

YIELD STABILITY OF NEW HYBRID RICE ACROSS LOCATIONS

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ABSTRACT

The adaptation of hybrid rice varieties mostly are in specific location and season, but there are some of the varieties have a wide adaptation then adopted by the farmer in the large area. Replicated yield trials were conducted to study the stability of hybrid rice yield and identify the best location to optimize their yield per ha. The trials were conducted in three location such as Sukamandi, Salatiga and Malang during two seasons in 2011. Data across location and season were analyzed by using AMMI and Eberhart Russel methods. The AMMI analysis showed that the IR79156A/PK88 was adaptable to favorable environments but unstable. This hybrid is always performing well and produce the higher yield compare to check variety. Some of other hybrids were good only in specific location, i.e. IR62829A/BP2280-1E-12-22 and IR58029A/BP2280-1E-12-22. Those hybrids produced higher yield in Salatiga and Malang, respectively. Seem to AMMI analysis, the result of Eberhart and Russell method also showed that IR79156A/PK81 was the best hybrid with regression slope (b) around 1 with the yield average higher than average of all hybrids. It indicated that this hybrid has a wide adaptation and probably can be cultivated in the wider ecosystem.

Keywords: AMMI; hybrid rice; stability; yield

INTRODUCTION

Plant breeders invariably encounter genotype x environment interactions (GEIs) when testing varieties across a number of environments. Depending upon the magnitude of the interactions or the differential genotypic responses to environments, the varietal rankings can differ greatly across environments.

Genotype-environment interaction (GEI) in hybrid rice (*Oryza sativa* L.) varieties is the differential response of genotypes to changing environmental conditions. Some researchers reported

that hybrid rice varieties may not produce uniform yields across different environment as a result of the existence of genotype x environment (G x E) interaction (Satoto *et al.*, 2010; Sreedhar *et al.*, 2011; Widyastuti and Satoto, 2012; Satoto *et al.*, 2013).

Univariate and multivariate statistical stability are the two major methods to analyse genotype x environment interactions and phenotypic stability (Lin *et al.*, 1986). Some of the methods have been suggested for analyzing the genotype x environment interaction and yield stability of a genotype. Finlay and Wilkinson (1963) stated that bi considers a cultivar stable if its response to environments is parallel to the mean response of all cultivars in the trial. Varieties with regression coefficient $b_1=0$, shows the relationship between fluctuations in yield and changes in the environment. The higher coefficient value ($b_i > 1.0$), the higher level of response of a variety. In the case when ($b_i < 1.0$), a variety shows a weaker response to environmental conditions than the average pool of the varieties under study. Eberhart and Russell (1965) revealed that S^2_d considers a cultivar stable if the residual mean square from Finlay and Wilkinson's regression model is not significant. The stability characteristics of a genotype will be higher, if the sum of yield deviation squares of genotype is low. A genotype is defined stable if having a coefficient regression over the environments close to 1.00 ($b_i=0$) and the minimum deviations from the regression of $S^2_d=0$.

The multiplicative interaction model was first introduced by Crossa (1990), then adapted to the agricultural framework as AMMI by Gauch and Zobel (1996). The main additive effect and multiplicative interaction (AMMI) analysis is a model that combines both additive and multiplicative components of a two way data structure that allows a breeder to obtain precise prediction on potential genotype and environmental effects on it (Akter *et al.*, 2014). This method has proven effective because it intercepts a large part of the

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GEI sum of square, it obviously separates main and interaction AMMI effects. The analysis not only serves an estimate of the total G x E interaction effect of each genotype but further partitions it into the environmental effects due to the interaction of the individual (Ebdon and Gauch, 2001). It combines the analysis for the genotypic and main environmental effect with several graphically represented interactions for principal component analysis (IPCA). Thus, it helps to summarize the pattern and relationship of genotypes, the environment, and their interaction. The aim of this research was to establish yield stability parameters in eighteen hybrid rice combination and to select the most valuable ones for the development of a stable variety.

MATERIALS AND METHODS

Eighteen new promising hybrid rice were used as testing materials compared to Hipa10 as hybrid check variety and Ciherang as popular inbred check variety. These hybrids rice derived from CMS introduced from IRRI namely IR580 25A, IR62829A, IR68885A, IR68897A, IR79156A and IR80151A.

