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Yield Stability of Sixteen Rice Genotypes in White Nile Sate, Sudan

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Abstract: The objective of the present investigation was to analyze the pattern of Genotype x Environment (G x E) interaction for grain yield of sixteen rice genotypes using Additive Main effects And Multiplicative Interaction (AMMI) model. Genotypes were grown at two locations (Ed-duim and Kosti, White Nile State, Sudan) for two years. Main effects due to environment (E), genotypes (G) and GxE interaction (GEI) were significant ($p \leq 0.01$), with highest variation (63.3%) accounted for by environmental effects. The first Interaction Principal Component Axes (IPCA 1) was significant ($p \leq 0.01$) and contributed 72.4% of the total GEI. The biplot was identified genotypes and testing environments that exhibited major sources of GE interaction as well as those that were stable. YUNLU 33 was identified as the best genotype (higher yielding and stable).

Key words: Rice; AMMI model; biplot; yield stability

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important crops. Globally it is grown extensively in tropical and sub-tropical regions of the world. More than half of the people on the globe depend on rice as their basic diet and, generally extensively consumed in the producing countries. Sudan has a total estimated potential rice area for more than 300,000 hectares. If this area is properly utilized it would suffice the local consumption demand to fill the gap for non-course food grain. Rice production in the Sudan has been practiced mainly in the southern states since it was introduced. In the northern states, particularly in the Gezira, the crop was introduced by the technical assistance of China in 1973 through 1980. During that period, 12000 hectares were cultivated under irrigated system and attained 3.5 to 7.6 t/ ha. In the White Nile State the crop had been cultivated under irrigation and is being cultivated as a flooded crop. Low yields of 0.98-1.2 t /ha were obtained using traditional cultivars with low inputs that are not adequate to enhance productivity. Identification of genotypes that show minimum interaction with the environment or possess greater yield stability is an important consideration in areas where environmental fluctuations are considerable. Grain yield in rice is an expression of different yield components under given environmental conditions. Therefore, yield stability is not dependent on the genotype alone, but on the interaction of genotype with the particular environment.

Several statistical methods have been developed for the analysis of genotype by environment interactions (GEI) and phenotypic stability (Crossa 1990; Flores *et al.* 1998). The regression technique has been widely used (Eberhart and Russell 1966; Perkins and Jinks 1968) due to its simplicity and the fact that its information on adaptive response is easily applicable to locations (Annicchiarico1997).

Additive main effects and multiplicative interaction (AMMI) has been proved to be a suitable method for depicting adaptive responses (Gaush and Zobel 1989; Ariyo 1999). AMMI analysis has been reported to have significantly improved the probability of successful selection and has been used to analyze G x E interaction with greater precision in many crops (Bradu 1984). The model combines the conventional analysis of variance for genotype and environment main effects with principal components analysis to decompose the GEI into several Interaction Principal Component Axes (IPCA). With the biplot facility from AMMI analysis, both genotypes and environments are plotted together on the same scatter plot and inferences about their interaction can be made.

The objective of this study was to quantify genotype x environment interaction for grain yield and the stability of 16 rice genotypes in four environments, using the AMMI model.

MATERIALS AND METHODS

Plant materials

Sixteen rice genotypes were used in this study (Table 1). The genotypes were introduced from IRRI (International Rice Research Institute), WARDA (West African Rice Development Association) and China by the National Rice Research Program, Agricultural Research Corporation (ARC), Wad Medani, Sudan.

Field trials

The experiment was carried out during the rainy seasons (June to October) of 2008 and 2009 at two locations [Ed-duim (long. 32°20′E, lat. 13° 39′ N) and Kosti (long 32° 46,′ lat 13° 6′ N)] White Nile State, Sudan. At each location, the genotypes were grown through direct seeding, in a randomized complete block design with three replications. The size of each plot was 6 m^2 made up of 6 rows. The row to row and plant to plant spacing was 25 cm. Triple super phosphate was applied atthe rate of 43kg P_2O_5/ha during land preparation. Urea (46% N) was applied at the rate of 86 kg/ ha in two equal doses, the first at tillering and the second at panicle development (booting) stage. The plots were hand- weeded regularly to minimize weed competition.

