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DEVELOPMENT OF STABLE AND HIGH-YIELDING RICE (*ORYZA SATIVA* L.) GENOTYPES FOR SUBOPTIMAL AGROECOSYSTEMS

S. YURIYAH[1], L. HERLINA[2*], H. AFZA[1], J. PRASETIYONO[2], A. DADANG[3], Y.N. ANDARINI[1], and A. MARUAPEY[4]

[1]Research Center for Food Crop, National Research and Innovation Agency, Indonesia
[2]Research Center for Applied Botany, National Research and Innovation Agency, Indonesia
[3]Directorate of Scientific Collection Management, National Research and Innovation Agency, Indonesia
[4]Sorong Muhammadiyah University, West Papua, Indonesia
[*]Corresponding author's email: tydars66@gmail.com
Email addresses of co-authors: siti093@brin.go.id, higa.afza@brin.go.id, joko038@brin.go.id, a.dadang68@gmail.com, yusi003@brin.go.id, ajangmarpy@gmail.com

SUMMARY

Stable and high-yielding rice (*Oryza sativa* L.) cultivars are essential for improving productivity in marginal environments such as Papua, Indonesia. Ten rice genotypes, including elite and advanced breeding lines, underwent evaluation across two contrasting sites—Muara (favorable) and Papua (suboptimal)—to estimate genetic variability, heritability, stability, and tolerance indices. Significant genotype-by-environment interactions were evident for key agronomic traits, particularly plant height, productive tiller number, and 1000-grain weight. Moderate to high heritability (H^2 = 0.593–0.745) indicated a strong genetic control, with the productive tiller number showing the greatest variability (GCV = 14.68%, PCV = 23.80%). Stability analyses using the Eberhart-Russell and AMMI (additive main-effects and multiplicative interaction) models identified the genotype 12F as highly adaptable and high yielding, 1F and 54F as broadly stable, and 58F and 44F as consistently stable under stress-prone conditions. The stress tolerance index (STI) supported these findings, confirming combined yield potential and environmental resilience. Although based on two locations, this study provides valuable preliminary insights for developing rice cultivars adapted to suboptimal agroecosystems.

Keywords: Adaptability, heritability, genotype stability, stress tolerance index, suboptimal agroecosystem

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Key findings: Significant genotype-by-environment interactions were noteworthy for primary agronomic traits, underscoring the importance of multi-environment assessment of rice (*O. sativa* L.). Stability analysis identified 12F as the most promising genotype, providing high yields and considerable adaptability.

INTRODUCTION

Rice (*Oryza sativa* L.) is a vital staple sustaining food security across Southeast Asia, including Indonesia, where diverse agroecological zones offer both opportunities and challenges for varietal development (Dhanushkodi *et al*., 2022; Zhai *et al*., 2023). Suboptimal agroecosystems, often characterized by poor soil fertility, fluctuating water regimes, and environmental stress conditions, pose significant constraints to rice productivity (Liu *et al*., 2020). These marginal environments remain underutilized in breeding programs due to the complexities of the genotype-by-environment interaction (GEI) and limited information on varietal adaptability (Shamsudin *et al*., 2016; Prasada, 2020; Kaur *et al*., 2023). Identifying rice genotypes with stable yield performance under such conditions must be a key breeding priority.

Conventional breeding has substantially improved yield potential under favorable environments, yet developing genotypes combining high yield and stability under marginal conditions remains a major challenge (Pour-Aboughadareh *et al*., 2022). Multienvironment trials enable assessment of both mean performance and phenotypic stability across contrasting conditions (Mau *et al*., 2019; Xu *et al*., 2024). Biometrical approaches, such as the Eberhart and Russell regression model, additive main effects and multiplicative interaction (AMMI), and genetic parameter estimates (heritability and genotypic and phenotypic coefficient of variation), provide insights into genetic control and environmental sensitivity, facilitating selection of broadly or specifically adapted genotypes (Kumar *et al*., 2024).

