

Genotype \times environment interaction, and stability analysis in lowland rice promising genotypes

Azri Kusuma Dewi^{1,4*}, M. Ahmad Chozin², Hermanu Triwidodo³, Hajrial Aswidinnoor^{2*}

¹Graduate School of Plant Breeding and Biotechnology, Faculty of Agriculture, Bogor Agricultural University, Jl. Meranti Kampus IPB Darmaga Bogor 16680, Indonesia

²Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, Jl. Meranti Kampus IPB Darmaga Bogor 16680, Indonesia

³Department of Plant Protection, Faculty of Agriculture, Bogor Agricultural University, Jl. Kamper Kampus IPB Darmaga 16680, Indonesia

⁴Center for Application of Technology Isotopes and Radiation-Indonesian Nuclear Energy Agency, Jl. Lebak Bulus Raya 49, Jakarta 12440, Indonesia

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Abstract

This assessing of genotype \times environment interaction is one important step for accurate rice promising genotypes evaluation in large multi-environment trials. In this study, ten rice promising genotypes and two Indonesian rice varieties were grown in nsix environments during 2011 plant season to determine the grain yield stability and adaptability. The experiment used randomized complete block design with three replications. Yield stability and adaptability of yield performance were analyzed by using coefficient regression (bi), general mean of yield and deviation of regression by Finlay-Wilkinson and Eberhart-Russell method and other parameters of stability and AMMI model. From the current study, it is concluded that among rice promising genotypes that identified superior performance genotypes i.e. IPB 107-F-5-1-1, IPB 115-F-3-2-1, IPB 116-F-44-1-1, IPB 116-F-46-1-1, IPB 117-F-4-1-1, and IPB 149-F-8-1-1 were stable for two or more stability parameters and combination with high yield potential. Further analysis based on YS_i only select four of the above genotypes i.e. IPB 115-F-3-2-1, IPB 116-F-44-1-1, IPB 117-F-4-1-1, and IPB 149-F-8-1-1, that could be recommended to farmers based on their performance of stability and high yield potential during selection. Based on AMMI biplot analysis, genotypes IPB 116-F-3-1-1, IPB 116-F-46-1-1, IPB 116-F-44-1-1 and IPB 149-F-8-1-1 were more stable and have minimal interaction with environment. Whereas, genotypes IPB 117-F-4-1-1 and IPB 107-F-5-1-1 was gave indication to adapt at specific environmental condition.

*Corresponding Author: Azri Kusuma Dewi ✉ azridewi@yahoo.co

Introduction

Rice (*Oryza sativa* L) is a primary food source for many people and play important role for food security and sovereignty in Indonesia. Rice grain yield, as a function of total global rice production, has a major impact on the supply and price stability of rice. Though more than 200 rice varieties have been released as national varieties in Indonesia, and only few varieties with stable performance continue to be under cultivation even after several years of release. Therefore, multi-location trials need to be done before the rice promising genotype released as national varieties and passed on to farmers as end users. Varieties of rice developed in the plant breeding will eventually planted by farmers in various different environments. The results of multi-location trials of promising rice lines often reflects differences in grain yield in each location that the highest yield of a genotype in one location often showing is inconsistent in other locations. This is caused by the interaction between genotypes and environment, making it difficult for plant breeders in selecting the best genotype.

The yield stability is one of the most desirable properties of a genotype to be released as a variety for cultivation. Stability is a complex product of genetic yield potential to stress conditions. Research on yield stability, or genotype \times environment interaction (GEI), is necessary to evaluate the consistency of rice grain yield and, for plant breeders, to develop cultivars that respond optimally and consistently across years and diverse agro-ecological conditions. The yield stability is influenced by several factors, such as environmental factors, agricultural managements and pest pressures (Hu and Buyanovsky, 2003; Berzsenyi and Dang, 2008). Breeding genotypes that are adapted throughout a reasonable large geographical area and that show some degree of stability from year to year is a major problem facing plant breeders. As a result, several methods of measuring and describing genotypic response across environments have been developed a utilized. For this purpose, multilocal trials, over a number of years are conducted (Luthra *et al.*, 1974).

