Evaluation of Performance and Yield Stability Analysis Based on AMMI and GGE Models in Introduced Upland Rice Genotypes Tested Across Northwest Ethiopia

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Abstract: *Multi-environment rice evaluation trials were conducted in eight environments across Northwest Ethiopia to select promising varieties that can be cultivated by farmers. Sixteen upland rice genotypes were planted in a randomized complete block design of three replications in each location. Data were analyzed using combined analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI) and GGE bi-plot analysis. The MMI analysis of variance for grain yield (kg ha^{-1}) of 16 upland rice genotypes revealed that the main effects of genotypes (G) and environments (E) accounted for 53.8% and 26.8 % of the treatment SS, respectively. The G x E interaction also accounted for 19.4% of the treatment SS. The mean grain yield value of genotypes averaged over environments indicated that WAB450-1-B-P-462-HB (G11) had the highest (4085.8 kgha^{-1}), followed by ARCCU3Fa11-L1P1-B-B-1 (G4) and ARCCU2Fa11-L2P1-B-B-1(G9) with grain yield of 3975.8 and 3853.3 kgha^{-1},respectively. As revealed by AMMI and GGE bi-plots, the genotype G11 was identified as specifically adapted to Fogera (Woreta areas). Following evaluation of candidate genotypes (G11, G4 and G9) and collecting farmers feedback , the National Variety Release Committee also recommended G11 as variety for cultivation in Fogera and other areas of similar cultivation conditions.*

Keywords: *Upland rice, AMMI, GGE bi-plot, G × E interaction.*

INTRODUCTION

Compared to other African countries, rice cultivation in Ethiopia is a recent phenomenon, most probably started in the late 1960s. Currently, the crop showed increasing trends in terms of area, total production and productivity. The country has a highly potential land of 5million ha for rain fed rice cultivation [1]. In Ethiopia, rice is used in the preparation of local foods such as *injera, dabbo, genffo, kinchie* and *shorba* [2]. Moreover, the crop is means of employment and income source to the farming community. Low productivity, diseases occurrence and erratic rain fall pattern 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 moisture stress and low soil fertility [1]. In Ethiopia, multi-environment variety trials have been conducted primarily to identify high yielding varieties of wider adaptation that are early maturing and resistant to major diseases of rice. Multi-environment trials allow breeders to select the best-performing genotype for their target regions by assessing the relative performance of genotypes under a variety of locations and environmental conditions [3].

Genotypes tested in different locations and over years have significant fluctuations in yield due to variations in soil fertility, unpredicted rainfall and presence of other biotic and abiotic stresses [4]. Such differential response of genotypes to different environmental conditions is termed as genotype by environment interaction (GEI). GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values [5]. Hence, GE interaction must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments [6].

Through determining GEI effects, several methods of estimating phenotypic stability and adaptability are often used [7, 8]. However, the additive main effects and multiplicative interaction (AMMI) [9] and the genotype main effects plus genotype by environment interaction effects (GGE-Biplot) [10] are the two most frequently used tools for multi-environment trials data analysis. Hence, the present

experiment was executed to evaluate the performance and stability of introduced upland rice genotypes for wider and /or specific recommendation for cultivation in North-West Ethiopia.

MATERIALS AND METHODS

Planting Materials, Experimental Design and Test Locations

Including one check, a total of 16 introduced (from Africa Rice Centre) upland rice genotypes (Table 2) were evaluated from 2010 to 2012 at four locations consisting of eight environments. The locations where the trials were conducted differ in soil type, altitude, temperature, rainfall received per annum (Table 1). At each location, the trial was laid out in a randomized complete block design (RCBD) of three replications. Each plot had six rows of 5 m long with spacing of 0.2 m between rows. Fertilizer (UREA and DAP) was applied as per the recommendation of each respective location. Total DAP was applied at planting while urea was applied one third at planting, one third at tillering and the remaining one third at panicle initiation. Seed rate of 60 kg ha^{-1} was used and seeds were directly drilled in a row. Plantings were done in the main rainy season following the optimal dates in each respective location.

