RESULTS

A detailed analysis of yield-related traits under different management systems revealed significant G × M interactions. Traits, such as panicle length, panicle weight, 1000-grain weight, single-plant yield, and grain yield, varied notably across systems. Conventional management showed the highest mean performance, while organic management offered moderate yields with greater trait stability. No-input management recorded the lowest yields and highest variability, indicating greater stress sensitivity. Plant height was tallest under OM, whereas CM favored root and panicle development.

Additive main effects and multiplicative interaction (AMMI) biplot

The AMMI analysis disclosed significant effects for genotype, management, and G × M interaction (Table 2). The genotype and environment (different management systems) were highly significant ($p < 2e^{-16}$), indicating notable genetic variation and environmental influence. Although the G × M is also significant ($p = 0.000941$), suggesting that genotype performance varies across managements.

GGE biplot - genotype performance and adaptability

Evaluation across management systems unveiled distinct performance trends of Kattuyanam, ASD19, Sennar20, Navera, Kalanamak, and Pokkali, which exhibited high adaptability and superior yield potential across all environments, as indicated by a positive PC1 axis. In contrast, KR09003, Mappillai Samba, CR1009, CO(R)50, Thuyamalli, CO(R)52, and PY7 showed lower overall performance, with a negative PC1, indicating limited adaptability unless implementing targeted improvements. Stable genotypes, including ADT39, KR09008, HUR1, IR36, IW Ponni, ADT43, IR50, Kuzhiadichan, HUR2, KR10023, Swarna Sub1, Karunkuruvai, and Karudan Samba, displayed minimal G × M interaction. It signified yield as largely environmentally dependent, and even high-performing genotypes tend to express their full potential under favorable conditions (Figure 1a).

Environment-specific genotypic performance

Under OM and NM conditions, genotypes such as Thuyamalli, CO(R)50, CO(R)52, PY7, ADT46, and Kichili Samba exhibited positive interactions along PC2, indicating niche adaptation to low-input systems despite a modest mean performance. Conversely, genotypes such as KR09003, KR10019, CR1009, Mappillai Samba, KKL(R)-1, ADT38, KR09011, ADT49, and Maudamani expressed a negative position along PC1, underperforming in CM but showing promise under OM and NM. Stable performers like Karudan Samba, HUR2, Karun Kuruvai, BPT5204, Poongar, KR10023, IR36, KR09011, and Thanga Samba demonstrated minimal interaction effects, suggesting wide adaptability and consistent performance across management systems, with environments ranked based on genotype performance (Figure 1b).

