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Stability analysis of grain yield in rice genotypes across environments of Jimma Zone, Western Ethiopia

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Genotype by environment interaction (GEI) is a major complication in plant breeding. An assessment of genotypes across diversified environment and season is important for releasing of varieties. The objective of the study was to evaluate the effects of GEI in fourteen NERICA rice genotype and their adaptation in two years at three locations in the production year 2009 and 2010. The trial was laid out in randomized complete block design with three replications. The combined analysis of variance revealed significant (P<0.01) environments, genotypes and genotype by environment interaction effect and environment captured 91.4% of the total variability. The additive main and multiplicative interaction further explained the genotype by environment interaction by decomposing in to two significant interaction principal components. The fourteen rice genotypes were best explained by the additive main effects and multiplicative interaction (AMMI) 1 that gives model fitness of 98.1%. The polygon view of the Genotype and genotype by environment interaction (GGE) bipolt analysis showed that the environments fall in to two sectors and the genotype NERICA 4 was wining genotypes in all of the environment except E4 (Gomma, 2010). The additive main effect and multiplicative interaction biplot 1 and polygon view of the GGE (Genotype and genotype by environment interaction) biplot showed that the genotype NERICA 4 were consistently higher yielder in all the environments in the study.

Key words: Additive main effects and multiplicative interaction (AMMI), Genotype and genotype by environment interaction (GGE), grain yield, upland rice.

INTRODUCTION

Rice (*Oryza sativa*) belongs to the family *poaceae*. It is the most widely consumed major food crop for a large part of the world's human population next to wheat. It is the grain with the second-highest worldwide production. According to WARDA (2004) rice is grown and consumed in about 39 countries of Africa. Fuelled by population growth and consumer preference, the demand for rice in West and Central Africa (WCA) is growing at the rate of 6% per annum, which is faster than anywhere else in the world, while the production increases at the rate of 4%

per annum. Africa consumes a total of 11.6 million tons of milled rice per year (FAO, 1996), of which 3.3 million tons (33.6%) is imported. Oteng and Sant Anna (1999) reported that among the 39 African countries that produce and consume rice, only ten have attained appreciable levels of rice self-sufficiency (75 to 99.9%), but the remaining 29 are heavy importers with self-sufficiency levels ranging between 0 and 62.8%). Therefore, it is obvious that rice production in Africa including Ethiopia has to increase to meet the high

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Table 1. Agro-ecological description of rice experimental locations.

Parameter	Locations		
	Eladale	Gomma-2	Shebe
Latitude	7°42' N	7°57' N	7°28' N
Longitude	36°48' E	36°38' E	36°25' E
Altitude (m a.s.l)	1813	1497	1370
Annual rainfall (mm)	1616	1470.4	1400
Annual maximum temperature (^{o}C)	28.4	29.5	30
Annual minimum temperature (^{o}C)	12.4	13.5	14
Soil type	clay	clay	clay loam
pH	5.53	6.15	6.37

demand in Africa.

The cultivation of rice in Ethiopia is of a recent history. However, its use as food and cash crop is well recognized. Rice in Ethiopia is one of the food security commodities and its expansion is also linearly increasing in different parts of the country (MoA, 2010). The country is endowed with a range of agro- ecological zones that suit to rice production with an estimated potential of more than 20 million hectares. Volume of rice production in Ethiopia is also increasing (MoA, 2010) with national average yield rise of 1.8 ton per hectare (CSA, 2005) to 2.9 ton per hectare (CSA, 2013). This is less than attainable yield in other African country such as in Kenya which is 2.2 to 4.3 tons per hectare as reported by Atera et al. (2011) and Kega and Maingu (2011). Low rice productivity in Ethiopia is attributed to shortage of high yielding varieties, terminal water deficit, low soil fertility and environmental fluctuations (MoA, 2010).

Ethiopia is a country of great environmental variation (MoA, 2010). When environmental differences are great, it may be expected that genotype by environment interaction will also be high. As a result it is not only average performance that is important in genotype evaluation, but also the magnitude of genotype by environment interactions, that is, one cultivar may have the highest yield in some environments while a second cultivar excel in others (Fehr, 1991; Gauch and Zobel, 1997).