Table 1. *Description of experimental locations.*

Location	Elevation (m)	Latitude	Longitude	Annual rain fall (mm)	Mean temperature (^{o}C)		Soil type
					Min.	Max.	
Woreta	1810	11^{0}58'N	37 ^{0} 41' E	1300	11.5	27.9	vertisol
Pawe	1050	11^{0}9'N	36 ^{0} 3' E	1457	17.2	32.7	cambisol
Metema	750	12°54'N	36°15'E	1100	22	29	vertisol
Maitsebri	1350	13°05'N	38°08'E	1296	15	36	vertisol

Source: [11] and [12]

Table 2. *Genotypes used in the study.*

No	Genotype	Genotype code	Source
1	ARCCU3Fa9-L6P1-B-B-2	G1	AfricaRice
2	ARCCU12Fa1L4P7-19-1-1-B1	G2	AfricaRice
3	ARCCU12Fa1L6P7-19-1-1-1-B1	G3	AfricaRice
4	ARCCU3Fa11-L1P1-B-B-1	G4	AfricaRice
5	ARCCU3Fa6-L3P9-B-B-3	G5	AfricaRice
6	ARCCU12Fa1L6P7-2-1-1-2-B	G6	AfricaRice
7	ARCCU12Fa1L6P7-24-1-1-2-B	G7	AfricaRice
8	ARCCU12Fa1L6P7-2-1-1-3-B	G8	AfricaRice
9	ARCCU2Fa11-L2P1-B-B-1	G9	AfricaRice
10	WAB880-1-38-20-17-P1-HB	G10	AfricaRice
11	WAB450-1-B-P-462-HB	G11	AfricaRice
12	WAB878-6-37-5-1-P1-HB	G12	AfricaRice
13	WAB878SG41	G13	AfricaRice
14	WAB880-1-32-1-2-P1-HB	G14	AfricaRice
15	IRAT112	G15	AfricaRice
16	AD048 (**check**)	G16	Adet research centre

Data Collection and Statistical Analysis

Data were collected for days to heading, days to maturity, panicle length, plant height, filled grains/panicle, fertile tillers/plant, grain yield, and 1000 seed weight. Grain yield (t ha^{-1}) was estimated based on adjustment at 14% moisture level on the basis of four central harvestable rows. The grain yield and other agronomic parameters were subjected to analysis of variance using the SAS version 8.1software. The grain yield data were also subjected to the Additive Main Effect and Multiplicative Interaction (AMMI) analysis. The GGE-biplot analysis was also used for ranking genotypes based on grain yield performance and stability and also for detecting wider and /or specifically adapted genotype(s).

RESULTS AND DISCUSSION

Analysis of Variance and Agronomic Performance

The combined analysis of variance for grain yield and other agronomic characters showed significant differences (P≤ 0.01) due to main effects such as genotypes and test locations. The analysis for year

effect also revealed significant variation (P≤ 0.01) among genotype in terms of all characters except in grain yield (Table 3). The genotype x location interaction effect was significant (P ≤ 0.01) for days to heading, days to maturity, panicle length, plant height and grain yield whereas genotype x year interaction found to be significant only for days to heading, days to maturity and plant height. On the other hand the location x year interaction showed significant variation (P ≤ 0.01) for all characters considered. Significant effect of location x year interaction emphasizes that influence of locations on grain yield of rice genotypes during years are obviously different.

