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HYBRID RICE STABILITY STUDIES IN INDONESIA

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SUMMARY

Hybrid rice has the potential to increase rice productivity per unit area by exploiting the phenomenon of heterosis to out-yield their inbred counterparts. Information based on genotype–environment interaction is highly helpful for selecting environment-specific genotypes by assessing the genotypes in various environments. The present research aimed to study the grain yield of rice genotypes under genotype–environment interactions at different locations and to select high-yielding hybrid rice genotypes. Twelve rice genotypes comprising eight promising rice hybrids, two hybrid rice check cultivars (Sembada 188 and Supadi 56), and two inbred check cultivars (Inpari 30 and Inpari 20) were studied in multilocation yield trials during 2019 at five locations in West Java Province (Sukamandi, Karawang, and Kuningan) and Central Java Province (Cilacap and Sragen), Indonesia. The trial at each location was planted in a randomized complete block design with four replications. Four stability models, i.e., Francis and Kannenberg (1978), Finlay and Wilkinson (1963), Eberhart and Russell (1966), and additive mean effects multiplicative interaction (Gauch, 2013) were used to identify high-yielding and stable rice genotypes. Pooled analysis of variance revealed that locations, genotypes, and genotype–environment interactions had significant ($P < 0.01$) effects on grain yield. Rice hybrids, i.e., 6802, 6803, 6808, 6809, and 418089, performed well with higher mean yield than environmental mean yield. Among the high-yielding hybrid rice genotypes, the hybrid 6809 (10.30 tons ha^{-1}) was classified as highly stable and widely adoptable to all locations on the basis of stability analyses.

Keywords: Genotype–environment interaction, stability models, grain yield, rice hybrids, check genotypes

Key findings: Genotype–environment interaction in combination with stability models can be used to assess different rice genotypes under diverse environments and to select the best-performing genotype in the existing environment. Rice hybrids and check genotypes showed varied yield responses across different environments through genotype–environment interaction. On the basis of stability analyses, the rice hybrid 6809 was found to be high yielding and classified as a stable and well-adapted genotype under existing environmental conditions.

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INTRODUCTION

Rice production in Indonesia has fluctuated within the last decade. Average rice production in Indonesia from 2009 to 2019 varied from 4.98 tons ha^{-1} to 5.34 tons ha^{-1} (BPS, 2020). Therefore, increasing rice productivity is the main challenge for breeders to fulfill the rice needs of the country. However, the limited germplasm with high yield potency and the quantitative genes responsible for enhanced grain yield have become the next challenges in rice cultivar development. Hybrid rice technology can be used as an alternative for increasing rice productivity by utilizing hybrid vigor. Compared with their related parental inbred lines, F_1 hybrids are more vigorous due to heterosis and provides 15%–30% more grain yield (Akter *et al*., 2015; Widyastuti *et al.,* 2017).

In Indonesia, rice is grown on various types of land that have various biophysical properties, such as climatic, edaphic, and biotic stresses (Sitaresmi *et al.,* 2012). Hybrid rice is mostly cultivated in low-to-medium land irrigated rice fields. The expansion of planted area may cause differences in environmental conditions that affect productivity. Therefore, breeders are attempting to develop rice hybrids that can adapt to diverse environments.

Genotype–environment interaction effects occur when the performance of the genotypes is influenced by different environments. Consequently, phenotypic differences among genotypes vary from one environment to another; however, the best genotype might somehow be stable across environments (Bustos-Korts *et al.,* 2019). Genotype–environment interactions can be used to provide facts about the environmental conditions required by a particular genotype with good yield. However, cultivar adaptability has limitations that are related to large environmental variants. Widyastuti *et al.* (2015) assessed some promising hybrids in the lowlands of Java Province, Indonesia, and revealed that all of the best-performing rice hybrids performed differently at each location and season. Ran *et al.* (2018) stated that soil, climate, terrain, and the rice cultivars themselves are the environmental factors that affect grain yield at different locations and environments.

The estimation of the adaptability and stability of rice genotypes at various locations is important to determine the influence of genotype–environment interactions on quantitative traits (Sreedhar *et al.*, 2011). Sitaresmi *et al.* (2016) stated that the maximum yield potential of rice cultivars could be increased in the optimum environment, i.e., when rice cultivars are planted in an environment that is suitable for their optimal genetic requirements. Providing the estimates of grain yield potential and the adaptation of hybrid rice cultivars to various environments are vital for preparing adoption technology (Tabanao *et al.,* 2015), which involves using the appropriate technology package to achieve F_1 hybrid rice production.

Many stability models are available for studying genotype–environment interactions (Sitaresmi *et al.*, 2019; Kang, 2020). Stability analysis is a tool for identifying the performance of different cultivars in various environments and guides the plant breeders in selecting promising lines. Laksmi *et al*. (2014) explained that the identification of stable and superior rice genotypes under various environmental conditions is necessary to obtain stable genotypes with high yield potential. A stable genotype can produce constant yield and is less affected by environmental changes that might be due to different locations or seasons.

Univariate and multivariate statistical stability are the two major methods for analyzing genotype–environment interactions and phenotypic stability in different crop genotypes (Lin *et al.,* 1986). Stability analysis can be performed by using the models of Finlay and Wilkinson (1963); Eberhart and Russell (1966); Francis and Kannenberg (1978); and Gauch (2013), who used the additive main effects and multiplicative interaction (AMMI) model. AMMI a is a model that combines the additive and multiplicative components of a two-way data structure that allows a breeder to obtain a precise prediction of potential rice genotype and environmental effects on it (Akter *et al.,* 2014). The contribution of each genotype and each environment to genotype–environment interaction is assessed by the use of the biplot graph display in which yield means are plotted against the IPCA1 scores of rice and other crops (Zobel *et al.,* 1988; Akter *et al.,* 2015). It can identify the groups of rice genotypes that can adapt broadly or specifically (Widyastuti *et al.,* 2012). On the basis of the above facts, the present research aimed to analyze the genotype–environment interaction for grain yield of 12 rice genotypes at five different locations and to select high-yielding hybrid rice.