Several methods of estimating phenotypic stability and adaptability across environments by determining genotype by environment interaction effects are often used (Crossa, 1990; Gauch, 1992). The additive main effects and multiplicative interaction (AMMI) model (Gauch et al., 2008) and the genotype main effects plus genotype by environment interaction effects (GGE - Biplot) model (Yan and Hunt, 2002) are the two models increasingly applied for multi-environment trials evaluation. The present study was undertaken to understand the nature and magnitude of GE interaction and to identify high yielding and widely and/or specifically adapted upland rice genotypes in South West Ethiopia.

MATERIALS AND METHODS

The experiments were conducted during the main cropping season of 2009 and 2010 at three locations (Eladale, Gomma-2 and Shebe) of the Jimma University research sites and the description of testing site is given in (Table 1). The trial was laid out in randomized complete block design (RCBD) with three replications with plot size of 6 m^2 (1.2H5 m). Five-rows per plot was used in all trials. Spacing between blocks and plots was 1 m and 0.5 m, respectively. Planting was carried out by hand drilling by using dry and clean seeds at a rate of 60 kg ha^{-1} in rows spaced 25 cm apart. Thinning was also carried out at 3 to 4 leaf stage to maintain single plant per hill at a spacing of 10 cm. The detailed description of the rice genotypes used in the study is given in (Table 2).

Chemical fertilizers were applied at a rate of 64 kg N and 46 kg P$_2$O$_5$ ha^{-1} as Urea and Di-ammonium phosphate (DAP) at each location. Nitrogen was applied in two splits: half at sowing and half at booting stage. Total recommended rate of P$_2$O$_5$ was applied basal at once during planting. Three times manual weeding was carried out at different crop stages (20, 40 and 60 days after sowing). Other management practices were applied as per recommendation for each location.

Statistical analysis

The data collected on grain yield for the 14 genotypes of rice were subjected to AMMI analysis using SAS version 9.2 (SAS Institute, 2008) after testing the ANOVA assumptions. The AMMI model is as follows:

$$Y_{ij} = \mu + G_i + E_j + \left(\sum_1^n k_n U_{ni} S_{ni} \right) + Q_{ij} + e_{ij}$$

Where: (i = 1, 2..........19: j = 1.......6)
Y_{ij} = The mean performance of the ith genotype in the jth environment
μ= The grand mean.
G_i = Additive effect of the ith genotype (genotype mean minus the grand mean)
Kn = eigen value of the PCA axis n,
E_j = Additive effect of the jth environment (environment mean deviation).
Uni and Snj = Scorer of genotype i and environment j for the PCA axis n.

Table 2. List of genotypes tested across locations.

Genotypes	Line Code	Parent age	Year of release in Ethiopia	Remark
NERICA 14	WAB 880-1-32-I-2-PI-HB	WAB 56-50/CG 14	2010	-
NERICA 3	WAB 450-I-B-P-28-HB	WAB 56-104/CG 14	2006	-
NERICA 4	WAB 450-I-B-P-91-HB	WAB 56-104/CG 14	2006	-
NERICA 7	WAB 450-I-B-P-20-HB	WAB 56-104/CG 14	-	-
NERICA 12	WAB 450-I-B-P-20-HB	WAB 56-50/CG 14	-	-
NERICA 13	WAB 880-1-38-20-28-PI-HB	WAB 56-50/CG 14	-	-
NERICA 2	WAB 880-1-38-20-17-PI-HB	WAB 56-104/CG 14	2007	-
NERICA 18	WAB 881-10-37-18-12-P3-HB	WAB 181-18/CG 14	-	-
NERICA 1	WAB 450-I-B-P-38-HB	WAB 56-104/CG 14	2007	-
FOFIFA 3730	CNA4137	Not available	-	-
FOFIFA 3737	CNA4196	Not available	2010	-
FOFIFA 4129	Not available	Not available	-	-
X-JIGNA	Local check	Local check	-	Local check
Gumara	IAC-164	Not available	1999	Standard check

Q_{ij} = Residual for the   after filtering n multiplicative components,

and

e_{ij} = error.