The three way interaction of genotype x location x year revealed significant variation ((P ≤ 0.01) only in days to heading, panicle length, filled grains per panicle and grain yield (Table 3). The significant genotype x location x year interaction effects for grain yield demonstrated that genotypes responded differently to the variation in locations and years indicating the necessity of testing rice genotypes at multiple locations and over yeas

Table 3. *Combined mean grain yield and yield related parameters of 16 upland elite rice genotypes evaluated at four locations from 2010 to 2012 cropping seasons in North west Ethiopia*

No	Genotype	Code	DTH	DTM	PL(cm)	PH(cm)	FGP	FTP	GY (kg/ha)	TSW(g)
1	ARCCU3Fa9-L6P1-B-B-2	G1	79.0cd	115.0bcd	27.5ab	78.4b	96.4de	4.7f	3035.b	28.3bcd
2	ARCCU12Fa1L4P7-19-1-1-B1	G2	74.0h	114.5bcd	23.2ef	66.3gh	87.4e	5.7bc	2099.5de	24.6ij
3	ARCCU12Fa1L6P7-19-1-1-1-B1	G3	74.8gh	115.3bc	23.3ef	68.5fg	93.7de	5.1cdef	1929.5e	25.0hi
4	ARCCU3Fa11-L1P1-B-B-1	G4	79.2	114.8bcd	24.8cde	70.6ef	109.5ab	6.1b	3975.8a	29.2ab
5	ARCCU3Fa6-L3P9-B-B-3	G5	79.9c	115.1bc	24.7de	74.6cd	95.6de	4.8ef	2288.6cd	26.4fg
6	ARCCU12Fa1L6P7-2-1-1-2-B	G6	78.5cde	114.3bcd	25.7bcd	77.4bc	99.7cd	4.7f	2264.5cd	26.0fgh
7	ARCCU12Fa1L6P7-24-1-1-2-B	G7	79.3	113.5bcd	26.0abcd	68.7fg	99.9cd	5.5bcde	2365.7cd	24.0j
8	ARCCU12Fa1L6P7-2-1-1-3-B	G8	78.0de	114.3bcd	27.0ab	77.2bc	102.1bcd	4.7f	2225.8cde	26.0gh
9	ARCCU2Fa11-L2P1-B-B-1	G9	84.0b	123.8a	27.8a	83.4a	116.3a	7.3a	3853.3a	29.2ab
10	WAB880-1-38-20-17-P1-HB	10	79.5cd	115.4b	24.5de	72.3de	94.7de	5.0def	3057.5b	30.0a
11	WAB450-1-B-P-462-HB	G11	79.5cd	112.8d	24.5de	71.4ef	105.8bc	6.1b	4085.8a	28.0cde
12	WAB878-6-37-5-1-P1-HB	G12	76.3fg	114.4bcd	22.5f	61.0i	95.2de	5.6bcd	2484.6c	25.6ghi
13	WAB878SG41	G13	77.0ef	113.1cd	22.0f	63.1hi	95.1de	5.1cdef	2420.3c	25.0hi
14	WAB880-1-32-1-2-P1-HB	G14	78.7cd	114.5bcd	23.6ef	67.2g	94.0de	5.6bcd	3169.0b	27.1ef
15	IRAT112	G15	80.0c	114.3bcd	22.4f	66.5g	89.7e	5.6bcd	2482.4c	29.0abc
16	AD048 (check)	G16	91.6a	124.4a	26.7abc	82.7a	87.8e	5.8b	3327.4b	27.2def
	Mean		79.3	115.6	24.8	71.8	97.7	5.5	2816.5	26.8
	CV (%)		3.67	3.29	13.24	7.86	16.52	22.44	19.62	7.58
	Genotype (G)		***	***	***	***	***	***	***	***
	Location (L)		***	***	***	***	***	***	***	***
	Year (Y)		***	***	***	***	***	***	NS	***
	G x L		***	***	***	***	NS	NS	***	NS
	G x Y		***	***	***	***	*	NS	NS	NS
	L x Y		***	**	***	***	***	***	***	**
	G x L x Y		***	NS	***	NS	***	NS	***	NS

Note: *,**, *** significant at 5%, 1% and 0.1% respectively, NS= not significant, DTH=days to heading, DTM= days to maturity, PL= panicle length, PH= plant height, FGP= field grains per panicle, FTP=fertile tillers/plant, GY= grain yield (kg/ha), TSW= 1000 seed weight (g).