The level of performance of any character is a result of the genotype (G) of the cultivar, the environment in which it is grown (E), and the interaction between G and E (GEI). Genotype \times environment interaction (GEI) exists when the responses of two genotypes to different levels of environmental stress are not consistent (Allard and Bradshaw, 1964). G \times E interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments, to help plant breeders in selecting varieties. Instability is the result of cultivars response in different environments which usually indicates a high interaction between genetic and environmental factors (Jusuf *et al.*, 2008; Lone *et al.*, 2009). Grain yield depends on genotype, environment and management practices and their interaction with each other (Messina *et al.*, 2009). Under the same management conditions, variation in grain yield is principally explained by the effects of genotype and environment (Dingkuhn *et al.*, 2006). Interaction between these two explanatory variables gives insight for identifying genotype suitable for specific environments. The environmental effect is typically a large contributor to total variation (Blanche *et al.*, 2009).

Lestari *et al.* (2010) reported that there was significant different stability and adaptability of 35 aromatic new plant type rice lines across different environments. Similarly, Sreedhar *et al.* (2011), evaluate 60 hybrid rice cultivars for yield and its component stability across three different agro-climatic zones, and also found that stability in single plant yield was due to plasticity and stability in yield components. In the study of Mosavi (2013) in some rice promising genotypes, showed that highly significant yield differences among rice genotypes, environment and genotype by environment interaction. Some rice genotypes were adjudged stable when different yield stability parameters were considered.

The analyses of genotype \times environment has focused on the identification of stable genotype for

cultivation. Various statistical procedures have been proposed to find out the stability of new cultivars. One of the most frequently used stability measures is based on a regression model (Yates and Cochran 1938). However, it was developed by Finlay (Finlay and Wilkinson 1963) to describe the adaptation of individual varieties to changing environment and while Eberhart (Eberhart and Russell 1966), used b-values as measures of environmental response and deviations from regression as measures of stability. Several of these statistics have been summarized and compared by Lin (Lin *et al.*, 1986) who pointed out that stability statistics fall into four groups depending on whether they are based on the deviation from the average genotype effect or on the genotype by environment term and whether or not they incorporate a regression model on an environment index. Other workers have suggested use of parameters like Coefficient of Variation, Wricke's ecovalence and AMMI Stability Value as measures of stability. Further, the simultaneous selection for yield and stability in crop performance is also used based on Kang's modified rank-sum method. This yield-stability statistic (YS_i) component is basically based on Shukla's (1972) stability-variance statistic (σ_{i2}). The Additive Main Effects and Multiplicative Interaction (AMMI) model has found more use recently since it incorporates both the classical additive main effects model for GxE interaction and the multiplicative components into an integrated least square analysis and thus becomes more effective in selection of stable genotypes (Crossa *et al.*, 1991; McLaren and Chaudhary, 1994; Ariyo, 1998; De Cauwer and Ortiz, 1998; Haji and Hunt, 1999; Ariyo and Ayo-Vaughan, 2000; Taye *et al.*, 2000; Yan and Hunt, 2001).

The present study was conducted to assess the extent of some promising rice genotypes by environment interaction for their yield stability and adaptability across different environments and to select lines having wide adaptation and/or specific adaptation to environment.

Material and methods

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Experimental design and plant materials

