RESEARCH ARTICLE

GRAIN YIELD STABILITY OF SWAMP RICE LINES ACROSS SWAMPLAND AGROECOSYSTEMS IN BENGKULU PROVINCE OF INDONESIA

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SUMMARY

Multi-environment experiment undertakings in 2020 recognized the stability and adaptability of promising swamp rice genotypes on five types of swampland agroecosystems. Grain yield data recording occurred on 10 swamp rice favorable lines and two check cultivars, transplanted on swamps consisting of alluvial mud, lowland peaty, lowland peat, middle estuarine tidal, and lower estuarine tidal swamp, then subjected to a combined analysis of variance. The AMMI model employed illuminated the effects of environments on a genotype's grain yield stability across the surroundings. Among the tested conditions, alluvial mud and lowland peat swamps showed as the most predictable environments for rice grain yield evaluation, with the former also representing a rich surrounding, whereas the latter a poor one, despite their provided weak genotype discrimination. Lowland peaty swamp was also a productive environment and conferred strong genotypic discrimination. Both middle and lower estuarine tidal swamps were less fruitful and had rationally durable genotype discrimination. Rice lines UBPR 1, UBPR 8, UPBR 2, and UBPR 4 indicated more desirable than the check cultivars (Inpara 6 and Inpara 4) for grain yield and stability across the test environments. The lines UBPR 3 and UBPR 10 enunciated desirable adaptive performance at the lowland peaty swamp.

Keywords: Swamp rice lines, promising lines, agroecosystem, lowland swamp, tidal swamp, genotype by environment interaction, AMMI model

Key findings: The swampland's environmental conditions differing in typologies manage the rice grain yield. Comparatively, some genotypes outperformed others in response to changing agroecological conditions. Relatively stable and adapted genotypes emerged from lowland peaty swamps.

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INTRODUCTION

Rice is the primary staple food for more than 95% of the Indonesian population, with a total consumption of 31.737 million MT of milled rice and about 93.95 kg per capita consumption annually (PUSDATIN, 2022). After two decades, the prediction for milled rice consumption due to population growth will reach 31.7 million t (Octania, 2021). During 2021, rice cultivation covered about 10.66 million ha, with a total production of 54.65 million MT (31.33 million MT milled rice), and irrigated lands account for 80% of the area, contributing 93% of the total production (BPS, 2022). However, numerous irrigated fields have continued to disappear, resulting in the gradual change in land uses caused by urban sprawl and agglomeration, with the rate of field conversion reaching about 100,000 ha annually, causing disproportion to the establishment of new rice fields (Mulyani *et al.*, 2016). If this prodigy continues without providing alternative production areas, it could endanger Indonesia's food supply in the forthcoming years.

In 33.4 million ha of swamplands, nine to 10 million ha had been identified as potential areas for crop production (Nursyamsi and Noor, 2013). Even so, their existence remains idle and needs further optimization. Although society has long known rice production on swampland as a crucial part of local culture, the grain yield is less than 3 t/ha (Rumanti *et al.*, 2018; Khairullah *et al.*, 2021). In contrast, the average grain yield of irrigated rice fields has reached 5.1 t/ha (BPS, 2022). Such low productivity is commonly due to poor soil physicochemical properties inherent in swampy environments, including flooding, high soil acidity (lowland swamp), or iron pyrite toxicity and salinity (tidal swampland), which limits crop productivity. Relatedly, seeing swamp rice breeding as an indispensable endeavor to bridge the yield gap between irrigated fields and marshes will ensure food security for Indonesia's community, in particular, and generally, the world.

Rice grain yield is a complex quantitative parameter with high genotype by environmental interaction effects, resulting from different genotype responses to various inherent biotic and abiotic stress factors (Balestre *et al.*, 2010; Umadevi and Manonmani, 2018). This consequence becomes a bottleneck for the breeder in targeting future production areas for the newly developed rice breeding lines, as their relative performance can change with the changing environments. Multi-environment trials have the breeder generally conducting these to build a practical basis for the stability and adaptability of the genotypes across the targeted surroundings (Sitaresmi *et al.*, 2019). The study objective was to identify the stable and high-yielding swamp rice lines on different types of swampland agroecosystems and determine the areas where the promising rice lines would easily adapt.