Significant interaction differences of genotypes × year × location implied that application of stability analysis for identifying widely and/or specifically adapted rice genotype is essential. These results are in agreement with those of [13] and [14]**.**

In the current study, as depicted by (Table 3), the overall agronomic performance of 16 genotypes seems good in terms of characters considered. The mean grain yield of 16 genotypes ranged from 1929.5 (G3) to 4085.8kgha[-1](G11). The Genotypes G11, G4 and G9 with grain yield of 4085.8, 3975.8 and 3853.3 kg ha^{-1}, respectively were the three high yielding genotypes. Compared to the standard check (G16), the top high yielding three genotypes (G11, G4 and G9) gave grain yield advantage of 22.8%, 19.5% and 15.8%, respectively. Of tested 16 genotypes, only these three genotypes performed significantly above the standard check. The three genotypes also performed better in terms of 1000 seed weight and in filed grains per panicle (Table 3).

AMMI Analysis of Variance for G X E Interaction

The AMMI analysis is indicated in Table 4. The MMI analysis of variance for grain yield (kg ha^{-1}) of 16 upland rice genotypes evaluated across eight environments revealed that the main effects of genotypes (G) and environments (E) accounted for 53.8% and 26.8 % of the treatment sum of squares, respectively. The G x E interaction also accounted for 19.4% of the treatment SS. The analysis showed that variations due to G, E and G x E were significant ((P $\leq$ 0.001).

Table 4. *AMMI analysis of variance for grain yield of 16 upland rice genotypes.*

Source	D.f	SS	MS	% explained SS
Total	383	404064795	1054999	
Block	16	9391336	586958*	
Treatments	127	325163496	2560342***	
Genotypes (G)	15	175089532	11672635***	53.8
Environments(E)	7	87116278	12445183***	26.8
G x E	105	62957685	599597***	19.4
IPCA 1	21	22441471	1068641***	35.6
IPCA 2	19	17061325	897964**	27.1
IPCA 3	17	11184475	657910**	18.8
IPCA 4	15	4911284	327419NS	
Residuals	33	7359130	223004NS	
Error	240	69509964	289625	

The large sum of squares for genotypes indicated that the genotypes were diverse, with large differences among genotypic means causing most of the variation in grain yield, which is in contrary with the findings of [15,16,1], in which the environments exhibited larger sum of squares than that of the genotypes. The presence of G x E interaction (GEI) was clearly demonstrated by the AMMI model, when the interaction was partitioned among the first three interaction principal component axis (IPCA) as they were significant in predictive assessment (Table 4). The first and the second interaction PCA were highly significant (P $\leq$ 0.001), capturing 35.6% and 27.1% of the total variation in the GxE interaction SS, respectively. The third interaction PCA was also significant (P $\leq$ 0.01), capturing 18.8% of GE interaction SS while the forth interaction PCA was not significant. The first three interaction PCA axes jointly accounted for 81.5% of the GxE interaction SS (Table 4).

AMMI Stability Analysis and Grain Yield Performance

In the current study, inconsistency in grain yield ranking was observed from environment to environment (Table5) which indicated the presence of possible crossover G x E interaction as described by Yan and hunt (2001). It is commonly reported that multi-environment data may constitute a mixture of crossover and non-crossover types of G x E interaction in which the former indicated the change in yield ranking of genotypes across environments and the later shows constant yield rankings of genotypes across environments [17, 18]**.** The environments mean grain yield ranged from 2131.1 for E7 to 3494.3 kaha^{-1} for E2 (Table 5).

