

# Agronomic performances and stability analysis of upland rice genotypes in North West Ethiopia

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**Abstract-** A field experiment was conducted at Woreta, Metema and Pawe of North West Ethiopia during the 2008/9 and 2009/10 cropping seasons. Sixteen upland rice genotypes including the standard check were evaluated with the objective of selecting stable and high-yielding, disease-resistant and early maturing varieties. The experiment was laid out in a randomized complete block design of three replications. Combined analysis of variance revealed significant variations in genotypes for most parameters except fertile tillers per plant. Mean squares due to the genotype  $\times$  location  $\times$  year interaction was significant for days to maturity, 1000-seed weight and grain yield ( $P < 0.01$ ). The highest grain yield of  $3.5 \text{ t ha}^{-1}$  was recorded by G15, followed by G7 ( $3.34 \text{ t ha}^{-1}$ ). In AMMI analysis, variations due to environments accounted for 52.48% of the treatment sum of square (SS) while genotypes and genotype  $\times$  environment interaction explained 12.06 % and 35.45% of SS, respectively. In GGE biplot, G15 and G7 respectively were the best genotypes in E1, E2, and E6. The Genotype G15 was relatively stable in grain yield across environments and it also showed relatively better resistance to major rice diseases. Hence, G15 could be recommended for cultivation by the farmers and this variety should be popularized in larger scale to make use of its merits.

**Index Terms-** AMMI, GGE, grain yield, upland rice

## I. INTRODUCTION

Rice (*Oryza sativa* L.) is a major food crop, ranking second to wheat among the most cultivated cereals in the world. It is a staple food for more than half of the world's population (International year of rice, 2004). Rice is also a traditional staple food in parts of West Africa and Madagascar, and it is increasingly becoming an important food in East, Central, and Southern Africa. In recent years, the relative growth in demand for rice is faster in SSA than anywhere else in the world (Balasubramanian *et al.*, 2007).

The cultivation of rice in Ethiopia is of a recent history. Currently, however, its use as food and cash crop is well recognized. Rice in Ethiopia is one of strategic 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 geographic and climatic conditions that suit to rice production with an estimated potential of more than 20 million hectares. Volume of rice production in Ethiopia is also on move (MoA, 2010) with national average productivity rise of

1.8 ton per hectare (CSA, 2005) to 2.9 ton per hectare (CSA, 2013).

Rice is a versatile crop and it offers a variety of uses. It is used in the preparation of local foods such as *injera*, *dabbo*, *genffo*, *kinchie* and *shorba* (Heluf and Mulugeta, 2006). In addition to the rice dish itself and local beverages like tella and katikalla either alone or mixed with other cereal grains, rice is means of employment to the farming community who were not growing rice before. The husk is used for fuel and feed while the bran and the straw are the most important animal feed.

Low productivity, diseases occurrence and environmental fluctuations are rice production constraints in Ethiopia. Low productivity, mainly in the upland rice production system, is attributed to, among other things, lack of high yielding varieties, terminal water deficit and low soil fertility (MoA, 2010). The National Rice Improvement Program has been conducting multi-environment variety trials since two decades ago primarily to identify high yielding varieties of wider adaptation that are early maturing and resistant to major diseases of rice.

Genotypes tested in different locations and over years have significant fluctuations in yield due to the response of genotypes to environmental factors such as soil fertility, unpredicted rainfall and /or the presence of other biotic and abiotic stresses (Kang, 1993). These fluctuations are often referred as genotype  $\times$  environment (GE) interactions. In the presence of GE interaction, the use of genotypic means across environments as criteria for selecting superior genotypes is not dependable (Kang, 1993). The GE interaction and yield stability analysis has, therefore, continued to be important in measuring varietal stability and suitability for cultivation across ecological zones and over seasons.

Several methods of estimating phenotypic stability and adaptability across environments by determining GE interaction effects are often used (Crossa, 1990; Gauch, 1992). However, 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 frequently used models for multi-environment trials evaluation. AMMI model of Gauch and Zobel (1988) considers environment (E), genotype (G), and GE interactions while the GGE Biplot of Yan (2001) considers only G and GE interaction as relevant to genotype evaluation and test environments evaluation.

Currently, upland rice is grown in a wide range of environments in Ethiopia where it is subjected to the influence of G  $\times$  E interactions. Hence, it is very important to study the nature

and magnitude of G x E interaction and stability of upland rice genotypes tested across locations and over seasons. The present study was, therefore, undertaken to understand the nature and magnitude of GE interaction and to identify high yielding, widely and /or specifically adapted and early maturing upland rice genotypes that are resistant to major rice diseases in North West Ethiopia.