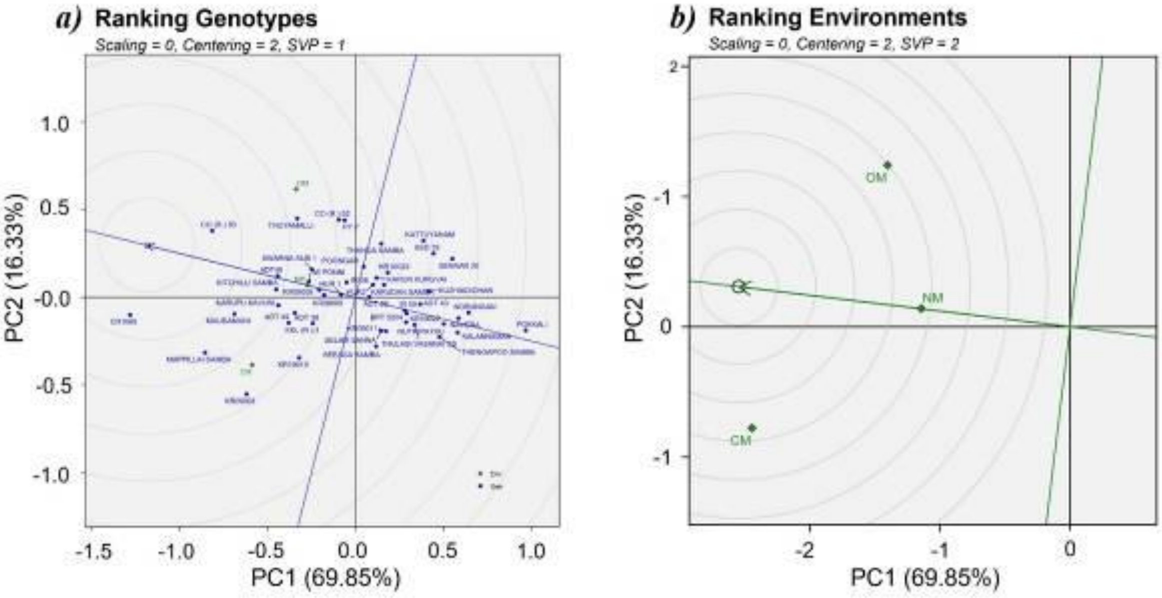

Figure 1*.* Ranking of genotypes (a) and environments (b) across three management systems: conventional, organic, and non-input systems. Environments' ranking was dependent on their impact on yield stability, while ranking genotypes was according to their performance across varying conditions. The plot highlights how different genotypes respond to each management system.

Environment ranking and discriminativeness

The biplot effectively assessed each environment's discriminative ability among the genotypes (discriminativeness) and reflected target conditions (representativeness) for genotype evaluation. OM positioned positively along PC2, indicating distinct interactions favoring specific genotypes, while NM near the origin reflected average performance with minimal GEI. CM, negatively aligned on PC2, showed contrasting management effects. All three managements were negative on PC1, suggesting below-average performance, although PC1 explained 69.83% of G + G × M variation, implying its major contribution in capturing differential genotype responses across environments. (Figure 2a).

Stability and high-performing genotypes

The GGE biplot revealed predominantly acute angles between genotype and environment vectors, indicating strong positive correlations and consistent performance across managements. Occasional obtuse angles suggested negative interactions, while right angles indicated neutral relationships, aiding identification of stable and adaptable genotypes. The PC1 and PC2 configurations further facilitated assessment of environmental discriminativeness and representativeness for effective selection (Figures 2b and 2c).

Genotypes, such as Kattuyanam, Thanga Samba, ASD19, Sennar 20, Poongar, KR10023, Karun Kuruvai, Karudan Samba, and Kuzhiadichan, combined high performance with stability, making them ideal for wide adaptation. CO(R)52, PY7, Thuyamalli, and CO(R)50 showed a moderate performance but high stability, suiting low-input systems. Genotypes like CR1009, Mappillai Samba, KR09003, KR10019, KKL(R)-1, ADT49, ADT38, Maudamani, and Karuppu Kavuni excelled under high-input conditions but lacked broad adaptability, suggesting their relevance in targeted breeding programs.

