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## Comparative Performance of Forty-Eight Rice Genotypes in Diverse Environments Using the Ammi and GGE Biplot Analyses

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### ABSTRACT

The study of Genotype×Environment Interaction (GEI) is critical for accurate cultivar evaluation in large multi-environment trials. Cultivars that exhibit high levels of mean performance and stability across a wide range of environmental conditions are desirable for rice production. The goal of this study was to examine the relative discriminatory abilities of AMMI and GGE stability models in selection for grain yield and stability among lowland rice genotypes. Forty-eight rice genotypes were tested for genetic variability and stability of performance in twelve environments in Nigeria, Benin Republic and Togo between 2008 and 2009. Statistical analysis was performed using Additive Main effect and Multiplicative Interaction (AMMI) and Genotype+Genotype×Environment (GGE) biplot models. The analysis of variance revealed significant ( $p = 0.05$ ) GEI effect. Mean grain yield of the rice genotypes ranged from 2148 kg ha<sup>-1</sup> for genotype TOG 5681 to 4469 kg ha<sup>-1</sup> for NERICA-L28. Ouedeme environments in Benin Republic were the most stable and ideal for rice cultivation while Ibadan sites were the most variable. Mega-traits and the best yielding rice genotypes in each mega-environment were revealed by the GGE biplot analysis. Furthermore, NERICA-L12, NERICA-L33, NERICA-L42 and NERICA-L56 were established as the most promising and stable genotypes across the test environments. FKR 19, NERICA-L49 and NERICA-L48 performed best for the grain thickness and 1000 grain weight mega traits while FARO 51 (CISADANE) performed best for grain width mega-trait. The best genotype for the grain length was NERICA-L55. Stability model of GGE biplot was observed to be more effective and informative in mega-environment analysis compared to AMMI analysis.

**Key words:** AMMI, genotype, GGE biplot, mega-environment, phenotype, rice, stability

### INTRODUCTION

Rice (*Oryza sativa* L.) has become a commodity of strategic significance and the fastest-growing food source in Africa. Its adoption as a principal staple food is increasing and is now grown and consumed in more than 40 African countries (Nwanze *et al.*, 2006; Ogunbayo *et al.*, 2007). The world population is expected to reach 8 billion by 2030 and rice production must be increased by 50% in order to meet the growing demand (Khush and Brar, 2002). The demand for rice in

sub-Saharan Africa is expected to grow substantially as the population is currently growing at the rate of 3-4% per annum and rice consumption is growing faster than that of any major food. Thus, to attain rice self-sufficiency and meet the future demand resulting from population growth, productivity in rice production has to be increased (Ogunbayo *et al.*, 2007; Akinwale *et al.*, 2011). Therefore, by exploiting the good adaptation and stability of yield and its components in rice genotypes, it would be possible to develop/identify high yielding and well adapted varieties. Genotypes that provide high average yields with minimum Genotype by Environment Interaction (GEI) have been gaining importance over increased yields. Plant breeders invariably encounter Genotype×Environment Interactions (GEIs) when testing varieties across a number of environments. In order to meet up the demand, development of high yielding genotypes with desirable agronomic traits for diverse ecosystem is therefore a necessity. Two frequently used statistical analyses are the Additive Main effects and Multiplicative Interaction (AMMI) model and the genotype main effects and genotype×environment interaction effects (GGE) model (Gauch, 2006). AMMI is the model of first choice when main effects and interaction are both important and this method integrates analysis of variance and Principal Component Analysis (PCA) into a united approach. These two statistical analyses (AMMI and GGE) have been used widely to visualize genotype×environment interaction and both of them integrate some features. Gruneberg *et al.* (2005) showed that AMMI, the multivariate tool was highly effective for the analysis of MET. In recent years, this method has often been used by international agricultural development agencies. The GGE provides visual evaluation of the data by creating a biplot that simultaneously represents mean performance and stability as well as identifying mega-environments (Ding *et al.*, 2007; Kang, 1993; Yan, 2001; Yan and Kang, 2003). The differences of the two methods, GGE biplot analysis is based on environment-centered Principal Component Analysis (PCA), whereas AMMI analysis is referred to double centered PCA. Moreover, GGE biplot is more logical and biological for practice than AMMI in terms of explanation of PC1 score which represents genotypic effect rather than additive main effect.

The goal of this study was to examine the relative discriminatory abilities of AMMI and GGE stability models in selection for grain yield and stability among lowland rice genotypes.

## **MATERIALS AND METHODS**

**Experimental sites, genotypes and procedures:** Forty-eight rice varieties that included 37 interspecific (*O. glaberrima*×*O. sativa indica*) and 11 intraspecific (*O. sativa indica*×*O. sativa indica*) crosses were evaluated in 2008 and 2009 wet seasons at the International Institute of Tropical Agriculture (IITA) Ibadan (Nigeria), Africa Rice Center (AfricaRice) Ouédémé (Benin Republic) and Farmers field in Kpalime (Togo). All the varieties used for the experiment were collected from the lowland breeding unit and genebank of Africa Rice Center, Cotonou, Benin. Field evaluation was carried out under irrigated lowland, valley bottom and valley fringe conditions. Randomized Complete Block Design (RCBD) with three replications was used in all locations and years. Each plot size was 1×5 m with 20 cm within and between row. Five rows per plot and inter-plot spacing of 40 cm was used. Seeds were sown directly for valley bottom and valley fringe environments at 2 seeds per hill and latter thin to one plant. Nursery beds were prepared for the irrigated plots and seedlings were transplanted at 21 days old. NPK (15-15-15) fertilizer was applied as basal application at the rate of 200 kg ha<sup>-1</sup> before transplanting and top dressed with urea at the rate of 65 kg ha<sup>-1</sup> at the tillering stage followed by of 35 kg ha<sup>-1</sup> at booting stage. The plots were hand-weeded regularly to minimize weed infestation.