## II. MATERIALS AND METHODS

A total of 16 advanced upland rice genotypes were used for this study. The genotypes comprised ‘WAB450-24-2-2-P33-HB (G1), WAB880-SG6 (G2), WAB880-SG14(G3), WAB880-SG37(G4), WAB880-SG38(G5), WAB880-SG39(G6), WAB880-SG02(G7), WAB880-SG47(G8), WAB880-SG35(G9), WAB880-SG70(G10), WAB880-1-32-1-1-P2-HB(G11), WAB880-1-38-13-1-1P1-HB(G12), WAB960-B-11A1-1(G13),

WAB910-B-14AB-1(G14), WAB515-B-16A1-2(G15)’ and ‘AD01 (G16)’ as standard check.

The study was conducted over two seasons (2008 and 2009) at three rice research stations of Woreta, Metema and Pawe in North west Ethiopia (Table 1) under rainfed conditions between June and December. The location-year combinations represent six environments i.e Woreta 2008(E1), Metema 2008 (E2), Pawe 2008(E3), Woreta 2009(E4), Metema 2009 (E5), and Pawe 2009 (E6). At each location, trials were manual-planted in a randomized complete block design of three replications with seeding rate of 60 kg ha<sup>-1</sup>. Plot size was 5 m × 1.2 m with six rows for each entry. The spacing was 1.0 m, 0.30 m and 0.20 m between blocks, plots and rows, respectively. Fertilizer application was 46 kg N ha<sup>-1</sup> and 46 kg P<sub>2</sub>O<sub>5</sub> ha<sup>-1</sup>. The P<sub>2</sub>O<sub>5</sub> was applied all at planting while N was applied in three splits i.e 1/3 at planting, 1/3 at tillering and the remaining 1/3 at panicle initiation. Weeding was done by hand two to three times starting from 25-30 days after sowing depending on infestation level.

**Table 1. Description of the test locations in North West Ethiopia**

Location	Latitude	Longitude	Altitude (m)	Annual rainfall (mm)	Mean temperature (°C)		Soil type
					Min.	Max.	
Woreta	11° 58' N	37° 41' E	1810	1300	11.5	27.9	Vertisol
Metema	12° 54' N	36° 15' E	750	1100	22	29	Vertisol
Pawe	11° 9' N	36°3'E	1050	1457	17.17	32.75	Cambisol

Data on days to 50% heading, days to 85% physiological maturity, panicle length(cm), plant height(cm), fertile tillers per plant, filled grains per panicle, %of filled grains per panicle, grain yield(g/plot) and 1000 seed weight(g) were collected from the middle four rows. Grain yield obtained on plot bases was converted into ton ha<sup>-1</sup> and adjusted at 14% grain moisture content. Disease data were collected based on 0-9 scale following IRRI standard evaluation system (IRRI, 1996); where 0 stands for immune, 1 for highly resistant, 2 for resistant, 3 and 4 for moderately resistant, 5 and 6 for moderately susceptible, 7 for susceptible, and 8 and 9 highly susceptible. The grain yield and other agronomic parameters were subjected to analysis of variance using the SAS 2002 package. The yield data were also subjected to the Additive Main Effect and Multiplicative Interaction (AMMI) analysis using gene stat. The GGE biplot

analysis was also used for detecting the winner genotype at each environment.

## III. RESULTS AND DISCUSSION

### 1.1. Combined analysis of variance

The results of combined analysis of variance for grain yield and other agronomic parameters revealed highly significant (p<0.001) variation in main effects such as genotypes (G), locations (L) and years (Y). Mean squares due to genotype × location interaction was also significant for grain yield and 1000 seed weight (p<0.01) (Table 2).