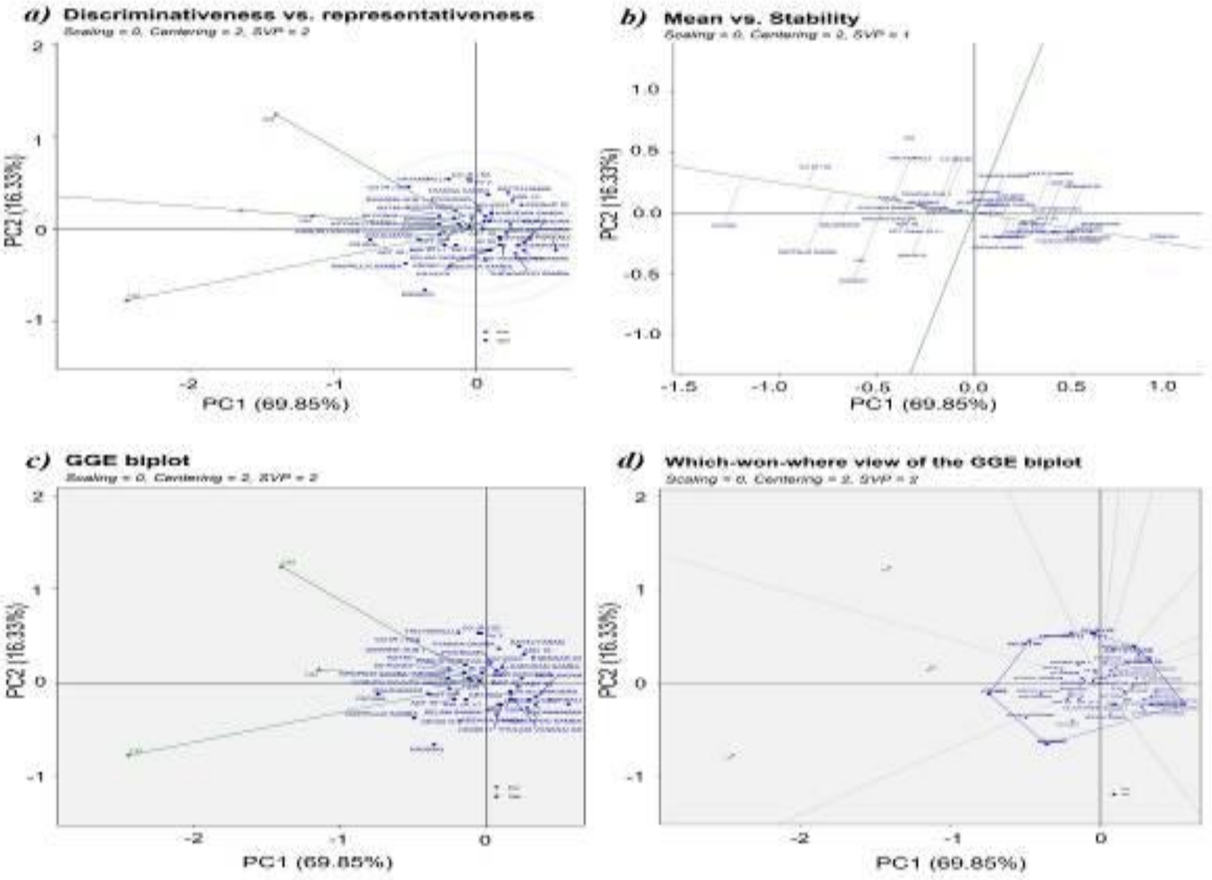

Figure 2. (a) Discriminativeness vs. representativeness plot, (b) Mean vs. stability plot, and (c) GGE biplot showing genotype × environment interaction among 46 rice genotypes under three management systems (conventional, organic, and low-input). (d) "Which-Won-Where" view of the GGE biplot highlights genotype adaptability and performance across environments. Genotypes near the ideal point indicate high yield and stability, while those farther away exhibit environment-specific responses.

Which-Won-Where biplot in genotype-environment analysis

Under OM, genotypes such as CO(R)50, Thuyamalli, and PY7 are notable as the best performers, with Swarna Sub1, ADT46, IW Ponni, CO(R)52, HUR2, and IR36 also exhibiting favorable interactions with OM environments. For NM within the sector defined by the vertex CR1009, emerge as a top performer, followed by KR09008, Kitchili Samba, KR09009, and ADT39, with locations in proximity to the NM environment. It suggests their moderate adaptation and even demonstrates comparable performance with OM management. In CM, CR1009 and KR09003 are the leading genotypes, while Karupu Kavuni, ADT38, Maudamani, ADT49, KKL(R)-1, Seeraga Samba, and KR10019 follow as strong contenders (Figure 2d).

Standard test evaluation parameter

The comparative analysis of genotype performance across the three management systems revealed key insights into their discriminating power, representativeness, and desirability (Tables 3 and 4). CM and OM exhibited the highest discriminating power (2.17 ± 1.24 and 2.17 ± 1.10, respectively),

Table 3. Standardized test evaluation parameters for different management.

