



GENOTYPE× ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY IN LOWLAND RICE (*Oryza sativa* Linnus) IN NIGERIA

Tolorunse, K. D., Gana, A. S., Ajaye, O. F. and Zubairu, Y.

Department of Crop Production, Federal University of Technology, Minna

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ABSTRACT: This study evaluated grain yield stability and genotype × environment interactions among rice genotypes across diverse Nigerian lowland environments. The experiment was carried out across five different locations. Treatments were 12 rice genotypes. Data were collected on plant height, number of tillers, 50% flowering, number of panicles, 1000 grain weight, panicle length and grain yield. Data collected were subjected to analysis of variance. The grain yield data was subjected to Additive Main effect and Multiplicative Interaction (AMMI) analysis, Genotype by Genotype by Environment Interaction (GGE). The results revealed that there were significant differences at $p \leq 0.05$ for all traits measured for genotype, environment and genotype by environment interaction. The first two interaction components explained over 86% of the G×E variation. FARO 67 was identified as the most stable genotype, while SC2019, SC2024, and SC2028 showed broad adaptability and are recommended for adoption.

Keywords: Rice genotypes, Grain yield, Stability, Genotype × environment interaction, Lowland rice

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops which serves as staple food in many countries of the world, Nigeria inclusive (Ricepedia, 2020). Rice belongs to the family poaceae and genus *Oryza*, the two cultivated species are *Oryza sativa* and *Oryza glaberrima*. It is an instantaneous energy source, due to its main component, being carbohydrates (starch). According to Sharief *et al.* (2015) more than ninety percent of the world rice production comes from Asia. Rice production in Africa has been characterized by low yield, average grain yield is as low as 2.2 mt/ha compared to a potential yield of 10 mt/ha. This low yield has been attributed to several abiotic and biotic factors. Nigeria

has six different environments that are suitable for cultivating rice: mangrove swamp, deep inland water, rain-fed lowland, upland, irrigated lowland, and hydromorphic. The Lowland (Rain-fed or irrigated) and Hydromorphic ecologies are the most prevalent in the nation and produce most of the rice per unit area (in hectares) (Bashir *et al.*, 2018). Rice production is influenced by seasonal and environmental factors and as well as the genotypic composition of the plant. The grain yield of rice is based on two major factors, which are the genotype and the environment in which the rice is being cultivated. Leon *et al.* (2016) reported that the performance of any character in a particular genotype, is a combined effect of that particular genotype, the environment and the interaction between the two factors (genotype and environment), this gives an insight in identifying genotypes suitable for specific environments. Rice, being one of the most consumed foods in Nigeria, has been faced with a lot of challenges. Most of the varieties available have selective habitat

*Corresponding Author E-mail: kehinde.tolorunse@futminna.edu.ng:
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characteristics and their yield differs greatly according to the environment used in their cultivation. It has been established that varieties that are stable across varied environments are better for breeding programme (Andrew *et al.*, 2014). Rice had moved from staple crop to crop for food security, the high increase in the demand of rice by the teeming populace may not be complemented by the supply system, therefore, development of stable and high yielding variety with good trait such as grain type, aroma, disease resistance, tolerance to abiotic stress is of high importance. The development of new varieties that will be stable across various agroecological zones and having good traits is of utmost importance to farmer in Nigeria. Over the years the two major cultivated varieties (FARO 44 and FARO 57) by farmers had been faced with a lot of challenges such as reduction in yield potential, breaking down of genes making them susceptible to biotic and abiotic stress. (Bashir *et al.*, 2018). Therefore, the objective of this study was to evaluate genotype by environment interaction across major rice growing zones in Nigeria.