**Table 2: Mean square of grain yield and other agronomic parameters for 16 upland rice genotypes tested across locations and over years in Ethiopia**

Source	Df	Mean squares				
		days to maturity	fertile tillers per plant	filed grains per panicle	grain yield (kgha <sup>-1</sup> )	1000 seed weight (g)
Replication	2	7.5ns	2.8ns	142.3ns	1416540.1*	0.2ns
Genotype (G)	15	71.5***	3.0ns	691.6**	1596938.4***	17.5***
Location (L)	2	34128.8***	77.0***	7598.7***	34810637.3***	41.6***
Year (Y)	1	975.***	32.3***	3476.4***	12686814.5***	161.0***
G×L	30	9.4ns	2.1ns	319.6ns	1085539.8**	4.6**
G×Y	15	43.5***	1.7ns	390.5ns	962597.7*	5.6**

L×Y	2	319.8***	19.0***	33525.4***	10961325.5***	90.7***
G×L×Y	30	14.4**	1.4ns	411.0ns	780015.1**	5.2**
Error	190	8.3	2.2	302.8	54610.5	2.2

\*, \*\*, \*\*\*= Significant at p<0.05, p<0.01 and p<0.001, respectively ns= non-significant

The genotype × location × year interaction showed significant variation for days to maturity 1000, grain yield and thousand seed weight p<0.01) (Table 2). AMMI analysis of variance for grain yield revealed that effects due to environments, genotypes and their interaction were significant (P<0.001) indicating that environments were diverse and genotypes respond variably (Table 3). Of the treatment sum of square (SS), only 52.48% was explained by the environment while 12.06% and 35.45% was justified by the genotype and GE interactions, respectively (Table 3). A large SS for environments indicated that the environments were so diverse, with large differences among environmental means. Naveed *et al.* (2007) reported that environments accounted for the largest proportion followed by GE interactions and genotypes. In the present study, the magnitude of GE interaction sum of squares was nearly 3 times larger than that of genotypes, indicating substantial differences in genotypic response across test environments (Table 3).

IPCA 3	15	8408183	560546NS	11.94
Residuals	11	1239553	112687NS	1.76
Error	180	67196699	373315	

IPCA= Interaction principal component analysis axes, NS= non-significant

Based on AMMI analysis, IPCA1 and IPCA2 were highly significant (P<0.001), capturing 57.42% and 22.5% of the total interaction SS, respectively. The IPCA3 explained a further 11.94% of interaction SS. Guach and Zobel (1988) reported that AMMI with only the first two interaction principal component axes was the best model for prediction assessment. On the other hand, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four interaction principal component axes. In the present study, however, even IPCA3 was not significant and hence was not relevant for prediction assessment. Therefore, the interaction of the 16 upland rice genotypes with six environments was best predicted by the first two principal components axes of genotypes and environments.

**Table 3. AMMI analysis of variance for grain yield (t ha<sup>-1</sup>) of 16 upland rice genotypes tested at six environments in Ethiopia**

Source	Df	Sum of Squares	Mean squares	Variation Explained (%)
Total	287	305181921	1063352	-
Blocks	12	39395722	3282977***	-
Treatments	95	198589499	2090416***	-
Genotypes (G)	15	23955182	1597012***	12.06
Environments (E)	5	104228646	20845729***	52.48
G × E	75	70405671	938742***	35.45
IPCA 1	19	40426920	2127733***	57.42
IPCA 2	17	15844038	932002***	22.50

**1.2. Agronomic performances and disease reaction**

The agronomic performances and disease reactions of 16 upland rice genotypes is shown on Table 4, 5 and 6. In genotypes, mean grain yield ranged from 2.22 t ha<sup>-1</sup> (G12) to 3.5 t ha<sup>-1</sup> (G15). Only two genotypes; G 7(3.33 tha<sup>-1</sup>) and G15 (3.50 tha<sup>-1</sup>) significantly out yielded the check G16 (2.69 tha<sup>-1</sup>) (Table 6). Compared to the check, G15, G14 and G7 were early maturing genotypes (Table.4). Based on diseases reaction, genotypes exhibited immune to moderately resistant (0.2-3) reactions to major rice disease such as leaf blast, panicle blast, brown spot and bacterial leaf blight (Table.5) which implied these genotypes, especially G15 and G7 with best combined mean yield, could be grown across locations with insignificant yield loss.