Papua Province represents a typical suboptimal agroecosystem where rice production constraints result from limited infrastructure, acidic soils, and high environmental variability (Beding *et al*., 2021; Cahyono and Altanjung, 2023; Saa, 2024). Identifying genotypes capable of stable performance under such conditions is critical for expanding cultivation and strengthening regional food security.

This study evaluated advanced breeding lines and released cultivars across two contrasting environments in Indonesia to assess genetic variability, GEI, and yield stability. Stability, defined as consistent genotypic performance across environments, incurred analysis using an integrated framework combining AMMI, Eberhart-Russell regression, and the stress tolerance index (STI). This multi-model approach provides complementary insights into yield stability and stress resilience, essential for developing rice cultivars suited to suboptimal agroecosystems.

MATERIALS AND METHODS

Experimental sites and plant materials

The study, conducted during the main planting season, comprised two agroecological distinct environments in Indonesia. The first site, Muara (6.6175°S, 106.7923°E; Bogor Regency, West Java), represents a well-managed lowland area with fertile alluvial soils, adequate irrigation, and stable rainfall typical of humid tropical lowlands. The second site, Sorong (4.2121°S, 104.5500°E; West Papua Province), typifies a suboptimal agroecosystem with acidic soils (pH < 5.5), irregular rainfall, and low-input management common to marginal areas of eastern Indonesia. These contrasting environments were choices to evaluate genotype × environment interactions (GEI).

Ten rice genotypes tested comprised six advanced breeding lines (1F, 7F, 12F, 44F, 54F, and 58F) and four released cultivars (Inpari10, Inpari13, Ciherang, and Situbagendit). The advanced lines originated from national breeding programs previously evaluated under low-pH and nutrient-deficient conditions to ensure baseline tolerance. Experiments at both sites followed a randomized complete block design with three replications.

Traits' measurement

The recording of standard agronomic and yield-related traits continued following the International Rice Research Institute (IRRI)'s Standard Evaluation System. Traits included plant height (PH, cm), productive tillers per plant (PT), days to 50% flowering (DFF), days to 85% maturity (DM), 1000-grain weight (TGW, g), filled grains per panicle (FG), empty grains per panicle (EG), and grain yield (YLD, kg ha^{-1} dry weight basis). Data averaging per plot occurred across replications.

Analysis of variance and genetic parameters

The study performed two-way ANOVA to partition variation among genotypes, environments, and their interactions. Genotypic ($\sigma^2 g$), G × E ($\sigma^2 ge$), and error ($\sigma^2 e$) variances entailed estimations. Broad-sense heritability (H^2) calculation followed Falconer and Mackay (1996):

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{ge}^2}{e} + \frac{\sigma_e^2}{re}}$$

Where *e* is the number of environments, and *r* is the number of replications.

Genotypic (GCV) and phenotypic (PVC) coefficients of variation also involved calculations to assess the genetic variability.

Stability and adaptability analysis

Genotypic stability and adaptability analyses used the additive main effects and multiplicative interaction (AMMI) model (Gauch, 2006) and the Eberhart-Russell (1966) regression model. These complementary methods separate additive and multiplicative effects, assessing genotypic responses across environments. With only two environments, deviations from regression (S^2di) were not interpretable (df = 0); thus, only considering regression coefficients (β) and mean yields $\beta \approx 1$, indicating average adaptability; $\beta > 1$ signifies adaptability to favorable environments; and $\beta < 1$ implies adaptability to stress-prone conditions.

The AMMI model combined ANOVA and principal component analysis (PCA) to visualize adaptability patterns. As AMMI analysis typically benefits from larger multienvironment datasets (≥5 sites), its employment here was as a descriptive, exploratory tool (Yan and Tinker, 2006). Trait-specific stability attained further assessment via the coefficient of variation (CV%) across environments. The stress tolerance index (STI) quantified yield performance with stress relative to optimal conditions (Fernández, 1992):

$$STI = (Yp \times Ys)/(\bar{y}p)^2$$

Where *Yp* = yield under favorable (Muara) conditions, *Ys* = yield under suboptimal (Papua) conditions, and $\bar{y}p$ = mean yield under favorable conditions. Genotypes with STI > 1.0 tended to be high-yielding and stress-tolerant.