Field experiments were conducted in the 2011 dry season (DS) and in the 2011 rainy season (WS) at three location i.e. Sukamandi West Java (Alluvial, 16 m above the sea level), Batang Central Java (Alluvial, 200 m above the sea level) and Malang (Alluvial, 400 m above the sea level), Indonesia. In each location-season site, 18 hybrids were tested compare to Hipa10 as hybrid check and Ciherang as inbred check varieties in a field experiment by using Randomized Complete Block Design (RCBD) with three replications. The plot size was 3 x 5 m². Each plot consisted of ten rows with 25 hills per row. The area was plowed and harrowed. Fertilizer of 300 kg urea/ha, 100 kg TSP/ha, and 100 kg KCl/ha were applied in the field and according to the recommended time and doses. After land preparation, the experimental plots were laid out and labeled accordingly. Twenty-one days old seedlings were planted in each designated plot. Each of the twenty-six genotypes was transplanted in each block using one-two seedling per hill, with planting space of 20 x 20 cm. Hand weeding was done when weeds were observed growing after the rice plants have recovered. Normal cultural practices were followed. The crop was protected from insect pest and diseases through chemical

control as and when needed. Harvesting was done when 85% of the grains were straw (i.e. yellow) colored and hard dough stage. Each plot harvested after cutting one row at border, off-type and abnormal plant.

The grain yield and its components (i.e. the length of the panicle, productive tiller number per hill, filled grains number per panicle, unfilled grains number per panicle, percentage of filled grains per panicle (seed set), and 1000 filled grains weight) were observed. Data of grain yield and yield components were analyzed using IRRISTAT (version 4.4) and the analysis of variance in RCBD was used to determine treatment differences. Groups of plant types were compared based on the least significant difference test (LSD) at the 5%. AMMI analysis and Eberhart Russel method were carried out using the IRRISTAT program. Standard heterosis (SH) was calculated as equation below by using of the standard variety Ciherang as the popular variety in Indonesia.

$$SH (\%) = \frac{\overline{F1} - \overline{SV}}{\overline{SV}} \times 100$$

where $\overline{F1}$ and \overline{SV} are the mean of F1 progenies and standard variety Ciherang in all replications.

RESULTS AND DISCUSSION

The combined analysis of variance is presented in Table 1. Genotype (G), environment (E) and genotype x environment interaction (GxE) were significant ($P \leq 0.01$) for grain yield. The source of variation due to the environments was the largest proportion (54.17%) followed by interaction of G x E (23.49%), and genotypes (21.99%). It means that the productivity grain yield of hybrid rice is depending on the environments and the genotypes of hybrid. The G x E interactions led to changes in the ranking of a genotype in one environment to another. The significant G x E interaction effects revealed that genotypes responded differently to the variation of environmental conditions and the yield performance of the genotypes was varied in different locations. Similar findings were also reported by Sitaesmi *et al.* (2012), Satoto *et al.* (2013) and Kulsum *et al.* (2014) in rice. But, this condition also make the difficulties in selecting promising lines to release as a variety.

Table 1. The combined analysis of variance for grain yield at 6 environments

Source of variation	Degree of freedom	Sum square	Mean square	Explained sum square (%)
Total	284	355.390		
Replications	2	0.129		
Environment (E)	5	192.53	38.506**	54.17
Genotype (G)	19	78.154	4.113**	21.99
G x E	95	83.471	0.879*	23.49
Error	190	1.107	0.006	

Remarks: * = significant at 5% level, ** = significant at 1% level

Table 2. Grain yield and environment index of eighteen hybrid rice combinations in six testing locations, 2011