**Table 4. Agronomic performance of 16 upland rice genotypes tested at six environments in North West Ethiopia**

Genotypes	Days to maturity	85% Panicle length (cm)	Plant height (cm)	Fertile plant	tillers/	Filled panicle	grains/ 1000 seed wt. (g)
G1	118.8	19.0	94.6	6.55	100.5	27.0	
G2	114.3	18.9	91.2	5.58	101.4	28.6	
G3	114.7	19.8	93.8	6.03	104.8	28.6	
G4	116.1	20.3	96.0	5.83	101.3	27.8	
G5	114.8	20.4	88.8	6.03	111.8	27.1	
G6	113.7	19.6	92.4	5.88	107.9	27.1	
G7	116.2	19.6	87.7	6.34	102.6	28.6	
G8	113.7	19.7	90.9	6.13	103.5	29.1	
G9	115.4	20.5	91.6	6.27	99.9	27.8	

G10	117.7	18.8	90.3	6.10	92.4	26.5
G11	115.4	29.2	92.4	6.55	96.9	27.0
G12	117.9	19.3	92.9	6.98	91.9	27.8
G13	114.3	18.3	92.7	6.04	113.3	29.7
G14	112.2	18.1	78.4	6.01	96.7	26.0
G15	112.7	18.7	79.8	6.03	108.6	27.8
G16(check)	118.4	19.8	100.6	6.93	98.6	27.6
Mean	115.4	20.0	90.9	6.2	102.0	27.8
CV (%)	2.5	30.8	9.42	21.56	17.07	5.3
LSD (0.05)	1.8	NS	5.6	NS	11.4	0.9

NS= not significant

In this study, except G15 which ranked first in three environments (E2, E5 and E6), different genotypes produced the highest grain yield in different environments. Genotypes G14, G2, and G7 for instance, possessed the highest mean yield in environments E1 (Woreta208), E3 (Pawe2008), and E4 (Woreta

2009), respectively (Table 6). On the other hand, most genotypes performed well at E3 and E6 which might be attributed to uniform rain fall distribution and favorable air temperature in the growing seasons.

**Table 5. Average diseases score (0-9) for 16 upland rice genotypes tested at six environments in North West Ethiopia**

Genotypes	Leaf blast	Panicle blast	Brown spot	Bacterial leaf blight
G1	3.0	1.0	2.7	2.0
G2	1.0	1.0	2.3	2.0
G3	1.6	1.0	2.0	1.6
G4	1.6	1.0	3.0	2.0
G5	1.6	1.0	2.7	2.0
G6	1.0	1.0	2.3	2.0
G7	0.4	1.0	2.0	1.3
G8	1.3	0.6	2.3	2.3
G9	3.0	2.3	2.7	2.0
G10	2.3	1.0	3.0	2.0
G11	2.6	2.3	3.0	2.0
G12	2.3	1.6	3.0	2.0
G13	1.0	1.0	2.3	2.0
G14	0.6	1.0	2.3	1.3
G15	0.5	0.2	1.3	1.2
G16(check)	2.3	2.3	3.0	2.0
Mean	1.6	1.2	2.5	1.9

**Table 6. Grain yield (t ha<sup>-1</sup>) performance of 16 upland rice genotypes tested across six environments in North West Ethiopia**

Genotypes	Environments						Mean yield	Rank
	E1	E2	E3	E4	E5	E6		
G1	2.71	2.41	3.34	2.19	2.11	4.20	2.83	10
G2	3.16	2.14	4.46	2.03	1.68	3.96	2.91	7
G3	4.27	2.48	3.95	2.30	2.46	2.81	3.05	3
G4	4.15	2.47	3.24	2.34	2.25	3.08	2.92	6
G5	2.54	1.99	3.52	1.89	1.58	3.78	2.55	14
G6	3.36	2.58	3.64	2.41	2.32	3.94	3.04	4
G7	4.28	2.99	3.34	3.42	2.34	3.64	3.34	2
G8	3.69	2.10	4.04	2.39	1.40	3.25	2.81	12
G9	3.57	2.34	3.63	2.18	2.30	2.94	2.83	10
G10	4.21	2.32	3.34	1.51	2.33	3.67	2.89	9
G11	1.49	2.24	3.78	2.31	2.23	3.52	2.59	13
G12	1.03	2.08	2.49	1.44	2.44	3.81	2.21	15
G13	3.87	2.52	2.99	1.42	2.91	3.70	2.90	8
G14	4.81	2.48	2.76	1.67	2.46	3.46	2.94	5

G15	3.55	<u>3.11</u>	4.09	2.88	<u>3.03</u>	<u>4.33</u>	3.50	1
G16(check)	3.07	2.36	3.13	2.32	2.29	2.96	2.69	13
Mean	3.36	2.42	3.48	2.17	2.26	3.56	2.87	

E1=Woreta2008, E2=Metema2008, E3=Pawe2008, E4=Woreta2009, E5=Metema2009, and E6=Pawe2009

### 1.3. GGE-biplot analysis

GGE biplot best identifies G x E interaction pattern of multi-environment data and clearly shows which variety performs best in which environments. In the present study, the first principal component axis (PC1) explained 33.93 % of total variation while PC2 explained 25.83%. Thus, the two axes together accounted for 59.76 % of the GGE variation for grain yield (Figure 1, 2, 3 and 4). The GGE biplot results are presented in three sections. The first section presents the results of “which won-where” to identify the best genotypes for each environment. And the second section deals with the results of ‘ideal genotype and mean performance and stability’ while the third section presents results of ‘test environments relationship’ (discriminating power and representativeness of the test environments).