The GGE biplot was computed according to the formula given by Yan et al. (2000).

$$y_{ij} - \mu - \beta_j = \lambda_1 \xi_{1i} \eta_{1j} + \lambda_2 \xi_{2i} \eta_{2j} + \varepsilon_{ij}$$

Where: y^{ij} is the mean for the i-th genotype in the j-th environment, μ is the overall mean, β is the effect for the j-th environment, λ^1 and λ^2 are the singular values of the first and second principal components (PC1 and PC2), ξ^1 and ξ^2 are the eigenvectors of i-th genotype for PC1 and PC2η^1 and η^2 are the eigenvectors of the j-th environment for PC1 and PC2.

RESULTS AND DISCUSSION

Combined analysis for individual environment

The testing environment E1 (Eladale, 2009) and E2 (Eladale, 2010) were lower yielding environments ranging from 5.24 to 10.93 Qt/ha while, the testing environment E3 (Gomma, 2009) and E4 (Gomma, 2010), were moderately yielding environment ranging from 22.13 to 43.02 Qt/ha. The testing environments E5 and E6 were higher yielding ranging from 41.16 to 60.09 Qt/ha (Table 3). The genotype NERICA4 was consistently higher yielder in most of the environments.

Combined analysis of variance

The combined analysis of variance revealed that the genotype, environment and genotype × environment interaction were significant (P ≤ 0.01) (Table 4). The total

sum of square explained by the environment was 91.4% followed by genotype by environment interaction 2.9% while the genotype explained least only, 2.4%. The magnitude of the environment was 37.92 times greater than the genotype, implying that most of the variation in grain yield was due to the environment. This could be attributed to unequal distribution of rainfall during growing season. The significant genotype by environment interaction effects showed that genotypes responded differently to the variation in environmental conditions of location which indicated the need for testing rice varieties at multiple locations. This also exhibited the difficulties encountered by breeders in selecting new varieties.

AMMI analysis of variance

The significant genotype by in environment was further decomposed in to interaction principal component analysis (Table 5). The first interaction principal component (IPCA1) captured 56.07% and the second (IPCA2) further explained 38.16% and the two interaction principal components cumulatively explained 94.23% of the genotype by environment interaction.

Based on Gollob (1968) F-test the two interaction principal components was significant (P<0.01) while the IPCA3 was not significant. Thus, according to this test for the genotype by environment interaction of the 14 upland rice genotypes with six environments was best predicted by the first two interaction principal components axes. The genotype and environment main effect grossly explained 93.76% and the interaction principal component (IPCA1) explained 4.34% of the data in the genotype by environment interaction and the AMMI one gives a best model fitness of 98.10% and the remaining 1.9 might be attributed to noise. The 14 upland rice data were well explained using the AMMI one.

Table 3. Combined analysis of variance for individual environment.

Genotypes	Environments					
	E1	E2	E3	E4	E5	E6
NERICA14	7.38	9.33	26.58	31.73	44.44	43.2
NERICA3	6.67	6.67	37.16	41.16	60.36	56.98
NERICA4	8.09	7.29	43.02	42.22	60.09	60.09
NERICA7	6.84	7.47	29.51	34.49	58.04	57.42
NERICA12	5.24	7.56	28.71	31.91	57.51	54.4
NERICA13	7.29	8	22.13	26.04	53.78	49.33
NERICA2	6.31	4.53	22.58	26.76	51.56	50.49
NERICA18	6.22	8.44	30.31	34.4	44.18	41.16
NERICA1	4.53	4.71	30.93	35.73	52.36	49.51
FOFIFA3730	7.47	9.16	24.36	30.67	54.13	50.31
FOFIFA3737	8.09	10.93	27.29	32.8	57.87	54.22
FOFIFA4129	6.22	7.2	31.47	32.98	56.09	48.44
X-Jigna	8.53	13.07	25.42	32.53	49.6	44.09
Gumara (IAC-164)	6.31	9.6	24.89	28.09	48.8	43.2

Table 4. Combined analysis of variance of grain yield for 14 lowland rice genotypes evaluated at six environments.