Data processing and visualization

All data processing used R software (v4.1.0) and Excel. Two-way ANOVA and variance components underwent computation in R, while deriving heritability, GCV, and PCV resulted from variance estimates. AMMI and regression analyses employed the *agricolae* package (v1.3-6), which also generated a PCA biplot. Trait-specific stability gained expression as CV% across locations.

RESULTS

Genotypic variation

Significant variation was evident among the 10 rice (*Oryza sativa* L.) genotypes for agronomic and yield traits across both environments (Table 1). Analysis of variance revealed highly significant effects of genotypes, environments,

Table 1. Analysis of variance for agronomic and yield traits of rice genotypes tested across two locations (Muara and Papua).

Source	d.f.	PH	PT	DFF	DM	TGW	FG	EG	YLD
Genotype (G)	9	9.95***	3.30*	1.02ns	0.79ns	4.34**	0.48ns	4.99**	2.41*
Location (L)	1	0.58ns	0.66ns	465.57***	368.17***	24.20***	33.89***	21.54***	10.52**
G × L	9	8.79***	2.53*	0.34ns	0.21ns	1.46ns	1.97ns	4.39**	2.50*
Residual	20	–	–	–	–	–	–	–	–

Notes: PH = Plant height; PT = Productive tiller; DFF = Days to 50% flowering; DM = Days to 85% maturity; TGW = 1000-grain weight; FG = Filled grains; EG = Empty grains; and YLD = Dry yield. Significance levels: ns = not significant; $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***).

Table 2. Mean performance of the rice genotypes for agronomic and yield-related traits across two locations (Muara and Papua).

Genotype	Location	YLD (kg ha^{-1})	EG (no.)	FG (no.)	TGW (g)	DM (days)	DF (days)	PT (no.)	PH (cm)
1F	Muara	3166.67	21.00	93.97	26.47	117.67	97.33	31.13	106.33
1F	Papua	3595.00	19.00	100.00	30.00	65.00	51.00	34.00	120.20
7F	Muara	2755.00	35.10	94.47	29.27	135.00	94.67	20.33	104.83
7F	Papua	3600.00	17.00	120.00	30.00	65.00	50.00	33.00	95.40
12F	Muara	3165.00	23.23	95.07	26.73	136.00	106.33	24.67	101.93
12F	Papua	4832.00	21.00	141.00	27.00	71.00	50.00	29.00	91.80
44F	Muara	3948.33	34.03	104.63	24.00	129.33	95.00	23.87	102.63
44F	Papua	3682.00	6.00	115.00	27.00	65.00	50.00	22.00	91.20
54F	Muara	3033.33	36.30	103.33	26.07	129.33	93.67	21.07	101.53
54F	Papua	3494.00	45.00	109.00	30.00	65.00	48.00	16.00	98.50
58F	Muara	3455.00	23.30	89.53	25.00	130.33	98.00	25.67	98.27
58F	Papua	3830.00	8.00	112.00	29.00	65.00	52.00	16.00	108.00
Ciherang	Muara	3058.33	40.77	93.67	24.07	131.67	97.00	21.73	106.53
Ciherang	Papua	2605.00	51.00	118.00	24.00	65.00	50.00	13.00	115.20
Inpari10	Muara	2946.67	30.03	91.13	27.80	134.67	102.00	22.80	95.57
Inpari10	Papua	4362.00	5.00	150.00	29.00	65.00	48.00	17.00	101.60
Inpari13	Muara	2766.67	50.50	87.27	25.17	128.67	93.67	23.33	100.47
Inpari13	Papua	3715.00	2.00	153.00	29.00	65.00	49.00	28.00	106.60
Situbagendit	Muara	3753.00	27.60	92.87	24.53	133.33	98.33	23.80	98.40
Situbagendit	Papua	3220.00	21.00	110.00	31.00	65.00	52.00	19.00	95.50