#### 1.3.1. Which-won-where pattern analysis

In the which-won-where concept of GGE biplot, genotype markers furthest from the biplot origin are connected with straight lines to form a polygon such that markers of all other

genotypes are contained in the polygon. To each side of the polygon, a perpendicular line, starting from the origin of the biplot is drawn and extended beyond the polygon so that the biplot is divided into several sectors. The markers of test environments are separated into different sectors and the genotype at the vertex for each sector is the winner genotype at environments included in that sector.

According to the biplot in Figure 1, the vertex genotypes were G15, G13, G12 and G8. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang, 2003). In this biplot, environments are also divided into different sectors. The first sector represents E1, E2 and E4; with genotype G15 as the best yielder genotype and the second sector represents E5 and E6; with genotype G13 as the most favorable while the third sector represents E3; with genotype G8 as the winner genotype. The other vertex genotype, G12 which was located far away from all of test environments, implied that it did not yield well at any of the test environments (Figure 1).

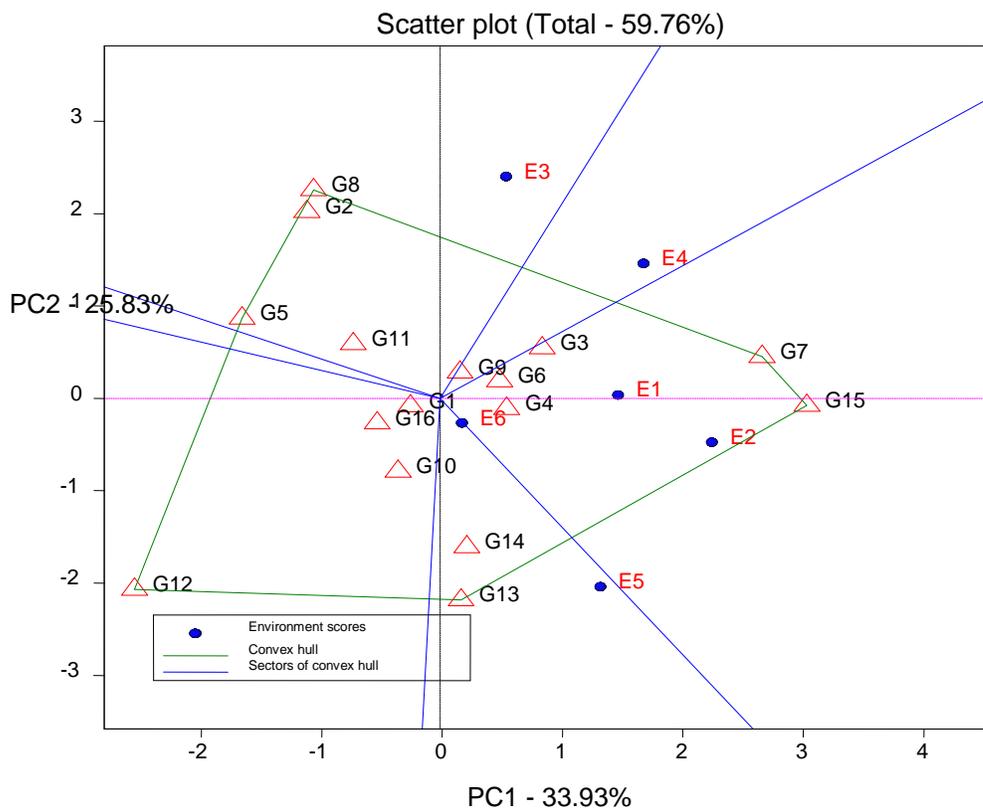


Figure 1. GGE biplot of 16 rice genotypes for grain yield based on which won where pattern

