Genotype × Environment Interaction and Stability Estimate for Grain Yield of Upland Rice Genotypes in Nigeria

Maji AT[1], Bashir M[2], Odoba A[1], Gbanguba AU[1] and Audu SD[1]*

[1]National Cereals Research Institute Badeggi, Niger state. Nigeria
[2]National Biotechnology Development Agency, Lugbe, Abuja, Nigeria

Abstract

Genotype × environmental interaction and stability estimate were investigated on grain yield of 30 upland rice varieties at Sabon Daga, Amakama, Yandev and Uyo in 2003. The experiments were laid out in a randomised complete block design with three replications. AMMI Anova for grain yield revealed no significant different among genotypes ($P < 0.01$), but there is significant difference on environments and the interaction. The significant different on the interaction indicates that, the genotypes respond differently across the different environments. The partitioning of GGE through GGE biplot analysis showed that principal component1 and principal component 2 accounted for 62.21% and 28.57% of GGE sum of squares respectively, explaining a total of 90.78% variation. AMMI 2 biplot revealed that, genotype ART16-9-3-15-3-B-1-1 (8) gave the highest mean yield of 2925 kg/ha with high main additive effect better than the check varieties. Hence, the genotype would be considered more adapted to wide environments than the rest of genotypes. Environments, such as Sabon Daga and Amakama could be regarded as a more stable site for high yielding rice varieties compare to the other locations.

Keywords: Genotype; Stability; ANOVA

Introduction

Rice (*Oryza sativa* L.) is the second most important cereals crop, grown in more than 144 million farm worldwide, most certainly than any other crop on a harvested area of about 162 million ha [1] .The author also reported that, global rice production rise more than tripled between 1961 and 2010, with a compound growth rate of 2.24% per year, most of the increase in rice production was due to higher yields, which increase at annual average rate of 1.74%, compared with an annual average growth rate of 0.49% for area harvested. He further stated that, per capital consumption of rice continues to grow fast particularly in most sub-Saharan Africa, where high population growth with changing consumer preferences is causing rapid expansion in rice consumption. In countries such as Kenya, Niger, Nigeria and Tanzania people are moving away from maize and cassava to rice as their income rises. Along with strong population growth, the rapid rise in per capita consumption also contributed to such rapid growth in rice demand.

In Nigeria, rice is a leading staple crop cultivated in virtually all the agro-ecological zones of country, from the mangrove and swamps environment of the coastal areas, to the dry zones of the Sahel in the North [2]. On the other side, the demand for rice has been soaring over years, since mid 1970's rice consumption in Nigeria has risen tremendously growing by 10.3% per annum, as a result of accelerating population growth rate, increasing per capita consumption, rapid urbanization, increase income levels, and associated changes in family occupational structures [2-4]. GRISP [1] reported that, Nigeria is blessed with three major rice production environments and their coverage is rainfed lowland (69.0%), irrigated lowland (2.7%) and rainfed upland (28.3%). More than 90% of Nigeria's rice is produced by resource poor small-scale farmers, while the remaining 10% is produced by cooperate/commercial farmers.

Upland rice is grown in rainfed, naturally well drained soils without surface water accumulation, normally without pyretic water supply, and normally not bunded. In the upland environment, rice cultivation is challenged by drought, low adoption of improved varieties, soil acidity and general soil infertility, poor weed control, limited capital investments, labor shortages and low mechanization, resulting in low

yield range from 1.0 to 1.7 t/ha compared with a potential of 2.0-4.0 t/ha. Most upland rice is grown on small subsistence farms with few purchased inputs and most production is for family consumption. Therefore developing high yielding upland varieties combine with tolerant to biotic and abiotic stress will contribute substantially to poverty alleviation, especially, for resource constrained households and can increase household food security.