Multi environment trials on twelve lowland rice genotypes were conducted during the 2011 cropping season at six environmental conditions; Bogor, Maros, Gunung Kidul, Sragen, Rangkasbitung and Purbalingga. Twelve rice genotypes (ten rice promising genotypes; IPB107-F-5-1-1, IPB107-F-65-3-1, IPB113-F-2-1-1, IPB115-F-3-2-1, IPB116-F-3-1-1, IPB116-F-44-1-1, IPB 116-F-46-1-1, IPB 117-F-1-3-1, IPB 117-F-4-1-1, IPB 149-F-8-1-1 and two rice national varieties Ciherang and IR64 as control plant) were planted in a plot of 4 m x 5 m. The experiment was laid out in a randomized complete block design with three replications. 15-20 days old seedlings were transplanted with 10 cm x 20 cm x 40 cm spacing and 1-2 seedlings per hill. Fertilizer (N-P-K, 100-200-100 kg/ha) was applied at the time of planting and 100 kg/ha of N was top dressed twice once at 30 and again at 60 days after transplanting. Data was collected at flowering and maturity stages, observations were recorded on plant height (cm.), days to 50% flowering, panicle length (cm.), panicle number per plant, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility percentage 1000-grain weight and grain yield per plot (Kg/Plot) was then used to estimate yields in tones per hectare.

Statistical analysis

Test of homogeneity of variance using Bartlett test that compares calculated *chi-square* value by *chi-square* table. If variances of all environments were found to be homogenous, then combined analysis of variance was proceeded to look at G x E and stability of the genotypes across all environments. The stability of yield performance for each genotype was calculated by regressing the mean yields of individual genotypes on environmental index (Finlay and Wilkinson, 1963) and deviations from regression were calculated, stability model according to Eberhart and Russell (1966). For linear regression, the following model was used:

$$Y_{ij} = \mu + G_i + E_j + b_i E_j + d_{ij} + e_{ij}$$

where Y_{ij} is the observed mean yield of the i^{th} genotype in the j^{th} environment ($i = 1, \dots, g; j = 1, \dots, e$),

μ is the mean, G_i is the effect of genotype i , E_j is the effect of environment j , b_i is the linear regression coefficient of the i th genotype on environmental index, d_{ij} is deviation from regression, and e_{ij} is the average of the random errors associated with the i th genotype and j th environment (Eberhart and Russell, 1966). Stability of yield performance of genotypes was also estimated using other parameters like coefficient of variation CVi% (Francis and Kannenberg 1978), genotypic/environmental variance (S_2), Wricke's ecovalence W_i (Wricke, 1962), where a low value for that parameters indicates that genotype have high relative stability. This analysis is followed with simultaneous selection for yield and stability based on Kang (1993) method. The AMMI model, which combines standard analysis of variance with PC analysis (Zobel *et al.*, 1988), was used to investigate of $G \times E$ interaction. In AMMI model the contribution of each genotype and each environment to the GEI is assessed by use of the biplot graph display in which yield means are plotted against the scores of the IPCA1 (Zobel *et al.* 1988). The AMMI model is:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \sum_N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij} + \varepsilon_{ijk}$$

where Y_{ijk} is the observed mean yield of genotype i in environment j ; μ is the grand mean; α_i is the genotype main effect; β_j is the environment main effect; λ_n is the eigenvalue of the interaction principal component analysis (IPCA); n , γ_{in} , and δ_{jn} are the genotype and environment scores for the IPCA axis n ; ρ_{ij} is interaction residual; N is the number of IPCA retained in the model; and ε_{ijk} is the random error term.

Results and discussion

Grain Yield

Bartlett's test for homogeneity of residuals variance was used and result show the non significance ($P > 0.01$) of Chi squares statistics was an indication of variances homogeneity and so combined analysis of variance was done. The environmental means for grain yield across six locations are showed in box plot graph (Figure 1). Genotypes contribute to high diversity for grain yield was found at environment 3

(Maros), while narrow diversity at environment 2 (Rangkas). Mean grain yield of the genotypes varied in every environment with ranged from 4.788 ton ha⁻¹ for environment 4 to 6.598 ton ha⁻¹ for environment 6, with a grand mean of 5.640 ton ha⁻¹. Variations of this result might have caused by several factors such as soil fertility, structure, texture and rainfall. Unpredictable environmental factors such as temperature and rainfall even at a single location may contribute to genotype by environmental interaction over year. In the multi-location trials, the environments at which the field experiments were conducted where geographically and temporally different; thus, a large effect due to environment was expected. Therefore testing genotypes over different location differing in unpredictable environmental variation is a suitable approach for selecting stable genotypes (Eberhart and Russel 1966).