MATERIALS AND METHODS

The present research involved 12 rice genotypes and was conducted during 2019 at five different locations in West Java Province (Sukamandi, Karawang, and Kuningan) and Central Java Province (Cilacap and Sragen), Indonesia. The climatic and topographic conditions of the five locations are as follows: Sukamandi is located at an altitude of 15 m above sea level (ASL) with monthly average temperature of 26 °C–28 °C and humidity of 78%–84%. Karawang is located at 5 m ASL and has a monthly average temperature of 27 °C, humidity of 80%, and annual rainfall of 1100– 3200 mm year^{-1}. Kuningan is located at 570 m ASL and has a monthly average temperature of 18 °C–32 °C and annual rainfall of 3000–4000 mm year^{-1}. Cilacap has an altitude of 30 m ASL, monthly average temperature of 22 °C–32 °C, and humidity of 80.6%, whereas Sragen has an altitude of 141 m ASL, monthly average temperature of 19 °C–31 °C, and annual rainfall of 3000 mm year^{-1}. Twelve rice genotypes comprising eight new promising hybrids, two hybrid check cultivars (Sembada 188 and Supadi 56), and two inbred check cultivars (Inpari 30 and Inpari 20) were used in the study (Table 1).

Table 1. Rice breeding materials used in the study.

Rice genotypes	Institution	Note
Rice hybrids		
6802	Nusantara Pertanian Indonesia	Hybrid rice genotype
6803	Nusantara Pertanian Indonesia	-do-
6808	Nusantara Pertanian Indonesia	-do-
6809	Nusantara Pertanian Indonesia	-do-
6810	Nusantara Pertanian Indonesia	-do-
418089	Nusantara Pertanian Indonesia	-do-
418092	Nusantara Pertanian Indonesia	-do-
418096	Nusantara Pertanian Indonesia	-do-
Check genotypes		
Sembada 188	Biogene Plantation	Hybrid check cultivar
Supadi 56	Primasid	-do-
Inpari 30	Indonesia Center for Rice Research	Inbred check cultivar
Inpari 20	Indonesia Center for Rice Research	-do-

All the rice genotypes were transplanted in a randomized complete block design (RCBD) with four replications at each location. Each rice genotype was transplanted in a subplot with dimensions of 4 m × 5 m with a plant spacing of 20 cm × 20 cm The fertilizers urea, SP-36, and KCL were applied at the rates of 250:100:100 kg ha^{-1}, respectively. Fertilizers were used in three split doses. All of the SP-36 and KCl and one-third dose of N (urea) were spread 1 week after planting (WAP), whereas the remaining N was applied at 4th and 7th WAP. All the rice genotypes were harvested when 80%–85% of the rice panicles per plot turned yellow and were at the hard dough stage. After threshing, the seeds were collected for the estimation of grain yield per plot. The grain yield was estimated and corrected at 14% moisture content and converted into dry grain yield per hectare (tons ha^{-1}).

The homogeneity test of the cultivars was performed via the Bartlett test. Analysis of variance was conducted by using SAS 9.0 and STAR programs. A least significant difference (LSD) at the 5% level of significance was used to ascertain the significant differences between rice genotypes and check cultivars. Stability analyses were conducted after obtaining significant differences in the genotype–environment interactions. Stability analyses were used to determine the stability of the rice hybrid genotypes across five locations.

Stability analyses were performed for grain yield by using several models, i.e., PBSTAT-GE 2.3 (www.pbstat.com), on the basis of the stability analysis according to Francis and Kannenberg (1978) and regression coefficients (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). Multivariate analysis based on the AMMI biplot was also conducted to identify the principal component-based stability analysis (Gauch, 2013).

RESULTS

The P-value obtained through the Barlett test for the combined response was 0.407. If the P-value was greater than 0.05, then the residual cultivar was fulfilled. The combined analysis of variance for the grain yield of 12 rice genotypes comprising eight rice hybrids and four checks grown at five locations was utilized to measure the interactions and main effects among and within the source of variations (Table 2). Moreover, the genotype–environment interaction effects were identified.

The F-values of the genotypes, environments, and genotype–environment interactions revealed significant ($P \leq 0.01$) differences for grain yield. Combined analysis revealed that the environments contributed 20.28% to the total sum of squares, genotype effects contributed 32.59%, and genotype–environment interaction effects contributed 21.22% (Table 2).

The coefficient of variation (CV) ranged from 5.79% (Sukamandi) to 13.07% (Cilacap) (Table 3). Among the promising hybrid rice genotypes, the hybrid 6802 showed the highest grain yield across locations, and the average grain yield was significantly different from the grain yield of all the check cultivars. Among the promising hybrid rice genotypes, the hybrid 6802 showed the highest grain yield and overall locations (11.09 tons ha^{-1}). Three other rice hybrids, i.e., 6809 (10.30 tons ha^{-1}), 6803 (10.14 tons ha^{-1}), and 418089 (10.08 tons ha^{-1}) also followed the above promising rice hybrid and performed better than the check cultivars by producing higher grain yield. The hybrid check cultivar Sembada 188 (10.04 tons ha^{-1}) also out-yielded the inbred line Inpari 30 (8.67 tons ha^{-1}).

Table 2. Combined analysis of variance for the grain yield of rice genotypes at five locations.

Source of variance	d.f.	S.S.	M.S.	F-value	Pr > F	S.S. Proportion (%)
Environments (E)	4	150.65	37.66	13.42**	0.00008	20.28
Replications (Environments)	15	42.10	2.81	0.13**	0.00020	5.67
Genotypes (G)	11	242.04	22.00	6.14**	0.000006	32.59
G × E Interaction (GEI)	44	157.62	3.58	3.93**	0.0000009	21.22
Error	165	150.29	0.91			
Total	239	742.71				

Note: ** highly significant at the level <0.01; E = environments or locations, d.f. = degrees of freedom; SS = sum of squares, MS = mean square.