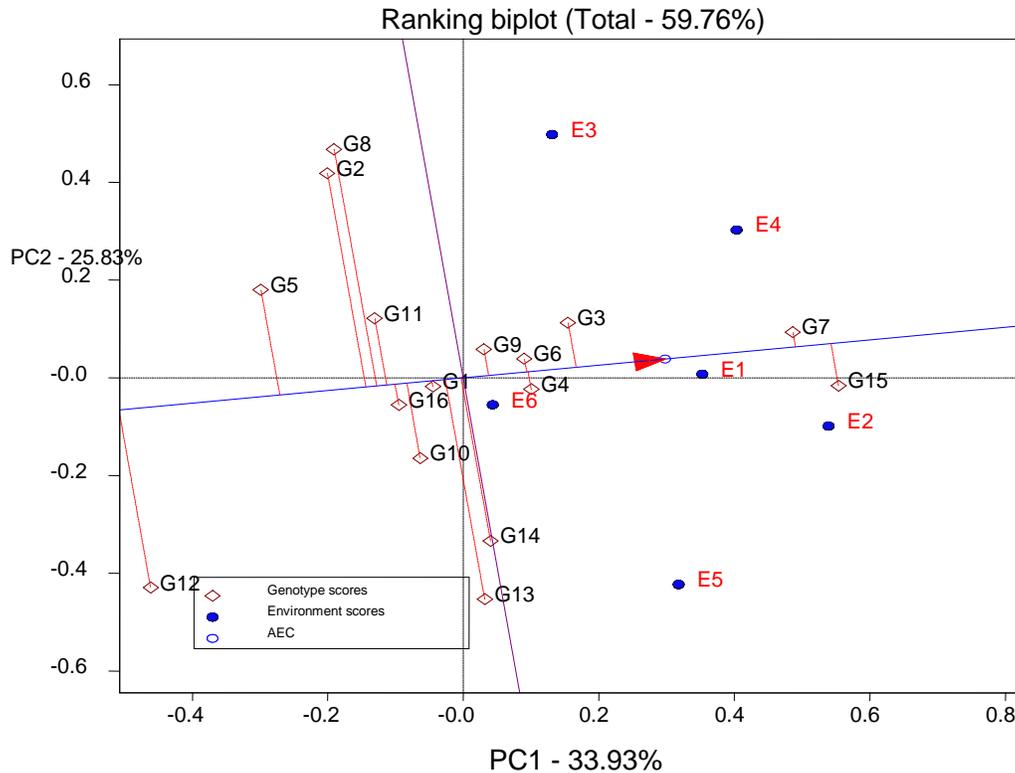
#### 1.3.2. Mean performance and stability analysis

Ranking of sixteen upland rice genotypes based on mean yield performance and stability is presented in Figure 2. The single arrow line passing through the biplot origin and the average environment indicated by the small circle is the average

environments coordinate (AEC) axis, which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang, 2003). This line points towards higher mean yield across environments. Hence, in the present biplot, G15 produced the highest mean yield while genotypes G7, G3, G4, G6 and G9

were the next high yielding genotypes in that order. However, the remaining genotypes had below average mean yield (Figure 2). The line which passes through the biplot origin and perpendicular to the AEC axis shows measure of stability. Either direction away from the biplot origin, on this axis, indicates

greater GE interaction and poor stability or vice versa (Kaya *et al.*, 2006). Thus, the genotypes with the highest yield performance and relatively better stability were G15, G7, G3, G4, G6 and G9. Conversely, genotypes G14, G13, G11, G2, G8 and G5 were not only low yielding but also less stable (Figure 2).