In AMMI-I biplot (Figure1), If a genotype or an environment has a IPCA1 score of nearly zero, it has small interaction effects and considered as stable. When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative [19]**.** Genotypes and environments on the same parallel lines have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yields than those of left hand side. Accordingly, among the upland rice genotypes, G11, G1, G4, and G10 generally exhibited high yield of positive IPCA1 score, out of which G11 and G1 had high IPCA1 scores in which G11 being the overall best genotype. Hence, the G11 was identified as specially adapted and the highest yielding genotype to the corresponding environments (Figure 1). On the other hand G9, G16 and G14 were high yielding genotypes with negative IPCA1 scores. Of 16 genotypes, G9, G10, G8, G15, G2, G6 and G13 were with near zero IPCA scores and hence have less interaction with the environments out of which only G9 and G10 had above average yield performance. Among environments, E6, E3, E4, and E8 exhibited near zero IPCA1 score and hence had small interaction effects indicating that all the genotypes performed well in these locations. Of the environments, however, E6 and E3 were most favorable environments for most genotypes while E2, E7 and E1 were good for only few genotypes[20] and [21] reported similar pattern of interactions

Table 5. *Predicted mean yield estimates of 16 upland rice genotypes across eight environments and stability indicators of AMMI analysis*

No	Genotype	Code	E1	E2	E3	E4	E5	E6	E7	E8	Mean	IPCA1	IPCA2
1	ARCCU3Fa9-L6P1-B-B-2	G1	2910	2985	3002	**3117**	3320	3297	2644	3005	**3035.0**	17.945	-10.915
2	ARCCU12Fa1L4P7-19-1-1-B1	G2	1425	3135	3531	1632	2263	2232	1732	2303	**2281.6**	-2.906	-18.299
3	ARCCU12Fa1L6P7-19-1-1-1-B1	G3	1299	2286	**4464**	1610	1952	2355	2018	1836	**2227.5**	10.349	-10.658
4	ARCCU3Fa11-L1P1-B-B-1	G4	**4290**	3930	2328	**3823**	**4281**	**5099**	**2949**	**3242**	**3742.8**	15.178	11.896
5	ARCCU3Fa6-L3P9-B-B-3	G5	1698	2819	2594	1695	2605	3204	1689	2467	**2346.4**	5.450	-6.968
6	ARCCU12Fa1L6P7-2-1-1-2-B	G6	1624	2665	3925	2307	1789	3062	1691	2298	**2420.1**	2.819	2.757
7	ARCCU12Fa1L6P7-24-1-1-2-B	G7	1960	3666	3331	2189	2245	2524	1328	2400	**2455.4**	-12.164	-8.634
8	ARCCU12Fa1L6P7-2-1-1-3-B	G8	1337	2739	3927	2102	1888	3458	1781	1881	**2389.1**	0.775	6.486
9	ARCCU2Fa11-L2P1-B-B-1	G9	**3948**	**4943**	2075	2993	**3948**	**4424**	**3111**	**3160**	**3575.3**	-4.034	3.536
10	WAB880-1-38-20-17-P1-HB	G10	2775	3369	2079	3043	2681	4152	2107	2802	**2876.0**	3.798	12.126
11	WAB450-1-B-P-462-HB	G11	**4408**	3811	**4192**	**3652**	**3952**	**4614**	**3713**	**4071**	**4051.6**	21.996	4.239
12	WAB878-6-37-5-1-P1-HB	G12	1151	3919	2132	2859	2667	2878	1639	2437	**2460.3**	-16.394	-19.786
13	WAB878SG41	G13	1819	3080	2680	2595	2547	2806	2094	2056	**2459.6**	2.689	-10.458
14	WAB880-1-32-1-2-P1-HB	G14	2322	**4819**	2614	2813	2407	3944	2194	2700	**2976.6**	-23.873	8.047
15	IRAT112	G15	1825	2777	2620	2119	1496	4170	1822	2320	**2393.6**	1.156	24.980
16	AD048 (**check**)	G16	3198	**4964**	**4300**	2972	2982	4128	1586	2863	**3374.1**	-22.784	11.651
	Mean		**2374.3**	**3494.2**	**3112.1**	**2595.1**	**2688.9**	**3521.7**	**2131.1**	**2615.1**			
	IPCA1		16.353	-44.026	-6.661	-0.081	10.193	1.669	19.150	3.403			
	IPCA2		12.991	-9.148	20.731	-6.546	-21.539	29.332	-13.919	-11.902			