Table 3. Grain yield of rice hybrids and check genotypes at five locations.

Rice genotypes	Grain yield across locations (tons ha^{-1})					Means
	Sukamandi	Karawang	Kuningan	Cilacap	Sragen	
6802	10.83 cd	13.35 abcd	8.68	11.23 abcd	11.36 abcd	11.09 abcd
6803	9.93	12.55 bcd	8.35	9.15 bd	10.71 bd	10.14 bcd
6808	9.58	12.10 bcd	8.25	9.33 bd	10.33 bd	9.92 d
6809	10.40 cd	11.73 bc	9.68 c	9.68 bd	10.05 bd	10.30 bcd
6810	9.7	7.3	8.15	7.68	6.19	7.8
418089	10.30 cd	12.08 bcd	8.4	9.30 bd	10.32 bd	10.08 bcd
418092	9.05	11.7	8.35	7.33	10.00 bd	9.29
418096	9.78	8.28	8.55	7.7	7.05	8.27
Sembada 188	10.43	11.38	9.5	9.2	9.68	10.04
Supadi 56	9.83	9.63	9.03	9.3	8.15	9.18
Inpari 30	9.23	10.53	7.93	6.68	8.98	8.67
Inpari 20	8.63	8.03	8.3	7.6	6.8	7.87
Means	9.8 d	10.72	8.6	8.68 c	9.13 d	9.39 cd
CV (%)	5.79	10.29	10.17	13.07	10.77	10.17
LSD$_{0.05}$	0.68	1.32	1.05	1.36	1.18	0.5

Note:. Numbers within the same column followed by a letter, 'a' indicates yield significantly higher than Sembada-188, while letter 'b' indicates yield significantly higher than Supadi-56, 'c' indicate yield significantly higher than Inpari 30, 'd' indicate yield significantly higher than Inpari-20 according to LSD test at ɑ 5%. CV: coefficient variation. LSD: least significant differences.

Table 4. Mean grain yield and stability parameters of rice hybrids and check genotypes at five locations.

Rice genotypes	Yi (tons ha^{-1})	bi	S^2_{di}
6802	11.09	1.48^{ns}	1.18**
6803	10.14	1.62*	0.47*
6808	9.92	1.40^{ns}	0.45*
6809	10.30	0.94^{ns}	-0.18^{ns}
6810	7.80	0.11^{**}	1.95**
418089	10.08	1.46^{ns}	0.06^{ns}
418092	9.29	1.61*	0.76^{**}
418096	8.27	0.36^{*}	1.03**
Sembada 188	10.04	0.97^{ns}	-0.20^{ns}
Supadi 56	9.18	0.37*	0.20^{ns}
Inpari 30	8.67	1.47^{ns}	0.29^{ns}
Inpari 20	7.87	0.20^{**}	0.39*
Environment mean yield	9.39	-	-

Yi: Yield means over all environments; bi: coefficient of regression; S^2 *di*: sum of squares deviation from regression; ns = nonsignificant.** = significantly different from 1 at an ɑ level of <0.01 * significantly different from 1, significantly different at an ɑ level of <0.05**.

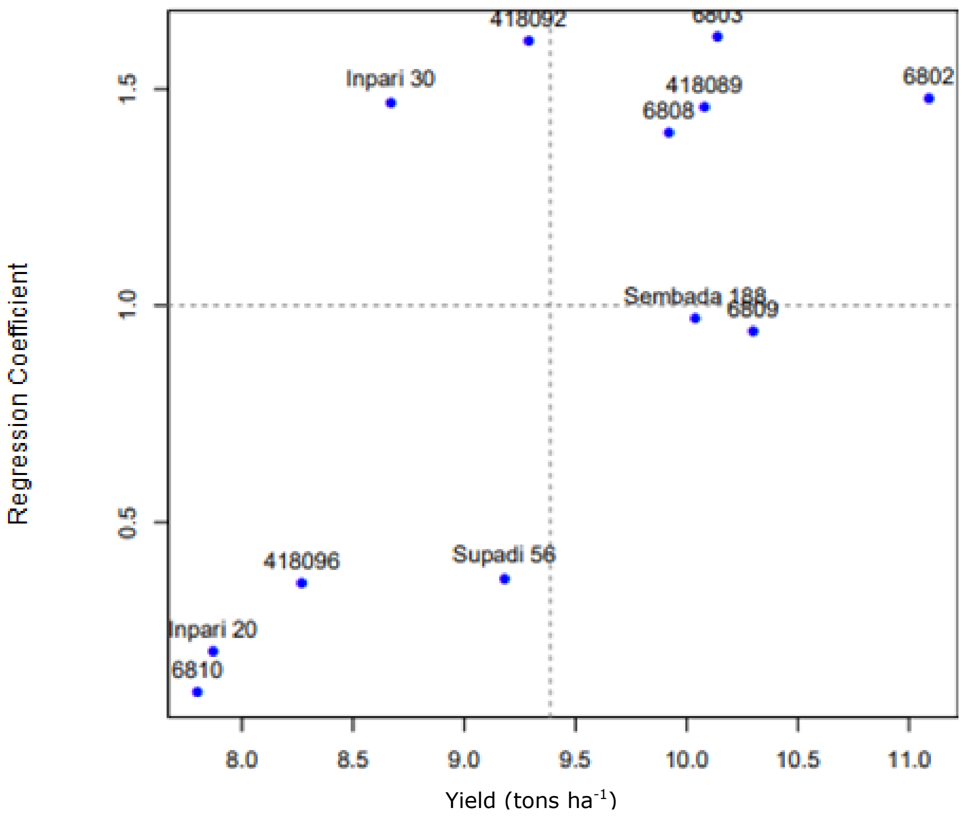

Figure 1. Distribution of grain yield (tons ha^{-1}) of 12 rice genotypes and regression coefficients.