MATERIALS AND METHODS

Experimental setup

A set of 12 swamp rice genotypes consisting of 10 promising lines and two released swamp rice cultivars as the check cultivars served as samples in this study (Table 1). The lines generated from crosses involved Bengkulu swamp rice heirlooms (Hanafi Putih, Batubara, Harum Curup, Tigo-tigo, and Lubuk Durian) and irrigated lowland rice cultivars released by the National Nuclear Agency of Indonesia (Diah Suci, Bestari, and Sidenuk). The trials ran from May to September 2020 on five types of swampland agroecosystems in Bengkulu Province, Indonesia (Table 2). E1 is a shallow swampland near a lake with irrigation and drainage systems. E2 and E3 are swamp peatlands differing in peat thickness and decomposition level, where E2 is distinctly sapric peat with a thickness of less than 30 cm, and E3 is a floating mat of mixed hemic and fibric peats with a thickness of more than 50 cm. E4 and E5 are estuarine swamplands near river banks that differ in retaining brackish water from tides. E4 locates 1 m higher toward the upper estuary compared with E5, but E4 has a concaved contour. A randomized

Table 1. Swamp rice genotypes used in the experiment.

Genotypes	Code	Parentage
UBPR 1	G1	Hanafi putih / Sidenuk
UBPR 2	G2	Batubara / Harum Curup
UBPR 3	G3	Tigo-tigo / Harum Curup
UBPR 4	G4	Tigo-tigo / Sidenuk
UBPR 6	G5	Diahsuci / Lubuk Durian
UBPR 7	G6	Harum Curup / Sidenuk
UBPR 8	G7	Sidenuk / Lubuk Durian
UBPR 9	G8	Lubuk Durian / Hanafi putih
UBPR 10	G9	Tigo-tigo / Bestari
UBPR 11	G10	Harum Curup / Bestari
Inpara 4	G11	-
Inpara 6	G12	-

Table 2. Description of the various environments used in the study.

Locations	Code	Geographic Coordinate	Altitude (masl)	Swampland Type	Soil Morphology	Hydrochemistry
Semarang	E1	E 102° 18' 8.7" S 3° 47' 18.1"	16.3	Alluvial mud swamp	Alluvial with confined peat	Freshwater
Kandang Limun 1	E2	E 102° 16.7' 17.9" S 3° 45' 17.8"	8.4	Lowland peaty swamp	Peaty soil	Freshwater
Kandang Limun 2	E3	E 102° 16' 13.9" S 3° 45' 26.7"	7.1	Lowland peat swamp	Peat soil	Freshwater
Pasar Seluma 1	E4	E 102° 30' 49.3" S 4° 8' 8.7"	6.4	Middle estuarine tidal swamp	Sandy silt	Brackish water
Pasar Seluma 2	E5	E 102° 30' 40.7" S 3° 8' 3"	5.1	Lower estuarine tidal swamp	Sandy silt	Brackish water

complete block design in each location had three replications assigned to 100 plants from each genotype on 2.5 m × 2.5 m plots spaced 0.5 m apart with a 1 m inter-block distance.

Transplanting of 21-day-old seedlings at 25 cm × 25 cm planting distance ensued in all locations in one week. Basal fertilizers' application at transplanting consisted of 69:72:51 kg NPK ha^{-1}, with top dressings of 23 kg N ha^{-1} applied four and eight weeks after transplanting. The management of rice crops at all the sites engaged normal cultural practices. Harvesting followed as the grains were fully mature. Individually collecting the grain yield data for all the genotypes at each location came from the plants at eight inner rows of each plot having a 14% water content. The resulting grain yield data gained converting to tons/ha for further analysis.

Data analysis

The grain yield data went through a combined analysis of variance across environments to determine the significance of genotypes (G), environments (E), and the genotype-by-environment interaction (GEI) effects. The analysis performed used PROC GLM of SAS v9.4 based on the following model (SAS Inst. Inc., Cary, NC):

$$Y_{ijk} = \mu + G_i + E_j + B_{k(j)} + (GE)_{ij} + \varepsilon_{ijk}$$

Where Y_{ijk} is the response of the ith genotype at j^{th} environment and k^{th} block within the jth environment; μ is the overall mean of observations; G_i is the ith genotype effect; E_j is the jth environment effect; $B_{k(j)}$ is the kth block

effect within the jth environment; $(GE)_{ij}$ is the interaction effect of the ith genotype and the jth environment; ijk is the experimental error assumed to normally and independently distributed with mean zero and variance.