MATERIALS AND METHODS

The experiment was conducted at National Cereals Research Institute Badeggi (Latitude 9° 45'57" N and Longitude 6° 8'36"E Southern Guinea Savannah of Nigeria) and some of its outstations in Kebbi (12°29'28" N and 4°15'53" E Sudan Savannah), Bacita (9° 7'06"N, 4°9'58"E Southern Guinea Savannah), Warri (5°31'30"N and 5° 46'9"E Tropical Rainforest) and Akure in a farmers field (7° 27'77"N and 5° 15' 97" Tropical rain forest) during 2023 rainy season. Seeds were sourced from rice breeding gene bank of National Cereals Research Institute Badeggi. The following rice genotypes were collected: SC2002, SC2003, SC2009, SC2010, SC2019, SC2022, SC2024, SC2027, SC2026, SC2028, FARO 44 (check) and FARO 67 (check). The treatments were the 12 rice genotypes fitted into a Randomized Complete Block Design (RCBD) in three replications across locations. The plot size was maintained at 5m x 2m and 20 cm by 20 cm inter and intra row spacing for each treatment. The Nursery was sited where there was proper drainage, exposure to sufficient sunshine, and close proximity to the main field. A raised seedbed was made, 10 meters long, 1 meter wide. The rice seeds were sown in the seedbed. Each genotype was tagged with it appropriate designation. Weed in the nursery was

manually removed by hand pulling after seedling emergence. Rice seedlings were transplanted twenty-one days after seeding at one seedling per hole, at a depth of three centimetres, and a spacing of 20 cm by 20 cm. Before transplanting, the nursery bed as a whole was suitably moistened to soften the compacted soil to allow simple uprooting and to minimize harm to the roots of the rice seedlings which was followed by the distribution of the rice lines to the plots that were allotted to them on the randomized complete block design experimental layout. Orizo Plus (whose active ingredients are 2-4 dichlorophenoxy acetic acid (0.75kg/ha) and 3',4'-dichloropionanilide (1.3kg/ha) was used for the control of weeds at 3-4 weeks after transplanting. Supplementary hand weeding was carried out to control weed at 42 days after transplanting. Fertilizer was applied at recommended rate of 80 kg N, 40 kg P₂O₅ and 40 kg K₂O per hectare. N P K 15:15:15 was used to supply total amount of phosphorus and potassium and a proportion of the Nitrogen needed. Urea fertilizer was used to supply the remaining portion of Nitrogen fertilizer in a split dose at tillering and panicle initiation stages. Data were collected on plant height which was taken from ground level to the tip of the longest panicle and was measured at maturity, number of tiller per plant was counted for each plot at maturity, a quadrat was used and the entire tillers of all rice plant in the quadrat were counted. Days to 50% flowering; this was from sowing to when half of the plant population in each plot are at anthesis, number of panicle in which metre square quadrat was used and the entire rice plant panicle within the quadrat was counted as panicle per square meter. 1000 grain weight was taken from each genotype evaluated, sun dried to 13% moisture content and weighed on an electronic scale with sensitivity between 0.01 and 500g. Panicle length was taken from the base of the panicle to the tip of the top most grain of the panicle (using centimetre ruler) at maturity and grain yield which is the weight of threshed grains per plot was measured and expressed in kilogram per hectare. Data from each locations were subjected to analysis of variance (ANOVA) individually to identify the variations in genotypes at each location. A combined ANOVA was done to average genotype effect, location effect and the interactions between genotypes and environments. The mean separation was performed using Duncan's Multiple Range Test

(DMRT). ANOVA from Additive Main Effects and Multiplicative Interaction (AMMI) and regression model was computed for grain yield. Genotype by environment interaction was quantified using pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, genotype by environment interaction and pooled error). The genotype by environment interaction analysis using Eberhart and Russell regression model was computed by using Plant Breeding (PB) tool version 1.3 statistical software

(Eberhart and Russel 1966). AMMI biplot and GGE biplot was used to determine which genotypes is most stable across test environment.

RESULTS

Table 1 revealed the mean square value of some measured traits, the result showed genotype, environment and genotype by environment interaction (GEI) were significantly different ($P \leq 0.05$) for all measured traits.