Stability analyses

Stability analyses were performed through Finlay–Wilkinson (1963), Eberhart and Russell (1966), and Francis–Kannenberg (1978) analyses. Finlay–Wilkinson (1963) analysis was based on bi-values. The bi-values for grain yield ranged from 0.11 to 1.62. The bi-values of four rice hybrids and one check cultivar, i.e., 6802, 6808, 6809, 418089, and Sembada 188, were not significantly different from 1 (Table 4 and Figure. 1). Four rice genotypes, i.e., 6810, 418096, Supadi 56, and Inpari 20, yielded bi-values less than 1 (bi < 1) and exhibited above-average stability. The two rice hybrids 6803 and 418092 and the inbred line Inpari 30 had bi-values of more than 1 (bi >1) and were classified as genotypes with below-average stability.

The linear regression coefficient (bi) and the sum of squares deviation from regression (S^2di) are used in Eberhart–Russell (1966) stability analysis. Genotypes with a bi-value equal to 1 and S^2di equal to 0 were considered as stable genotypes (Table 4). The rice hybrids 6809, 418089, and check hybrid Sembada 188 were identified as stable genotypes. The rice hybrid 6809 obtained the highest grain yield (10.30 tons ha^{-1}) relative to the average grain yield (9.39 tons ha^{-1}) with the regression coefficient and regression deviation values of 0.94 and −0.18, respectively. These rice genotypes were found to be suitable for cultivation in all environments.

Table 5. Stability parameters for rice hybrids and check genotypes based on Francis and Kannenberg (1978).

Rice genotypes	Yi (tons ha^{-1})	CVi	Group
6802	11.09	15.03	II
6803	10.14	15.88	II
6808	9.92	14.42	II
6809	10.30	8.24	I
6810	7.80	16.44	IV
418089	10.08	13.6	II
418092	9.29	17.95	IV
418096	8.27	12.35	III
Sembada 188	10.04	8.71	I
Supadi 56	9.18	7.14	III
Inpari 30	8.67	16.7	IV
Inpari 20	7.87	8.98	III
Environment mean yield	9.39	12.95	

Yi: average grain yield at 5 locations; CVi: coefficient of genotypic diversity.

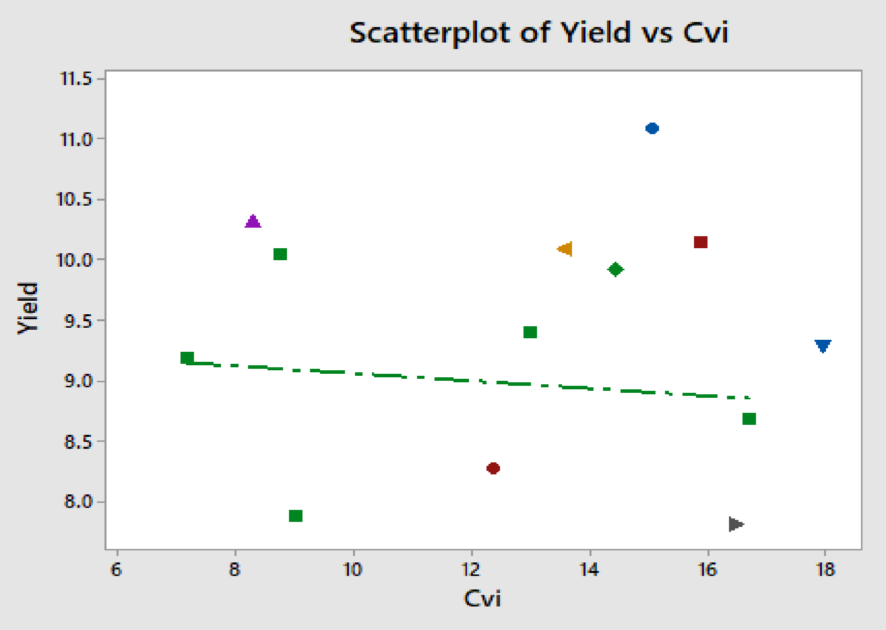

Figure 2. Coefficient of diversity and average grain yield.

Stability analysis based on Francis–Kannenberg (1978) parameter analysis divided the rice genotypes into four groups (Table 5 and Figure 2). Group I consisted of rice genotypes, namely rice hybrid 6809 and check hybrid Sembada 188, with grain yields that were higher than average and CVi that were less than average. The group I genotypes were considered more stable than all other genotypes. Group II consisted of the rice genotypes 6802, 6803, 6808, and 418089 that had grain yields and coefficient of genotypic diversity (CVi) values that were higher than average. Group II rice genotypes were high-yielding but were less stable than group I genotypes. Group III consisted of the rice genotypes

418096, Supadi 56, and Inpari 20 that had grain yields and CVi values that were lower than average values. Group IV consisted of genotypes, i.e., 6810, 418092, and Inpari 30, that had grain yields that were lower than average and CVi values that were higher than average. Genotypes belonging to group IV were found to be unstable genotypes.

AMMI

The AMMI of 12 rice genotypes assessed at five locations showed significant genotype–environment interactions for grain yield. The breakdown of interactions into four interactions among the main components (PC) showed that only PC 1 and PC 2 were significant (Table 6). The significant contribution of variance could be explained by each of the main components of interaction (PC) i.e., 82.70% of PC 1 was significant at the level of 0.01%, whereas PC2 with 14.40% was significant at the level of 0.05%. PC 3 and PC 4 were nonsignificant and described only 2.90% of the total sum of squares and thus did not help in the prediction of valid observations.