The combine analysis of variance revealed highly significant differences for grain yield among environment and genotype \times environment interaction, while among genotype was significant, indicated differential performances of genotypes over environments (Table 1). These results are supported by data mean square of E, G, and GEI were accounted significant for 19.641, 1.640, and 1.688 respectively. The significant and relatively large percentage of the total variation attributable to $G \times E$ interaction suggests that genotypes responded differentially to environment for rice grain yield. Similar reports on rice were earlier made by Blanche *et al.* (2009), Misra *et al.* (2010), Sreedhar *et al.* (2011), Mosavi *et al.* (2013), and Kulsum *et al.* (2013), where in all studies reveal that GEI was significant, indicating differential response of genotypes to changes in environment and some genotypes show stable performance over the range of environment. Furthermore, Blanche *et al.* (2009) stated that generally effects due to G and GEI were greater than for E than has been shown in other studies (Samonte *et al.* 2005, Wade *et al.* 1999). This may be due to the wide range of cultivars included in their present study, which included different levels of homozygosity, grain types, and origins of development.

Table 1. Combine analysis of variance for grain yield at six environments.

Source of Variation	Degree of freedom (df)	Sum Square (SS)	Mean Square (MS)	F-ratio
Environment (E)	5	98.205	19.641	22.20**
Replication (Envir)	12	8.843	0.737	0.83
Genotype (G)	11	18.039	1.640	1.85*
G x E (GEI)	55	92.836	1.688	1.91**
Error	132	116.791	0.885	
CV (%)	16.7			

Note: * = significant at 5% level; ** = significant at 1% level; CV = Coefficient of Variance.

Table 2. Estimates of different stability parameters for 12 genotypes grain yield (t/ha) at six environments.

Genotypes	Mean	Variance (S ₂)	CV (%)	Wi	bi	S ² di
1 IPB 107-F-5-1-1	5.578	1.266	16.216	16.216	1.059	1.581
2 IPB 107-F-65-3-1	5.363	1.413	7.789	1.459	1.528*	1.767
3 IPB 113-F-2-1-1	5.306	0.914	7.256	0.711	1.208	1.143
4 IPB 115-F-3-2-1	5.873	0.782	13.634	2.806	0.703	0.978
5 IPB 116-F-3-1-1	5.871	2.404	11.037	4.127	1.947*	3.005
6 IPB 116-F-44-1-1	5.791	1.164	13.540	2.493	1.110	1.455
7 IPB 116-F-46-1-1	5.418	0.022	3.063	2.771	0.012*	0.028
8 IPB 117-F-1-3-1	5.053	0.423	8.482	0.962	0.712	0.529
9 IPB 117-F-4-1-1	5.647	0.442	7.658	0.944	0.733	0.553
10 IPB 149-F-8-1-1	5.977	1.090	12.590	2.283	1.080	1.362
11 CIHERANG	6.037	1.068	15.954	3.852	0.773	1.335
12 IR64	5.762	1.746	19.822	5.269	1.135	2.183
Average	5.640	1.061	11.42	2.58	1.00	1.33

In the present study the 1000-grain weight, number of filled grains/panicle and number of whole grains/panicle of each genotype is the most important of yield component trait that contributing to yield (Figure 2, 3 and 4). Each trait is positively associated and contributed to grain yield. Regarding this trait, the result indicating that environmental factors were strongly influences that character. In figure 2, each genotype showed different result in each environment, where 1000-grain weight of each genotype in the environment SGN (Sragen) exhibited significantly lower than other environments. In figure 3 and 4, among the genotypes, ten genotypes G1, G2, G3, G4, G5, G6, G7, G8, G9 and G10 exhibited higher result for number of whole and filled grains per panicle in RKS (Rangkasbitung) environment, while the other genotypes G11 and G12 are lower in that environment. The report was made by Sreedhar *et al* (2011), revealed that genotype x environment interactions were significant for yield characters include number of filled grains per panicle and 1000-grain weight implying differential respon of genotypes under three locations for these characters.