The stability analysis performed followed the AMMI model (Zobel *et al.*, 1988):

$$\hat{Y}_{ij} = \mu + G_i + E_j + \sum_1^k \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where $\hat{Y}_{ij}$ is the expected response of ith genotype in the jth environment; μ = the overall mean of all observations, G_i is the ith genotype effect; E_j is the jth environment effect; and λ_k, $_{ik}$, and γ_{jk} are singular value, genotype eigenvectors, and environment eigenvectors for the principal components (PCA); and εij is the residual associated with i^{th} genotype and j^{th} environment.

Running the analysis used PBTools v1.4 (available at http://bbi.irri.org/products). The AMMI stability values (ASV) calculations for each genotype were according to Purchase *et al*. (2000) to rank the rice genotypes based on their stability as follows:

$$ASV = \sqrt{\left[\frac{SS\ IPC1}{SS\ IPC2}(IPC1_{score})\right]^2 + (IPC2_{score})^2}$$

where SS IPC1 and SS IPC2 are the sums of squares for IPC1 and IPC2, respectively, resulting from the decomposition of G × E interaction sum of squares, while IPC1 and IPC2 scores refer to the distance and direction of a genotype from the origin of the IPC1 and IPC2 axes, respectively.

RESULTS

Mean performance

The grain yield of 12 rice genotypes in five swampland agroecosystems is in Table 3. Overall, the observed maximum grain yield showed under E1 (8.03 t/ha), followed by E2 (5.35 t/ha), E5 (4.03 t/ha), and E4 (3.65 t/ha), whereas the least yield was at the E3 (2.13 t/ha). The incompatible performance of the rice genotypes is notable from their ranking as varied across the environments. The coefficient of variation (CV) signifies the extent of variability among the genotypes concerning their mean performance in each ecosystem. In this case, the lowest variability appeared in E1 (10.27%), followed by E5 (18.81%), E3 (19.00%), and E4 (25.34%), whereas the highest was in E2 (38.92%).

Table 3. Mean grain yield (t/ha) and rank order of 12 swamp rice genotypes tested in five swampland agroecosystems.

Genotypes	E1	Rank	E2	Rank	E3	Rank	E4	Rank	E5	Rank
G1	8.70	4	7.24	3	2.89	1	5.47	1	3.72	7
G2	9.06	1	5.37	7	1.81	9	3.67	6	4.54	4
G3	9.06	1	8.35	2	2.77	2	4.50	2	4.42	5
G4	8.04	6	6.02	5	2.29	5	4.45	3	5.29	1
G5	7.40	9	3.76	9	1.69	12	3.11	9	3.54	9
G6	8.83	3	3.15	10	1.72	11	4.20	4	4.62	3
G7	7.88	8	6.19	4	2.08	6	3.45	7	3.63	8
G8	7.98	7	2.33	12	1.87	8	3.86	5	3.92	6
G9	8.62	5	8.60	1	2.36	3	3.08	10	5.13	2
G10	6.69	12	2.77	11	1.73	10	3.14	8	3.33	10
G11	7.32	10	5.41	6	2.31	4	3.00	11	3.03	12
G12	6.92	11	4.95	8	2.01	7	1.90	12	3.16	11
Means	8.03		5.35		2.13		3.65		4.03	
CV (%)	10.27		38.92		19.00		25.34		18.81	

Table 4. Combined analysis of variance and partitioning GEI effect by AMMI analysis for grain yield of 12 swamp rice genotypes tested on five swampland agroecosystems.