Management	Discriminating Power Mean ± SD	Representativeness Mean ± SD	Desirability Mean ± SD
CM	2.17 ± 1.24	0.46 ± 0.15	5.36 ± 4.36
NM	2.16 ± 0.98	0.54 ± 0.16	4.59 ± 3.28
OM	2.17 ± 1.10	0.53 ± 0.14	4.30 ± 2.35

†CM – Conventional Management; NM – No input Management; OM – Organic Management; SD – Standard Deviation.

Table 4. Summary of ideal genotypes and genotypes with stable and high mean yields in different management.

Management	Ideal_Genotype	Stable_Genotype	High_Mean_Genotype
CM	KKL(R)-1	IR50	KKL(R)-1
NM	BPT5204	Thuyamalli	Mappillai Samba
OM	Poongar	Kuzhiadichan	Karudan Samba

†CM – Conventional Management; NM – No input Management; OM – Organic Management.

though CM showed greater variability. NM had a slightly lower discriminating power (2.16 ± 0.98) but the highest representativeness (0.54 ± 0.16), indicating stronger alignment with average genotype performance, followed by OM (0.53 ± 0.14) and CM (0.46 ± 0.15). Although CM recorded the highest desirability index (5.36 ± 4.36), its high variability reduced reliability, whereas NM (4.59 ± 3.28) and OM (4.30 ± 2.35) offered more consistent and stable selection potential.

In CM, genotypes CR1009 and KKL(R)-1 demonstrated high grain yield, with Kalannamak identified as the most stable. Under NM, CO(R)52 and CR1009 showed strong adaptability, KR09008 was most stable, and CO(R)52, Kattuyanam, and Pokkali exhibited high yields. In OM, CO(R)50, Karun Kuruvai, and Karuppu Kavuni were the top-performing genotypes, with ASD19 showing the highest stability. Notably, CR1009 (CM and NM) and CO(R)50 (OM) emerged as ideal genotypes, while Kalannamak, KR09008, and ASD19 represented valuable stable resources across management systems.

Multivariate analysis of variance

The performed MANOVA demonstrated that genotypes, management systems, and their interaction all exerted highly significant effects on the combined set of response variables, with a $p < 0.001$ threshold across all four test statistics (Tables 5 and 6). The consistency in significance across Wilks' Lambda, Pillai's Trace, Roy's Largest Root, and Hotelling-Lawley Trace strengthens the reliability of these findings, as each test has different sensitivities to assumption violations and effect size structures.

Management systems dominated multivariate trait variation, with high F-values in Roy's Root and Hotelling-Lawley tests, which are sensitive to the presence of strong effects in one or more canonical variates. Genotypes were significant, indicating genetic composition contributed to phenotypic variance, while the G × M interaction showed moderate, significant effects, signifying differential responses and the need for stability evaluation.

DISCUSSION

Selecting suitable test environments is crucial in rice breeding, as they significantly affect trait expression and genotype differentiation (Prado *et al.,* 2024). The GGE biplot's interpretation used the average environment coordination (AEC) method, an approach by Ajay *et al.* (2022). It effectively integrates mean performance with stability to evaluate genotype-by-environment interactions (GEIs). These primarily have the governance of variations in soil fertility status, nutrient availability, and management practices across CM, OM, and NM systems. In this method, the AEC abscissa identifies high-yielding, stable

Table 5. MANOVA for genotype, management, and their interaction effects.

Genotype					
MANOVA test	Statistic value	F Value	numDf	den Df	Pr (>F)
Wilks	0.0000060	14.244	450	2649.3	$< 2.2e^{-16}$ ***
Pillai	5.6092	7.864	450	2770	
Roy	54.867	337.73	45	277	
Hotelling-Lawley	73.900	43.72	450	2662	
Management					
MANOVA test	Statistic value	F Value	numDf	den Df	Pr (>F)
Wilks	0.0142979	197.329	20	536.0	$< 2.2e^{-16}$ ***
Pillai	1.5401	90.083	20	538	
Roy	28.820	775.25	10	269	
Hotelling-Lawley	30.165	402.71	20	534	
Genotype x Management					
MANOVA test	Statistic value	F Value	numDf	den Df	Pr (>F)
Wilks	0.0000463	5.240	890	2697.2	$< 2.2e^{-16}$ ***
Pillai	5.6499	4.042	890	2770	
Roy	13.341	41.52	89	277	
Hotelling-Lawley	26.381	7.89	890	2662	

†***significance at the 0.1% level.