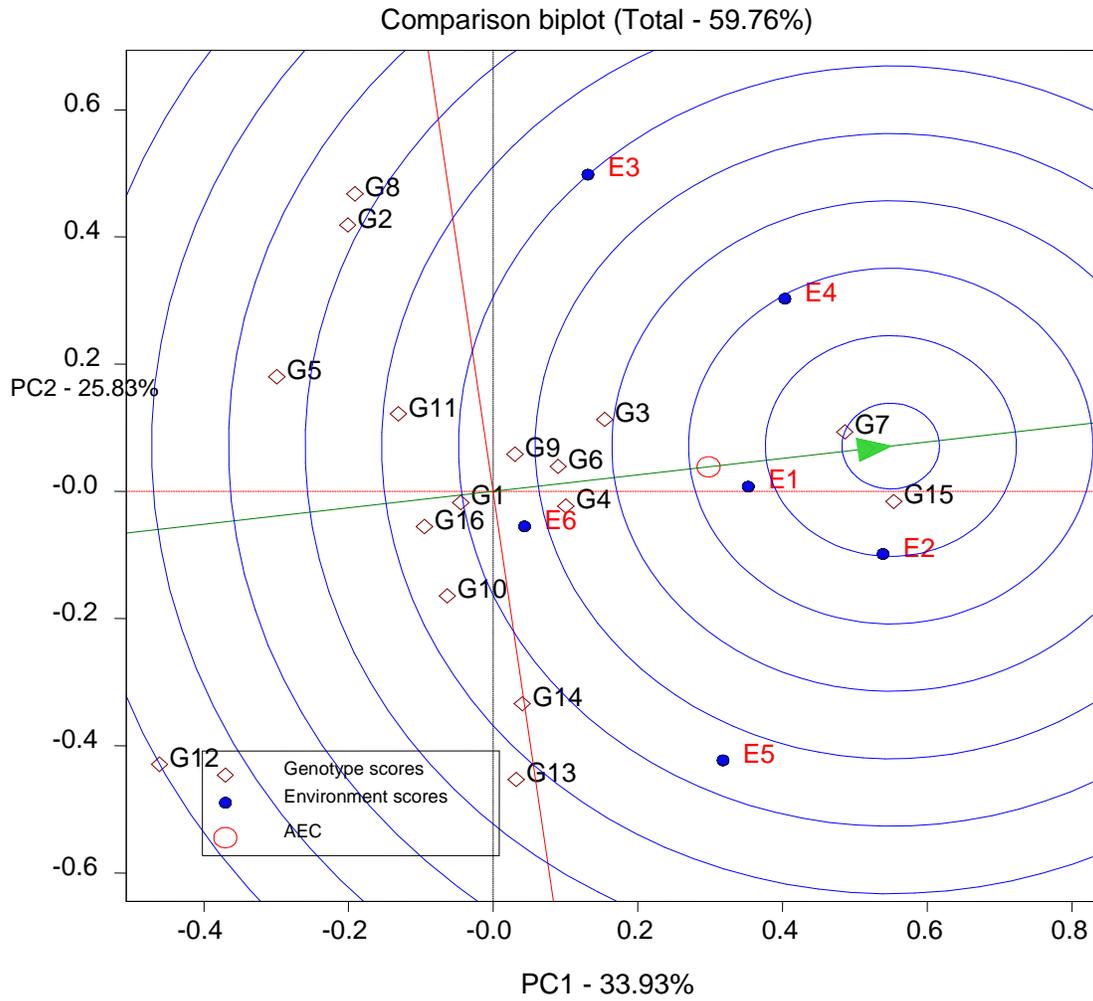


**Figure 2. Average-environment coordination (AEC) view of the GGE biplot for ranking of 16 rice genotypes based mean yield performance and stability**

### 1.3.3. Genotypes relative to ideal genotype and test environments relationship

The ideal genotype and comparison of other genotypes with ideal genotype is presented in Figure 3. An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003). Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero GE interaction, as represented by an arrow pointing to it (Figure 3). A particular genotype is more desirable if it is located closer to the ideal genotype. Accordingly, genotype G7 and G15 are located closer to the ideal genotype and therefore, they are most desirable of all the tested genotypes. Genotypes G3, G4 and G6 are the next desirable genotypes in that order while the rest genotypes are not desirable (Figure 3).

Figure 4 shows summary of the interrelationships among the six test environments. The lines that connect the biplot origin and the markers of the environments are called environment vectors. Favorable test environments should have large PC1 scores (more discriminating of the genotypes) and near-zero PC2 scores (more representative of an average environment) (Yan, 2001). Based on this argument, environment E2 had large PC1 score and relatively smaller PC2 score and hence it best discriminates genotypes and most representative test environment. Environment E1 is most representative as it had near zero PC2 score but less discriminating ability compared to E2. On the other hand, E3 and E5 had good discriminating ability but not representative (Figure