Numerous statistical methods have been developed for the analysis of Genotype by Environment Interactions (GEI) and phenotypic stability [5-8]. Regression technique has been widely used [9,10] due to its ease and the fact that its information on adaptive response is easily applicable to locations. The Principal Component Analysis (PCA) method that shows the mean squares of the principal components axes [11] has also been used. [12] Zobel *et al.* compared the traditional statistical analysis such as Analysis of Variance (ANOVA), Principal Component Analysis (PCA) and Linear Regression with AMMI analyses, and showed that the traditional analyses were not always effective in analyzing the multi-environment trial data structure. The ANOVA is an additive model that describes main effects effectively and determines if GE interaction is a significant source of variation, but it does not provide insight into the patterns of genotypes or environments that give rise to the interaction. The PCA is a multiplicative model that contains no sources of variation for additive G or E main effects and does not analyze the interactions effectively. The linear regression method uses environmental means, which are frequently a poor estimate of environments, such that the fitted lines in most cases

account for a small fraction of the total GE and could be misleading [13-15].

Additive main effects and multiplicative interaction (AMMI) has been proved to be a suitable method for depicting adaptive responses [15-17]. AMMI analysis has been reported to have significantly improved the probability of successful selection [17] and has been used to analyse GxE interaction with greater precision in many crops [13,15,18]. The model combines the conventional analysis of variance for genotype and environment main effects with principal components analysis to decompose the GEI into several Interaction Principal Component Axes (IPCA). With the biplot facility from AMMI analysis, both genotypes and environments are plotted together on the same scatter plot and inferences about their interaction can be made.

This study, reports the use of AMMI model to analyse yield data of thirty genotypes of upland rice evaluate in four locations. The objectives is (1) to determine the nature and magnitude of G × E interaction effect on grain yield in diverse environment (2) to determine environment where upland rice genotypes would be adapted and produce economically competitive yield.

Materials and Methods

Thirty upland rice varieties selected from breeding task force upland mega environmental trial (MET) of 2012 are composed as preliminary yield trial (PET) in National Cereals Research Institute, Badeggi rice breeding unit, evaluated during 2013 cropping season at four locations as shown in Table 1. The experiment was conducted in a randomised complete block design in three replication, The plot size was 4 m × 3 m square with 20 cm inter and intra row spacing. Fertilizer application was 40 kg N, 40 Kg P_2O_5 and 40 Kg K_2O at transplanting, while additional 40 kg N per ha was used as top dressing at vegetative and panicle initiation in equal split. Weed control was by chemical at 21 days after transplanting (DAT) using a formulation of Propanil and 2-4-D (Orizo Plus[(R)]), and was followed by hand weeding at 43 days after transplanting. Grain yield was recorded after harvest at 14% moisture content and was subjected to analysis of variance (ANOVA) using Crop Stat statistical package. In order to determine the effect of genotype × environment interaction on rice grain yield, the data was further subjected to an additive main effect and multiplicative interaction (AMMI), GGE-biplot and Boxplot analysis using Breeding View (BV) statistical package.

Results and Discussion

AMMI analysis of variance

The fit of an additive model to the rice grain yield data are presented in Table 2. It showed that, there is no significant difference in genotypes main effect. However, significant differences (P<0.01) exist among environments and genotypes × environment (G × E) interaction, PCA1 and PCA2 main effects. The environments are characterised by the average performance of the genotypes at a particular environment and the results indicates that, the environments differ significantly. Marcos et al. [19] reported that, environmental difference is not a major concern, but the differences that exist between the genotypes. No significant genotype main effect indicates that genotypes are not different in their mean performance across environment. Although genotypic and environmental scores are deemed to represent genetic and environmental qualities, they come from a mathematical procedure, a principal components analysis on the GEI [12,20] that maximizes the variation explained by the products of the genotypic and environmental scores. The first two PCA explains most of the variation,

in grain yield. This is reflected in Table 2, which shows the results from the AMMI model to the grain yield data. In the AMMI model, GEI is explained by two axes (principal component 1, PCA1, and principal component 2, PCA2) that are highly significant respectively, both with an associated (P<0.001). Thus the interaction of the 30 genotypes across four environments was best predictable by the first two principal components.