Table 6. Standard test evaluation parameter for the traits observed under each management.

MGT	GY	SPY	TGW	PH	RL	RV	PL	PW	TT	SV	DAF
CM	1.1 ± 0.51	22.02 ± 9.09	32.28 ± 8.05	104.39 ± 23.72	20.66 ± 3.72	22.16 ± 7.1	24.56 ± 3.78	2.73 ± 1.03	16.9 ± 3.27	37.4 ± 3.51	94.72 ± 11.34
NM	0.72 ± 0.32	17.45 ± 7.2	23.84 ± 5.88	100.11 ± 23.96	23.3 ± 5.35	21.05 ± 10.81	20.85 ± 2.71	2.41 ± 0.71	14.76 ± 2.67	37.69 ± 3.9	96.91 ± 9.54
OM	1.07 ± 0.37	18.43 ± 4.09	23.62 ± 5.19	104.83 ± 20.76	22.19 ± 4.22	21.53 ± 7.93	21.56 ± 2.66	2.32 ± 0.75	16.84 ± 2.44	34.95 ± 4.1	95.65 ± 11.63

†CM – Conventional Management; NM – No input Management; OM – Organic Management
Grain yield (GY), Single plant yield (SPY), 1000-grain weight (TGW), Plant height (PH), Root length (RL), Root volume (RV), Panicle length (PL), Panicle weight (PW), Number of tillers at three growth stages (TT), Chlorophyll content SPAD value (SV), and Days to 50% flowering (DAF).

genotypes, whereas the perpendicular distance from the AEC ordinate represents each genotype's contribution to GEI. Additionally, the angles between genotype and environment vectors provide insights into their correlations, where acute angles indicate positive associations, obtuse angles denote negative relationships, and right angles reflect no correlation. Kunwar *et al.* (2024) reported that using the AEC method, genotypes with high mean performance and low GEI contribution could have a clear distinction from less stable genotypes. This demonstrated that multi-environment biplot analyses accurately identify broadly adaptable versus niche-adapted genotypes, providing reliable selection guidance.

In line with this, the present biplot clearly separated the three management systems: OM aligned with PC2, highlighting favorable genotype-trait associations; NM clustered near the origin, reflecting average performance with minimal GEI; and CM positioned negatively along PC2. It showed a strong discrimination due to contrasting input levels. A negative association of all environments with PC1 suggested below-average performance; proximity to the origin indicated stability (Khan *et al.*, 2021). Accordingly, Kattuyanam, Thanga Samba, ASD19, Sennar 20, Navera, Kalannamak, Pokkali, Poongar, KR10023, Karun Kuruvai, Karudan Samba, and Kuzhiadichan demonstrated both a high mean performance and stability. Sapkota *et al.* (2024) found that these genotypes consistently maintained yield stability across multiple environments, confirming their suitability for both high- and low-input systems. In contrast, CO(R)50, PY7, Thuyamalli, ADT38, CR1009, Mappillai Samba, KR09003, KR10019, KKL(R)-1, ADT38, ADT49, Maudamani, and Karuppu Kavuni displayed niche adaptation under low-input or conventional systems. Derbew (2024) reported that environments with contrasting inputs can discriminate genotype performance effectively and emphasized the importance of PC1 and PC2 in summarizing GEI patterns.