Source of variation	df	Ss	MS	% explained
Reps. Within Env.	12	1649029.4	137419.1	0.18
Environment (E)	5	834063799.7	166812759.9**	91.40
Genotype (G)	13	21558325.3	1658332.7**	2.36
Genotype by environment interaction	65	26576002.6	408861.6**	2.91
Residual	156	28698801.560	183966.677	3.14

Table 5. AMMI (Additive main effects and multiplicative interaction) analysis of variance for grain yield.

Source of variation	df	SS	MS	Variation explained (%)
Environment (E)	5	834063799.7	166812759.9**	91.40
Rep (environments)	12	164909029.4	137419.1**	18.07
Genotype (G)	13	21558325.3	1658332.7**	2.36
Genotype by environment interaction	65	26576002.6	408861.6**	2.91
PCA1	17	14900792.7	876517.2**	56.07
PCA2	15	10141075.5	676071.7**	38.16
PCA3	13	831351.5	63950.1[ns]	3.13
PCA4	11	512378.0	46579.8[ns]	1.93
PCA5	9	190404.9	21156.1[ns]	0.72
Residual	156	28698801.560	183966.677	-
Grand mean	3007.926	-	C.V (%) = 14.26	-

AMMI 1 biplot analysis

The interaction principal component 1 (IPCA1) represented in the y- axis where as the genotype and environment mean represented on the x- axis in the so-called AMMI1 biplot (Figure 1). Genotypes or Environments located in the right side of perpendicular line have higher yields than those on the left side.