Box Plot is a convenient way of graphically depicting group of numerical data through their qualities. It displays varieties in samples of a statistical population without making any assumptions of the underlying statistical distribution [21]. The spacing between the different parts of the box indicates the degree of dispersion (spread) of the data and allows visually estimate of inter-quartile mean, median and mode. Result in Figure 1 is showing the distribution pattern of grain yield of 30 rice genotypes across four environments. The result revealed that, Sabon daga has the highest mean grain yield of 3692 kg/ha (Table 3) with large variance followed by Amakama with mean yield of 2940 kg/ha, while Yandev and Uyo discriminate less between genotypes with mean of 1719 and 1846 kg/ha, respectively. This is reflected in

Location	Longitude	Latitude	State	Agro-Ecological Zones
Sabon Daga	$09^0.73'$ N	$06^0.52'$ E	Niger	Southern Guinea Savannah
Amakama	$05^0.29'$ N	$07^0. 33'$ E	Abia	Rain Forest zone
Uyo	$04^0. 50'$ N	$07^0. 56'$ E	Akwa Ibom	Rain Forest zone
Yandev	$08^0.47'$ N	$07^0.22'$ E	Benue	Southern Guinea Savannah

Table 1: Geographic description of coordinates of the trial location in 2013 cropping season.

Source	d.f.	s.s.	m.s.	v.r.	F pr
Genotypes	29	3120724	107611	1.20	0.2529
Environments	3	79273389	26424463	295.33	<0.001
Interactions	87	7784210	89474	3.37	<0.001
IPCA 1	31	4842595	156213	5.88	<0.001
IPCA 2	29	2224187	76696	2.89	0.0035
Residuals	27	717428	26571		

Table 2: AMMI analysis of variance for grain yield of 30 rice genotype across 4 environments.
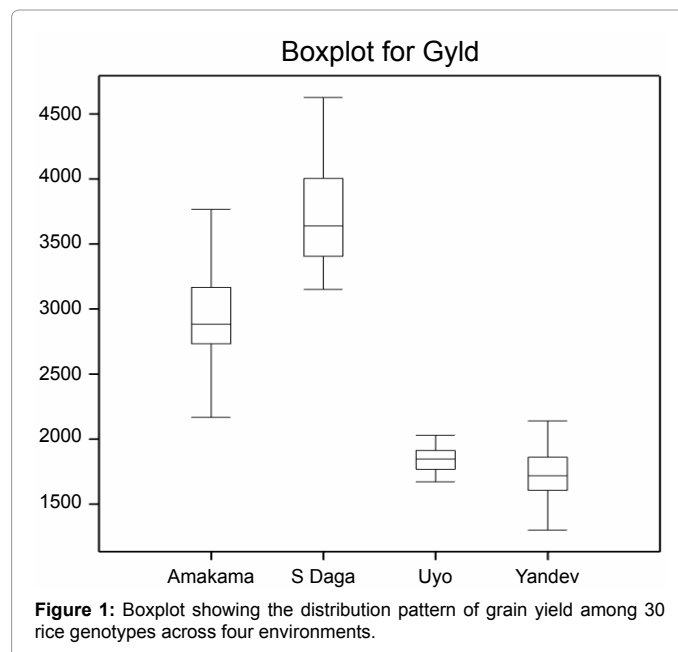

Figure 1: Boxplot showing the distribution pattern of grain yield among 30 rice genotypes across four environments.

Location	Range	Lower quartile	Upper quartile	Std. d	Mean	%cv	s. sq
S Daga	1477	3405	4004	398.4	3692	10.79	4603301
Amakama	1600	2733	3167	406.3	2940	13.82	4787551
Uyo	358	1768	1911	98.7	1846	5.35	282616
Yandev	839	1606	1861	206.1	1719	11.99	1231466

Table 3: Showing the statistical distribution of environmental performance.

the smaller variance Przystalski [22] reported that, the genetic variance tends to be larger in better environments than in poorer environments.