**Data collection and analysis:** Morphological data were collected for twenty-two quantitative and qualitative characters at appropriate growth stage of rice plant following the Standard Evaluation System (IRRI, 2002). The characters that were evaluated included days to 50% flowering, days to 85% maturity, plant height, number of tiller at 60 days, number of panicles per m<sup>2</sup>, grain yield, panicle length, panicle exertion, plant vigor, panicle shattering, panicle threshability, hairness, awning, primary panicles branching, secondary panicles branching, leaf length, leaf width, flag leaf angle, basal leaf sheath colour, grain length, grain width and 1000-grain weight. The characters that were evaluated are as shown in Table 1. The data collected on 22 agro-botanical traits from the rice accessions were subjected to statistical analysis using SAS/PC version 9 package (SAS, 2000). The Additive Main Effect and Multiplicative Interaction (AMMI) model. Zobel *et al.* (1988) was performed using MATMODEL 2.0 (Gauch and Zobel, 1996; Gauch, 2006). In the analysis, each combination between the location and a year was considered as an environment, therefore making a total of 6 environments for each ecology. The AMMI model equation is written as:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}$$

For the additive parameters,  $Y_{ge}$  is the yield for genotype (g) in environment (e),  $\mu$  is the grand mean,  $\alpha_g$  denotes genotype deviation,  $\beta_e$  indicates environment deviation,  $\lambda_n$  is the singular value for component n,  $\gamma_{gn}$  is the eigenvector value for g,  $\delta_{en}$  is the eigenvector value for e and the residual term is  $\rho_{ge}$ . The GGE model is written as:

$$Y_{ge} - \beta_e - \mu = v_{ge} = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}$$

Table 1: List of characters studied in the experiment and the respective abbreviations

Characters	Abbreviation
Plant vigor	PV
Number of tiller at 60 days	NmTiller
Flowering date	Flwdays
Maturity date	Matdays
Plant height (cm)	PltHght
Panicle exertion	PanExt
Panicle shattering	PSht
Panicle threshability	Pthres
Yield (gms)	Yld
Hairnes	Hairnes
Panicle number/m <sup>2</sup>	Pan_m
Awning	Awning
Panicle length (cm)	Panlght
Primary branch panicle	Prybrpan
Secondary branch panicle	Secbrpan
Leaf length (cm)	Lflgth
Leaf width (cm)	Lfwdth
Flag leaf angle	FlaglAng
Base tiller coloration	Bastlcol
Grain length (mm)	Grlght
Grain width (mm)	Grwidth
1000 grain weight (gms)	1000 grwt

where  $V_{ge}$  is environment-centred yields and  $Y_{ge}-\beta_e$  is the nominal yields in the AMMI literature (Gauch and Zobel, 1996).

The model uses the analysis of variance (ANOVA) approach to study the main effects of genotypes and environments and a Principal Component Analysis (PCA) for the residual multiplicative interaction between genotypes and environments.

The GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and GGE concept (Gauch and Zobel, 1996; Yan *et al.*, 2000) was also used to visually analyze the results of SREG analysis of MET data. This methodology uses a biplot to show the two factors (G plus GE) that are important in cultivar evaluation and that are also the sources of variation in SREG model analysis of MET data (Yan *et al.*, 2000, 2001). The GGE biplot shows the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data (the yield variation due to GGE) to singular value decomposition (Yan *et al.*, 2000). In this study, GGE biplots were used to compare the performance of different genotypes at an environment, compare the performance of a genotype at different environments, compare the performance of two genotypes at all environments, identify the highest yielding genotypes at the different mega-environments and identify ideal cultivars and test locations.

## RESULTS

Table 2 presents combined analysis of variance for flowering days, maturity days, plant height, panicle/m<sup>2</sup> and yield of 48 rice genotypes at 12 environments. Significant replicate effects were observed for flowering days, maturity days, plant height, panicle/m<sup>2</sup> and yield. The result indicates that the rice genotypes varied significantly with respect to all traits. The location, genotype×location were highly significant to all traits except panicle/m<sup>2</sup>. The two years differed significantly with respect to all traits meaning that climatic changes were observed during the study. Significant genotype×year effects were observed for flowering days and maturity days but non-significant G×E effects were observed for plant height, panicle/m<sup>2</sup> and yield meaning that the last three traits remained similar over the two years. Location×year interaction reported highly significant effects for all the five traits meaning that the location of experiments differed in the two years of the study. Table 3 presents the Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for seed yield per plot in forty-eight genotypes tested across 12 environments (6-locations by 2-seasons). The result showed a strong evidence that, Environment (E),

Table 2: Mean squares of the combined analysis of variance for yield and related characters of rice accessions at 12 environments (6-locations by 2-seasons)

Source	df	Flowering days	Maturity days	Plant height	Panicle/m <sup>2</sup>	Yld (kg)
Rep	2	405.57**	320.90*	935.73*	17802.79**	3172332.00*
Genotype	47	573.99**	445.64**	2510.16**	3224.97*	4241473.00**
Location	5	3415.67**	3293.76**	16468.86**	58159.07**	478999838.00**
Genotype×Location	235	39.00**	59.01**	431.84**	1640.01 <sup>ns</sup>	2045861.00**
Year	1	598.55**	987.06**	11891.26**	2518782.18**	214102592.00**
Genotype×Year	47	55.59**	74.22*	60.48 <sup>ns</sup>	1076.35 <sup>ns</sup>	1323782.00 <sup>ns</sup>
Location×Year	5	11053.14**	4314.64**	6147.59**	662751.43**	337035964.00**
Genotype×Location×Year	235	56.47**	48.14 <sup>ns</sup>	60.66 <sup>ns</sup>	1267.41 <sup>ns</sup>	1876652.00*
Error	1150	23.14	39.26	107.85	1895.73	1411702.00