Source of variation	d.f.	SS	MS	F-value	% SS$_{total}$	% SS$_{GEI}$
Environments (E)	4	707.98	176.99	216.72**	69.6	
Block/Environment	10	16.94	1.69	2.07*	1.7	
Genotypes (G)	11	64.55	5.87	7.19**	6.3	
G × E Interaction (GEI)	44	138.69	3.15	3.86**	13.6	
IPC1	14	106.79	7.65	9.34**		77.0
IPC2	12	20.39	1.70	2.08*		14.7
Residual	18	11.51	0.64	0.78		8.3
Error	110	89.84	0.82	-	8.8	
Total	179	1018.00				

*, ** denote significance at 5% and 1% of probability level by F test, respectively.
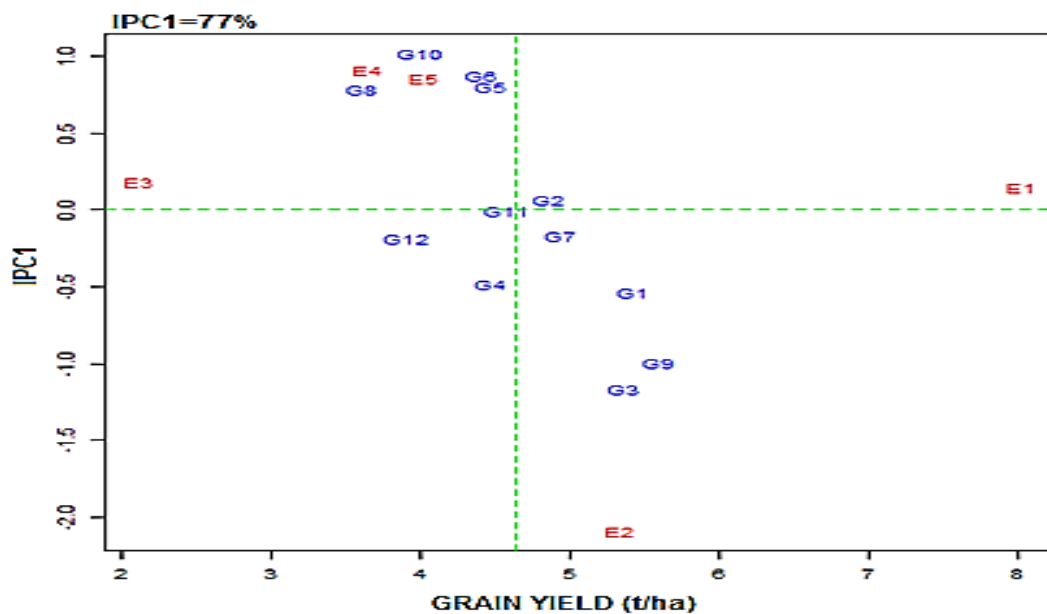

Figure 1. AMMI-1 biplot of 12 swamp rice genotypes for grain yield across five swampland agroecosystems.

Analysis of variance

Combined analysis of variance revealed significant (p < 0.01) differences for genotypes, environments, and G × E interaction (Table 4). The environmental effects are vital contributing as the major source of variation in grain yield by capturing 69.6% of the total sum of squares, followed by GEI (13.67%), and genotypes (6.3%). Further partitioning the GEI effect into principal components using the AMMI model revealed that only the first two IPC showed significance.

The IPC1 accounted for 77.0% of the GEI sum of squares and was far greater than IPC2 (14.7%). The remaining IPCs were just noise since their mean squares were not significant, accounting for only 10% of the total sum of squares.

AMMI-1 biplot

The AMMI-1 biplot is a graph plotted from the environment and genotype means as the abscissa against their corresponding IPC1 scores as the ordinate (Figure 1). The graph

helps interpret the relationship between additive main effects (E and G) and G × E interaction effects. The dislodgment of environments and genotypes along the abscissa revealed variations in the main influences, while the displacement along the ordinate indicates the differences in the interaction impacts. Amongst the environments, the projection of E1 and E3 was on the farthest end of the abscissa in opposite directions, placing them near the zero ordinate, suggesting that these two environments combined the largest main effects with the smallest interaction outcomes, with E1 representing the most productive environment and E3 the least productive one. The E2 positioned at the lower right of the graph indicated that this surrounding combined a moderate main effect with a large interaction influence. The E4 and E5 plotted at the upper left of the graph implied a similar feature, i.e., less productive environments with a moderate high G × E.