A desirable property of the AMMI model is that, the genotypic and environmental scores can be used to construct powerful graphical representations called biplots [19] that help to interpret the GEI, the biplot showing both genotypes and environments in the same plot. The author further stated that, biplots facilitate the exploration of relationships between genotypes and/or environments. Genotypes that are more similar to each other are closer to each other in the plot than genotypes that are less similar. The same is true for environments. Genotypes/environments that are alike tend to cluster together. Result in Figure 2 indicates that, S Daga location has the highest mean yield 3692 kg/ha, while ART12-1L6P7-8-1-B-1 (2) is the genotype with the highest mean yield. The result also shows that, there is no correlation between Amakama and Yandev/ Uyo locations. The projection of ART12-1L6P7-8-1-B-1 (2) and ART16-9-3-15-3-B-1-1 (8) on to S Daga axis reflects the higher mean yield performance of the genotypes. Similarly in Amakama genotype ART3-9L9P3-1-B-2 (22) and ART2-6L6P6-1-B-1(10) performed best in the location, while genotype ART12-1L6P7-8-1-B-1 (2) and ART16-9-3-15-3-B-1-1 (8) has positive interaction with S Daga. It is also predicted that, genotype ART3-3L12P9-1-1-B (15), ART3-7L9P8-3-B-B-2(20) and ART3-6L3P9-B-B-2 (16) has negative GEI values in S Daga because their projections were towards the negative direction of S Daga arrow. Also genotype FARO55 (23), ART16-22-1-1-2-B-1-1 (7) and WAB706-27-K5-KB-2 (28) have negative interaction with Amakama location. Generally, there was a poor yield performance in Yandev and Uyo locations as shown in Figure 2.

AMMI 2 biplot display

In the AMMI 2 biplot, (Figure 2) the environmental scores (locations) are joined to the origin by side lines. Sites with short vectors do not exert strong interactive forces (Uyo and Yandev). While those that long vectors exert strong interaction (S.Daga and Amakama). Weikai Yan reported that, a short vector indicates a location in which there is a small range of genotype performance.

The vertical Y axis is showing the best one dimension measure of the GE effect for each genotype. Thus, genotypes close to the X axis have a small GE effect, while those far away the X axis in either the positive or negative directions has a large GE effect. Figure 2 shows that, genotype ART10-1L12P2-1-B-1(1) and ART16-16-5-23-1-B-1-1 (6) has a small GE effect, which is considered stable and less influenced by the environments.

Weikai Yan reported that, If the angle between two genotype vectors is less than 90 degrees, then the genotypes are positively correlated, tending to do well, or badly, in the same environment. But if the angle between the vectors of two genotypes is greater than 90 degrees, then they tend to perform differently over the trial environments. If the angle between two genotype vectors is 90 degrees, their performance is independent, of each other. Figure 2 shows that, ART16-9-3-15-3-B-1-1 (8), ART3-9L9P3-1-B-2 (22) and ART3-6L3P9-B-B-3 (17) are

positively correlated. However, there is negative correlation between ART16-9-3-15-3-B-1-1 (8), ART10-1L12P2-1-B-1 (1) and ART16-16-5-23-1-B-1-1(6). Also, there is no correlation between ART16-9-3-15-3-B-1-1 (8) and ART3-12L11P2-B-B-1 (11) ART16-12-22-4-1-B-1-1 (5), ART3-8L6P6-5-B-2(21) and FARO58 (24). The ideal genotype is the genotype with high performance combined with good stability.

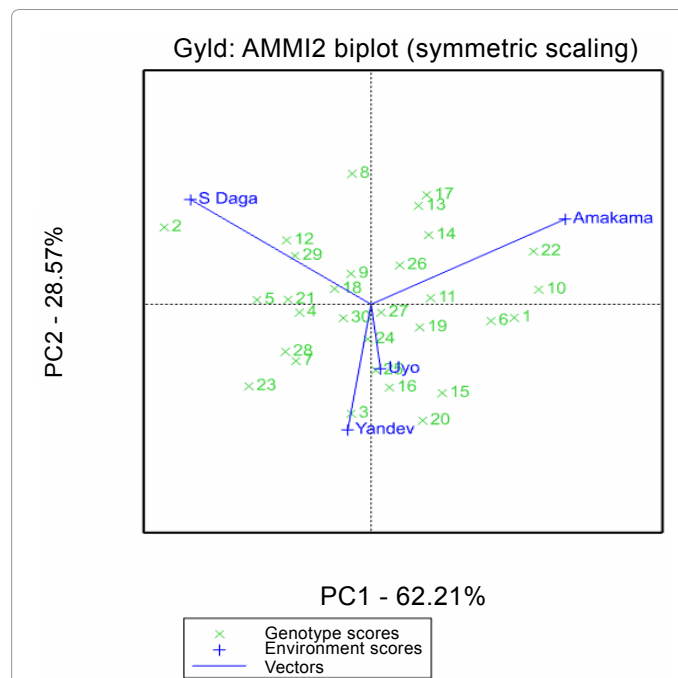GGE biplot also allows the partitioning of environment into