Table 1 Mean square value of some lowland rice parameters measured across different environment

Sources Of Variations	50% Flowering	Panicle length	Plant height	Tiller Count/M ²	Panicle Count/M	1000 Grain Weight	Grain Yield/Hectare
Environment	1402.59**	54.81**	705.83**	7905.34**	100453.23**	294.03**	101530433.67**
Genotype	118.58**	38.60**	255.14**	42498.01**	8564.85**	123.58**	7815181.65**
Genotype *Environment	18.39**	7.29**	118.72**	17619.60**	2368.54**	4.24**	5834598.93**
Error	2.16	0.97	4.55	713.86	777.06	1.21	6342.28

*=significantly different at $P \leq 0.05$ **=significantly different at $P \leq 0.01$

Table 2 indicated mean grain yield performance of rice genotypes which were significantly different at $P \leq 0.05$ across various environment in which they were tested. In Akure rice grain yield ranged from 3296.75kg/ha to 8991.75 kg/ha

with genotype FARO 44 being the genotype with the highest grain yield while genotype SC2010 had the lowest grain yield in that environment. FARO 44 Mean grain yield was significantly different from other genotypes.

Table 2 Mean grain yield performance of rice genotypes across different location

Genotype	Akure	Bacita	Badeggi	Kebbi	Warri
SC2024	5907.25 ^h	7791.58 ^f	4791.67 ^c	5666.67 ^d	8041.75 ^c
SC2022	5471.50 ⁱ	5750.00 ^j	4875.00 ^c	4687.50 ^e	5505.00 ^h
SC2010	3296.75 ^k	7875.00 ^{ef}	5208.33 ^a	5916.67 ^c	5482.50 ^h
SC2026	7412.75 ^d	9437.17 ^b	4437.50 ^e	6337.50 ^b	7356.00 ^d
SC2019	6493.25 ^g	8437.50 ^d	5300.00 ^a	6250.00 ^b	6520.00 ^f
SC2003	5991.00 ^h	8604.17 ^c	3916.67 ^f	5635.42 ^d	6063.25 ^g
SC2009	8016.00 ^c	6458.33 ⁱ	1729.17 ⁱ	4197.92 ^f	8093.75 ^c
SC2002	4306.25 ^j	7937.42 ^e	4612.50 ^d	5656.25 ^d	8486.25 ^b
SC2027	6701.75 ^f	8479.17 ^d	4645.83 ^d	5937.50 ^c	6745.75 ^e
SC2028	7146.00 ^e	7333.08 ^g	5025.83 ^b	5552.08 ^d	7257.25 ^d
FARO 44	8991.75 ^a	6625.00 ^h	2666.67 ^h	4020.83 ^g	9024.50 ^a
FARO 67	8344.25 ^b	10666.58 ^a	3750.00 ^g	6583.33 ^a	8396.75 ^b
MEAN	6506.54	7949.58	4246.60	5536.81	7247.73
SE±	60.42	50.39	33.67	61.78	68.68
CV	1.31	0.90	1.12	1.58	1.34

Table 3 Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance

Source of Variation	df	Sum of Square	Mean Square	% explained
Environment (E)	4	406121734.67	101530433.67**	
Genotype (G)	11	85966998.16	7815181.65**	
Genotype*Environment interaction	44	256722352.75	5834598.93**	
IPCA1	14	176143800.20	12581700.00**	68.60
IPCA2	12	46742207.30	3895183.90**	18.20
IPCA3	10	32915042.40	3291504.20**	12.80
IPCA4	8	921302.90	115162.90*	0.40
IPCA5	6	0.00	0.00	0.00

Df = Degree of freedom, IPCA= Interaction Principal Component Axis

Table 3 presents the Additive Main Effect and Multiplicative Interaction (AMMI) analysis of variance. The Interaction Principal Component Axis 1 (IPCA1) accounted for 68.6% of the total variation explained by genotype by environment interaction sum of squares. IPCA2 explained 18.20% of the total variation, while IPCA3 explained 12.80%. These

three principal components (IPCA1, IPCA2, and IPCA3) were found to be significant and provided sufficient explanation for the genotype by environment interaction. Figure 1 shows GGE biplot genotype view. It revealed that the bold line with double arrow head measured the degree of stability while the dotted blue line measured average yield.