The cumulative genotype–environment effects of the sum of squares for PC 1 and PC 2 explained 97.10% of the total genotype–environment sum of squares. This result showed that the interaction of the 12 genotypes at five locations was predicted by the first and second components of the genotypes and environments. The biplot of the AMMI model for grain yield illustrated the effects of interaction between genotypes and environments (Figure 3). The rice hybrids 6802, 6803, 6808, 6809, and 418089 had the highest grain yield and interaction score in the same direction (PC1).

Genotype–environment interactions were also shown by AMMI biplot 2 (Figure 4). The imager line of the PC1 and PC2 factor values can form the coordinates of the location of each genotype. The biplot indicated that the line connecting the grooves to the central point (0,0) as the point of intersection of the source dividing the biplot into four quadrants and showed the closeness of the relationship between the genotypes and environments, where short lines connecting the genotype with the central point indicate a high level of the stability of the genotype (Figure 4). The rice genotypes Sembada 188 and 6809 were found as stable hybrids because they approach the centeral point. The genotype–environment interaction has a positive interaction effect if the PC value has the same direction and a negative interaction if it is in the opposite direction. The rice hybrid 6802 produced the highest grain yield, whereas the hybrid 6810 provided the lowest grain yield. Positive interactions revealed that these cultivars could adapt and grow well in an environment that has the same score sign of PC1. The rice genotypes 6810, 418096, Inpari 20, and Supadi 56 showed positive interactions at three locations, namely, Cilacap, Kuningan, and Sukamandi. The rice genotypes Inpari 30, 418092, 418089, 6808, 6803, and 6802 had positive interactions at two locations, i.e., Sragen and Karawang. The rice genotypes Sembada 188 and 6809 exhibited less interaction with the environment because their PC 1 score was close to zero (Figure 4).

The main component is a vector of variability that is used to determine the position of the variable of an object. The use of the main components that are standardized in the form of the eigen factor (eigenvalue) illustrates the diversity of the data, which include the main components in the vector. PC 1 and PC 2 had an eigenvalue of more than 1. PC 1 and PC 2 were recorded with eigenvalues of 4.3073 and 1.1339, respectively (Table 7).

Table 6. AMMI analysis of variance for grain yield in rice hybrids and check genotypes across five locations.

Source of variation	d.f.	S.S.	M.S.	F value	Explained S.S. (%)
Environments (E)	4	150.65	37.66	13.42**	
Replications (Environments)	15	42.10	2.81	0.13**	
Genotypes (G)	11	242.04	22.00	6.14**	
G × E Interaction (GEI)	44	157.62	3.58	3.93**	
PC1	14	130.32	9.31	10.22**	82.70
PC2	12	22.74	1.89	2.08*	14.40
PC3	10	4.47	0.45	0.49ns	2.80
PC4	8	0.10	0.01	0.01ns	0.10
Error	165	150.29	0.91	-	-

E: location (environment); PC : principal component analysis; ** = significant at an α level of <0.01;
* significant at an α level of <0.05; ns = nonsignificant; d.f. = degrees of freedom.

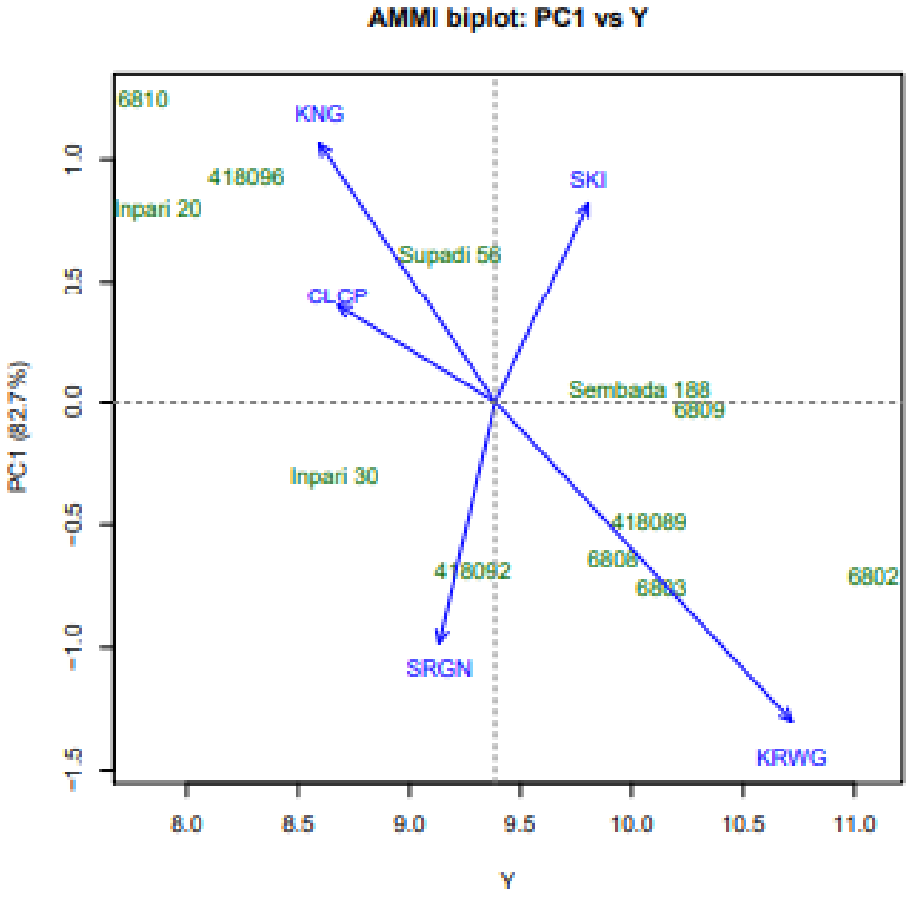

Figure 3. Biplot AMMI-1, locations: KNG = Kuningan, SKI = Sukamandi, CLCP = Cilacap, SRGN = Sragen, KRWG = Karawang.

