Analysis of Genotype x Environment Interaction Effect and Yield Stability on Improved Rice Genotypes in Central Java Using Graphical GGE-Biplot Method.

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ABSTRACT

GGE-Biplot method was used to analyze data of grain yield of 10 improved rice genotypes evaluted at eight paddy fields environments during the wet and dry seasons of 2008 – 2009. The objectives of this study was to demonstrate the utility of GGE-biplot model analysis in evaluating the significance and magnitude of the GE effect on grain yield of improved rice genotypes and to determining the yield stability of improved rice genotypes in several paddy field environments in Central Java, Indonesia. Experiments were conducted using a randomized completely block design with three replications at each environment. Results indicated that environment (E), G and GE had significant effect on rice grains yield. Environment explained 42.86% of the total (G + E + GE) variation, whereas G and GE explained 18.63% and 38.51% of the total variation, respectively. The first two principal components (PC1 and PC2) were used to create a two-dimensional GGE-biplot and these principal components explained 50.57% and 24.30% of the GGE sum of squares, respectively. Cimelati genotype has the highest grain yield, but unstable. The Sintanur genotype is the best of genotype, combining high stability with high grain yield, therefore can be recommended for cultivation in any of the environments in Central Java. Gombong environment was the best representative of the overall environments and the most powerful environment to discriminate the genotypes.

Keywords: Rice, yield, genotype × environment interaction, GGE-biplot

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INTRODUCTION

Understanding the genotype × environment interaction (GEI) has long been a key issue for plant breeders and geneticists. Crop performance, the observed phenotype, is a function of genotype (G), environment (E) and genotype × environment interaction (GEI). Understanding the structure of genotype x environment interaction is important in plant breeding programs because a significant GEI can seriously impair efforts in selection of genotypes and cultivars development programs (Yan and Racjan 2002). Information on the structure of GEI is particularly needed to determine if they need to develop cultivars for all environments of interest or if they should develop specific cultivars for specific target environments. GEI is said to occur when different cultivars or genotypes respond differently to diverse environment (Suwarto and Nasrullah, 2011).

Genotype × environment interaction is commonly observed as differential ranking of cultivar performances among locations or years. Researchers have long been aware of the various implications of GEI in breeding program. Genotype x environment interaction is important only when it is significant and cause significant change in genotypes ranks in different environment (Crossa, 1990). Genotype × environment interaction has a negative impact on heritability. Knowing the effect of GEI, as well as the estimate of its magnitude relatives to the magnitude of G and E effects is very important for efficient breeding program. Therefore, understanding the structure and nature of GEI is particularly useful to breeders as it help determine whether to develop cultivars for all environments or to develop specific cultivars for specific target environments (Bridge, 1989).

Biplots are useful for summarizing patterns of response that exist in the original data. Biplots graph scores of environments and genotypes of the first bilinear term against scores of environments and genotypes of the second bilinear term. Genotypes and environments scores are represented as vectors in a two-dimensional space. The genotypes and environments vectors are drawn from the origin (0, 0) to the end points determined by their scores. An angle less than 90^0 or larger than 270^0 between a cultivar vector and a site vector indicates that the genotype had a positive response at that environment. A negative genotype response is indicated if the angle is between 90° and 270°. The cosine of the angle between two environments (or genotypes) approximates the phenotypic correlation of the two environments (or genotypes) with an angle of zero indicating a correlation of +1, an angle of 90° (or -90°) a correlation of 0 and an angle of 180° a correlation of –1.

A standard biplot of the SREG model was reported by Yan et al. (2000). He proposed to connect the scores of the furthest cultivars in the biplot such that they are at the corners of an external polygon and, for each side of the polygon, drawing a line segment perpendicular to that side that passes through the origin. These line segments subdivide the polygon into sectors involving different subsets of sites and cultivars. The genotype that is at the corner of one sector is the best performer in the sites included in that sector. Sites located far away from the origin discriminate the cultivars more than those near the origin.