\*, \*\*Significant at 5 and 1% probability levels, respectively

Table 3: Additive Main effect and Multiplicative Interaction (AMMI) model analysis of variance for rice yield in forty-eight accessions tested across 12 environments (6-locations by 2-seasons)

Source	df	Sum of squares	Mean square	Total sum of squares (%)	Treatment (%)	G×E(%)
Total	1726	7097293236.77	4111989.13			
Treatment	575	5471072240.27	9514908.24**	77.1		
Genotype	47	192681506.17	4099606.51**		3.5	
Environment	11	4299546982.94	390867907.54**		78.6	
G×E	517	978843751.17	1893314.80**		17.9	
IPCA 1	57	267371718.91	4690731.91**			27.3
IPCA 2	55	232488363.78	4227061.16**			23.8
IPCA 3	53	130469255.67	2461684.07**			13.3
IPCA 4	51	102507705.53	2009955.01*			10.5
IPCA 5	49	80847056.65	1649939.93			8.3
IPCA 6	47	70716162.42	1504599.20			7.2
IPCA 7	45	40623835.32	902751.90			4.2
Residual	160	53819652.89	336372.83			
Error	1151	1626220996.50	1412876.63	22.9		

\*, \*\*Significant at 5 and 1% probability level, respectively

Genotype (G) and Genotype-by-Environment (G×E) interaction were highly significant ( $p < 0.01$ ), as E and G, respectively accounted for 78.6, 3.5 and 17.9% of the total variation. The total sum of square due to G×E interaction was mainly explained by the first two principal component axes (IPCA1 and 2) which were significant and respectively accounted for 27.3 and 23.8% of the sum squares. The IPCA1 mean square was almost four times larger than the error mean square. The IPCA 3 and IPCA 4 were equally significant and accounted for 13.3 and 10.5% of the G×E interactive sum of squares, respectively.

The genotype and environment mean yields of 48 rice accessions as well as their first principal axes scores (interaction) from the AMMI analysis is presented in Table 4. Plot yield ranged from (1965 g) for NERICA-L6 to (4582 g) for WITA 7 in environment 1. In Environment 2, seed yield per plot was highest for IR 75871-8-14-21-WAB1 (4956 g) and lowest was 967g for TOG 5681. In environment 3, seed yield per plot(4539 g) was observed in BW348-1 while lowest yield (1708 g) was observed in TOG 5681.

All the genotypes reacted differently in the twelve environments with regards to seed yield per plot. TOG 5681 exhibited a consistent low yield across environments with an average yield of 2148 g. The highest average seed yield across all environments of 4469 g was recorded for NERICA-L28 followed by NERICA-L14 with 4382 g. TOG 5681 had the least mean yield of 2148 g per plot. Generally, environment 12 recorded the highest yield mean per plot of 5495 g relative to other environments. This was followed by mean seed yield of environment 9 with value of 5058 g. The two ecologies valley fringe (E6) and valley fringe (E8) at Ibadan and Kpalime in 2009 recorded the least mean yields which were 2712 and 2007 g, respectively. FKR 19 had the largest interaction (-33.951) and was obviously the most dynamic whereas NERICA-L12 has the least interaction (0.971) and thus, the most stable across the twelve environments. However, environment 12 with largest PCA score (65.835) was the most unstable, while environment 9 with PCA score (0.241) appeared to be the most stable.

Table 4: Genotype and environment mean yields of 48 rice accessions and their first PCA scores from AMMI analysis