Figure 2: Biplot of AMMI for 30 rice genotypes across four environments.
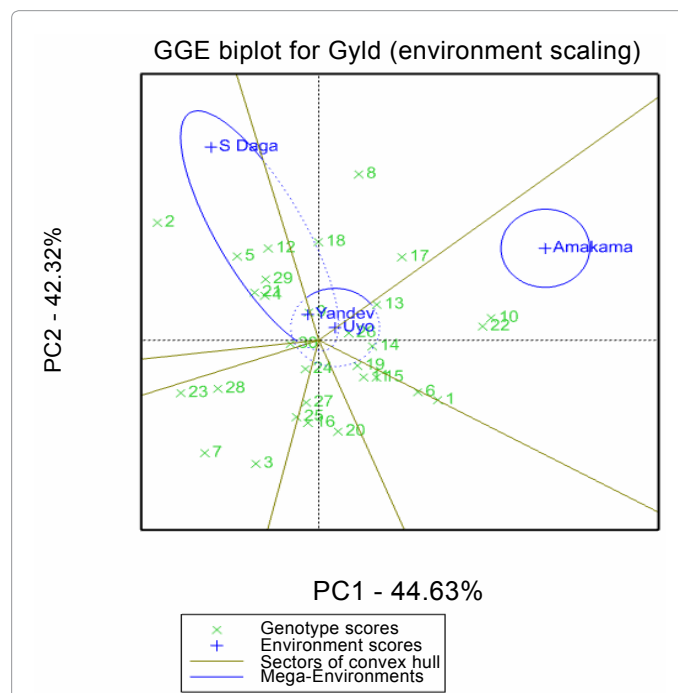

Figure 3: GGE biplot for best rice genotypes in different environments for grain yield.

groups. In this study, three environmental groups are identified as shown in the Figure 3. S Daga and Amakama in the upper part are two different environments, while Yandev and Uyo close to each other at the origin form one similar environment. The partitioning of GGE through GGE biplot analysis of grain yield showed that, PC1 and PC2 accounted for 44.63% and 42.32% of GGE sum of squares respectively, explaining a total of 86.95% variation. GGE biplot shows the cosine of the angle between two environment vectors is proportional to the correlation between those two environments that is an angle of less than 90 degrees. The environments are positively correlated [21]. The result in Figure 3 shows a negative correlation between S Daga and Amakama indicating that different genotypes performed differently across the two environments. The distance between S Daga and Amakama in the GGE biplot is related to the independence of the genotype performance in the two environments, while the closeness of Yandev and Uyo location signifies that genotypes response patterns are similar in yield performance. Therefore to save resources, it is better to select only one location out of this group for further trials, Yandev location could be selected in group 3 as it has the longest vector (Tables 4 and 5).