Statistical analysis

Analysis of variance was done for the combined analysis of variance across the test environments of location and years. A combined ANOVA and AMMI analysis was processed using the program GENSTAT Discovery Edition 4. The AMMI model is:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \alpha_{in} y_{in} + R_{ij}$$

Where:

Y_{ij} is the grain yield of the i^{th} genotype in the j^{the} environment; μ is the grand mean; g_i is the deviation of the genotype mean from the grand mean; e_i is the deviation of the environment mean from the grand mean; λ_n is the eigenvalue of the n^{th} PCA; α_{in} and y_{in} are the genotype and environmental interaction principal components eigenvectors (PCAg and PCAe, respectively) for axis *n*; N is the number of IPCA retained in the model; and R_{ij} is the residual. The principal advantage of AMMI is that the interaction can be modeled by only one or two PCA-axes.

AMMI uses ordinary ANOVA to analyze the main effects (additive part) and principal component analysis (PCA) to analyze the non-additive residual left over by the ANOVA (Gauch 1993). In the analysis, each combination of single location and year was considered as an environment.

The interaction is the genotype PCA score multiplied by that of the environment. When a genotype and an environment have the same sign on their respective first PCA axis, their interaction is positive; if different, their interaction is negative. An AMMI plot is a graph where aspects of both genotypes and environments are plotted on the same axis so that interrelationship can be visualized. It provides a pictorial view of the transformed GxE interaction (Kempton 1984) for easy interpretation. In a biplot, where PCA 1 score is on the vertical axis and the mean yield on the horizontal, genotypes that appear almost on a perpendicular line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Similarly, environment that occurrs almost on a perpendicular line has similar means and those on horizontal lines have similar interaction patterns. Genotypes or environments with large PCA 1 scores, either positive or negative, have large interactions, whereas genotypes with PCA 1 score of zero or nearly zero have smaller interaction (Crossa *et al.* 1990). The biplot of the first two IPCA axes demonstrates the relative magnitude of the GEI for specific genotypes and environments. The further away from the axes center a genotype or environment is, the larger the GEI.

Table 1. Grain yield (t/ha) of sixteen rice genotypes grown in four environments and the first IPCA scores for the G x E interaction as derived from AMMI analysis

Genotypes	Genotype code	E1	E2	E3	E4	Genotype mean	IPCA 1
NERICA 2	G1	3.1	1.2	2.1	3.5	2.5	-0.329
NERICA 4	G2	3.1	2.3	2.9	6.6	3.7	0.592
NERICA 5	G3	2.8	1.3	2.3	2.1	2.1	-0.904
NERICA 12	G4	2.9	3.0	4.0	2.3	3.1	-1.379
NERICA 14	G5	4.9	2.6	3.5	4.9	4.0	-0.333
NERICA 15	G6	3.8	1.6	2.4	4.9	3.2	0.068
NERICA 17	G7	2.6	1.4	2.2	3.8	2.5	-0.216
YUNLU 22	G8	3.2	1.3	2.0	5.5	3.0	0.417

Table 1. Cont.

Genotypes	Genotype code	E1	E2	E3	E4	Genotype mean	IPCA 1
YUNLU 24	G9	3.0	1.7	2.3	6.1	3.3	0.589
YUNLU 26	G10	2.3	1.7	2.2	6.0	3.1	0.598
YUNLU 30	G11	4.0	1.9	2.8	4.0	3.2	-0.401
YUNLU 33	G12	3.3	2.5	3.2	5.4	3.6	0.035
YUNLU 34	G13	3.6	1.5	2.1	5.9	3.3	0.532
WAB880-1-38-19-8	G14	4.7	1.2	2.0	5.2	3.3	0.229
WAB891SG12	G15	2.9	1.4	2.1	4.8	2.8	0.143
WAB-1-38-19-14-P2-HB	G16	4.0	1.7	2.4	5.7	3.5	0.356
	Environment mean	3.4	1.8	2.6	4.8		
	IPCA 1	-0.294	-0.663	-0.914	1.872		

RESULTS AND DISCUSSION

Analysis of variance

Results of analysis of variance is presented in Table 2. Genotype, location, genotype x location, year, year x location and year x location x genotype were significant for rice grain yield. Such statistical interaction results from changes in the relative ranking of the genotypes or changes in the magnitudes of differences among genotypes from one environment to another. The significant L x G effects demonstrated that genotype responded differently to the variation in environmental conditions of location, and indicated the necessity of testing rice genotypes at multiple locations. This shows the difficulties encountered by breeders in selecting new genotypes for release; these difficulties arise mainly from the masking effects of variable environments (Goncalves *et al*. 2003). Thus, it is important to study adaptation patterns, genotypes response and their stability in multi-location trials.