Notes: YLD = dry yield; EG = empty grains; FG = filled grains; TGW = 1000-grain weight; DM = days to 85% maturity; DFF = days to 50% flowering; PT = productive tillers; and PH = plant height.

and their interactions for most traits, particularly plant height, the productive tiller number, grain yield, and spikelet sterility. Genotypes 1F and 7F produced more tillers in Papua, whereas 44F and Situbagendit maintained stable plant heights across both sites, indicating contrasting responses of plasticity versus stability.

Mean performance (Table 2) reflected similar trends. The genotype 12F achieved the highest grain yield in Papua (4,832 g plot^{-1}) but a moderate yield in Muara, while Situbagendit yielded best in Muara. Cultivars Inpari10 and Inpari13 also performed well in Papua. These crossover responses illustrate strong environmental influence on yield expression and adaptation patterns.

Traits association and yield determinants

Trait-yield relationships varied between environments. In Muara, early flowering reduced spikelet sterility and supported higher yields, while longer maturity favored grain

Table 3. Percentage contribution of agronomic and yield-related traits to the first five principal components (PC1–PC5) based on PCA of rice genotypes evaluated across Muara and Papua environments.

Traits	PC1	PC2	PC3	PC4	PC5
PH	0.01	11.55	59.03	14.93	1.43
PT	0.02	32.89	34.91	2.18	0.63
DFF	25.28	5.49	0.19	0.65	2.53
DM	25.39	4.45	0.03	0.34	1.18
TGW	10.91	6.08	1.91	45.59	2.61
FG	17.38	0.15	0.33	9.66	58.57
EG	12.18	17.97	0.59	8.87	1.13
YLD	8.82	21.41	3.00	17.76	31.90

Notes: YLD = dry yield; EG = empty grains; FG = filled grains; TGW = 1000-grain weight; DM = days to 85% maturity; DFF = days to 50% flowering; PT = productive tillers; and PH = plant height.