Plot/ No.	Genotype	Environment												First PCA Mean score	
		1	2	3	4	5	6	7	8	9	10	11	12		
1	Bw 348-1	2300	3541	4539	3974	4499	3120	3387	2167	5098	5918	2147	7017	3976	17.606
2	FARO 44 (SIPI-692033)	2156	2528	2324	5568	2583	3605	4367	1967	6976	7246	4748	7234	4275	25.554
3	FARO 51 (CISADANE)	2538	3372	2741	3704	2871	2267	5067	1933	6917	6280	3627	5483	3900	9.301
4	IR 75866-18-30-19-WABI	3047	4367	2628	4319	3332	4474	4600	1667	6712	5797	2690	4601	4019	-1.896
5	IR 75866-2-18-23-WABI	3377	3779	3210	4452	2720	4303	5393	2133	6169	3865	3824	5097	4027	-6.892
6	IR 75871-4-29-13-WABI	3535	3458	2832	5737	2092	4087	5633	1767	4082	5556	3815	4444	3920	-8.664
7	IR 75871-8-14-21-WABI	2654	4956	3290	4931	2696	4618	5167	2367	4492	3502	4015	4420	3926	-18.157
8	NERICA-L6	1965	3017	3414	3634	4667	1798	5433	1700	4778	3623	3036	6763	3652	8.727
9	NERICA-L7	3175	3496	3008	4194	3626	3949	4993	1500	4806	7126	3600	6449	4160	21.887
10	NERICA-L8	3388	3868	3202	4517	2261	3485	4520	1600	4865	5797	3634	5918	3921	7.080
11	NERICA-L9	3234	3272	2690	3548	2705	3143	6113	1467	4487	6401	5196	6461	4060	21.805
12	NERICA-L12	3152	3173	2780	4280	2511	3093	7033	1533	4126	4327	4020	5423	3779	0.971
13	NERICA-L14	3801	2668	2837	4456	2906	3763	6800	2333	5392	6159	4468	7005	4382	20.396
14	NERICA-L15	3619	4125	2791	4573	2875	2445	6400	2133	4852	5797	4460	6703	4231	14.058
15	NERICA-L17	3620	3953	2856	4259	2554	1909	5900	2100	4423	6401	4775	5966	4060	13.297
16	NERICA-L18	3437	3470	3042	4978	2928	1931	5667	1833	3745	5676	3881	6063	3888	8.244
17	NERICA-L19	3741	3849	2882	4386	2895	1657	6487	2333	5007	4710	4156	6932	4086	14.129
18	NERICA-L20	3976	3687	3265	6175	3133	2687	6587	2000	4407	5676	3297	6715	4300	10.170
19	NERICA-L26	4502	2859	3076	5088	4239	2213	4433	1700	6428	5435	3205	5857	4086	9.626
20	NERICA-L28	4077	3745	3040	4252	2634	3570	4920	2033	6209	6280	4420	8454	4469	26.999
21	NERICA-L32	3056	3498	3824	4610	2588	2826	4267	1533	5036	4348	4323	6401	3859	5.200
22	NERICA-L33	3711	3274	2714	5418	3027	2794	5067	1600	5004	4106	4555	6618	3991	2.407
23	NERICA-L34	3538	2946	2826	5741	2326	2927	3500	1633	5276	4831	4100	7089	3894	15.207
24	NERICA-L36	3596	3814	3119	4398	2599	3665	5067	1500	5168	4831	4716	6655	4094	7.581
25	NERICA-L37	4027	3354	2528	5225	2896	1664	4267	1867	5706	1932	2907	4831	3434	-21.464
26	NERICA-L38	3816	3492	2811	5790	3022	2318	4067	1933	5392	1691	4370	6993	3808	-6.854
27	NERICA-L39	3407	2774	3140	4196	2297	3000	2867	2067	4233	2657	2823	4469	3161	-16.819
28	NERICA-L40	3267	3890	2727	4414	3216	1905	4467	2433	4161	2778	4825	5556	3637	-9.242
29	NERICA-L41	3317	4571	2615	4835	2966	2260	3600	2800	6075	3502	5190	6232	3997	-6.749
30	NERICA-L42	3756	3698	2371	5245	2462	2629	3720	2267	4987	5193	3481	6582	3866	4.333
31	NERICA-L45	4254	3214	2712	5426	3349	2324	2933	2267	4043	3623	3326	5966	3620	-8.788
32	NERICA-L46	2930	2940	3050	6673	3261	2182	3800	2267	5355	3986	4465	5592	3875	-8.422

Table 4: Continue

Plot/ No.	Genotype	Environment												First PCA score	
		1	2	3	4	5	6	7	8	9	10	11	12		
33	NERICA-L48	3321	3046	3424	6106	3296	1860	4033	1933	4886	3865	3604	4082	3621	-19.344
34	NERICA-L49	3326	4509	2767	5683	4889	3232	4000	2267	5987	4348	5384	4891	4274	-15.226
35	NERICA-L50	3462	3142	2874	4153	2198	1687	4433	1633	6295	4589	3804	4408	3557	-5.669
36	NERICA-L53	3070	4063	3948	4793	3220	2449	5240	1900	5624	3502	4063	3684	3746	-20.875
37	NERICA-L54	2981	3376	3355	3734	2530	1862	5333	1833	5957	4710	3941	5326	3753	3.481
38	NERICA-L55	2880	3618	2913	4271	2981	3987	5560	1933	5470	4348	2941	4227	3761	-5.930
39	NERICA-L56	2811	3453	3707	5372	3851	2371	4600	2367	5804	6884	3950	4722	4158	1.480
40	NERICA-L60	2750	3472	3457	4185	3303	2588	4430	2367	4393	5495	3608	5121	3764	2.865
41	SUAKOKO 8	2895	3490	2934	4626	3277	1731	4120	2700	4629	6039	2428	4541	3618	-1.976
42	TOX 4004-43-1-2-1	3560	2797	3819	6128	3581	2628	4233	2633	4681	4952	3058	3128	3766	-20.768
43	WITA 7	4582	3950	3622	5435	3400	2097	4760	2433	4109	3895	2768	4867	3824	-17.822
44	TOG 5681 (Parent)	2822	967	1708	2713	2619	900	2620	1667	2229	2415	830	4287	2148	-10.891
45	IR 64 (Parent)	2945	3124	2474	4351	2648	2728	4333	1733	4473	4408	4347	5483	3587	1.977
46	WITA 4 (Check)	3553	4284	3747	6326	2595	2680	4733	2833	4406	6884	4686	3056	4149	-15.587
47	FKR 19 (Check)	3305	2388	2948	5071	2004	2128	5600	1967	4727	4227	3583	797	3229	-33.951
48	FKR 54 (Check)	3188	3099	4057	5128	2562	2642	5927	1700	4700	6763	5204	5157	4177	7.605
	Mean	3321	3446	3042	4814	2996	2712	4802	2007	5058	4838	3839	5495		
	First PCA	-15.098	-18.607	-15.038	-34.603	-10.299	-10.26	8.989	-21.114	0.241	48.672	1.283	65.835		

NB: IRIB-08: Irrigated Ibadan 2008 (Environment 1), VFKP-08: Valley fringe Kpalime 2008 (Environment 2), VFKP-09: Valley fringe Kpalime 2009 (Environment 3), VBOD-08: Valley bottom Ouedeme 2008 (Environment 4), VBOD-09: Valley bottom Ouedeme 2009 (Environment 5), VFOD-08: Valley fringe Ouedeme 2008 (Environment 6), VFOD-09: Valley fringe Ouedeme 2009 (Environment 7), IRIB-09: Irrigated Ibadan 2009 (Environment 8), VBIB-08: Valley bottom Ibadan 2008 (Environment 9), VBIB-09: Valley bottom Ibadan 2009 (Environment 10), VFIB-08: Valley fringe Ibadan 2008 (Environment 11), VFIB-09: Valley fringe Ibadan 2009 (Environment 12), PCA: Principal Component Analysis