AMMI analysis

The AMMI analysis of variance of grain yield (t/ha) of 16 rice genotypes tested in four environments showed that 63.3 % of the total variation was attributable to environmental effects; only 10.9 % to genotypic effects and 25.7 % to G x E interaction effects (Table 3). The result showed that the environment main effect (E) was the most important source of variation, due to its large contribution to the treatment sum of squares for yield. The G x E sum of squares was two times larger than that for genotypes, which determined substantial differences in genotypic response across environments.

The presence of GEI was clearly demonstrated by the AMMI model, when the interaction was partitioned between the first two Interaction Principal Component Axes (IPCA). The IPCA1 explained 72.4% of the interaction sum of squares in 37% of the interaction degrees of freedom. Similarly, the second principal component axis (PCA2) explained 19.3% of the GEI sum of squares. They cumulatively captured 91.7% of the total GEI SS, using 32 df. This implied that the interaction of the 16 genotypes of rice with four environments was predicted by the first two principal components of genotypes and environments, which is in agreement with the recommendation of Sivapalan *et al.* (2000). This is also in concordance with the results of Van Oosterom *et al.* (1993), where as much as the first five IPCA were significant. However, this agrees with the findings of Gauch and Zobel (1996) who recommended that the most accurate model for AMMI can be predicted using the first two IPCA. These results indicate that the number of the terms to be included in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment (Kaya *et al*. 2002).

A large variation among the studied genotypes for grain yield and their interaction to the environment was determined. The highest average grain yield was obtained in environment E4 (Kosti 2009) followed by environment E1 (Ed-duim 2008), whereas environment E2 obtained the lowest yield (Table 1). Environment E4 exhibited the largest absolute PCA 1 score (i. e. had the highest variability in interaction), whereas the smallest score was shown by environment E1 (i.e. had the least variability in interaction). This indicated that relative ranking of genotypes was more stable at E1 than at E4, making it difficult to recommended a specific genotype for E4.

Among genotypes, YUNLU 33 revealed the smallest PCA 1 score (0.035) (Table 1), indicating its least variability in interaction, while NERICA 12 showed the largest score (-1.379), pointing to its highest variability in interaction.

The AMMI analysis provides a biplot (Figure 1) of main effects and the first principal component score of interaction (IPCA1) of both genotypes and environments. The differences among genotypes in terms of direction and magnitude along the X- axis (yield) and Y axis (IPCA 1 scores) are important. In the biplot display, genotypes or environments that appear almost on a perpendicular line of the graph had similar mean yields and those that fall almost on a horizontal line had similar interaction. Thus the relative variability due to environments was greater than that due to genotype differences. Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. Consequently, NERICA 4, NERICA 14, YUNLU 33, and WAB-

1-38-19-14-P2-HB were generally high yielding (3.7, 4.0, 3.6 and 3.5 t/ha, respectively) with NERICA 14 being the best with yield of 4.0 t/ha. In contrast, NERICA 2, NERICA 5, NERICA 17 and WAB891SG12 were generally low yielding genotypes.

Genotypes or environments with large negative or positive IPCA scores have high interactions, while those with IPCA scores near zero (close to the horizontal line) have little interaction across environments and vice versa for environments (Egesi and Asiedu 2002) and are considered more stable than those further away from the line. The best genotypes should be high–yielding and stable across environments. The four genotypes stability ranking based on lower PCA1 was YUNLU 33 (0.035), NERICA 15 (0.068), WAB891SG12 (0.143) and WAB880-1-38-19-8 (0.229). Hence, YUNLU 33 was identified as the best genotype (higher yielding and stable).

NERICA 14 and NERICA 4 showed the highest grain yield (4.0 and 3.7 t/ha) respectively, and high IPCA score (-0.33 and 0.59), indicating large interaction exhibited by this two genotypes.