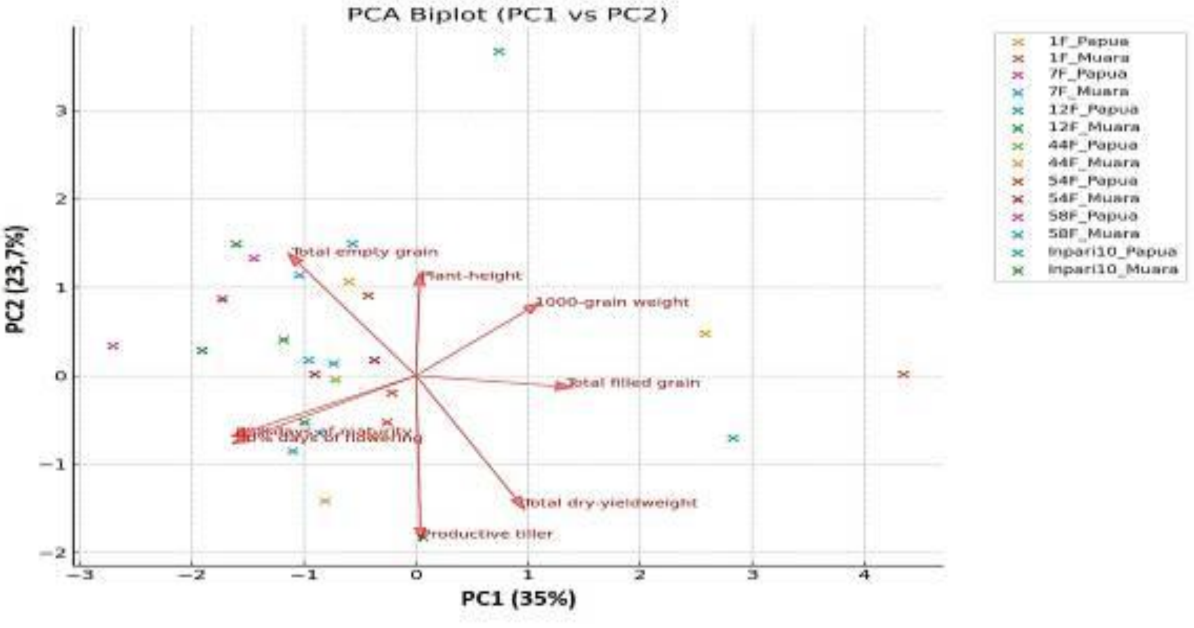


Figure 1. Principal component analysis (PCA) biplot of rice genotypes evaluated in Muara and Papua environments, showing separation along phenology-yield (PC1) and reproductive efficiency (PC2) axes.

filling. A yield-grain size trade-off was evident as heavier grains showed an association with reduced productivity. Conversely, in Papua, prolonged maturity and larger grains significantly enhanced yield, whereas spikelet sterility reduced it. Regression analysis confirmed these patterns. In Muara, shorter cycles promoted the grain yield, while in Papua, maturity duration (β = +2.670) and 1000-grain weight (β = +0.677) were the strongest yield determinants.

Multivariate analysis

Principal component analysis (PCA) summarized the interrelationships among traits (Table 3). The first two components explained 58.7% of the total variance (Figure 1). PC1 represented a maturity–yield axis driven by days to flowering, days to maturity, and filled grains, whereas PC2 corresponded to reproductive efficiency through a productive tiller number, yield, and empty grains.

Table 4. AMMI principal components scores and stress tolerance index (STI) of rice genotypes evaluated under favorable (Muara) and suboptimal (Papua) environments.

Genotype	PC1 Score	PC2 Score (≈0)	Yp (Muara)	Ys (Papua)	STI
12F	+833.18	≈ 0	3165.00	4832.00	1.49
1F	−42.69	≈ 0	3166.67	3595.00	1.11
44F	−533.89	≈ 0	3948.33	3682.00	1.42
54F	−19.82	≈ 0	3033.33	3494.00	1.03
58F	−80.40	≈ 0	3455.00	3830.00	1.29
7F	+251.94	≈ 0	2755.00	3600.00	0.97
Ciherang	−666.12	≈ 0	3058.33	2605.00	0.78
Inpari10	+655.23	≈ 0	2946.67	4362.00	1.25
Inpari13	+325.01	≈ 0	2766.67	3715.00	1.00
Situbagendit	−722.45	≈ 0	3753.00	3220.00	1.18

Note: Genotypes with STI > 1.0 exhibit superior performance under both favorable and suboptimal environments.

The PCA biplot (Figure 1) revealed clear clustering between environments. Papua genotypes grouped on the negative PC1 axis, associated with taller plants, delayed flowering, and higher dry yield. Muara genotypes displayed more dispersion, with Inpari10 (Muara) occupying an extreme positive PC1–PC2 position, indicating a distinct phenotypic expression. Genotypes, such as 7F (Papua) and 44F (Papua), clustered tightly, reflecting phenotypic stability under suboptimal conditions. The separation of clusters confirmed strong genotype × location interaction and environment-driven trait differentiation.