E1= Woreta2010, E2= Pawe2010, E3= Woreta=2011, E4= Metema2011, E5= Pawe2011, E6= Woreta2012, E7= Pawe2012, E8= Maitsebri2012
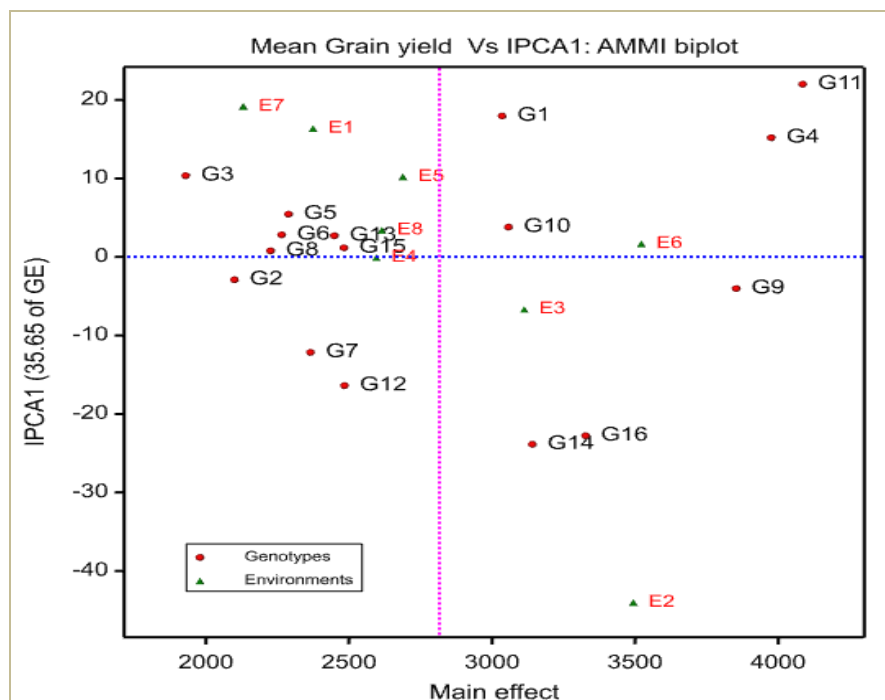

Figure 1. *AMMI biplot for grain yield (kg ha^{-1}) of sixteen upland rice genotypes (G) and eight environments(E) using genotypic and environmental scores. {E1= Woreta2010, E2= Pawe2010, E3= Woreta=2011, E4= Metema2011, E5= Pawe2011, E6= Woreta2012, E7= Pawe2012, E8= Maitsebri2012}*

In AMMI 2 biplot (Figure2), the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. Hence, environments E2, E6, E7 and E3 exerted strong interaction forces while the rest four did less. On the other hand, the genotypes near the origin are not sensitive to environmental interaction and