Accordingly, 3(NERICA 4), 5 (NERICA 12), 11(FOFIFA3737), and 2(NERICA3) were higher yielder genotypes greater than grand mean. The genotypes 7(NERICA 2), 6(NERICA 13), 10(FOFIFA3730), 12(FOFIFA4129) 14(Gumara IAC-164) G9), 13(X-Jigna), 1(NERICA 14) and 8(NERICA 18) was lower yielder less than the grand mean. When we look at the location-year combination, the environment E6 (Shebe, 2010) and E5
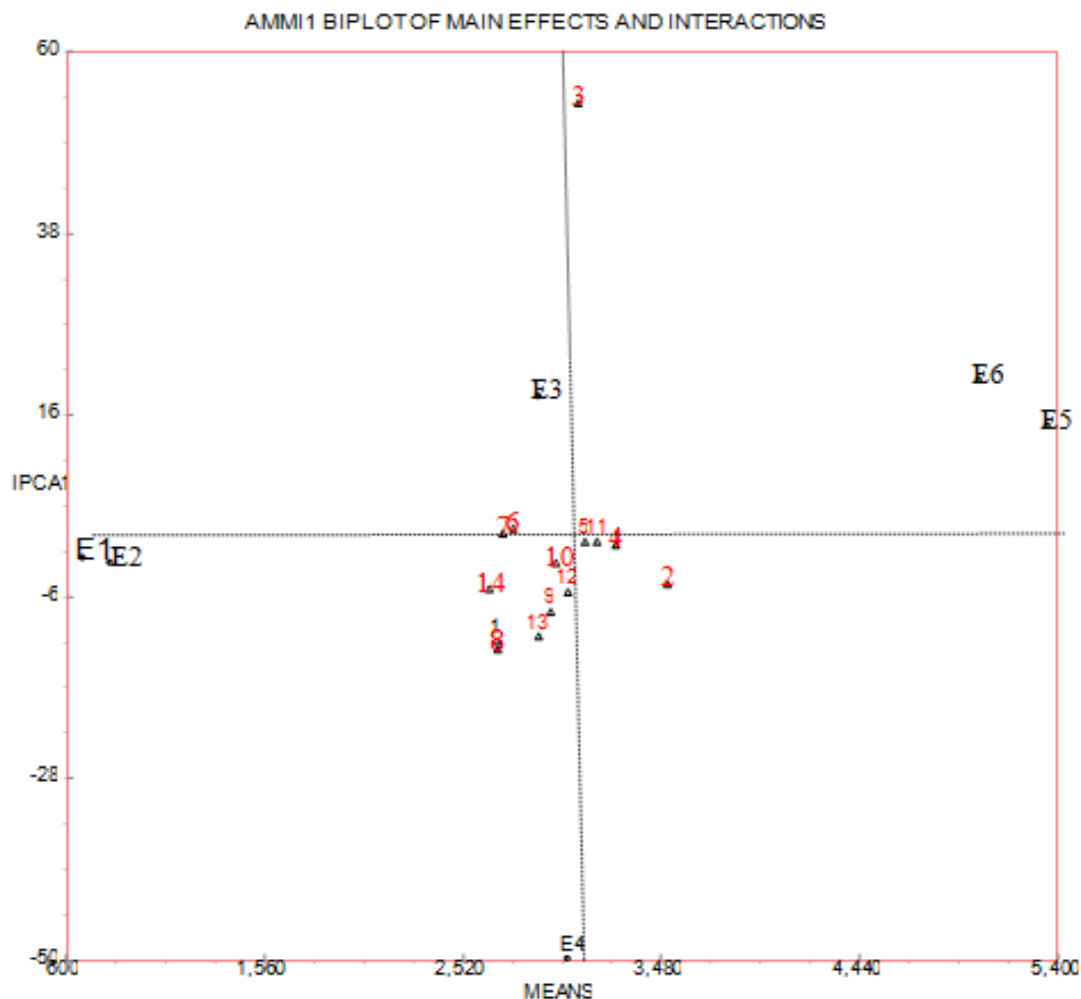
Figure 1. AMMI (Additive main effects and multiplicative interaction) biplot analysis of 14 rise genotypes in six environments. Genotypes plotted as 1, 2, 3 … and environments as E1, E2, and E3... A) Genotypes: 1= (NERICA 14), 2= (NERICA3) 3= (NERICA 4), 4= (NERICA 7), 5= (NERICA 12), 6=(NERICA 13), 7= (NERICA 2), 8=(NERICA 18), 9=(NERICA1), =(FOFIFA3730),11=(FOFIFA3737), 12=(FOFIFA4129) 13=(X-Jigna) and 14=(Gumara IAC-164) B) Environments: E1= (Eladale, 2009), E2 (Eladale, 2010) E3= (Gomma, 2009), E4=(Gomma, 2010), E5 = (Shebe, 2009) and (E6=(Shebe, 2010).