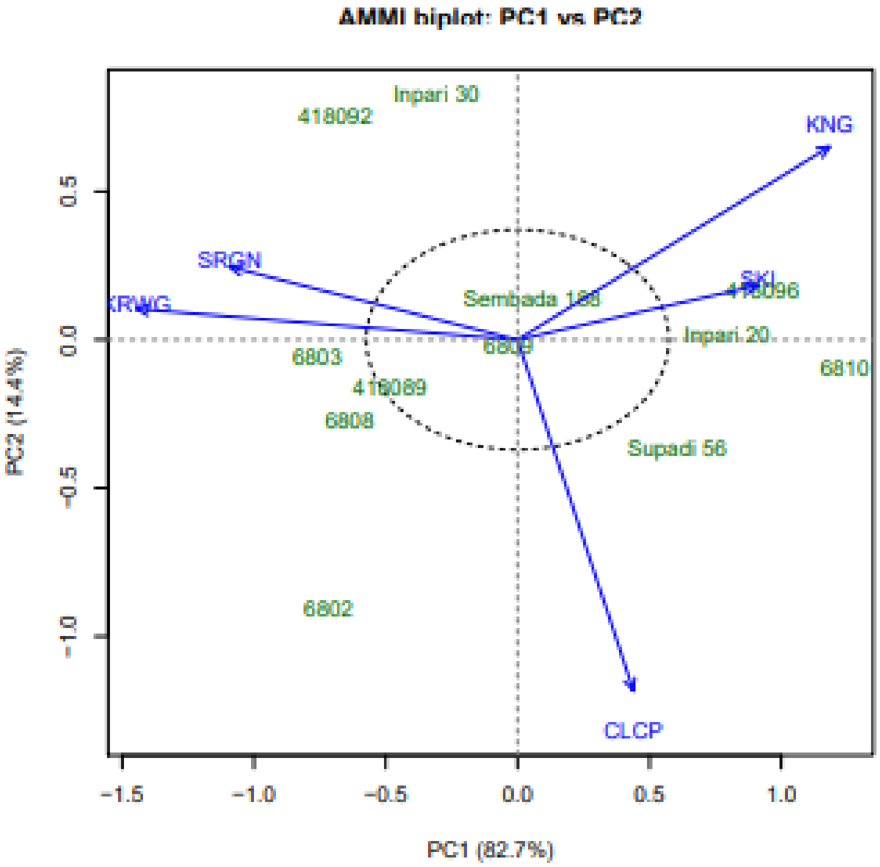

Figure 4. AMMI-2 biplot showing the interaction between rice genotypes and environments. In this plot, the ordinate is PC2, and the abscissa is PC1.

Table 7. Principal component analysis of eigenvalues at five locations.

Statistics/Locations	PC1	PC2	PC3	PC4
Proportion of variance	0.7179	0.189	0.0652	0.0279
Cumulative proportion	0.7179	0.9069	0.9721	1.000
Eigenvalue 5 locations	4.3073	1.1339	0.3914	0.1673
Sukamandi	−0.3967	−0.3634	0.4975	−0.6724
Karawang	−0.4276	0.4135	−0.2118	−0.077
Kuningan	−0.2616	−0.6806	−0.6777	0.0347
Cilacap	−0.4262	−0.2133	0.444	0.7282
Sragen	−0.4265	0.4159	−0.2206	−0.0931

PC1: principal component 1; PC2 : principal component 2; PC3 : principal component 3; PC4 : principal component 4.

DISCUSSION

Rice breeding programs mainly focus on developing high-yielding cultivars with wide adaptability to various environments. Breeders encounter genotype–environment interactions when several genotypes must be planted across diverse environments. Multienvironment trials could provide information for selecting the best genotype to be recommended in a target environment. Genetic factors, environment, and genotype–environment interaction are the main factors that determine crop productivity. The significant effect of the environment accounts for the highly differential genotypic responses over different environments. The variation in altitude, microclimate, annual rainfall, soil structure, moisture, and inputs across different environments is considered as a major underlying causal factor of genotype–environment interactions. Genotype–environment interactions lead to the successful evaluation of stable genotypes that can be used for general cultivation.

This study, the significant genotype–environment interaction indicated the varied performance of the genotypes over environments (locations). Rice genotypes significantly explained 32.59% of the total variation. The contribution of genotype–environment interaction to genotypic variation was small, whereas genotypes explained most of the variations. This situation indicated that rice genotypes were more important in governing the expression of grain yield. Past studies have noted that the interaction between rice genotypes and environment and genotype differences are due to adaptation to different environments (Akter *et al.*, 2015). Satoto (2016) also reported significant genotype–environment interaction effects that led to the varied responses of hybrid rice genotypes in diverse environments. Moreover, Sharifi *et al.* (2017) reported that rice genotypes and genotype–environment interactions are the major contributors to grain yield. The results showed that the genotype sum of squares were large, confirming its great role in managing grain yield. However, the existence of genotype–environment interaction in multienvironment trials is inevitable due to diversity of the rice germplasm and agroecosystem (Kulsum *et al*., 2015; Kartina *et al.*, 2019).

According to Finlay and Wilkinson (1963) stability analysis, five rice genotypes, i.e. 6802, 6808, 6809, 418089, and Sembada 188 showed wide adaptability across locations. However, the genotypes 6803, 418092, and Inpari 30 were adapted to optimal environments (bi > 1). Thus, the addition of inputs to optimized environmental conditions will provide support to produce high grain yields. The genotypes 6810, 418096, Supadi 56, and Inpari 20 were shown to be adapted to unfavorable environments (bi < 1). Thus, if inputs (low fertilizers, low soil fertility, and low irrigation) are not optimal, the yields of the genotypes will not decrease. In this case, the indication should be restricted only to farmers with low capital for rice crop management (Akmal *et al.,* 2014).