In this study, the mean performance coupled with the stability parameters of each rice genotype represented its stability are showed in Table 2. Stability parameters like regression coefficient (*bi*), and deviation from regression (*S²di*) of the genotypes were estimated following simple linear regression method “LR model” (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). Genotypes giving *b*-value close to unity are considered to be adapted to all environments, while those showing *b*-value greater than or less than unity would show specific adaptation to rich or poor environment, respectively, and the genotypes showing low and non-significant *S²di* values are considered to possess stability of performance over the range of environments. Average yield of the 12 genotypes ranged from 5.053 to 6.037 ton ha⁻¹ with a grand mean of 5.64 ton ha⁻¹ (Table 2.). Among the genotypes, IPB 115-F-3-2-1, IPB 116-F-3-1-1, IPB 116-F-44-1-1, IPB 117-F-4-1-1, IPB 149-F-8-1-1, and include Ciherang and IR 64 as two control varieties, gave above average yield. While the other genotypes are IPB 107-F-5-1-1, IPB 107-F-65-3-1, IPB 113-F-2-1-1, IPB 116-F-46-1-1, and IPB 117-F-1-3-1 have yield below a grand mean.

Yield Stability

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Table 3. YS_i for simultaneous selection for yield and stability in rice promising genotypes performance trials

Genotype	Mean Yield	Yield rank (Y')	Adjustment to Y'	Adjusted Y	Stability variance (σ_i^2)	Stability rating (S)	$YS_i = (Y+S)$
G1	5.576667	5	-1	4	2.206770	-4	0
G2	5.363333	3	-1	2	0.876546	0	2
G3	5.303333	2	-1	1	0.341454	0	1
G4	5.875000	10	1	11	1.847250	0	11 +
G5	5.871667	9	1	10	2.795862	-8	2
G6	5.788333	8	1	9	1.624146	0	9 +
G7	5.420000	4	-1	3	1.830102	0	3
G8	5.051667	1	-2	-1	0.526890	0	-1
G9	5.645000	6	1	7	0.511866	0	7 +
G10	5.975000	11	1	12	1.478694	0	12 +
G11	6.036667	12	1	13	2.599710	-4	9 +
G12	5.763333	7	1	8	3.625878	-8	0

Yield Mean: 5.639167
 YS Mean: 4.583333

LSD (0.05): 0.5194412

+ selected genotype on the basis of YS_i .**Table 4.** Mean squares from AMMI ANOVA of rice genotypes for yield.

Source	df	Sum of Squares	Mean of Squares	F-value	Prob > F	% of GxE
Environment (E)	5	98.21	19.64**	26.65	0.000	29.33
Rep (Env)	12	8.84	0.74	0.83	0.617	2.64
Genotype (G)	11	18.04	1.64*	1.85	0.051	5.39
G x E	55	92.84	1.69**	1.91	0.001	27.74
IPCA 1	15	31.92	2.13	2.41	0.004	(34.39)
IPCA 2	13	31.76	2.44	2.76	0.002	(34.21)
IPCA 3	11	19.88	1.81	2.04	0.029	(21.41)
IPCA 4	9	7.14	0.79	0.90	0.531	(7.69)
IPCA 5	7	2.14	0.31	0.35	0.932	(2.30)
IPCA 6	5	0.00	0.00	0.00	1.000	(0.00)
Error	132	116.79	0.88			
Total	215	334.71				100.00

*, **: Significant at 0.05 and 0.01 probability level, respectively.