Stability and adaptability

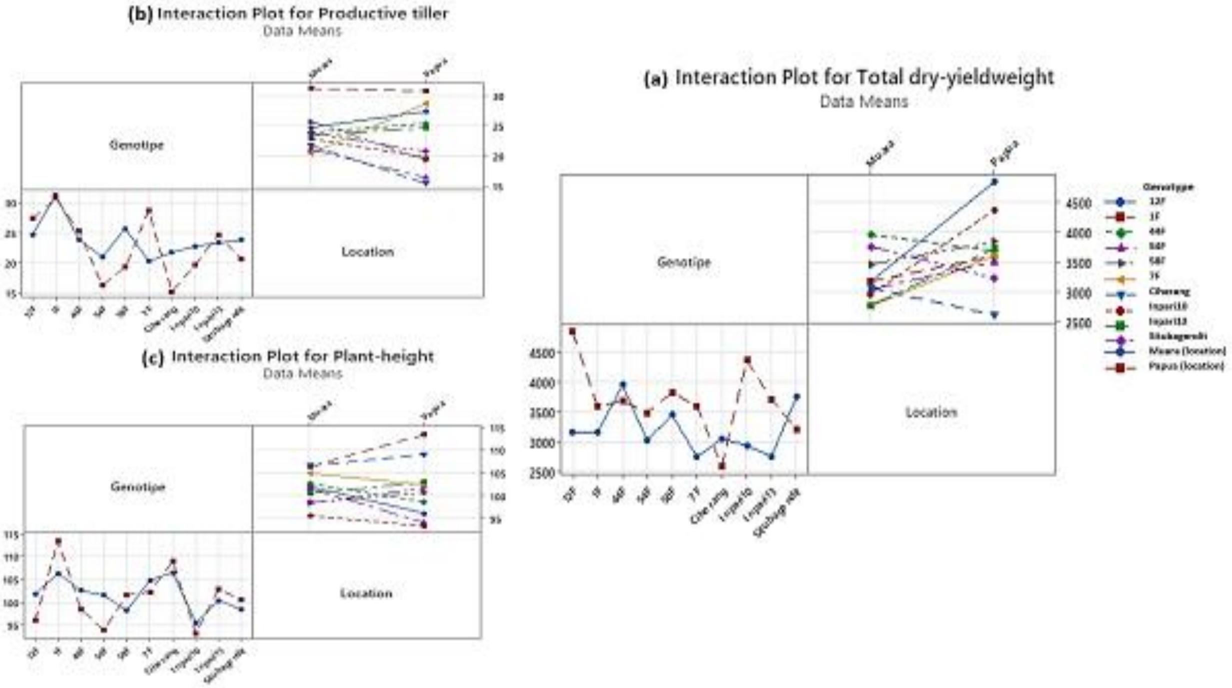
AMMI analysis (Table 4) identified differential adaptation strategies. Genotypes 12F and Inpari10 showed high positive PC1 scores, suggesting preference for favorable environments, such as Muara, whereas Ciherang and 44F exhibited negative scores, indicating site-specific adaptation limits. Genotypes 1F and 54F, with near-zero PC1 values, displayed broad adaptability. These patterns were consistent with the AMMI biplot for yield, tiller number, and plant height (Figure 2). Given only two environments, AMMI results acquired a descriptive interpretation rather than an inferential one, following the recommendations of Gauch (2006) and Yan and Tinker (2006). Nonetheless, they provided valuable preliminary insights into adaptability and GEI structure.

Trait-specific stability, based on the coefficient of variation (CV%), corroborated these trends. The genotype 12F showed the highest variability for flowering and maturity (CV = 50.96% and 44.41%, respectively), indicating strong environmental responsiveness. Conversely, 58F (PH CV = 2.38%) and 44F (PT CV = 4.22%) exhibited minimal variability, implying stability, while 1F and 54F displayed intermediate CV%, suggesting balanced adaptability. The stress tolerance index (STI) further supported these observations (Table 4). Genotypes 12F, 44F, 58F, and Inpari10 displayed STI > 1.0, demonstrating superior yield potential and stress tolerance across environments. Thus, these genotypes are promising candidates for improving rice productivity in suboptimal ecosystems.

Overall, although limited to two test environments, the integrated application of AMMI, Eberhart-Russell regression, and STI effectively identified genotypes with high-yield stability and adaptability. This multidimensional approach provides a practical framework for early selection in breeding programs targeting marginal agroecosystems and underscores the need for subsequent multi-location and multi-season validation before varietal release.