The results of the Eberhart and Russell (1966) stability analysis succeeded in the selection of three rice genotypes, i.e., 6809, 418089, and Sembada 188, that were stable in all environments. Therefore, these genotypes had an average capacity for growth in environments and were also considered as ideal rice cultivars with good performance in poor environments. The rice hybrid 6802 which provided the highest grain yield (11.09 tons ha^{-1}), had the maximum values for bi (1.48) and S^2d (1.18). Therefore, it was categorized as a genotype with below-average stability that was specifically adapted to favorable environments. This analysis did not identify rice genotypes with high mean yields and specific adaptability to unfavorable environments (Scapim *et al.,* 2000). A previous stability analysis explained the determination of stable genotypes based on linear regression coefficients (bi) and nonlinear (S^2d) components, and genotypes with bi = 1 and S^2d = 0 were considered as stable genotypes (Eberhart and Russell, 1966).

The Francis and Kannenberg (1978) approach is based on the formation of genotype groups with different environments. This stability analysis used the variability coefficient (CVi) for each genotype. On the basis of these categories, all the rice hybrid genotypes and check cultivars had low CVi. The analysis revealed that the rice hybrid 6809 and check hybrid Sembada

188 were the most stable hybrids because they had the lowest CVi and higher productivity than the average yield. Previous studies revealed that most of the stable cultivars were the genotypes that had higher grain yields than average while having a lower CVi than average (Francis and Kannenberg, 1978).

Univariate analysis does provide basic information on the interaction of the genotypes with a particular environment. Therefore, they cannot recognize promising genotypes in a specific agroecosystem. The multivariate analysis of genotype–environment interaction is an alternative method for identifying genotype stability (Crossa, 1990). In the AMMI model for genotypes, the genotype–environment interaction effects are divided on the basis of each environment (Gauch, 2013). AMMI analysis helps evaluate the interaction effect of a genotype in each location and to analyze the genotypes that are best suitable for a specific location. The analysis of variance showed significant mean squares due to genotypes, environments, and genotype–environment interactions, indicating broad diversity among the genotypes. Environmental variations were considerably higher than genotype effects, suggesting that genotype performance for grain yield was influenced by environmental factors. The maximum grain yield potential was obtained by the genotype that was planted in an environment that met the optimal genetic requirements for obtaining high grain yield

The present results revealed that PC 1 and PC 2 have larger sums of squares than other PC components. PC1 accounted for approximately 82.70% of the interaction SS, whereas PC2 explained 14.40% of the interaction SS. The F values for PC1 and PC2 were also significant at $P \leq 0.01$ and $P \leq 0.05$. Cumulatively, the mean squares for PC 1 and PC 2 could explain 97.10% of the total genotype–environment variation. These two PCs of the interaction were significant for the model with 26 degrees of freedom. By contrast, PC3 and PC4 were nonsignificant and could thus be ignored. This result revealed that the interaction of the 12 genotypes at five environments was predicted by the first and the second components of genotypes and environments (Widyastuti *et al.,* 2012). Given that AMMI analysis is based on genotype–environment interaction effects, the effects due to rice genotypes could be included or ignored (Sitaresmi *et al.,* 2019).

Biplot analysis is the interpretive tool for AMMI models. AMMI analysis can be used to determine the stable genotypes at all test sites or a specific rice genotype for a particular location. The AMMI biplot reflected the adaptability of the rice genotypes. The best-adapted genotype is the genotype that provides a high average yield and is located close to a central point. The rice hybrid 6809 was verified as the best-adapted genotype for all the locations and was found to be close to the check cultivar Sembada 188. The site Karawang was identified as the best location given that several rice genotypes showed high productivity at this location. Location-specific genotypes were illustrated through by plotting PC1 scores against the mean of genotype–environment interaction. The rice genotypes 6803, 418089, and 6808 were well adapted at Karawang, whereas the rice hybrid 418096 produced good yields at Sukamandi. The rice hybrids that showed the best performance in specific areas, such as Karawang and Sukamandi, could be recommended for general cultivation in these environments.

The rice hybrid 6802 provided the highest grain yield, whereas 6810 produced the lowest grain yield. A positive interaction indicates these rice hybrids could be more adaptable in an environment that has the same scores as PC1. The rice genotypes 6810, 418096, Inpari 20, and Supadi 56 had positive interactions at Cilacap, Kuningan, and Sukamandi. However, the rice genotypes Inpari 30, 418092, 418089, 6808, 6803, and 6802 had positive interactions at Sragen, and Karawang. Two rice genotypes, i.e., Sembada 188 and 6809 revealed less interaction with the environment considering that they had the lowest PC 1 scores that were close to zero. Sembada 188 and 6809 were found as the most stable rice hybrids at all locations.

The main component is a vector of variability for determining the position of the variable of an object. The use of the main components that were standardized in the form of the eigen factor value (eigenvalue) illustrates the diversity of data and includes the main components in the vector. Jolliffe (2002) stated that the eigenvalues prevent the effect of multicollinearity in determining characters in the multivariate regression.

CONCLUSIONS

The results indicated that genotypes, environments, and genotype–environment interactions had significant effects on grain yield. In accordance with stability models, the rice hybrid 6809 was identified as the best hybrid rice by producing the highest grain yield and stable performance across locations. AMMI was identified as the best analysis model for selecting the leading rice genotypes in a specific environment.

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REFERENCES

BPS (2020). The average rice production during 2009-2019. Indonesian Statistic Bureau, Jakarta, Indonesia.

Bustos-Korts D, Romagosa I, Borras-Gelonch G, Casas AM, Slafer GA, van-Eeuwijk F (2019). Genotype by environment interaction and adaptation. In: Meyers R. (eds) Encyclopedia of Sustainability Science and Technology. Springer, New York, NY.