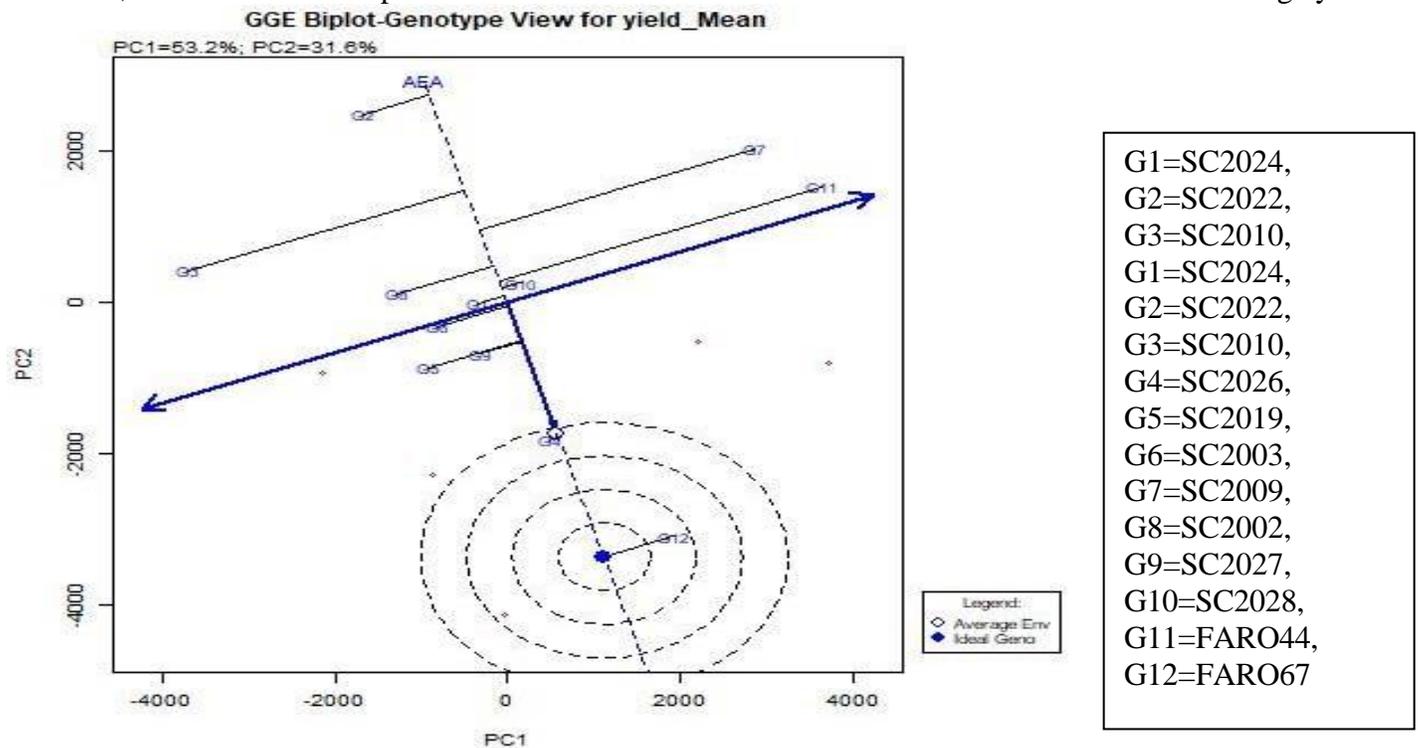


Figure 1 GGE biplot Ranking genotypes based on mean grain yield and stability across environments.