Genetic variability and heritability

Genetic parameters indicated strong selection potential for key yield traits (Table 5). Plant height exhibited the highest broad-sense


(b) Interaction Plot for Productive tiller
Data Means

(a) Interaction Plot for Total dry-yieldweight
Data Means

(c) Interaction Plot for Plant-height
Data Means

Figure 2. Genotype × environment interaction plots illustrating the performance of 10 rice (*Oryza sativa* L.) genotypes for (a) total dry yield weight, (b) productive tiller number, and (c) plant height across two contrasting environments—Muara (favorable lowland) and Papua (suboptimal, marginal). The plots depict differential genotype responses and adaptability patterns under these distinct growing conditions.

Table 5. Components of variance and broad-sense heritability estimates for agronomic traits in rice genotypes.

Trait	σ²g (Genotypic Var.)	σ²ge (G × E Var.)	σ²e (Error Var.)	Broad-sense heritability (H²)
TGW	1.67	0.34	3.19	0.63 (Moderate-high)
DFF	0.83	7.43	10.32	0.12 (Very low)
DM	5.40	1.59	32.74	0.37 (Low-moderate)
PH	23.60	4.08	24.16	0.74 (High)
PT	11.72	10.10	11.97	0.59 (Moderate)
EG	37.89	181.39	56.14	0.27 (Low)

Notes: TGW = 1000-grain weight; DM = days to 85% maturity; DFF = days to 50% flowering; PT = productive tillers; PH = plant height; and EG = empty grains.

heritability ($H^2 = 0.745$), followed by 1000-grain weight ($H^2 = 0.633$) and productive tillers per plant ($H^2 = 0.593$), suggesting substantial genetic control. Flowering time showed low heritability ($H^2 = 0.117$), reflecting a dominant environmental influence.

Similarly, genotypic and phenotypic coefficients of variation were maximum for productive tiller number (GCV = 14.68%, PCV = 23.80%), indicating strong genetic contribution with moderate environmental effects. Flowering and maturity traits had the lowest variability (GCV < 5%, PCV < 10%), suggesting a high environmental control. Collectively, these findings state that plant height, tiller number, and grain weight are reliable targets for direct selection in early breeding cycles.

DISCUSSION

Across both locations (Muara and Papua), rice (*Oryza sativa* L.) genotypes displayed marked variability in agronomic and yield traits. Significant genotype × environment interactions confirmed productivity was strongly environment-dependent. Traits, such as productive tiller number, plant height, and 1000-grain weight, exhibited moderate to high heritability, indicating strong genetic control and suitability for direct selection. In contrast, flowering and maturity were environmentally driven, aligning with previous findings that rice phenology is highly sensitive to photoperiod and temperature (Chen *et al*., 2021; Qiu *et al*., 2023; Zhao *et al*., 2023).

Compared with Muara, the Papua site generally promoted taller plants, more tillers, and greater filled-grain numbers but with reduced spikelet sterility. These results agree with reports showing stress-prone environments can extend reproductive duration and enhance grain filling in adapted genotypes (Saito *et al*., 2018; Barus *et al*., 2022). Such site-specific responses reflect complex physiological interactions underlying genotype × environment (G×E) variation.

Yield responses provided the clearest evidence of G×E effects. The genotype 12F produced the highest yield in Papua, whereas Situbagendit and Inpari10 excelled in Muara, demonstrating crossover interactions. In Papua, yield received primary effects from longer maturity, heavier grain weight, and lower sterility, while in Muara, early flowering and efficient assimilate partitioning were advantageous. Regression analyses supported these contrasting determinants, consistent with earlier studies showing extended grain filling under marginal conditions can improve yield in specific rice ideotypes (Thuy and Saitoh, 2017; Ladha *et al*., 2021). Physiological tolerance also contributed—in the acidic, low-nutrient soils of Papua, genotypes 12F, 44F, and 58F maintained high tiller numbers and low sterility—reflecting traits linked to nutrient-use efficiency and phenological flexibility. Barus *et al.* (2022) and Liu *et al.* (2020) have noted similar mechanisms of resilience in stress-adapted rice populations.