The GGE-biplot refers to genotype main effect (G) plus genotype by environment interaction (GE) which is the two sources of variation of the SREG model. The biplot from the SREG model shows that ideal genotypes should have large primary effects (high mean yield) and near zero secondary effects (more stable) and the ideal sites should have large primary effects (high power to discriminate cultivars) and small secondary effects. Such properties tend to occur if the primary effects of cultivars are highly correlated with the cultivar means(Yan et al. (2000; Crossa et al., 2002). The objectives of this study was to demonstrate the utility of GGE-biplot model analysis in evaluating the significance and magnitude of the GE effect on grain yield of improved rice genotypes and to determining the yield stability of improved rice genotypes in several paddy field environments in Central Java, Indonesia.

MATERIALS AND METHODS

Data collected in multi-location trials are intrinsically complex, thus they should be analyzed and presented in a form of which it is easy to be understood and interpreted with high accuracy. Many analysis methods have been developed to handle multi-location trials data, such as variant component, regression approach, Additive Main Effect and Multiplicative Interaction (AMMI) and most recently was Genotype and Genotype × Environment (GEI). Zobel et al (1988) compared the traditional statistical analysis, analysis of variance (ANOVA), principle component analysis (PCA) and linear regression, with AMMI analyses and showed that traditional analyses were not always effective in analyzing multiple-environment trial (MET) data structure. ANOVA is an additive model that describes main effects effectively and determines if GE is a significant source of variation, but it does not provide insight into the patterns of genotypes or environments that give rise to the interaction. Principal component analysis is a multiplicative model that contains no sources of variation for additive G or E main effects and does not analyze the interactions effectively. Linear regression method use E means, which are frequently a poor estimate of environments, such that the fitted lines in most cases account for a small fraction of the total GE. Linear-bilinear models are useful tools for analysing MET data and examining and interpreting GEI (Gauch and Zobel, 1997). Useful linear-bilinear models, among others, are the AMMI model and the Sites Regression (SREG) model.

The linear-bilinear AMMI model is represented by

$$\bar{y}_{ij.} = \mu + \tau_i + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij.}$$

and the SREG linear-bilinear model is given by

$$\bar{y}_{ij.} = \mu + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij.}$$

where $\bar{y}_{ij.}$ is the mean of the ith cultivar in the jth environments; μ is the overall mean; τ_i is the genotypic effect; δ_j is the site effect; $\lambda_k (\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_t)$ are scaling constants (singular values) that allow the

imposition of orthonormality constraints on the singular vectors for cultivars, $\alpha_{ik} = (\alpha_{1k},...,\alpha_{gk})$ and sites, $\gamma_{jk} = (\gamma_{1k},...,\gamma_{ek})$, such that $\sum_i \alpha_{ik}^2 = \sum_j \gamma_{jk}^2 = 1$ and $\sum_i \alpha_{ik} \alpha_{ik'} = \sum_j \gamma_{jk} \gamma_{jk'} = 0$ for $k \neq k'$; α_{ik} and γ_{jk} for k=1,2,3,… are called "primary," "secondary," "tertiary,". . . etc. effects of cultivars and sites, respectively; $\overline{\varepsilon}_{ij.}$ is the residual error assumed to be NID (0, σ^2/r) (where σ^2 is the pooled error variance and r is the number of replicates). Least squares estimates of the multiplicative (bilinear) parameters in the kth bilinear term are obtained as the kth component of the deviations from the additive (linear) part of the model. In the SREG model, the main effects of cultivars (G) plus the GEI are absorbed into the bilinear terms. Ten improve rice genotypes were used in this study. They were Bahbutong (G1), Cimelati (G2), Fatmawati (G3), Barumun (G4), Aeksibundong (G5), IR64(G6), Sintanur (G7), Bengawan Solo (G8), Maligaya Special (G9) and Gilirang (G10). Yield potential of these genotypes ranges from high (Fatmawati) to good (other genotypes), milling quality ranges from excellent (Cimelati) to average (IR64) and maturity ranges from very early (Maligaya Special) to mid-season (Barumun). These improve rice genotypes were evaluated at eight environments paddy field in Indonesia, namely; Kaliori (E1), Kutasari (E2), Redisari (E3), Kalikidang (E4), Banyumas (E5), Baturaden (E6), Gombong (E7) and Cilongok (E8) during the wet seasons of 2008 - 2009. At each environment, a randomized complete block design with three replications was used to arrange treatments. Each experimental plot sizes 2 x 10 m^2. Grain yield was obtained from a harvested area of 8.00 m^2 at the center of each plot.