Regression coefficient (b_i) values of genotypes ranged from 0.01 to 1.95, and only three genotypes namely IPB 107-F-65-3-1, IPB 116-F-3-1-1, and IPB 116-F-46-1-1 were significantly different from one (Table 2.). Two genotypes IPB 107-F-65-3-1, and IPB 116-F-3-1-1 with b_i -values were greater than unity (> 1.2), indicating better adaptability of these genotypes to rich environments and sensitive to environmental changes. The remaining one genotype IPB 116-F-46-1-1 had b_i -values less than unity (< 0.7), indicating specific adaptation to poor environments (Das *et al.*, 2010). Whereas other genotypes had b_i -values close to or equal with unity, indicating genotypes having wide adaptability to the environment. Stable varieties according to Eberhart and Russel (1966) are a

genotype which had high mean yield, regression coefficient (b_i) close to unity and deviation from regression (S^2_{di}) near to zero. A variety with high yield and meet both these criteria will have a good performance in all environments. The deviation from regression (S^2_{di}) among the genotypes ranged from 0.03 to 3.01. Only one genotype had deviation from regression (S^2_{di}) value was equal with zero namely IPB 116-F-46-1-1, indicating stability performance of these genotypes over environments. In general, when the adaptability parameters of mean yield, regression coefficient, and deviation mean square were considered, none of the genotypes exhibited general adaptability. Further, if considering mean and b_i -value of the genotypes jointly, six genotypes having

wide adaptability to the environment because they had a bi-values equal to one and the average score higher than general mean. A non-significant correlation between the deviation from regression (S^2di) and mean performance or regression coefficient (b_i) indicated that these stability parameters might be under the control of different genes located on different chromosomes (Reddy and Chaudhary, 1991; Singh *et al.*, 1995). Earlier, it is also reported by Grafius (1956) and Bradshaw (1965), that plasticity in one or more component characters might allow stability in the final character. It is inferred that alleles that confer broader adaptation might be involved to achieve yield and stability across environments.

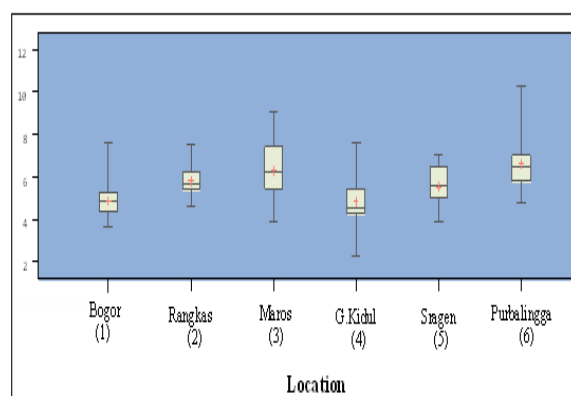


Fig. 1. Mean grain yield from twelve genotypes across at six environments.

Stability of performance of genotypes was also assessed by other stability parameters, i.e., CV, variance, and ecovalence (Wi). The genotypes showing lower values for these parameters are considered to possess stability of performance. The genotypic variance (S^2) and genotypic coefficient of variation (CV) indicated that IPB 116-F-46-1-1 was more stable since it has the least value for these parameters, but with respect to equivalence (Wi), genotype IPB 113-F-2-1-1 that had the least value of 0.711. However, estimating of those parameters would be a useful supplement to assessing stability by linear regression model. The differences in the stability parameters may be reflecting to types of stability through the stability models are broadly classified into three groups (Types I, II, and III) and stability parameter (Wi) which is a Type I stability measure, the regression coefficient (a Type II stability Dewri *et al.*

measure), and the mean square deviation from regression (a Type III measure) of the environmental index has found wide use as a stability measure (Lin *et al.*, 1986).

Further, the simultaneous selection for yield and stability (YS_i) is to selected genotype on basis of YS_i value. In Table 3, the mean YS_i is 4.58 and five genotypes with $YS_i \geq 6$ would be selected. Those genotypes are IPB 115-F-3-2-1 (G4), IPB 116-F-44-1-1 (G6), IPB 117-F-4-1-1 (G9), IPB 149-F-8-1-1 (G10) and CIHERANG (G11), and also recorded those genotypes had average yield higher than general mean.