**Figure 3. GGE biplot of ideal genotype and comparison of the genotypes with the ideal genotype**

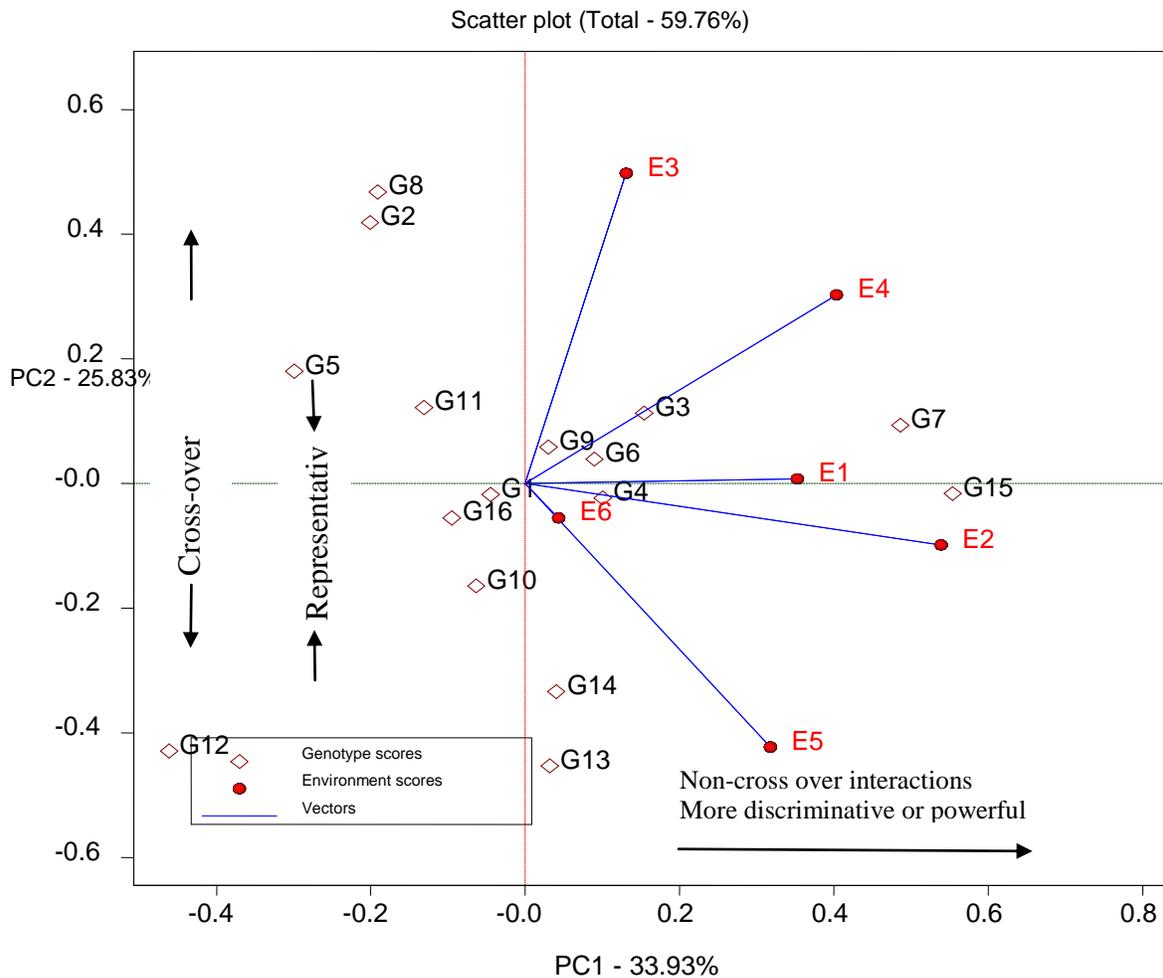


Figure 4. Vector view of GGE biplot for relationships among six test environments

#### IV. CONCLUSION

The combined analysis of variance revealed significant variations in genotypes, locations, years and their interactions. In AMMI analysis of variance, the magnitude of genotype by environment interaction for grain yield of 16 upland rice genotypes tested across six environments was larger than genotype main effect but smaller than that of the environment main effect signifying the deferential response of genotypes to the test environments. Genotypes showed immune to moderate resistance to major rice disease such as blast, brown spot and bacterial leaf blight.

In GGE biplot analysis, winner genotypes at each sector, performance and stability of genotypes were clearly investigated. Relationships among test environments were also observed. Based on the analysis, genotypes G15 and G7 were the first and second high yielding genotypes, respectively in E1, E2 and E4. Genotypes G15, G7, G3, G4, G6 and G9 were the highest yielding and most stable genotypes. The two genotypes, G7 and G15 were the closest to the ideal genotype and may be considered as the best genotypes. Hence, the present result suggested that G15 followed by G7 could be recommended for

production in agro-ecologies it was tested and other areas of similar conditions.

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