Based on the same criteria, rice genotypes G1, G4, G12, G7, G2, and G11 were consecutively anticipated near the origin of the coordinates to indicate that these genotypes were moderately productive and relatively stable. The genotypes G3 and G9, shown at the lower right, denoted that these genotypes were fruitful but less stable. However, genotypes G5, G6, G10, and G8 were moderately beneficial and less stable, as plotted in the upper left.

AMMI-2 biplot

The spatial pattern of the environments and rice genotypes on the coordinate plane of the first two IPCs shows in the AMMI-2 biplot (Figure 2). The graph indicates the levels of interaction effects among environments and genotypes and the degree of relationship among ecosystems. The strength of the GEI effects contributed by a given environment has a vector length representation. Short spoke indicates weak GEI effects and long spoke as strong. By such references, the E2 exerted the strongest interactive force, followed by E1, E4, E5, and E3.

In the biplot, the angle among the environments exhibited the degree and the direction of the correlation between them. An acute angle (<90°) indicates a strong positive correlation, while an angle close to 90° denotes non-correlation among environments.
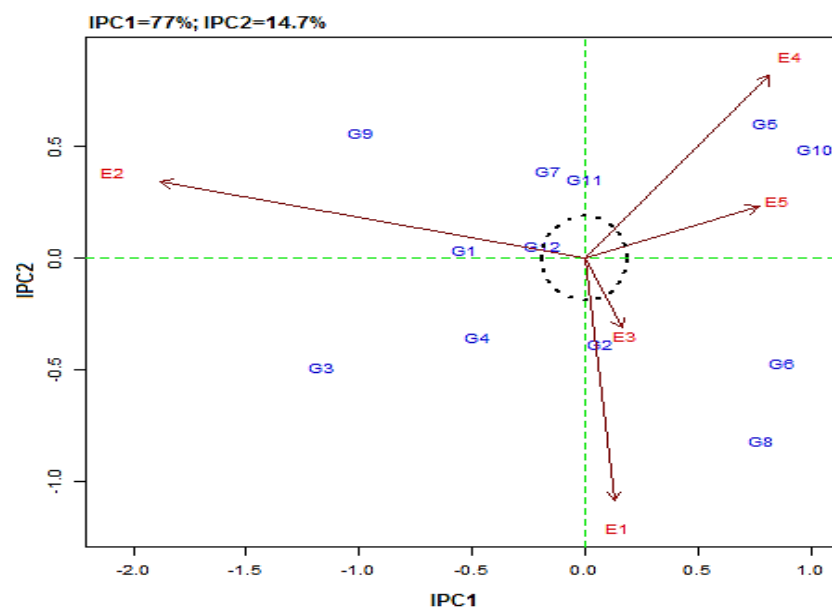

Figure 2. AMMI-2 biplot of 12 swamp rice genotypes for grain yield across five swampland agroecosystems.

Further, an obtuse angle (close to 180°) represents a strong negative association. Accordingly, the acute angle formed by the pairs of two environments, i.e., E1 and E3 and E4 and E5, signified that each match had a definite, strong correlation and had similarity in the genotype distinction. Conversely, a strong negative correlation resulted in E2 with the remaining test ecosystems and represented distinctive genotypic discrimination with all other test locations.

The genotypes' projection in different environments assessed genotypic responses to the changing environments. Genotypes observed in the circle or near the origin will tend to have similar reactions to all the test ecosystems, with those shown far away indicating varied patterns of responses across locations. Genotypes G12, G1, G11, G7, G2, and G4 clustering occurred near the origin and exhibited non-sensitive to environmental interactive effects. However, the remaining genotypes showed scattering away from the source, revealing that these genotypes were more sensitive with varying responses to environmental interaction effects.

AMMI stability value

The average grain yield for each genotype in five different environments with their corresponding IPC1 and IPC2 scores and AMMI stability values (ASV) are available in Table 5.

The mean grain ranged from 3.53 to 5.82 t ha^{-1}, with an overall mean of 4.64 t ha^{-1}. Seven promising rice lines, viz., G3, G1, G9, G4, G2, G7, and G6 surpassed the check cultivar (G11) for grain yield. The scores of IPC1 and IPC2 expressed the relative position of the genotypes, as shown in the IPC1 and IPC2 axes in the AMMI-2 biplot. Meanwhile, ASVs represent the Pythagorean distance of the genotypes from the origin of the coordinate plane of IPC1 and IPC2. The extent of the genotype ASV estimates ranged from 0.058 to 0.817, with an ascending order of ranking. Genotypes with minimum ASV values, regarded as highly stable, had G12 and G1 with the distinctively smallest ASVs occupying the lead and second-top ranking in yield stability.