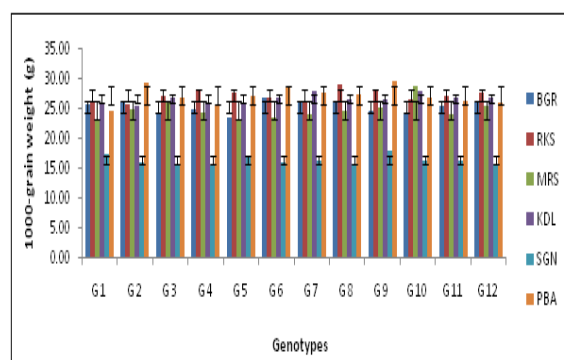


Fig. 2. 1000-grain weight in each genotype in each location.

In linier regression model that proposed by Eberhart and Russel (1966), the genotype showing high positive interaction at certain environments and negative interaction at others is likely to show high S^2di and would be considered unstable. That model does not provide critical analysis of interaction of genotypes in specific environments and does not help in identifying promising genotypes to take advantage of their high positive interaction with specific locations or specific agro-ecological or agro management conditions. Therefore, in AMMI analysis $G \times E$ interaction effect of each genotype is further partitioned into effects due to individual environments. Low $G \times E$ interaction of a genotype indicates stability of the genotype over the range of environments (Misra *et al.*, 2009). Thus, a genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore better suited for that environment. AMMI analysis permits estimation of

interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations (Das *et al.*, 2010).

AMMI analysis of variance of the genotype location data on yield showed that all the three components i.e. genotype (G), environment (E) and G×E interaction, were significant indicating broad range of diversity existed among genotypes (Table 4). Further the mean squares from AMMI analysis indicated variation among E and G×E showed highly significant different at level $P < 0.01$, whereas G showed significant at $P < 0.05$, this result similar with combine analysis of variance. GEI was further partitioned into six interaction principal component analysis axis (IPCA). The IPCA 1, 2 and 3 score are highly significant explaining 34.39%, 34.21 % and 21.41% respectively, from the total G×E interaction sum of squares, indicating the variability relating to GEI. The remaining three IPCA captured insignificant portion of variability which could be regarded as noise.

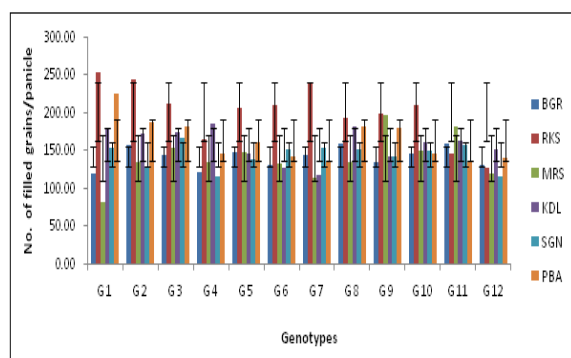


Fig. 3. Number of filled grains/panicle in each genotype in each location.

Figure (5) gives the AMMI II biplot for yield, where the IPCA 1 and IPCA 2 scores of genotype and environments are plotted against each other. This biplot permit easy visualization of differences in interaction effects. Genotypes that are near the line indicating tend to be environment-specific. The IPCA 1 component accounted for 34.39 % of G×L interaction, while IPCA 2 accounted for 34.21 %, and thus the AMMI II biplot gave a model fit of 68.6 %. Genotype is stable if the coordinate axes are close to or are in an ellipse. Distribution of genotype points in the AMMI II biplot revealed that the genotypes IPB 116-F-3-1-1, IPB 116-F-46-1-1, IPB 116-F-44-1-1 and Dewi *et al.*

IPB 149-F-8-1-1 scattered close to the origin or in an ellips, indicating of these genotypes more stable and have minimal interaction with environment. The remaining ten genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Judged by the distance of the environments from origin the interactive forces of environment 2, 3, 4 and 6 respectively were strong, while it was small at environment 5, and least at environment 1. Genotype IPB 117-F-4-1-1 and IPB 107-F-5-1-1 is located close to the line L4, indicating their specific adaptation to that environment (G. kidul). The same thing showed of genotype ciherang and IR64 as control varieties is specific adaptation to Maros environment. Furthermore, genotypes IPB 113-F-2-1-1 and IPB 115-F-3-2-1 showed strong positive interaction at Maros environment, and on the other hand, genotypes IPB 107-F-65-3-1 and IPB 117-F-1-3-1 showed the same indications at Purbalingga environment.