Conclusion

AMMI statistical model is a tool in selecting the most suitable and

S/no.	Genotype	Location Mean Grain Yield (Kg/ha)				Mean Grain yield (Kg/ha)
		Sabon Daga	Amakama	Uyo	Yandev	
1	ART10-1L12P2-1-B-1	3150	3333	1870	1611	2491
2	ART12-1L6P7-8-1-B-1	4627	2500	1743	1739	2652
3	ART15-4-14-63-2-B-1	3214	2367	1810	1678	2267
4	ART16-12-17-3-4-B-1-1	4004	2800	1849	1936	2647
5	ART16-12-22-4-1-B-1-1	4248	2767	1861	2028	2726
6	ART16-16-5-23-1-B-1-1	3225	3267	1810	1681	2496
7	ART16-22-1-1-2-B-1-1	3417	2167	1794	1369	2187
8	ART16-9-3-15-3-B-1-1	4429	3500	2016	1756	2925
9	ART16-9-4-17-3-B-1	3856	2967	1771	1708	2576
10	ART2-6L6P6-1-B-1	3405	3767	1854	1939	2741
11	ART3-12L11P2-B-B-1	3428	3067	1712	1611	2455
12	ART3-12L2P1-B-B-1	4255	2933	1804	1778	2693
13	ART3-1L6P5-1-B-1	3783	3300	1714	1450	2562
14	ART3-2L4P5-1-B-1	3599	3167	1910	1300	2494
15	ART3-3L12P9-1-1-B	3334	3100	1918	2083	2609
16	ART3-6L3P9-B-B-2	3291	2700	1767	1817	2394
17	ART3-6L3P9-B-B-3	3954	3500	2028	1494	2744
18	ART3-7L3P3-B-B-2	4132	3167	1843	2139	2820
19	ART3-7L9P8-1-B-B-2	3468	3067	1671	1861	2517
20	ART3-7L9P8-3-B-B-2	3166	2800	1931	1917	2454
21	ART3-8L6P6-5-B-2	4048	2767	1790	1894	2625
22	ART3-9L9P3-1-B-2	3423	3700	1992	1583	2675
23	FARO55(NERICA1)	3712	2200	1740	1833	2371
24	FARO58(NERICA7)	3576	2800	1986	1689	2513
25	FARO59(NERICA8)	3354	2667	1722	1756	2375
26	NERICA11	3680	3100	1768	1597	2536
27	NERICA18	3446	2733	1911	1394	2371
28	WAB706-27-K5-KB-2	3679	2367	1903	1606	2389
29	WAB788-16-1-1-2-HB	4121	2833	1993	1606	2638
30	WAB891-SG12	3732	2800	1887	1728	2537
	LSD @ 0.05%	NS	NS	NS	NS	NS
	% CV	19.7	24.3	7.4	10.2	14.3

Table 4: Mean grain yield of upland rice varieties across four location in Nigeria.

s/no.	Trt/no.	Genotype	Sensitivity	Mean	Mean square deviation
1	3	ART15-4-14-63-2-B-1	0.6666	2453	7633
2	13	ART3-1L6P5-1-B-1	0.7323	2267	22924
3	18	ART3-7L3P3-B-B-2	0.7335	2609	49011
4	28	WAB706-27-K5-KB-2	0.7814	2394	5782
5	22	ART3-9L9P3-1-B-2	0.8351	2374	5527
6	5	ART16-12-22-4-1-B-1-1	0.8481	2491	201906
7	7	ART16-22-1-1-2-B-1-1	0.8652	2496	141668
8	9	ART16-9-4-17-3-B-1	0.8931	2187	114581
9	29	WAB788-16-1-1-2-HB	0.8947	2371	199216
10	16	ART3-6L3P9-B-B-2	0.9020	2513	10073
11	10	ART2-6L6P6-1-B-1	0.9223	2517	52360
12	30	WAB891-SG12	0.9226	2741	337543
13	23	FARO55(NERICA1)	0.9326	2388	107737
14	4	ART16-12-17-3-4-B-1-1	0.9480	2371	38952
15	15	ART3-3L12P9-1-1-B	0.9724	2454	43037
16	25	FARO59(NERICA8)	0.9836	2537	8713
17	11	ART3-12L11P2-B-B-1	0.9957	2675	324508
18	1	ART10-1L12P2-1-B-1	1.0467	2647	55744
19	14	ART3-2L4P5-1-B-1	1.0767	2536	17852
20	26	NERICA11	1.0896	2625	68563

Table 5: Twenty environmentally sensitive rice varieties in grain yield across four upland rice growing environments in 2013 using AMMI analysis.

stable high yielding crop genotype 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 rice grain yield in the genotypes is attributed to environments. Most of the genotypes showed environment specificity. The mean grain yield value of genotypes averaged over environments indicated that ART16-9-3-15-3-B-1-1 (8) had the highest mean grain yield 2925 kg/ha. Genotypes ART10-1L12P2-1-B-1(1) and ART16-16-5-23-1-B-1-1 (6) has a small GE effect, which is considered as stable and less influenced by the environment.