Table 2. Analysis of variance of grain yield for sixteen rice genotypes grown in two locations in 2008-2009

Source	DF	SS	MS
Total	191	525.26	
Replications	2	2.48	1.24^{ns}
Year (Y)	1	56.66	56.66**
Locations (L)	1	4.91	4.91*
Genotypes (G)	15	42.06	2.80**
Y x L	1	180.77	180.77**
Y x G	15	22.27	1.48^{ns}
L x G	15	30.27	2.02*
Y x L x G	15	45.81	3.05**
Error	126	140.03	1.11

*= Significant at P≤0.05 level of significance

**= Significant at P≤0.01 level of significance

Ns= Not significant.

DF= degree of freedom; SS= sum of squares; MS= mean of sum squares.

Table 3. Additive main effect and multiplicative interaction analysis of variance for grain yield (t/ha) of the rice genotypes across environments

Source	DF	SS	MS	Explained%
Total	191	525.3		
Treatments	63	382.8	6.08**	72.9
Genotypes	15	42.1	2.8**	10.9
Environments	3	242.3	80.78**	63.3
Block	8	10.3	1.29^{ns}	1.9
Interactions	45	98.4	2.19**	25.7
IPCA 1	17	71.2	4.19**	72.4
IPCA 2	15	19.3	1.28ns	19.6
Residuals	13	7.9	0.61	2.0
Error	120	132.2	1.1	25.2

*= Significant at P≤0.05 level of significance

**= Significant at P≤0.01 level of significance

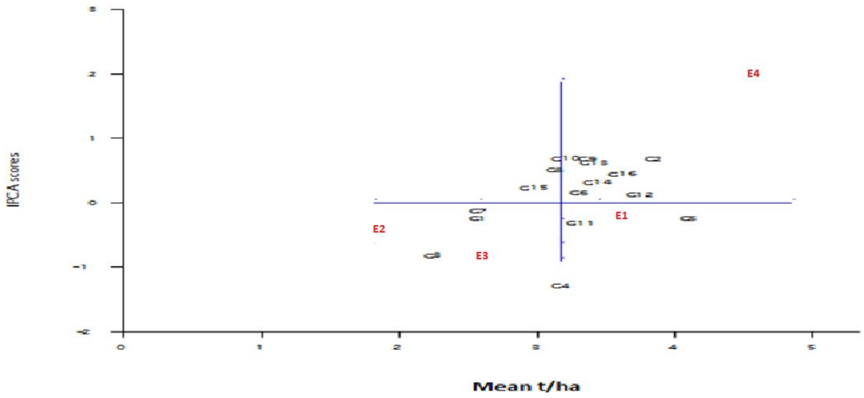

Fig. 1: AMMI -1 biplot for grain yield of rice genotypes in four environments: E1 Ed-duim 2008, E2 Kosti 2008, E3 Ed-duim 2009 and E4 Kosti 2009. Genotypes are indicated by letter codes (G1-G16).

CONCLUSION

The AMMI statistical model was very effective for studying GEI interaction and showed that the largest proportion of the total variation in grain yield was attributed to environments. The biplot identified genotypes and testing environments that exhibited major sources of GE interaction as well as those that were stable. YUNLU 33 was identified as the best genotype (higher yielding and stable).

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تحليل ثبات الإنتاجية فى ستة عشر طراز وراثى للأرز فى النيل الابيض ، السودان

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المستخلص: هدفت الدراسة لتحليل التفاعل بين الطراز الوراثى والبيئة لانتاجية الحبوب فى ستة عشر طرازاً وراثياً للأرز بتحليل AMMI. زرعت الطرز الوراثية لمدة عامين فى موقعين الدويم وكوستى النيل الابيض – السودان . التأثير الرئيسى لكل من البيئة ، الطراز الوراثى والتفاعل بينهما كان معنوياً ($P<0.01$) ، أسهمت البيئة بـ (63.3%) من التباين الكلى . محور المكون الأول (IPCA1) كان معنوياً واسهم بـ 72.4% من مجموع لكلية للتفاعل بين الطراز الوراثى والبيئة . biplot ميز الطرز الوراثية والبيئات المختبرة التى أظهرت تفاعل كبير بين الطراز الوراثى والبيئة من تلك التى أظهرت ثباتاً . حدد YUNLU 33 كأفضل طراز وراثى (أعلى إنتاجية وثباتاً) .