PC1 captured 69.83% of the total variation, underscoring its role in explaining genotype responses. Genotypes such as CO(R)50, PY7, Thuyamalli, and ADT38 displayed moderate yields but high stability, making them suitable for low- to medium-input conditions. Conversely, CR1009, Mappillai Samba, KR09003, KR10019, KKL(R)-1, ADT49, ADT38, Maudamani, and Karuppu Kavuni performed well under CM but lacked stability. It indicates their yield expression is strongly dependent on external nutrient supply and may not perform well under low-input systems where nutrient availability is inadequate. The "Which-Won-Where" GGE biplot visualizes crossover interactions, mega-environment differentiation, and genotype-specific adaptation, identifying top performers across environments and management systems (Olanrewaju *et al.,* 2021; Figure 2d). However, these findings are dependent on a single season and require multi-season validation to confirm their stability. According to Hashim *et al.* (2021), genotypes identified at the vertices of a polygon exhibit superior performance and strong adaptability to specific mega-environments, making them particularly well-suited for those conditions. Accordingly, OM had CO(R)50, Thuyamalli, and PY7; NM had KR09008, Kitchili Samba, and ADT39; and CM had CR1009, KR09003, and Karuppu Kavuni. CM showed the strongest discriminating ability; NM and OM offered better stability and representativeness, essential for selection in variable agroecological contexts. Evaluation metrics confirmed these patterns: CM produced higher trait values but with greater variability, whereas NM and OM provided better environmental representativeness and yield stability (Table 3).

MANOVA confirmed significant effects of genotype, environment, and G × M ($p < 2.2e^{-16}$), with the management system exerting the strongest influence on multivariate trait variation. Multivariate tests (Wilks' Lambda, Pillai’s Trace, Roy’s Largest Root, Hotelling–Lawley Trace) consistently supported genotype-driven variation, especially in plant height, tiller number, and root volume. These results, consistent with wheat studies in stress environments (Zencirci *et al.*, 2019), suggest CM favors high-yielding types, while NM and OM promote stability and resilience. Composite yield analysis and selection indices integrated with GGE insights enabled classification into three functional groups: broadly adapted genotypes suitable for all three environments, high-performing types under organic conditions, and those suited to no-input systems.

Genotypes identified as ideal, stable, or high-yielding varied by the management system: CR1009 and KKL(R)-1 were ideal under CM, CO(R)52 and CR1009 under NM, and CO(R)50, Karun Kuruvai, and Karuppu Kavuni under OM. NM and OM showed more stable and representative performance, while CM had the highest but most variable desirability index. Recent studies by Abdelrahman *et al.* (2022), Kapoor *et al.* (2023), and Jyoti *et al.* (2024) also highlighted that significant G × M interactions revealed genotype-specific responses, necessitating tailored variety selection to specific environmental and input conditions. Genotypes such as CO(R)50, PY7, and ADT38 demonstrated stable yields across all management regimes, reflecting broad adaptability and genetic resilience. Similarly, KKL(R)-1, Mappillai Samba, and Karudan Samba exhibited low genotype-by-environment interaction (GEI) values and high yield stability, probably due to efficient nutrient uptake and stress tolerance—traits valuable for breeding resilient cultivars suited to diverse environments. Under CM, genotypes such as KKL(R)-1, Mappillai Samba, CO(R)50, Kattuyanam, and KR10023 displayed strong yield stability, attributed to traits related to input responsiveness. However, their performance is closely dependent on external inputs, limiting their utility in low-input systems. Incorporating these traits into less productive accessions may enhance yield potential and resource-use efficiency in input-intensive systems. In organic systems, genotypes including KR10019, Mappillai Samba, Karudan Samba, and Poongar consistently recorded high yields and positive G × M, signifying their suitability for low-input environments. Their performance suggests underlying root traits, such as root length (cm), root volume (ml/hill) for improved nutrient cycling, and compatibility with organic amendments. As their AMMI scores confirm stability under organic conditions, further breeding is essential to ensure consistency across varied organic managements. NM favored genotypes like ADT46, Thuyamalli, CR1009, and CO(R)52, which showed high yield and strong GEI. Other genotypes like Mappillai Samba, Kattuyanam, Karuppu Kavuni, and Kitchilli Samba also exhibited high stability. These genotypes demonstrate drought resilience and efficient nutrient uptake, and introgressing these traits into less resilient lines can enhance performance under no-input conditions, supporting sustainable, low-cost rice production**.**