The genotype at the centre of the concentric circle is the ideal genotype which is also the most responsive genotype to a better environment. An ideal genotype is that genotype that is high yielding across all test environments and it is absolutely stable (Figure 1), FARO 67 was identified as the ideal genotype. Genotypes carrying longer vectors are unstable while genotypes with short vectors are stable genotypes. Genotype SC2026, SC2024 SC2027, SC2002, and SC2028 are the stable genotypes while Genotype SC2010, SC2009 and FARO 44 are unstable. Figure 2 shows GGE biplot Environment scaling which group the environment into 3 mega environments with Akure and Warri in the same group while Bacita and Kebbi belong to the same group and Badeggi alone in a separate group.

DISCUSSION

The result from evaluation of the rice genotypes revealed significant differences among all the traits studied across all the locations as shown in the result from the analysis of variance. This indicates a significant level of environmental influence among the studied traits. The combined analysis of variance revealed significant interaction between all the genotypes evaluated and the environment. Similar result was reported by Islam *et al.* (2020) when an experiment was conducted to determine the effect of genotype, environment and genotype by environment interactions on grain yield of some rice genotypes. Shrestha *et al.* (2020) reported highly significant difference for grain yield when stability analysis was carried out for Chinese hybrid rice which is in harmony with the result from this study. Bashir *et al.* (2018) reported significance difference for numbers of tiller per metre square among genotypes across location except for Warri, Enugu and Wushishi location when agronomic performance and Genotype by environment was carried out for some hybrid rice in Nigeria. AMMI analysis revealed that interactions of twelve genotypes and the five environments were predicted by the first two interaction principal component axis. The first and second interaction principal component axis accounted for more than 70% variation explained by genotype by environment interaction sum of square, which is in harmony with Abebe *et al.* (2023), where the first two interaction principal component axis explained more than 70% variation by the sum of square for genotype by environment interaction. Ghazy *et al.* (2023) reported

similar pattern of result when genotype by environment interaction was carried out on 34 rice genotypes. The Joint regression analysis of variance revealed significant differences among the test genotypes across the environments, indicating wide variations in the varieties used for the experiment and their responses to the test environments. Similarly, the test environments showed significant differences, suggesting variations in their quality across locations. The presence of highly significant sensitivity indicated the presence of genotype by environment interaction. The variance ratio indicated that the environment was the major source of variation, consistent with findings by Bashir *et al.* (2018). This study reported significant differences in genotypes, environments, and genotype by environment interaction in rice genotypes subjected to stability analyses, with the environment contributing more to the explained variation. This underscores the importance of considering genotype-environment interaction in crop breeding and management strategies to ensure optimal performance across diverse environmental conditions. Such insights from joint regression analysis can inform the selection of adaptable genotypes and the optimization of management practices to enhance crop productivity and stability across different environments, contributing to sustainable agricultural production and food security initiatives. GGE biplot environmental scaling revealed that the five locations were grouped into three. Genotypes in the same group behaved in similar pattern was reported by Kebede *et al.* (2023) where 9 environments were grouped into 4 mega environments when GGE biplot analysis of genotype by environment interaction and grain yield stability of oat (*Avena sativa* L.) was carried out. Bashir *et al.* (2018) reported similar result pattern where environments were grouped into three mega environment with Kebbi, Enugu, Warri and Wushishi in one group while Lafiyagi was alone in one group and kano also alone in a group when Agronomic Performance and Genotype \times Environment Interaction of some Hybrid Rice was carried out across diverse environment in Nigeria. Similar findings were also reported by Zhang *et al.* (2023) where 8 test sites were classified into two mega-environments using GGE biplot analysis for genotype assessment. GGE biplot revealed that the FARO 67 was the ideal Genotype because it was the genotype at the centre of the concentric circle,

followed closely by Genotype SC2026, SC2024, SC2027, SC2028. An ideal genotype is that genotype that is stable in performance and high yielding across all environment. Similar findings were reported by Zhang *et al.* (2023) where they identified cultivar YG35, ZZG21, and DT29 as the best performers for being the closest to the ideal cultivar.

CONCLUSION

The yield variation experienced across the environments was a clear indication of the presence of genotype by environment interaction and the diversity

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