STATISTICAL ANALYSIS

The collected data were analyzed using Proc.Mixed of SAS 9.1 where genotype was the fixed factor and growing seasons and locations were treated as random factors. The effects of G, E and GE were analyzed using Graphical GGE Biplot following Yan et al. (2001). The first two principal components (PC1 and PC2) were used to create a two-dimensional GGE-biplot.

RESULTS AND DISCUSSION

Soil iron content at the experimental environments ranged from high (70.43 g/kg) at Cilongok to low (24.42 g/kg) at Gombong, and soil pH ranged from high (7.88) at Gombong to low (4.02) at Cilongok (Table 1).

Table 1: Mean of Fe, NO$_3$-N, P, K contents in the soil and soil pH at the experimental locations in Central Java, Indonesia.

Factor	Kaliori	Banyumas	Kutasari	Baturaden	Redisari	Gombong	Kalikidang	Cilongok
	(E1)	(E5)	(E2)	(E6)	(E3)	(E7)	(E4)	(E8)
Fe (g/kg)	48.60	50.80	53.50	51.40	25.04	24.42	71.45	70.43
NO$_3$-N(%)	0.16	0.14	0.18	0.15	0.10	0.11	0.02	0.03
P (mg/kg)	535.42	588.43	724.40	799.42	453.43	462.35	268.45	288.32
K (mg/kg)	336.54	332.52	479.32	480.83	330.53	324.68	219.42	221.20
pH	4.50	4.02	6.12	6.02	7.80	7.88	4.10	4.04

Table 2: Rice grains grain yield (g) of 10 evaluated genotypes at eight environments in Central Java, Indonesia.

Genotype	Kaliori	Kutasari	Redisari	Kalikidang	Banyumas	Baturaden	Gombong	Cilongok
	(E1)	(E2)	(E3)	(E4)	(E5)	(E6)	(E7)	(E8)
Bahbutong (G1)	5063	5964	6335	5361	2543	6132	5213	3637
Cimelati (G2)	6304	6131	7401	4994	5202	6279	11811	3838
Fatmawati (G3)	9348	4551	4862	3561	1968	5120	5877	3233
Barumun (G4)	4286	5318	7631	4172	2619	4714	4089	4290
Aeksibundong(G5)	4754	5703	6629	4928	2794	6499	5371	4924
IR 64 (G6)	4943	5236	5710	3932	2561	6061	5362	3547
Sintanur (G7)	6106	5058	6524	5418	4205	6081	6260	4031
Bengawansolo(G8)	5176	4301	5911	4407	3695	6185	4609	3597
Maligaya (G9)	4290	4320	3583	3580	2353	3250	5742	3405
Gilirang (G10)	5767	6030	6371	4417	3959	4910	5084	3457
Average	5603	5261	6095	4477	3189	5523	5941	3795

Rice grain yield of improve rice genotypes was highly varied across environments (Table 2). Table 2 show the generally, the environment E3(Redisari) recorded the highest mean yield per plot (6095 g) relative to other environments. This was followed by mean seed yield in the environment E7 (Gombong) with value of 5941 g. The two environments both at environment E8 (Cilongok) and environment E5 (Banyumas) recorded the least mean grain yields, which were 3795 g and 3189 g respectively. The genotype G3 (Fatmawati) had recorded the highest mean yield per plot (8725 g) at environment E1 (Kaliori), but recorded the least mean grain yields (1968 g) at environment E5 (Banyumas).