CONCLUSIONS

The findings highlight the performance of selected rice genotypes across diverse management systems, emphasizing key traits like nutrient use efficiency, stress tolerance, and low GEI that support breeding for broad adaptability. Genotypes such as CO(R)50, PY7, and ADT38 performed consistently across conventional, organic, and no-input systems, while input-responsive types like KKL(R)-1 and Mappillai Samba excelled under conventional management. In organic systems, KR10019 and Poongar showed efficient nutrient use, and under no-input conditions, ADT46 and Thuyamalli demonstrated resilience through traits like optimal tillering, which highlights the need to integrate system-specific adaptive traits into less stable genotypes.

REFERENCES

Abdelrahman M, Shaheen A, El-Beltagy A, Mahfouz M (2022). Detection of superior rice genotypes and yield stability under different nitrogen levels using AMMI model and stability statistics. *Agronomy* 12: 1567. https://doi.org/10.3390/plants11202775.

Ajay BC, Manivannan N, Jadhav DR, Jayakumar P, Gowda MVC (2022). Higher order AMMI (HO-AMMI) analysis: A novel stability model to study genotype-location interactions. *Indian J. Genet.* 82: 25–30. https://doi.org/10.31742/IJGPB.82.1.4.

Ajay BC, Sebastià MT, Farshadfar E (2019). ammistability: R package for ranking genotypes based on additive main effects and multiplicative interactions stability parameters. *Indian J. Genet. Plant Breed.* 79(2): 457–466. https://doi.org/10.31742/IJGPB.79.2.10.

de-Mendiburu F (2023). agricolae: Statistical Procedures for Agricultural Research. R package version 1.3-7. https://CRAN.R-project.org/package=agricolae.

Derbew S (2024). AMMI and GGE biplot analysis for barley genotype yield stability and adaptability in multi-environment trials. *Agronomy* 14(3): 456. https://doi.org/10.1002/agg2.20565.

Esan VI, Oke GO, Ogunbode TO, Obisesan IA (2023). AMMI and GGE biplot analyses of Bambara groundnut (*Vigna subterranea* (L.) Verdc.) for agronomic performances under three environmental conditions. *Front. Plant Sci.* 13: 997429. https://doi.org/10.3389/fpls.2022.997429.

FAO (2020). World food and agriculture – statistical yearbook 2022. https://doi.org/10.4060/cb4477en.

Gawdiya S, Kumar D, Shivay YS, Bhatia A, Mehrotra S, Chandra MS, Kumawat A, Kumar R, Price AH, Raghuram N, Pathak H, Sutton MA (2023). Field-based evaluation of rice genotypes for enhanced growth, yield attributes, yield and grain yield efficiency index in irrigated lowlands of the Indo-Gangetic Plains. *Sustainability* 15(11): 8793. https://doi.org/10.3390/su15118793.

Hashim N, Begum H, Ahmed B, Rashid MM, Islam MR, Chowdhury SI, Ahmed S, Sultana S, Rahman MH (2021). Integrating multivariate and univariate statistical models to investigate genotype-environment interaction of advanced fragrant rice genotypes under rainfed conditions. *Sustainability* 13(8): 4555. https://doi.org/10.3390/su13084555.

Hudson AI, Odell SG, Dubreuil P, Tixier MH, Praud S, Runcie DE, Ross-Ibarra J (2022). Analysis of genotype-by-environment interactions in a maize mapping population. *G3 Genes Genomes Genet.* 12(3): jkac013. https://doi.org/10.1093/g3journal/jkac013.

ICAR-NRRI (2024). Package of practices for organic aromatic rice cultivation. ICAR-National Rice Research Institute, Odisha, India. Available at: https://icar-nrri.in/wp-content/uploads/2024/08/NRRI_Research-Bulletin-No-46.pdf.