those distant from the origins are sensitive and have large interaction. In the present study, G11, G15, G2, G1, G12, G14 and G16 had more responsive since they were away from the origin whereas the genotypes G8, G4, G10, G6, G9, G5, G3, G13 and G7 were close to the origin and hence they were less sensitive to environmental interactive forces while genotypes G9, G6 and G8 were the most closest to the origin and hence had almost no interaction forces.
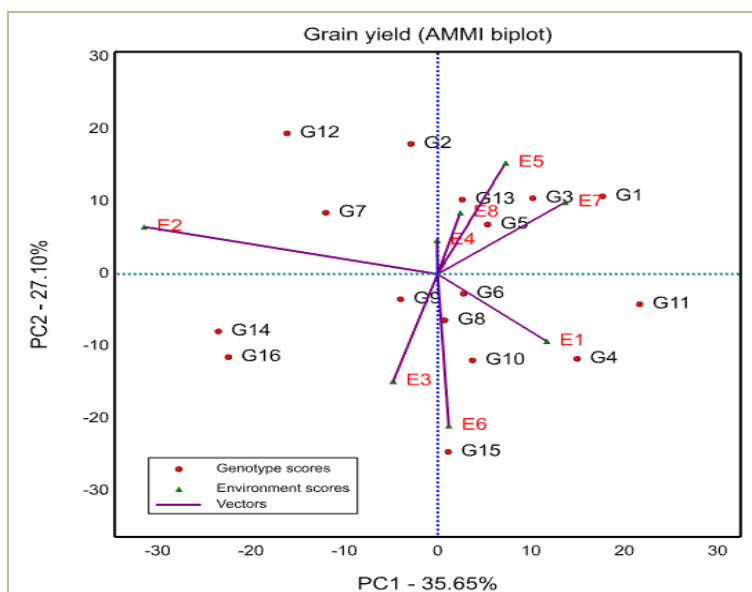

Figure 2. *AMMI-II biplot for grain yield (kg ha^{-1}) showing the interaction of PC1 against PC2 scores of sixteen upland rice genotypes (G) and eight environments(E). {E1= Woreta2010, E2= Pawe2010, E3= Woreta=2011, E4= Metema2011, E5= Pawe2011, E6= Woreta2012, E7= Pawe2012, E8= Maitsebri2012}*

GGE bi-plot Analysis

GGE bi-plot can best identify G x E interaction pattern of data and clearly shows which genotypes performs best in which environments, and thus facilitates mega-environment identification than AMMI. Otherwise, both GGE and AMMI models are equivalent as far as their accuracy is concerned [22]**.** The polygon view of the GGE bi-plot (shown in figure 3) indicates the best genotype(s) in each environment[10]. The vertex genotypes (G11, G9, G16, G7 and G3) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments. The vertex genotypes for each sector are the ones that gave the highest yield for the environments that fall within that sector. The genotype with the high yield in E7, E5, E4, E6, E3, E8 and E1 environments is G11, followed by G4, G9. In E2 the best genotypes is G14. The other vertex genotypes (G7 and G3), are poorest in all environments because there is no location in their sectors.
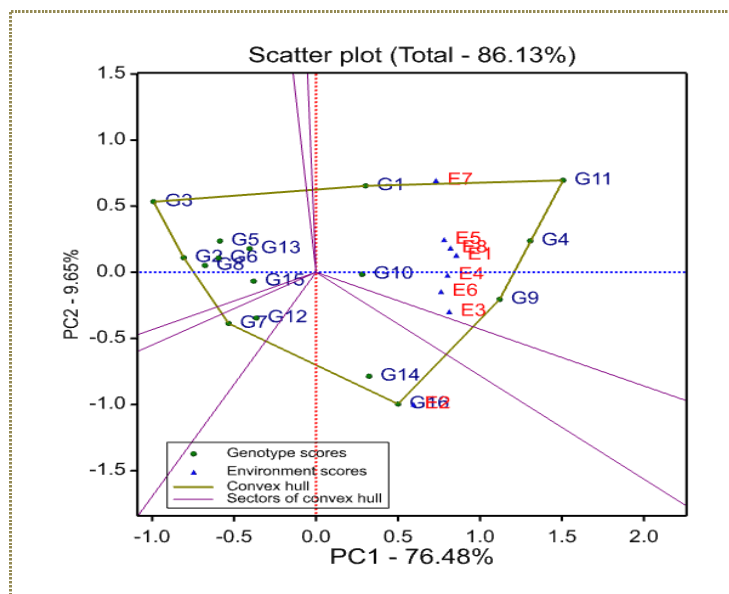