Analysis of variance showed that environment, genotype and genotype x environment interaction significantly influenced rice grain yield. Environment explained 42.86% of total (G + E + GE) variation,

whereas G and GE captured 18.63% and 38.51% respectively. Based on two-dimensional GGE-biplot, PC1 and PC2 explained 50.57% and 24.30% of GGE sum of squares. Effects of G, E and their interaction were significant on rice grain yield. The effect of GE was two times of the contribution of G (Table 3). Significance effect of genotype, environment and interaction genotype x environment are also reported in potato plants (Hassanpanah, 2010), hybrid rice cultivar (Sreedhar et al., 2011), aromatic rice mutants (Bughio et al ., 2002), barley (Jalata, 2011), oil palm (Okoye et al., 2011), Red Bean Elite Lines (Asfaw et al., 2008).

Table 3. Analysis of variance of the effects of genotype, environment, genotype×environment (GE) on rice grains grain yield.

Sources of variation	df	SS	MS	F value	P value	Model	SS(%)*
Environment	7	233776423.4	33396631.9	116.99	<.0001	Random	42.86
Replication (Env)	16	16706627.2	1044164.2	3.66	<.0001		
Genotype	9	101612403.1	11290267.0	39.55	<.0001	Fixed	18.63
Genotype x Env	63	210027410.6	3333768.4	11.68	<.0001	Random	38.51
Residual	144	41106267.5	285460.2				
Total	239	603229131.9					

* percentage from total SSG, E dan GE

Table 4. GGE biplot analysis of rice grains yield of 10 evaluated genotypes at eight environments in Central Java, Indonesia.

Principal Component	Eigen Values	Total Eigen Values (%)	Cumulative (%)
PC1	157594775.11	50.56	50.57
PC2	75738552.02	24.30	74.87
PC3	42335064.48	13.58	88.45
Residu	35971419,00	11.54	100,00
Total	311639810.34*		

*) Total eigen values = total SS of Genotype + (Genotype x Environment)

Identification of the best genotype in each environment

The eigenvalues obtained by the GGE biplot method can be observed in Table 4 and Table 5. The first principal component captured 50.57% of the sum of the square of genotype (G) + genotype-by-environment (GE), and the second 24.30%, with an accumulation of 74.87 % in the two principal components. Visualization of the "which-won-where" pattern of MET data is important for studying the possible existence of different environments in a region (Gauch and Zobel, 1997; Yan et al., 2001).

The polygon view of a biplot is the best way to visualize the interaction pattern between genotypes and environments and to effectively interpret a biplot (Yan and Kang, 2003). Based on Table 5, the vertex genotypes in this investigation were Barumun (G4), Cimelati (G2), Fatmawati (G3) and Maligaya (G9), the vertex genotype for each sector is the one that gave the highest rice grain yield for the environments that fall within that sector (Figure 1 and Figure 2). Another important feature of Figure 1 is that it indicates environment grouping, which suggests the possible existence of different environments. Only two sectors of the four sectors contained environments and these were identified as the two groups of environment. The group of environments that share the same best genotype (s) (identified as being located at the corner of the polygon) is termed the mega- environment (Yan et al. (2000; Yan and Hunt, 2002). Hence, Cimelati (G2) had the highest rice grains yield at Gombong environment (E7) and Fatmawati (G3) had the highest rice grains grain yield at Kaliori (E1).