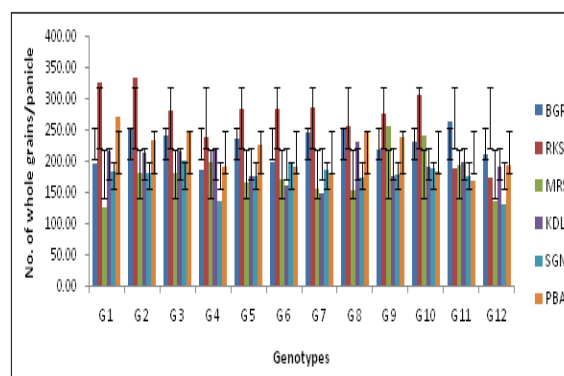


Fig. 4. Number of whole grains/panicle in each genotype in each location.

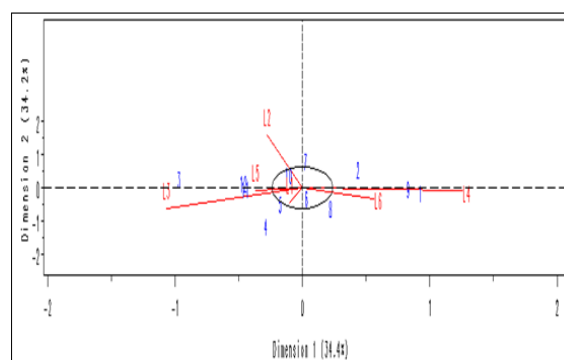


Fig. 5. AMMI II biplot of G×E interaction of 12 rice genotypes in six environments. Genotype; 1, 2, 3,...12; Environment; L1, L2, L3, L4, L5, L6 (Genotype and Environment names in Figure 1 & Table 2).

Generally, effects due to E and GEI were greater than for G, this may be due to the wide range of cultivars included in the present study have almost similar genetic background, which included different levels of homozygosity, grain types, and origins of development. Additionally, a relatively big proportion of variance attributable to E may be explained by the fact that trials were managed to achieve not optimal conditions for factors such as irrigation and fertilization. The specific adaptations of such a wide array of cultivars also contributed significantly to the GEI. Evaluation of genotype \times environment interactions is an important component of the variety development process and ultimately, cultivar selection. Effects due to E, G, and GEI were all significant contributors to grain rice yields. Multiple methods were employed to analyze stability, which, coupled with mean analyses, provided a good understanding of the adaptation level of rice genotypes across a diverse range of environments (Blanche *et al.*, 2009).

Conclusion

From the present investigation it is concluded that multiple methods were employed to analyze stability, which, coupled with mean analyses, provided a good understanding of the adaptation level of rice genotypes across a diverse range of environments. The yield stability across different environment varied among genotypes. Additionally, among rice promising genotypes that identified superior performance genotypes IPB 107-F-5-1-1, IPB 115-F-3-2-1, IPB 116-F-44-1-1, IPB 116-F-46-1-1, IPB 117-F-4-1-1, and IPB 149-F-8-1-1 were stable for two or more stability parameters and combination with high grain yield potential. Based on the simultaneous selection for yield and stability (YS_i) value there were four of above genotypes are selected i.e. IPB 115-F-3-2-1, IPB 116-F-44-1-1, IPB 117-F-4-1-1, and IPB 149-F-8-1-1. On the other hand, based on AMMI biplot analysis, genotypes IPB 116-F-3-1-1, IPB 116-F-46-1-1, IPB 116-F-44-1-1 and IPB 149-F-8-1-1 were more stable and have minimal interaction with environment. Whereas, genotypes IPB 117-F-4-1-1 and IPB 107-F-5-1-1 was give indication to adapt at specific

environmental condition.

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