No	Hybrid rice/check varieties	Grain yield (t ha ⁻¹) at across locations and seasons:						Mean
		Salatiga DS	Sukamandi DS	Malang DS	Salatiga WS	Sukamandi WS	Malang WS	
1	IR58025A/PK73	4.88	4.09	4.50	5.20	4.80	9.58	5.51
2	IR79156A/PK88	8.03*	7.39	8.34*	7.77*	7.87	9.28	8.11
3	IR79156A/PK81	6.66*	5.82	6.68	5.49	7.13	9.93	6.95
4	IR58025A/BP2872-3E-10-2	4.30	6.12	5.95	5.27	4.60	9.47	5.95
5	IR58025A/BP2872-3E-10-3	3.63	6.64	4.15	5.97	6.26	9.04	5.95
6	IR58025A/BP2276-5E-25-2	6.01	6.45	5.58	5.62	6.60	10.66	6.82
7	IR58025A/B1800-1F-19	5.98	6.77	8.72*	7.83*	7.35	11.43	8.01
8	IR58025A/B2080-2E-KN-6-1	3.99	6.26	7.08	6.39	6.74	12.12	7.10
9	IR58025A/BP1800-1F-18	4.04	6.15	6.00	5.61	4.49	10.09	6.06
10	IR62829A/CRS117	4.38	4.90	4.56	5.11	4.68	7.85	5.25
11	IR68897A/CRS125	5.40	6.49	5.31	5.29	6.28	9.90	6.44
12	IR62829A/BP1800-1F-18	5.80	5.83	5.42	5.70	7.35	9.39	6.58
13	IR68897A/BIO12-2-1	6.97*	7.12	6.63	5.19	8.19	10.28	7.40
14	IR62829A/BP2280-1E-12-22	5.99	6.80	7.93*	6.60	6.50	6.76	6.76
15	IR62829A/CRS125	6.19	6.56	4.98	6.44	6.72	9.76	6.77
16	IR68897A/CRS134	5.02	5.99	4.83	5.25	6.34	7.92	5.89
17	IR80151A/CRS87	6.73*	6.54	5.42	5.37	7.57	8.96	6.76
18	IR68885A/BIO12-3	4.59	4.23	4.24	4.51	4.77	7.35	4.95
19	Hipa10	5.59	7.10	7.38*	5.34	6.85	5.75	6.33
20	Ciherang	6.16	7.00	5.01	6.22	7.62	10.29	7.05
	Mean	5.52	6.21	5.93	5.81	6.44	9.29	6.53
	LSD (%)	0.33	1.87	2.04	0.80	1.56	1.82	
	CV (%)	3.66	18.20	20.69	8.36	14.63	11.49	
	Ij	-1.02	-0.32	-0.60	-0.72	-0.10	2.76	

Remarks: Value within column with *: significantly different at LSD 5% than Ciherang; Ij: Environmental index, DS: Dry season, WS: Wet season

Table 2 shows that the coefficient of variation ranged from 3.66% (Salatiga, DS 2011) to 20.69% (Malang, DS 2011). It means that grain yield data collected were valid for variance analysis. Different genotypes showed inconsistent performance across all environments. The genotypic mean of grain yield ranged from 4.95 to 8.11 t ha⁻¹. The hybrid IR79156A/PK88 yielded over the check variety Ciherang at three locations i.e. Salatiga and Malang at DS and Salatiga at WS, whereas IR58025A/B1800-1F-19 at two locations, i.e. Malang DS and Salatiga WS. Most hybrid rice

yielded grain were not significant than Ciherang. The average yields of eighteen hybrid combinations ranged from 4.95 to 8.11 t ha⁻¹, while that of Ciherang was 7.05 t ha⁻¹. All hybrids gave yield potential lower than Ciherang, except IR79156A/PK88, IR58025A/B1800-1F-19, and IR68897A/BIO12-2-1.

The value of environmental index (Ij) reflected the favorable and unfavorable environments for the yield character (Hasan *et al.*, 2011). According to Eberhart and Russell (1965), environmental index indicate relative land produc-

tivity; locations with higher environmental index are more suitable for plant growth than other locations with lower I_j value (Karimzadeh *et al.*, 2012). Tiawari *et al.* (2011) also stated that land is more productive when its I_j value is higher. Environment index values showed the importance of variability as well as the difference with other induced factors in detecting the performance of genotypes under different environments. The environmental mean from 5.52 to 9.29 t ha⁻¹ and averaged grain yield over environments and genotypes is 6.53 t ha⁻¹. Environmental index (I_j) of six environments ranged from -1.02 to 2.76 (Table 2). On the basis of the environmental index value in terms of negative and positive, Salatiga DS, Sukamandi DS, Sukamandi WS, and Salatiga DS are poor, and Malang are rich environment. Within the genotypes, six hybrids rice have higher average yields and these genotypes adapted to favorable environments, while genotypes IR79156A/PK88 and IR58025A/B1800-1F-19 adapted to poor environments (Table 2).

The mean of grain yield, standard heterosis than Ciherang and stability parameters

of the eighteen tested hybrid combinations and two check varieties are presented in Table 3. Standard heterosis most of all hybrid rice was negative except IR68897A/BIO12-2-1, IR58025A/B1800-1F-19, and IR79156A/PK88 i.e 4.96%, 13.62% and 15.04% respectively. Coefficient of regression (b_i) varied from -0.11 to 1.85. Coefficient of regressions of all hybrid combinations except IR79156A/PK88, IR58025A/BP2276-5E-25-2, IR58025A/B2080-2E-KN-6-1, IR62829A/BP2280-1E-12-22, and Hipa10 were significantly different from one, means that these hybrids were not stable. In 2011, by Eberhart and Russell's method, there were two genotypes with grain yield higher than grand mean showed specific adaptability to favorable environments ($b_i > 1$ i.e IR79156A/PK81, and IR58025A/B1800-1F-19), two hybrid had wide adaptability ($b_i = 1$, i.e. IR68897A/BIO12-2-1 and IR62829A/CR S125) and only one hybrid showed and unfavorable environments ($b_i < 1$ IR80151A/CRS87). The environments classified as favorable was Malang and as unfavorable were Sukamandi and Salatiga.