Table 5: Eigenvector 10 evaluated genotypes and the eight environments

Factor	Code	PC1	PC2
Genotype	G1	-6.6949	14.0855
Genotype	G2	75.6592	1.0191
Genotype	G3	-3.0385	-55.8263
Genotype	G4	-22.1983	24.1180
Genotype	G5	-4.2200	22.1122
Genotype	G6	-10.5239	2.3679
Genotype	G7	11.7081	5.8612
Genotype	G8	-13.2716	6.0049
Genotype	G9	-22.6269	-23.4176
Genotype	G10	-4.7934	3.6751
Environment	E1	17.3200	-47.0390
Environment	E2	12.1938	15.8090
Environment	E3	18.1617	36.3758
Environment	E4	10.9110	18.1802
Environment	E5	27.8259	13.6411
Environment	E6	15.8200	18.5939
Environment	E7	72.9678	-12.7241
Environment	E8	1.2050	14.6469

Mean of performances and stability genotypes

Yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2002; Yan 2002). In this method, an average

environment is defined by the average PC1 and PC2 scores of all environments, represented by small circle (Figure 3). Genotypes with above average rice grains yield means were Cimelati (G2), Sintanur (G7) and Aeksibundong (G5). A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of genotype, which means it is more variable and less stable across environments or vice versa. Sintanur (G7) was more stable as well as high yielding and it was the best genotype in terms of better rice grains yield mostly at Gombong environmet (E7).
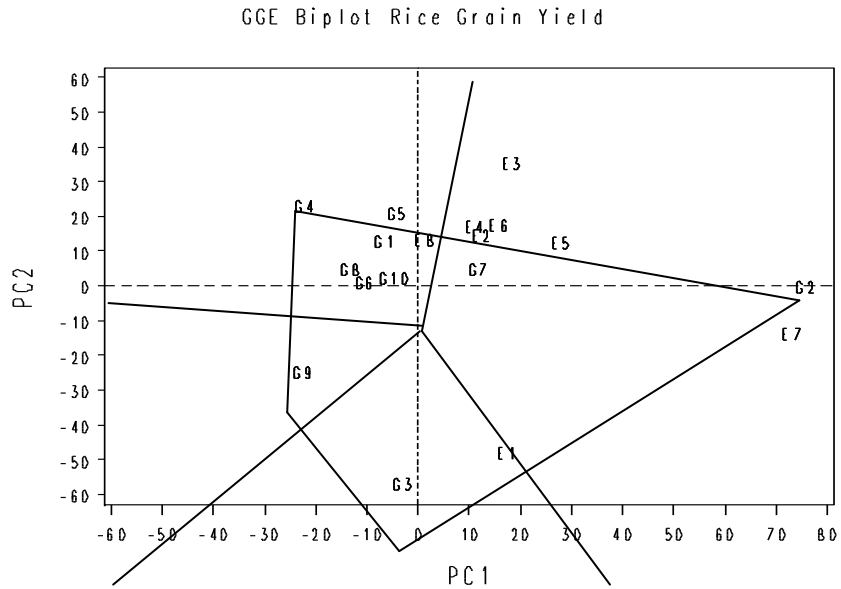
Figure 1: Genotype plus genotype x environment (GGE) biplot of the environment and their winning genotypes.
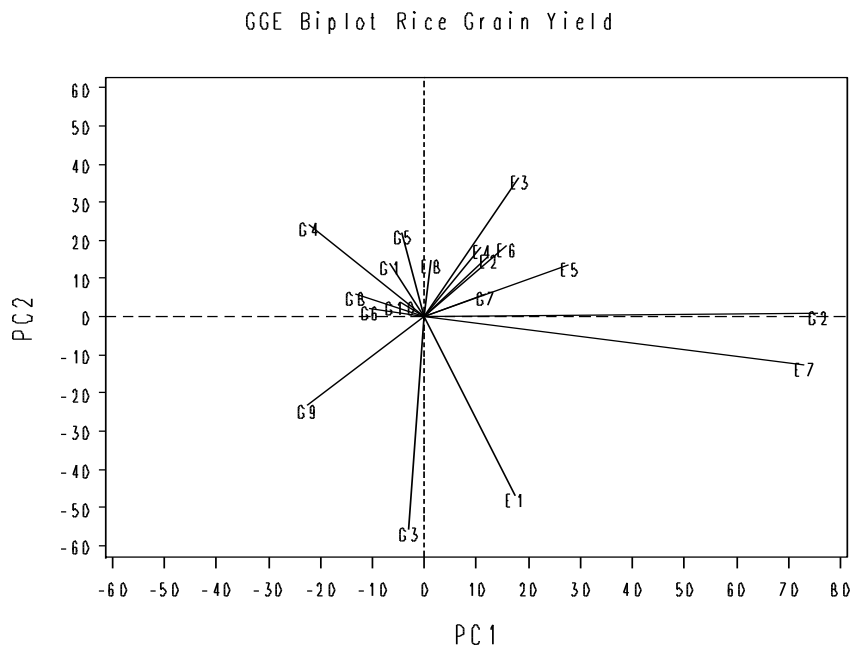