Multivariate analysis provided meaningful insights into genotype performance by separating rice genotypes along phenology-yield and reproductive-efficiency axes. The clustering of 12F_Papua and 44F_Papua suggested relative stability across specific environments, whereas the broader dispersion at Muara highlighted phenotypic plasticity under heterogeneous conditions. Consistent with earlier work, PCA and biplot methods effectively captured genotype × environment (G×E) interactions and revealed trait structures influencing adaptation (Zobel *et al.*, 1988; Annicchiarico, 2002; Yan and Tinker, 2006). Comparable applications in multienvironment trials by Yadawad *et al*. (2023) emphasize the utility of such visualization tools in identifying stable, high-yielding cultivars and representative testing sites.

Stability analysis complemented these findings by distinguishing broad adaptability from site-specific responsiveness. AMMI analysis indicated 12F and Inpari10 excelled under favorable conditions, whereas Ciherang and 44F were in the confines of narrower niches. Genotypes 1F and 54F—with near-zero PC1 scores—demonstrated wide adaptability, while 58F showed resilience to stress. The consistency across stability parameters (Eberhart-Russell regression and CV%) reinforces these observations. The STI added quantitative validation—genotypes 12F, 44F, 58F, and Inpari10 (STI > 1.0) combined high-yield potential with stress resilience, supporting Fernández’s (1992) concept of simultaneous selection for productivity and tolerance.

Although AMMI’s full inferential strength requires more than two environments, its descriptive application remains valuable for early-stage screening (Zobel *et al.*, 1988; Gauch, 2006). The Eberhart-Russell model continues to excel in differentiating predictable from unpredictable responses (Eberhart and Russell, 1966; Lin *et al*., 1986), and combining AMMI with CV% improves selection efficiency under adverse conditions (Purchase *et al.*, 2000; Annicchiarico, 2002). Together, these tools provide a multidimensional perspective on adaptability in small-environment trials.

Genetic parameter estimates reinforced the feasibility of selection. High heritability and narrow GCV-PCV gaps for plant height and grain weight signify reliable genetic control and minimal environmental interference—traits that respond effectively to direct selection. Similar outcomes have successful documentations in rice and other cereals (Burton and Devane, 1953; Johnson *et al*., 1955). In contrast, low heritability in phenological traits indicates strong environmental impact, requiring multienvironment testing for accurate adaptation assessment (Falconer and Mackay, 1996; Huang *et al*., 2021). Recent studies (Akinwale *et al*., 2011; Senguttuvel et al., 2021) recommend dual selection strategies: rapid genetic gain from highly heritable traits and long-term refinement of environment-sensitive traits through extended trials. Integration of multivariate, stability, and heritability analyses—as demonstrated by Lee *et al*. (2023) in Korean rice—provides a comprehensive framework for selecting regionally stable, high-performing genotypes.

Integrating these results, three groups of rice genotypes emerged as particularly valuable: 12F as a high-yielding, responsive type for favorable environments; 1F and 54F as broadly adaptable genotypes with consistent performance across locations; and 58F and 44F as stable performers in stress. This categorization provides a practical framework for variety release and parental selection. Importantly, the contrasting yield-trait relationship between Muara and Papua demonstrated that suboptimal environments were not uniformly detrimental; however, they can reveal adaptive traits that broaden the genetic base of breeding programs (Sabri *et al*., 2020).

CONCLUSIONS

This study demonstrated substantial genetic and environmental variability among 10 rice (*Oryza sativa* L.) genotypes evaluated across contrasting Indonesian agroecosystems. Significant genotype × environment interactions confirmed that performance was strongly site-dependent. Traits, such as plant height, tiller number, and 1000-grain weight, showed high heritability and strong potential for selection, whereas flowering and maturity were environment-dependent. Integrated stability analyses using AMMI, Eberhart-Russell regression, and the stress tolerance index consistently identified genotypes 12F, 44F, 58F, and Inpari10 as high-yielding and stress-tolerant, while 1F and 54F showed broad adaptability.

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