Figure 3. *GGE-biplot showing upland rice genotypes with respect to the environments*

Mean Grain Yield and Stability Performance

The ranking of 16 upland rice genotypes based on their mean yield and stability performance are shown in Figure 4. The line passing through the bi-plot origin is called the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments [23]. The line which passes through the origin and is perpendicular to the ATC represents the stability of genotypes. Either direction away from the bi-plot origin on this axis indicates greater GE interaction and reduced stability. For selection, the ideal genotypes are those with both high mean yield and high stability. In the bi-plot, they are close to the origin and have the shortest vector from the ATC.
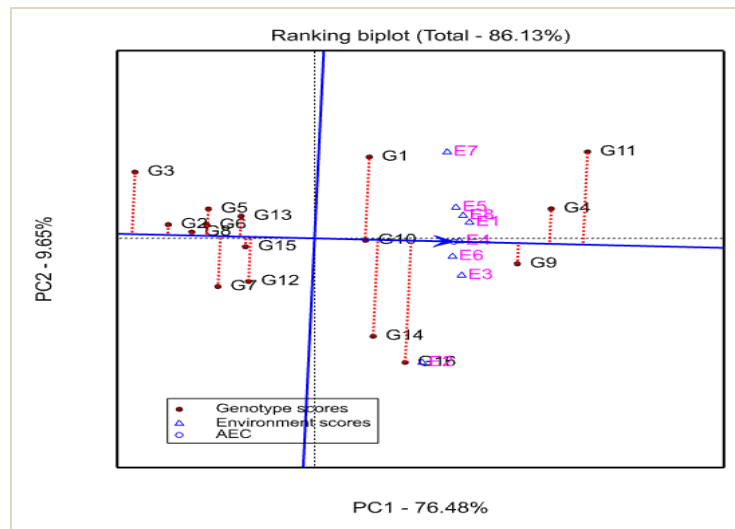
Figure 4. *Ranking genotypes based on mean grain yield and stability across environments*

As shown in Figure 4, the genotype G4, followed by G9, can be considered as genotypes with both high yield and stability performance. The genotypes with highest yielding performance but relatively with low stability was G11, whereas the genotypes with low yield and low stability were G16, G14, and G1. The other genotypes on the right side of the line with no arrow have yield performance greater than mean yield and the genotypes on the left side of this line had yields less than mean yield. Of the genotypes, G10 was the most stable, followed by G9 with better mean yield performance. According to this bi-plot (Figure 4), G11 can be recommended for specific adaptation whereas G4 and G9 relatively for wider adaptation.

CONCLUSION AND RECOMMENDATION

The results indicated that yield performance of upland rice genotypes were influenced by GE interaction effect, the environments and genotypes as well. Grain yield is a complex trait that is affected by a number of component characters along with the environment directly or indirectly. AMMI and GGE statistical models could be a great tool to select the most suitable and stable high yielding genotypes for specific as well as for diverse environments. In the present study, AMMI model has shown that the largest proportion of the total variation in grain yield was attributed to genotypes and somehow to environments. GGE bi-plot analysis also allowed to visualize the winner genotype at each sector and to identify high yielding and stable genotypes. The mean grain yield value of genotypes averaged over environments indicated that G11 had the highest (4085.8 kgha^{-1}), followed G4 with grain yield of 3975.8kgha^{-1}. As revealed by AMMI and GGE bi-plots, the genotype G11 was identified as specifically adapted to Fogera (Woreta areas). This is in line with the recommendation of the National Variety Release Committee of Ethiopia. The committee declare its decision on G11 to use as variety based on mean yield performance and farmers feedback. Therefore, G11 could be popularized in wider scale in Fogera and in other ecologies of similar conditions.

ACKNOWLEDGEMENT

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