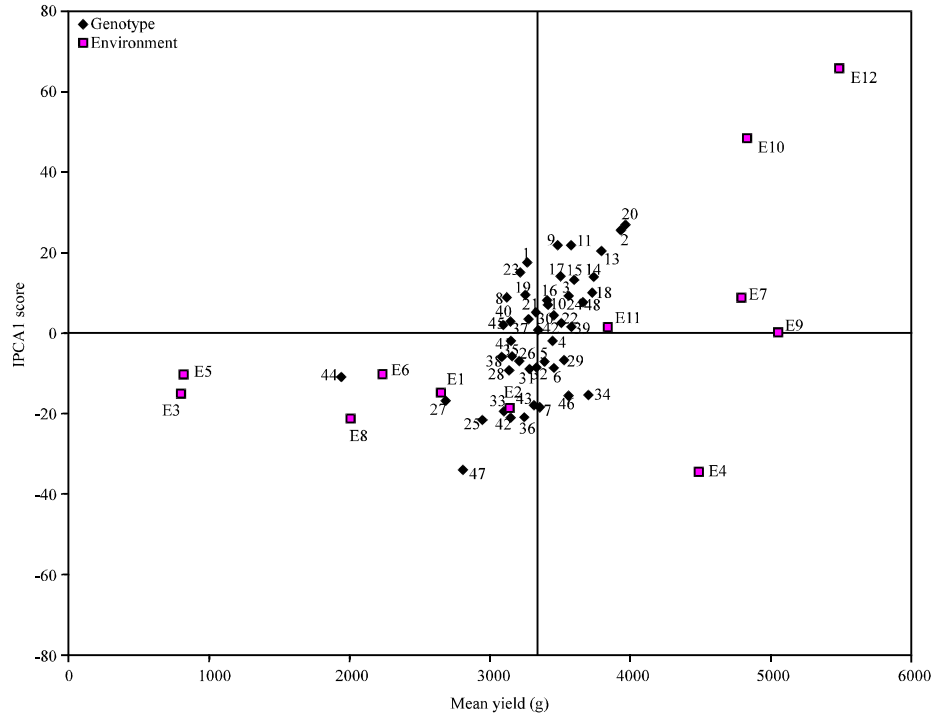


Fig. 1: Biplot of AMMI for 48 rice accessions evaluated in twelve environments (6-locations by 2-seasons)

Figure 1 represents the biplot of AMMI for 48 rice accessions in 12 environments. The y-axis represents the IPCA1 scores, while the x-axis represents the seed yield per plot (main effect) of the genotypes. NERICA-L56 was the overall best genotypes combining relative stability and high yield. Genotypes NERICA-L8, NERICA-L12, NERICA-L33, NERICA-L36, NERICA-L42 and FKR 54 were highly stable and above average in yield, while NERICA-L28 was above average in yield but relatively unstable due to large interaction. IR 64 and NERICA-L 60 had below average yield but were stable. The poorest of the genotypes due to instability and lowest yield were TOG 5681 and FKR 19. Environments (E1, E2, E3, E5, E6 and E8) had below average yield. The environment 9 and 11 were most stable, whereas environment 10 and 12 were most unstable producing large interactions.

Figure 2 shows the GGE biplot analysis of yield in forty-eight rice genotypes evaluated in twelve environments (6-locations by 2-seasons). The GGE biplot accounted for 51.5% of the total variation consisting of 31.3 and 20.2% of variance attributed to the first and second principal components (PC1 and PC2), respectively. Environments E1, E2, E3, E5 and E6 were the most ideal as most of the genotypes particularly IR 75866-18-30-19-WAB1, NERICA-L12, NERICA-L8, NERICA-L54 and NERICA-L26 performed well in these environments. This was followed by the Environments (E4, E7, E9 and E11) in which Genotypes FARO 51, NERICA-L9, NERICA-L14, NERICA-L15, NERICA-L17 and NERICA-L20 specifically did very well. Environment (E8) was the least ideal environment. TOG 5681 and FKR 19 performed poorly in all the 12 environments.

Figure 3 presents the ranking of accessions based on mean yield and stability of performance. It is a biplot of the 'ideal genotype' concept as it indicates desirability in terms of both crop stability and mean performance. The Average Environments Coordinate (AEC) which is the single arrowed