Adaptation maps

The pattern of genotype adaptation to environmental variations has its visualization on the adaptation map (Figure 3). Drawing the rice lines came from the predicted grain yield projection for each genotype against the environment's IPC1 scores. The displacement of environments along the IPC1 axis reflects their similarity in genotype discrimination, i.e., closer means were more similar, as shown by the two pairs of surroundings, i.e., E1 and E3 and E4 and E5. The rice lines' slope indicates the varied responses of the genotypes to

Table 5. Grain yield means and AMMI stability value (ASV) with ranking, the IPC 1 and IPC2 scores of 12 swamp rice genotypes across five swampland agroecosystems.

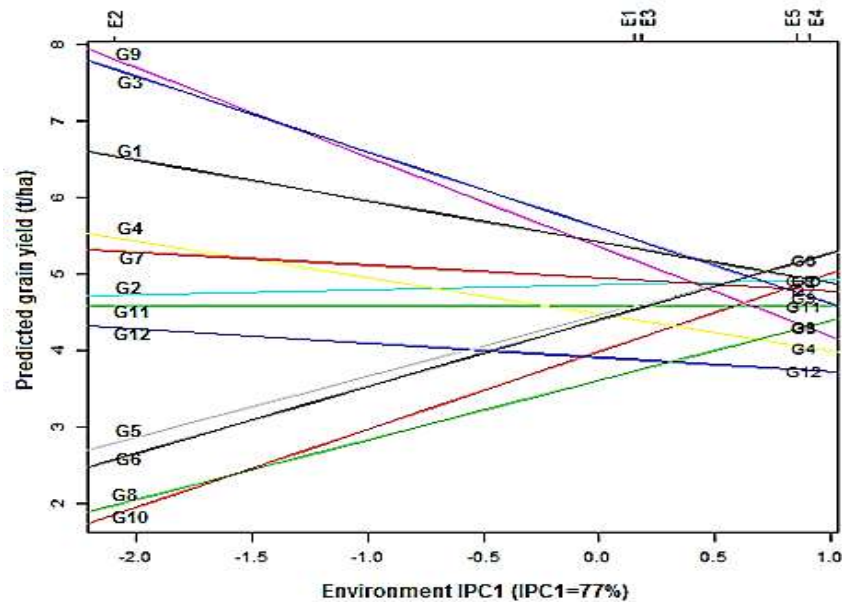| Genotype codes	Grain yield (t ha^{-1})	IPC1 Score	IPC2 Score	ASV	Rank
G1	5.60	-0.534	0.037	0.060	2
G2	4.89	0.065	-0.382	0.382	5
G3	5.82	-1.167	-0.489	0.500	9
G4	5.22	-0.479	-0.352	0.355	3
G5	3.90	0.798	0.608	0.612	11
G6	4.50	0.870	-0.469	0.476	7
G7	4.65	-0.169	0.394	0.394	6
G8	3.99	0.779	-0.814	0.817	12
G9	5.56	-0.991	0.565	0.572	10
G10	3.53	1.020	0.491	0.499	8
G11	4.21	-0.004	0.356	0.356	4
G12	3.79	-0.188	0.056	0.058	1

Figure 3. Adaptation map showing the predicted mean yields of 12 swamp rice genotypes across five swampland agroecosystems.

different ecosystems. However, lines G9 and G3 had sharp set down along the IPC1 axis. Similar features also resulted in the rice genotypes, viz., G10, G8, G6, and G5, but in the opposite direction. Additionally, rice lines G2, G11, G12, G7, G4, and G1 had reasonable slopes along the IPC1 axis.

DISCUSSION

Developing rice cultivars with higher grain yield and wider adaptability is the major goal of the breeders. However, it is not always easy to succeed, as the environments where the rice grows may operate distinctively in affecting the rice plant's genetic potential and productivity. The relevant multi-location rice experiments showed that average grain yield fluctuated across the test environments (Table 3). In each location, the perusal of the genotypic performances reveals the variability among the genotypes in producing grain yield. However, variations in the genotypic ranking across different environments also suggested that the genotypes' response differs over all the ecosystems (Crossa, 1990).