Table 3. Mean of yield, standard heterosis, coefficient regression, and deviation of regression for 18 hybrid rice and 2 check varieties tested in 6 environments in Indonesia, 2011

No	Hybrid rice/check varieties	Mean of Yield (t ha ⁻¹)	Standar heterosis than Ciherang (%)	b_i	S^2d_i
1	IR58025A/PK73	5.51	-21.84	1.40	0.61
2	IR79156A/PK88	8.11	15.04	0.38*	0.18
3	IR79156A/PK81	6.95	-1.42	1.10	0.48
4	IR58025A/BP2872-3E-10-2	5.95	-15.60	1.20	0.64
5	IR58025A/BP2872-3E-10-3	5.95	-15.60	1.20	1.14
6	IR58025A/BP2276-5E-25-2	6.82	-3.26	1.37*	0.14
7	IR58025A/B1800-1F-19	8.01	13.62	1.21	1.05
8	IR58025A/B2080-2E-KN-6-1	7.10	0.71	1.85*	0.80
9	IR58025A/BP1800-1F-18	6.06	-14.04	1.42	0.92
10	IR62829A/CRS117	5.25	-25.53	0.91	0.13
11	IR68897A/CRS125	6.44	-8.65	1.26	0.11
12	IR62829A/BP1800-1F-18	6.58	-6.67	1.04	0.33
13	IR68897A/BIO12-2-1	7.40	4.96	1.09	0.83
14	IR62829A/BP2280-1E-12-22	6.76	-4.11	0.02*	0.51
15	IR62829A/CRS125	6.77	-3.97	1.06	0.45
16	IR68897A/CRS134	5.89	-16.45	0.78	0.19
17	IR80151A/CRS87	6.76	-4.11	0.82	0.70
18	IR68885A/BIO12-3	4.95	-29.79	0.83	0.13
19	Hipa10	6.33	-10.21	-0.11*	0.93
20	Ciherang	7.05		1.21	0.61

Remarks: b_i coefficient of regression, S^2d_i standard deviation. Value within column with *: significantly different at LSD 5% to value Of 1.0

Table 4. AMMI analysis of variance for grain yield (t ha⁻¹) of the genotypes across environments

Source of variation	df	SS	MS	F	Explained (%)
Genotypes (G)	19	78.154	4.113		22.07
Environments (E)	5	192.532	38.506		54.36
G x E	95	83.471	0.878		23.57
IPCA 1	23	43.060	1.872	3.336**	51.59
IPCA 2	21	21.327	1.016	2.714**	25.55
IPCA 3	19	9.518	0.501	1.676**	11.40
IPCA 4	17	6.080	0.358	1.539*	7.28
G x E Residual	15	3.485			0.98
Total	119	354.158			

Remarks: ** significant at 5 and 1% probability by the F test

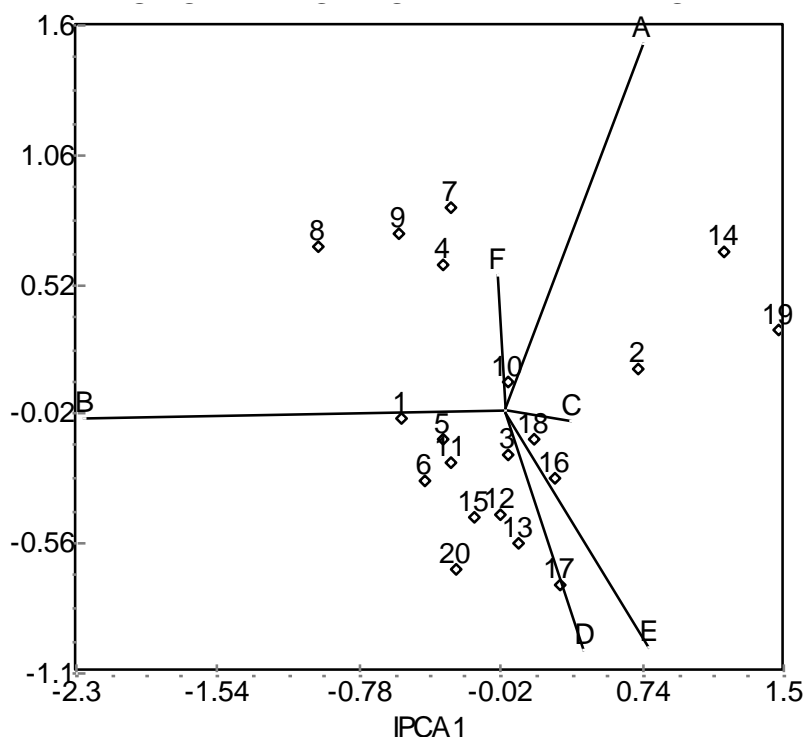
The AMMI analysis variance for grain yield (t ha⁻¹) of 20 genotypes tested in 6 environments showed that 54.36% of the total sum of square was attributable to environment effects, only 22.07% to genotypic effect and 23.57% of the total variation for grain yield (Table 4). The large sum of square of environments denotes that the environments were diverse and causing the variation in grain yield. The magnitude of the GEI sum of squares was 1.07 times larger than that for genotypes, which suggests that there were major differences in genotypic response across environments. This report is in harmony with the findings of Blanche *et al.* (2009), Hasan *et al.* (2011) and Tariku *et al.* (2013).