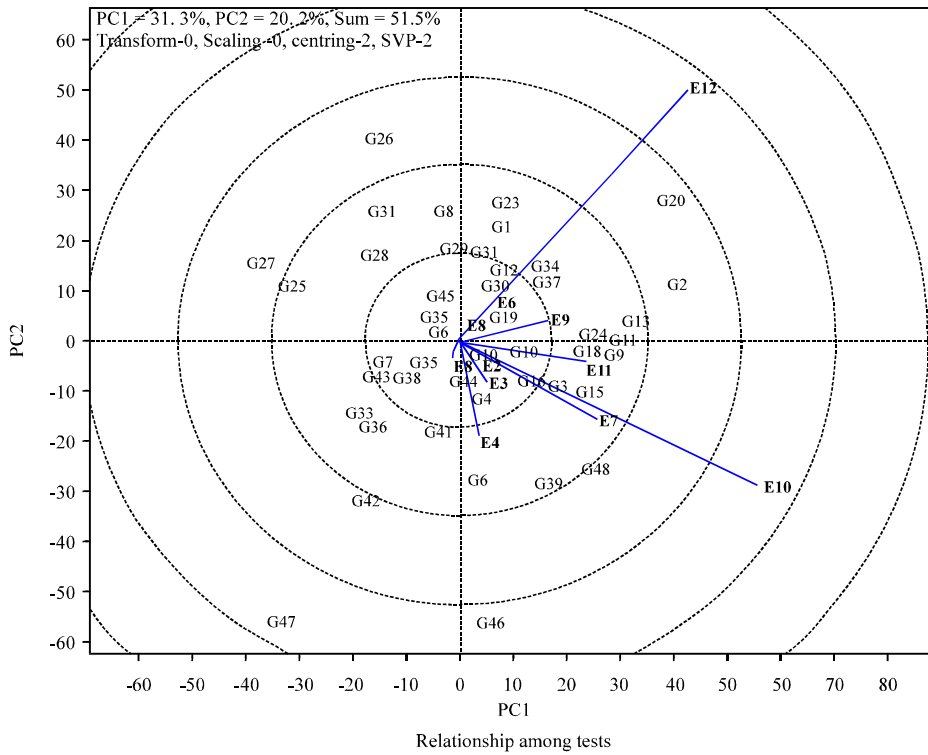


Fig. 2: GGE Biplot showing relationship among environments for grain yield

line that passes through the biplot origin is the abscissa. The AEC and the average environment represented by the small circle that represent the mean yield of genotypes. However, the AEC which is the double arrowed line that passes through the biplot origin and perpendicular to the abscissa represents the GE interaction or stability/instability of the genotypes. The single arrowed line points towards the direction of increasing mean yield and the two arrows on the AEC-ordinate points to greater GE interaction or lower stability (instability). Thus, four environments (E4, E7, E10 and E12) were very unstable but had better mean yield, the remaining environments were more stable but with reduced yield. NERICA-L8 was the best (most ideal) genotype. NERICA-L7, NERICA-L20, NERICA-L12 and FARO 51 were the most stable and close to the ideal genotype. These were followed by FARO 44, NERICA-L14 and NERICA-L28 that had above average mean yield but were relatively unstable. However, TOG 5681 and FKR 19 have no place as far as yield and stability is concerned. NERICA-L33 and IR 75866-2-18-23-WAB1 performed below average but stable.

The GGE biplot of the best genotypes in each of the environments for seed yield is presented in Fig. 4. The polygon view of the GGE-biplot explicitly displays 'which-won-where' i.e., (best genotype in each environment) and it is a summary of the GEI pattern of a multi-environment seed yield trial data. The polygon is formed by connecting the genotypes that are further away from the biplot origin such that all other genotypes are contained within the polygon. To each side of the polygon, a perpendicular line, starting from the origin is drawn and extended beyond the polygon, so that the biplot is divided into several sectors and the different environments that were separated into different sectors. There were seven sectors. The genotype at the vertices of each sector is the best performer at environments included in that sector, provided

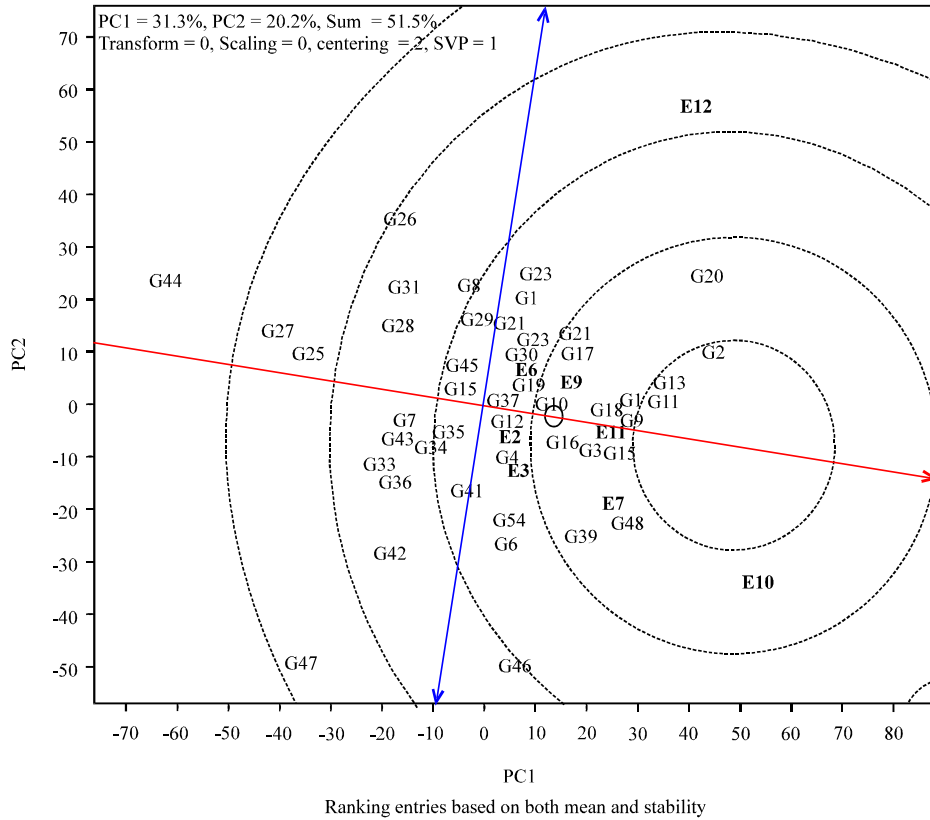


Fig. 3: GGE Biplot showing ranking of accessions based on both yield and stability of performance

that GGE is sufficiently approximated by PC1 and PC2. Hence, though there were seven sectors in all, four mega environments were identified. Environments (E1, E6, E9 and E12) constituted one mega environment with FARO 44 and NERICA-L28 as winning or the best genotypes in this environment. One other sector had E11 in the second mega-environment and E7 and E10 as the third mega-environment.