International Rice Research Institute (IRRI) (2013). Standard Evaluation System for Rice (SES). International Rice Research Institute, Los Baños, Philippines. Available at: http://www.knowledgebank.irri.org/images/docs/rice-standard-evaluation-system.pdf.

Jyoti SD, Singh RP, Kumar A (2024). Rice breeding for low input agriculture. *Front. Plant Sci.* 15: 1408356. https://doi.org/10.3389/fpls.2024.1408356.

Kapoor C, Raj C, Avasthe R, Basandrai D, Pattanayak AK, Aditya JP, Das SP, Sharma V, Singh M, Singh S (2023). Rice genetic resources for organic agriculture under hill ecology: Evaluation and usefulness. *Plant Genet. Resour.* 21: 123–134. https://doi.org/10.1017/S1479262123000576.

Khah EM, Memariani F, Asadi Fozi M (2019). Multienvironment testing for trait stability and G × E interaction in wheat breeding. *Front. Sustain. Food Syst*. 3: 82. https://doi.org/10.3389/fsufs.2019.00082.

Khan MMH, Rafii MY, Ramlee SI, Guevarra RB, Badruzaman M, Latif MA, Ahmad F, Al-Qurainy F. (2021). AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. *Verdc*.) genotypes under multi-environmental trials (METs). *Sci. Rep.* 11: 22791. https://doi.org/10.1038/s41598-021-01411-2.

Kunwar CB, Basnet B, Sunuwar S, Mahato DN, Chaudhari R, Upadhya J, Pokhrel P (2024). Unravelling genotype-by-environment interaction in maize using cutting-edge statistical tools: Innovative empirical selection for increased yield stability. *Ecol. Genet. Genomics* 32: 100249. https://doi.org/10.1016/j.egg.2024.100249.

Molitorisová A, Clemens S, Fresco L, Hubar-Kołodziejczyk A, Tosun J, Niggli U, Qaim M, Visser RGF, Weber APM, Wesseler J, Zilberman D, Purnhagen K (2025). New genomic techniques in organic production: Considerations for science-based, effective, and acceptable EU regulation. *Cell Rep. Sustain.* 2(6): 100405. https://doi.org/10.1016/j.crsus.2025.100405.

Olanrewaju OS, Oyatomi O, Babalola OO, Abberton M (2021). GGE biplot analysis of genotype × environment interaction and yield stability in Bambara groundnut. *Agron.* 11: 1839. https://doi.org/10.3390/agronomy11091839.

Porter HF, O'Reilly PF (2017). Multivariate simulation framework reveals performance of multi-trait GWAS methods. *Sci. Rep.* 7: 38837. https://doi.org/10.1038/srep38837.

Prado M, Famoso A, Guidry K, Fritsche-Neto R (2024). Optimizing multi-environment trials in the Southern US Rice belt via smart-climate-soil prediction-based models and economic importance. *Front. Plant Sci.*, 15, Article 1458701. https://doi.org/10.3389/fpls.2024.1458701.

R Core Team. (2024). R: A language and environment for statistical computing (Version 4.3.1). R Foundation for Statistical Computing. https://www.R-project.org/.

Srivastava AK, Kumar A (2022). Exploring organic farming: Advantages, challenges, and future directions. *Plant Sci. Arch*. 7(3): 9–13. https://doi.org/10.5147/PSA.2022.7.3.09.

Wodebo TF, Labuschagne MT (2023). Multienvironment testing for trait stability and G × E interaction in wheat breeding. *Front. Sustain. Food Syst.* 3: 82. https://doi.org/10.3389/fsufs.2019.00082.

Zencirci N, Ulukan H, Ordu B, Aslan D, Mutlu HT, Örgeç M (2019). Salt, cold, and drought stress on einkorn and bread wheat during germination. *Int. J. Secondary Metabol.* 6(2): 113–128. https://doi.org/10.21448/ijsm.543097.