(Shebe, 2009) were favorable located to the right of the perpendicular line whereas; E3, (Gomma, 2009) E1(Eladale, 2009), E2 (Eladale, 2010) and E4 (Gomma, 2009) were unfavorable testing environments (Figure 1).

GGE-biplot analysis

Mega environment classification and winning or stable genotypes for the testing locations

Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments (Yan and Kang, 2003). The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex (Yan et al., 2007). The GGE biplot for the two interaction principal component (IPCA1) and IPCA2 cumulatively captured 85.23% of the genotype and genotype by environment interaction.

The 2 (NERICA3) and 3(NERICA 4) was vertex genotypes and the genotype 3(NERICA 4) was winning genotype for all of the testing locations except E4 (Gomma, 2010) (Figure 2). When we consider mega environment (group of locations that consistently share the same winning varieties) classification the testing locations-year combination fall into two sectors E1 (Eladale, 2009), E2 (Eladale, 2010) E3 (Gomma, 2009 E5 = (Shebe, 2009) and (E6= (Shebe, 2010) incorporated in first sector whereas the testing environment E4 (Gomma, 2010) was in the second sector of the GGE biplot (Figure 2).
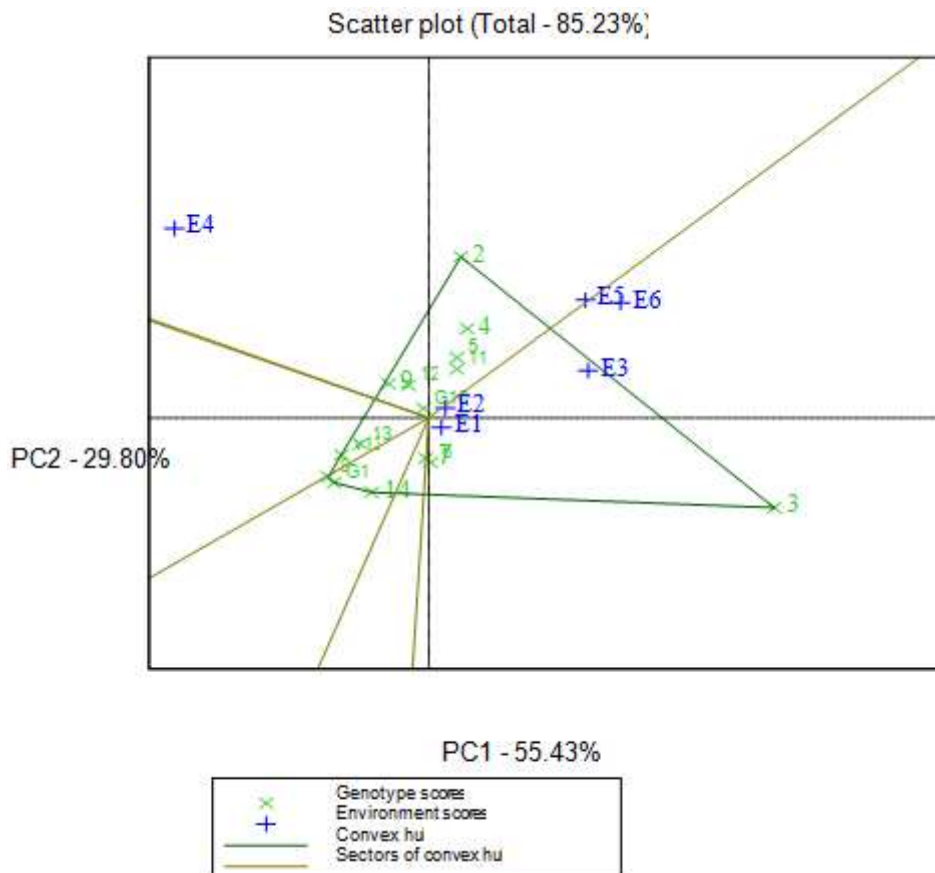
Figure 2. Which genotype wins where of the GGE biplot analysis of 14 rise genotypes in six environments. Genotypes plotted as 1, 2, 3 … and environments as E1, E2, and E3... A) Genotypes: 1= (NERICA 14), 2= (NERICA3) 3= (NERICA 4), 4= (NERICA 7), 5= (NERICA 12),6=(NERICA 13),7= (NERICA 2), 8=(NERICA 18),9=(NERICA1),10=(FOFIFA3730),11=(FOFIFA3737), 12=(FOFIFA4129) 13=(X-Jigna) and 14=(Gumara   IAC-164)   B) Environments: E1= (Eladale, 2009), E2 (Eladale, 2010) E3= (Gomma, 2009), E4=(Gomma,2010), E5 = (Shebe, 2009) and (E6=(Shebe, 2010).

Conclusions

The fourteen rice genotype were evaluated in six growing environments to quantify the magnitude of genotype by environment interaction. The combined analysis of variance revealed significant (P<0.01) environments, genotypes and genotype by environment interaction effect and environment captured 91.4% of the total variability. The additive main and multiplicative interaction further explained the genotype by environment interaction by decomposing in to two significant interaction principal components. The fourteen rice genotypes were best explained by the AMMI 1 that gives model fitness of 98.1%.The polygon view of the GGE bipolt analysis showed that the environments fall in to two sectors and the genotype NERICA 4 was wining genotypes in all of the environment except E4 (Gomma, 2010). The additive main effect and multiplicative interaction biplot 1 and polygon view of the GGE biplot showed that the genotype

NERICA 4 were consistently higher yielder in all the environments in the study. The two model families the additive main effect and multiplicative and polygon view of GGE biplot analysis are equally important in the analysis of genotype by environment interaction study.

Conflict of Interests

The authors have not declared any conflict of interests.

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