The winning (best) genotypes for the fourth mega-environment consisting of environments (E2, E3, E4 and E5) that overlaps with E8 were WITA 4 and FKR 54. The remaining sectors have no environment within them but contained 3 genotypes (NERICA-L26, TOG 5681 and FKR 19) on their vertices. These vertex genotypes without environment in the sectors were never high yielding genotypes at any environment. Moreover, they were poorest at all or some sites. However, genotypes within the polygon, particularly those located near the plot origin were less responsive than the vertex genotypes.

Figure 5 which is the polygon view of the GGE-biplot explicitly displays 'which-won-where' i.e best genotype in grain quality traits. The polygon is formed by connecting the genotypes that are further away from the biplot origin such that all other genotypes are contained within the polygon. To each side of the polygon, a perpendicular line starting from the origin is drawn and extended beyond the polygon, so that the biplot is divided into several sectors and the different grain quality traits were separated into different sectors. The genotype at the vertices of each sector is the best performer for the trait included in that sector, provided that GGE is sufficiently approximated by PC1 and PC2. Hence, though there were seven sectors in all, four mega traits were identified.

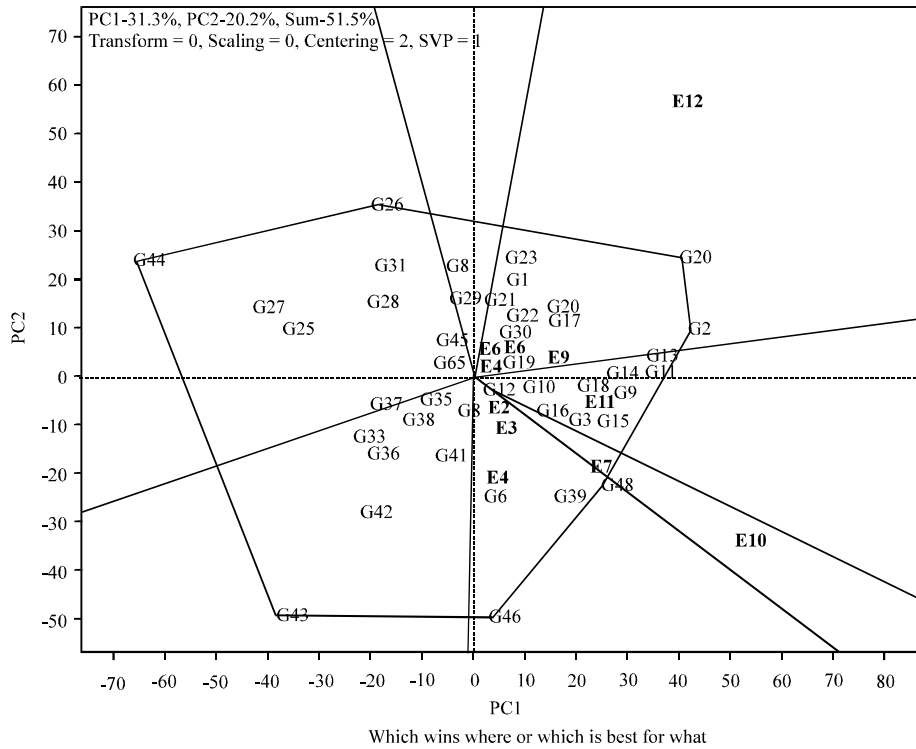


Fig. 4: GGE Biplot for best genotypes in different environments for grain yield

Grain shape was one mega trait with NERICA-L15 as winning or the best genotypes for this trait. The best genotype for the mega-grain length was NERICA-L55. FKR 19, NERICA-L49 and NERICA-L48 performed best under the grain thickness and 1000 grain weight mega traits while FARO 51 (CISADANE) performed best under grain width mega-trait. The remaining sectors have no grain quality traits within them but they contained genotypes TOX 4004-43-1-2-1 and FKR 19 on their vertices. However, genotypes within the polygon, particularly those located near the plot origin were less responsive relative to the vertex genotypes.

**DISCUSSION**

The selection of crops is preceded by multi-locational trials in which the performance of the best genotypes is determined and recommend to researchers and farmers. The interaction that exists between genotypes and environment in diverse environments makes selection of any genotype for recommendation a little challenging for breeders. Therefore, it is importance to analyze the interaction in order to determine the yield potential and stability of the rice genotypes (Yan *et al.*, 2001; Setimela *et al.*, 2007). The mean yield of rice genotypes used in this experiment over a two year period across the twelve environments differed substantially. This is indicative of the wide genetic background of the genotypes. This result agrees with earlier reports of Egesi (2001) and Brondani *et al.* (2006). The genetic make up of seed, effect of environment and field management practices have been reported to influence the morphology of a crop (Singh and Rachie, 1985).

The AMMI analysis had lower GxE interaction, thus NERICA-L8, NERICA-L12, NERICA-L33, NERICA-L36, NERICA-L42 and FKR 54 could be considered stable in any environment.