This concept has validation in the combined analysis of variance, where the highest portion of variation had control of the environments (Table 4). Past studies also reported similar, and the environmental effects comprised the largest among all sources of variation in the rice multi-environment studies (Nassir and Ariyo, 2011; Utami *et al*., 2020; Kartina *et al*., 2021). Therefore, screening the genotypes over heterogeneous environmental conditions is a valid approach for identifying stable genotypes (Eberhart and Russell, 1966).

Applying the AMMI model for retaining the first two IPCs to explain the GEI effects should be sufficient since both IPCs cumulatively explained 91.7% of the GEI variability. Neisse *et al*. (2018) deemed that 70% variability was the minimum proportion for the model to be reliable. Zobel *et al*. (1988) also considered AMMI with only two IPCs as the best predictive model. Thus, the estimates displayed in the AMMI-1 and AMMI-2 biplots and the adaptation map were close to the true values of the grain yield prediction and the same as in the ASV table.

The AMMI-1 biplot (Figure 1) and the AMMI-2 biplot (Figure 2) revealed the inherent

characteristics of the test environments for rice production, where E1 (alluvial peat swamp) represents the rich environments and E3 (lowland peat swamp) represents a poor environment. Alluvial soil is known to be rich in minerals and nutrients brought down by rivers and other bodies of water, which serves as a good crop soil (Mawardi *et al.*, 2020), while peat soil has a low fertility level (Septiyana *et al.*, 2017) and holds a variety of soil physical constraints (Herawati *et al.*, 2021). Aside from the productivity difference, however, both environments emerged similarly weak in discriminating the rice genotypes.

On rice production, the remaining test environments between E1 and E3 appeared with varied responses in genotypic discrimination. The E2 (lowland peaty swamp) also serves as a productive and highly discriminatory environment for the rice genotypes. However, the environments E4 and E5 (estuarine tidal swamps) were less fruitful but had reasonably strong genotypic discrimination. The biplots also revealed the productiveness and stability of the rice genotypes. Genotypes G1, G4, G12, G7, G2, and G11 occurred more productive and relatively stable across the environments. For productivity, the rice lines G1, G4, G7, and G2 also indicated better productivity and desirable than check cultivars (G11 and G12).

The AMMI model does not provide a quantitative stability measure (Gauch, 1992; Gauch and Zobel, 1997), whereas such gauges are important for ranking the genotypes based on grain yield stability. Adopting the AMMI stability value proposed by Purchase *et al.* (2000) aide in quantifying the rice genotypes in compliance with their grain yield stability (Table 5). The G12 and G1 were notably the most stable rice genotypes across the environments, although leading performers in producing grain yield. The same phenomena also came from findings by Sharifi *et al.* (2017) and Bii *et al.* (2020).

The adaptation map signifies the specific adjustment of the rice genotypes based on predicted grain yield over the tested environments (Figure 3). Attainment of the highest grain yield of genotypes G9 and G3 will surface in E2 (lowland peaty swamp), with the lowest in the estuarine marshes, while the genotypes G10, G8, G6, and G5 suggest the other way around. Compared with the rest of the rice genotypes, the G2, G11, G12, G7, G4, and G1 will better adapt in all the tested environments, as confirmed by the adaptation map.

CONCLUSIONS

The study revealed that environments are vital in determining rice grain yield. However, a considerable variation in genotype responses across ecosystems occurs, as indicated by significant genotype × environment interaction, suggesting that no genotype had persistently superior performance in all tested environments. These facts imply that breeding efforts in developing high-yielding rice for swampland agroecosystems are even more challenging. Nevertheless, the employed AMMI stability model showed that rice genotypes UBPR1 (G1), UBPR8 (G7), UPBR2 (G2), and UBPR4 (G4) proved more desirable than the check cultivars Inpara 6 (G12) and Inpara 4 (G11) based on their stability and grain yield. Genotypes UBPR 3 (G3) and UBPR 10 (G9) also showed promising adaptive performance under lowland peaty swamps (E2).

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