Results from AMMI analysis (Table 4) also showed that the first interaction principal component axis (IPCA 1) of the interaction captured 51.59% of the interaction sum of squares in 23.57% of the interaction degrees of freedom. Similarly, the second principal component axis (PCA 2) explained a further 25.55% of the GEI sum of squares. For further, PCA 1 and PCA 2 had larger sums of squares than that of genotypes. Cumulatively the mean squares for the PCA 1 and PCA 2 were able to explain 77.14% from the total GxE variation. This indicated that the interaction of the 18 rice genotypes with 6 environments was predicted by the first two components of genotypes and environments. This result was in conformity with the findings of Gauch and Zobel (1996) that the most accurate model for AMMI can be predicted using the first two IPCAs.

Biplot analysis is the interpretive tool for AMMI models. Hernandez and Crossa (2000) stated that a biplot resulted from genotypic and environmental scores of IPCA 1 and IPCA 2 of AMMI components. A biplot has four sections,

depending on signs of the genotypic and environmental scores. In AMMI 2 biplot (Figure 1), the IPCA scores for both the genotypes (numbers) and environments (alphabet) were plotted over the mean grain yield for the genotypes and the environments respectively. Sites with short spokes do not exert strong interactive forces, while those with long spokes exert strong interaction. The IPCA scores of a genotype in the AMMI analysis indicated the adaptability over environments. An example, the environments C and F had short spokes and it did not exert strong interactive forces. The genotypes that occur adjacent on the plot will tend to have similar yields in all environments while genotypes apart may be different in the average yield or show a different pattern of response over the environments. Therefore, the genotypes close to the origin were not sensitive to the interaction of the environment and the genotypes that far from the origins were sensitive and had large interaction.

In the present study, the hybrid rice IR79156A/PK88 (2), IR62829A/BP2280-1E-12-22 (14), and Hipa 10 (19) have specific adaptation to favorable environments. Considering only the IPCA scores, it became clear that IR79156A/PK88 (2), IR62829A/BP2280-1E-12-22 (14), and Hipa10 (19) were the more unstable genotypes, but they were well adapted to high-yielding or more favorable environments. The same result showed from analysis stability by Eberhart and Russel (Table 2). The hybrid IR62829A/CRS117 (10), and IR68885A/BIO12-3 (18) with a close to zero IPCA scores show that they were more stable but low yield. These genotypes were suitable for low input or Sreedhar unfavorable environments. Whereas IR79156A/PK81 (3) was the most stable hybrid with higher yield than overall genotypes tested.



Remarks: A: Malang DS, B: Malang WS, C: Sukamandi DS, D: Sukamandi WS, E: Salatiga DS, F: Salatiga WS
Figure 1. Interaction Biplot for AMMI2 Model Fit 77.1% of GxE

CONCLUSIONS AND SUGGESTIONS

The mean grain yield value of genotypes averaged over environments indicated that IR79156A/PK88 was the highest (8.11 t ha^{-1}) and IR68885A/BIO12-3 was the lowest yield (4.95 t ha^{-1}), respectively. The hybrid rice IR79156A/PK88 was adaptable to favorable environments with highest grain yield but unstable. IR79156A/PK81, IR68897A/BIO12-2-1, and IR62829A/CRS125 hybrid combinations had a regression coefficient nearest to one. It means that they were stable and adaptable to both favorable and unfavorable environments. IR80151A/CRS87 hybrid combinations was more adaptable to sub optimal environments. As a breeding, it is better to cluster the testing locations into homogenous groups used for breeding for specific adaptation and/or for broad adaptation.

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