Akmal, Gunarsih C, Samaullah MY (2014). Adaptasi dan stabilitas hasil galur-galur aromatik padi sawah di Sumatera Utara. *J. Penelitian Pertanian Tanaman Pangan* 33(1): 9-16.

Akter A, Hassan MJ, Kulsum MU, Islam MR, Hossain K, Rahman MM (2014). AMMI biplot analysis for stability of grain yield in hybrid rice (*Oryza sativa* L.). *J. Rice Res*. 2(2): 126-129.

Akter A, Hasan MJ, Kulsum MU, Rahman MH, Paul AK, Lipi LF, Akter S (2015). Genotype × environment interaction and yield stability analysis in hybrid rice (*O. sativa* L.) by AMMI biplot. *Bangladesh Rice J*. 19(2): 79-86.

Crossa J (1990). Statistical analysis of multi-location trials. *Adv. Agron*. 44: 55–85.

Eberhart SA, Russell WA (1966). Stability parameters for comparing varieties. *Crop Sci*. 6: 36-40.

Finlay KW, Wilkinson GN (1963). The analysis of adaptation in a plant breeding programme. *Aust. J. Agric. Res*. 14: 742-754.

Francis TR, Kannenberg LW (1978). Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Can. J. Plant Sci*. 58: 1029-1034.

Gauch HG (2013). A simple protocol for AMMI analysis of yield trials. *Crop Sci*. 53: 1860–1869.

Jolliffe IT (2002). Principal component analysis, 2nd edition. Springer Verlag, Inc., New York, USA.

Kang MS (2020). Genotype–environment interaction and stability analyses: an update. CAB International. *Quantitative Genetics, Genomics and Plant Breeding*, 140 2nd Edition (*ed.* Kang MS).

Kartina N, Purwoko BS, Dewi IS, Wirnas D, Sugiyanta (2019). Genotype by environment interaction and yield stability analysis of doubled haploid lines of upland rice. *SABRAO J. Breed. Genet.* 51(2): 191-204.

Kulsum MU, Hasan MJ, Akter A, Rahman H, Biswas P (2015). Genotype–environment interaction and stability analysis in hybrid rice: an application of additive main effects and multiplicative interaction. *Bangladesh J. Bot*. 42(1): 73-81.

Lakshmi BV, Veni BK, Chamundeswari N, Ramana JV (2014). Stability analysis of grain yield and its components in rice

(*Oryza sativa* L.) genotypes. *J. Rice Res*. 7(1&2): 10-15.

Lin CS, Binns MR, Lefkovitch LP (1986). Stability analysis: Where do we stand?. *Crop Sci*. 26(5): 894-900.

Ran Y, Chen H, Ruan D, Liu H, Wang S, Tang X, Wu W (2018). Identification of factors affecting rice yield gap in southwest China: An experimental study. *PLoS ONE* 13(11): e0206479.

Satoto, Rumanti IA, Widyastuti Y (2016). Yield stability of new hybrid rice across locations. *Agrivita* 38(1): 33-39.

Scapim, Alberto C, Oliveira, Rodrigues V, Braccini, Alessandro L, Cruz, Damião C, Andrade, Alberto C, Vidigal, Gonçalves MC (2000). Yield stability in maize (*Zea mays* L.) and correlations among the parameters of the Eberhart and Russell, Lin and Binns and Huehn models. *Genet. Mol. Biol*. 23(2): 387-393.

Sharifi P, Aminpanah H, Erfani R, Mohaddesi A, Abbasian A (2017). Evaluation of genotype × environment interaction in rice based on AMMI model in Iran. *Rice Sci.* 24(3): 173-180.

Sitaresmi T, Nafisah, Gunarsih C, Daradjat AA (2012). Analisis stabilitas hasil gabah galur-galur padi melalui pendekatan parametrik dan nonparametrik. *J. Penelitian Pertanian*. 31(2): 79-86.

Sitaresmi T, Gunarsih C, Nafisah, Nugraha Y, Abdullah B, Hanarida I, Aswidinnoor H, Muliarta IGP, Daradjat AA, Suprihatno B (2016). Interaksi genotipe × lingkungan terhadap hasil galur harapan padi sawah. *J. Penelitian Pertanian Tanaman Pangan* 35(2): 89-97.

Sitaresmi T, Suwarno WB, Gunarsih C, Nafisah, Nugraha Y, Sasmita P, Daradjat AA (2019). Comprehensive stability analysis of rice genotypes through multi-location yield trials using PBSTAT-GE. *SABRAO J. Breed. Genet*. 51(4): 355-372.

Sreedhar S, Reddy TD, Ramesha MS (2011). Genotype × environment interaction and stability for yield and its components in hybrid rice cultivars (*Oryza sativa L.*). *Int. J. Plant Breed. Genet*. 5(3): 194-208.

Tabanao D, Carampatana J, Pocsedio A, Gramaje L (2015). Multilocation adaptation tests of hybrid rice varieties in the Philippines. *Crop Protect. Newsletter* 40(2): 25-32.

Widyastuti Y, Satoto, Rumanti IA (2012). Pemanfaatan analisis regresi dan AMMI untuk evaluasi stabilitas hasil genotipe padi dan pengaruh interaksi genetik dan lingkungan. *Informatika Pertanian* 22(1): 21-27.

Widyastuti Y, Satoto, Rumanti IA (2015). Performance of promising hybrid rice in two different elevations of irrigated lowland in Indonesia. *Agrivita* 37(2): 169-177.

Widyastuti Y, Yunus M, Purwoko BS, Satoto (2017). Diversity and capability analyses of fertility restorer genes of cytoplasmic male sterile rice lines using SSR. *Indonesian J. Agric. Sci.* 18(2): 1-10.

Zobel RW, Wright MJ, Gauch HG (1988). Statistical analysis of a yield trial. *Agron. J.* 80: 388-393.