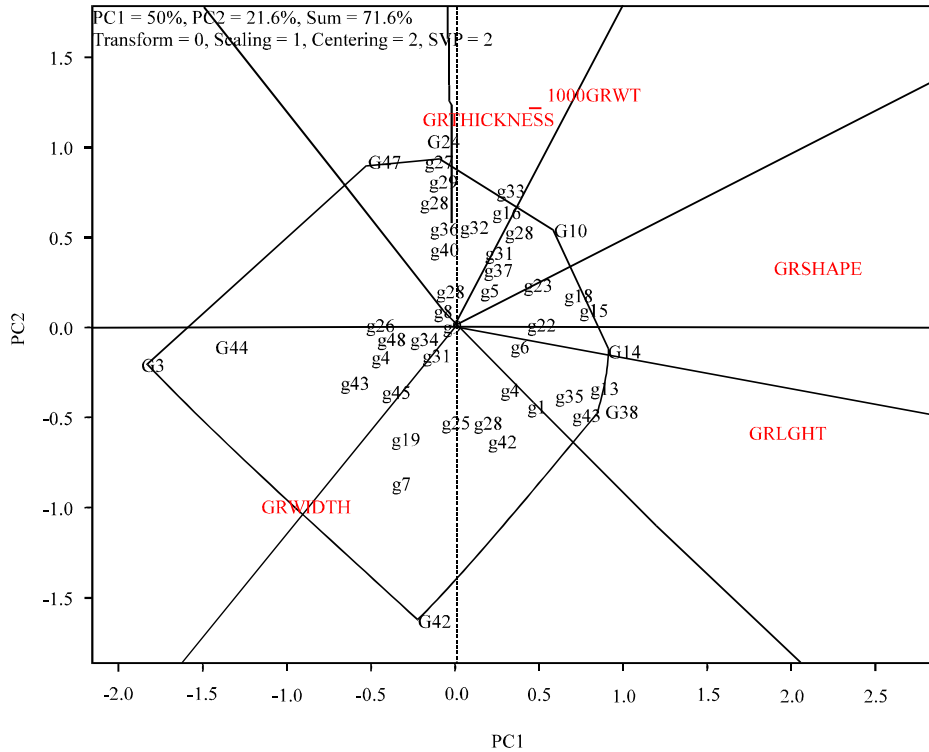


Fig. 5: GGE biplot for best genotype in different grain quality traits for rice grain

NERICA-L28 was above average in yield but had high interactions, indicating that it was unstable and responsive to changes in the environment. It can only be recommended for all the test locations provided that improved management practices and optimum climatic factors are in place. IR 64 and NERICA-L60 had yield below the average but stable. The poorest of the accessions due to instability and lowest yield were TOG 5681 and FKR 19 and as such they would require special attention to be able to perform well.

According to Yan *et al.* (2000), the stability of the cultivars is measured by their projection onto the double-arrow line (AEC y-axis) while the average yield of the cultivars is approximated by the projections of their markers on the AEC x-axis. NERICA-L8 was the best (most ideal) genotype, whereas NERICA-L7, NERICA-L20, NERICA-L12 and FARO 51 were identified as high yielding and more stable genotype.

GGE biplot was also used to compare the performance of the rice genotypes at the test locations. In the “which-won-where” polygon view, the vertex cultivar in each sector represents the highest yielding cultivar in the location that falls within that particular sector. A line drawn from the origin of the biplot and perpendicular to the side of the polygon effectively divided the test locations into seven sectors. This indicates that a single genotype had the highest yield in each mega-location and each mega-location provided similar information about the genotypes. Though, there were seven sectors in all, four mega environments were identified. Irrigated Ibadan ‘08 (E1), valley fringe Ibadan ‘09 (E6), valley bottom Ouédémé ‘08 (E9) and valley fringe Ouédémé ‘09 (E12) constituted one mega environment with FARO 44 and NERICA-L28 as wining or the best genotypes in this environment. One other sector had valley fringe Ouédémé ‘08 (E11) in the second mega-environment and valley fringe Kpalime ‘08 (E7) and valley bottom Ouédémé ‘09 (E10) as the third mega-environment.

The wining (best) genotype for the fourth mega-environment consisting of irrigated Ibadan '09 (E2), valley bottom Ibadan '08 (E3), valley bottom Ibadan '09 (E4) and valley fringe Ibadan '08 (E5) that overlaps with valley fringe Kpalime '08 (E8) were WITA 4 and FKR 54. The remaining sectors have no environment within them but contained the following genotypes on their vertices NERICA-L26, TOG 5681 and FKR 19. These vertex genotypes without environment in the sectors had low yield in all environments. Moreover, they were poorest at all or some sites. However, genotypes within the polygon, particularly those located near the plot origin, were less responsive than the vertex genotypes.

The best genotype for the mega-grain length was NERICA-L55. FKR 19, NERICA-L49 and NERICA-L48 performed best under the grain thickness and 1000 grain weight mega traits while FARO 51 (CISADANE) performed best under grain width mega-trait. Grain shape was one mega trait with NERICA-L15 as wining or the best genotypes for this trait. The remaining sectors have no grain quality traits within them and contained the following genotypes on their vertices TOX 4004-43-1-2-1 and FKR 19.

## CONCLUSION

The study of genotype×environment interaction is critical for accurate cultivar evaluation in large multi-environment trials. Cultivars that exhibit high levels of mean performance and stability across a wide range of environmental conditions are desirable for rice production.

However, it becomes difficult for breeders to determine which genotypes should be selected in the presence of GEI. In the current study, GGE biplots and AMMI were used to compare the performance of different genotypes at different environment. The results indicated that the yield performance of rice was highly influenced by GE interaction effects. The AMMI analysis was able to explain the GEI, however, investigation of GEI was observed to be more meaningful when used with Genotype (G).

The GGE biplot provided an excellent graphical presentation of MET data. It gave a reliable graphical display of the yield stability of cultivars in different environments, ranked environments based on relative performance of a given cultivar, identified the best cultivar in each environment, identified mega environments and evaluated environments based on discriminating ability and representativeness. Thus, GGE biplot was a useful tool because the concept of the analysis considers both and only G plus GE and not all of the phenotypic variation which may be misleading. Environmental component is irrelevant in making selection decision. Moreover, Genotype plus Genotype×Environment (GGE) biplot was able to identify which genotype performs best in a given environment and also which genotype had the highest stability in the test locations. GGE biplot view, therefore, is more effective and informative than AMMI in mega-environment analysis and GEI evaluation.

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