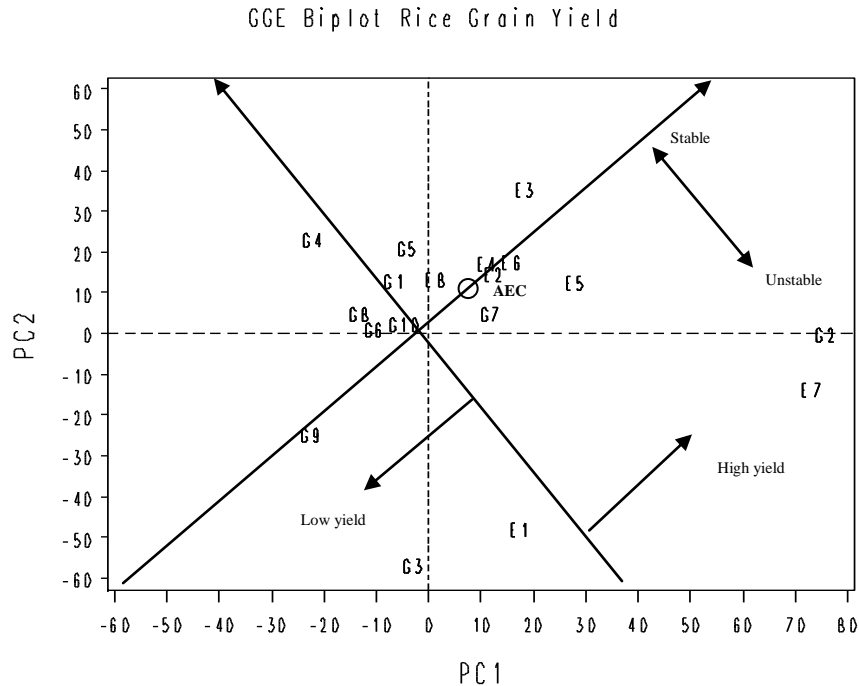**Figure 2: Vector view of an environment x genotype biplot**

GGE Biplot Rice Grain Yield

Figure 3: Average environment coordination (AEC) views of the GGE-biplot for the means performance and stability of genotypes.

CONCLUSIONS

The results indicated a significant effect of genotype by environment interaction on the expression of rice grains grain yield. Genotype, environment and their interaction represented 18.63%, 42.86% and 38.51% of total variance, respectively. Cimelati genotype has the highest grain yield, but unstable. The Sintanur genotype is the best of genotype, combining high stability with high grain yield, therefore can be recommended for cultivation in any of the environments in Central Java. Gombong environment was the best representative of the overall environments and the most powerful environment to discriminate the genotypes. GGE-biplot method analysis is useful to determine the relative performance of a genotype in a specific environment and comparison of performances of genotypes across environments, comparison of two genotypes in different environments and identify high yielding genotypes across environments, the best genotype and the best environment.

ACKNOWLEDGEMENT

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