References

1. GRISP (Global Rice Science Partnership) (2013). Rice almanac, 4th edition. Los Banos (Philippines) International Rice Research Institute: 283.

2. Akande SO (2002) An Overview of the Nigerian Rice Economy, NISER, Ibadan.

3. Akpokodje GF, Lançon O, Erenstein (2001) Nigeria's Rice Economy: State of the Art. Project Report - The Nigerian Rice Economy in A Competitive World: Constraints, Opportunities And Strategic Choices. Bouake: WARDA: 11-55.

4. UNEP (United Nations Environment Programme) (2005). Annual report; Division of Early Warning and Assessment (DEWA) Nairobi, 00100, Kenya

5. Hill, J (1975) Genotype- environment interaction- A challenge for plant breeding. J. Agri Science, Cam 85: 477-493

6. Lin CS, MR Binn, LP Lefkovitch (1986) Stability an alysis: Where do we stand. Crop Sci 26: 894-900.

7. Crossa J, Gauch HGJ, Zobel RW (1990) Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Science 30: 493-500

8. Flores GV, Daga A, Kalhor HR, Banerjee U (1998) Lozenge is expressed in pluripotent precursor cells and patterns multiple cell types in the Drosophila eye through the control of cell-specific transcription factors.Development 125: 3681-3687.

9. Eberhart SA, Russell WA (1966) Stability parameters for comparing varieties. Crop Sci 6: 36-40.

10. Perkins JM, Jinks JL (1968) Environmental and genotype-environmental components of variability. 3. Multiple lines and crosses.Heredity (Edinb) 23: 339-356.

11. Gauch HG, Furnas RE (1991) Statistical analysis of yield trials with MATMODEL. Agronomy Journal 83: 916-920.

12. Gauch HG (1988) Model selection and validation for yield trials with interaction. Biometrics 44: 705-15

13. Crossa J, Fox PN, Pfeiffer WH, Rajaram S, Gauch HG Jr (1991) AMMI adjustment for statistical analysis of an international wheat yield trial. Theor Appl Genet 81: 27-37

14. Zobel RW, Wright MJ, Gauch HG (1988) Statistical analysis of a yield trial. Agronomy Journal 80: 388-393.

15. Kayode A Sanni OJ, Ariyo DK, Ojo G, Gregorio, et al. (2009) Additive Main Effects and Multiplicative Interactions Analysis of Grain Yield Performances in Rice Genotypes Across Environments. Asian Journal of Plant Sciences 8: 48-53.

16. Gauch HG (1993) Matmodel version 2.0. AMMI and related analysis for two way data matrics. Micro computer power, Ithaca, New York, USA.

17. Gauch HG Jr, Zobel RW (1989) Accuracy and selection success in yield trial analyses.Theor Appl Genet 77: 473-481.

18. Gauch HG (1990) Using Interaction to Improve Yield Estimates. In: Kang MS (ed.) Genotype-by-Environment Interaction and Plant Breeding, Department of Agronomy, Louisiana State University, Baton Rouge, Louisiana, 141-150.

19. Marcos M, Jean-Marcel R, Fred A (2013) The statistical analysis of multi-environment data: modelling genotype-by-environment interaction and its genetic basis; Wageningen University, Netherland

20. Gabriel K (1978) Least squares approximation of matrices by additive and multiplicative models. J. R. Stat. Soc. B 40: 186-196

21. McDermott B, Coe R (2012). An Easy Introduction to Biplots for Multi-Environment Trials; Statistical Services Centre, University of Reading, UK and World Agroforestry Centre, Kenya

22. Przystalski M, Osman A, Thiemt EM, Rolland B,et al. (2008). Comparing the performance of cereal varieties in organic and non-organic cropping systems in different European countries. Euphytica 163: 417-433