

INTERNATIONAL JOURNAL OF AGRICULTURE, MANAGEMENT AND TECHNOLOGY



Vol 8(1) 2024

Published by
Federal College of Agriculture,
Ishiagu Ebonyi State

GGE Biplot for Genotype × Environment Interaction: Stability Studies of Hybrid Yam (*Dioscorea rotundata*) Genotypes in South East Nigeria.

Nnabue, I., Udeagbara, A. I., Ochuba, C. O. Edemodu, A.

ABSTRACT

The presence of genotype-environment interaction (GEI) influences production making in the selection of cultivars in a complex process. The two most used methods to analyze GEI and evaluate genotypes are AMMI and GGE Biplot, being used for the analysis of multi environment trials data (MET). Sixteen white yam (*Dioscorea rotundata*) genotypes with two checks (local and standard) in collaboration with and fourteen hybrids from IITA were evaluated in four environments using randomized complete block design (RCBD) with 3 replications. The environments were Umudike (Humid Rain Forest), Abakaliki (Derived Savanna/ Humid Rain Forest), Uyo (Humid Rain Forest) and Igbariam (Humid Rain Forest). The yield data were analyzed using AMMI and GGE statistical model. Both models were equivalent for the data's evaluation, permitting increased reliability in the selection of superior cultivars and test environments. Highly significant ($P < 0.001$) genotype (G), environments (E) and G x E effects were observed on yield of the tested genotypes. Genotype accounted for 19.05, environment 21.4 and G x E 11.4% of the total sum of squares. Genotype TDr1302100 was the top most-yielding genotype and the most stable across the environments among the 16 genotypes.

Key words: AMMI, G X E, hybrid, yams

Introduction

Yams are starchy tuberous vegetables that belong to the *Dioscoreaceae* family. They are widely cultivated for their edible underground tubers and are a staple food in many tropical and subtropical regions. Yams are distinct from sweet potatoes, although the terms are often used interchangeably in some regions, leading to confusion. The scientific name for yams is *Dioscorea*, and there are over 600 species within this genus. Yams are characterized by their large, cylindrical tubers that can vary in size, shape, and color. The outer skin is usually rough and scaly, while the flesh inside can range from white to yellow, pink, or purple. Yams are climbing plants with heart-shaped leaves and produce long vines. Yams are a crucial food source in many parts of Africa, Asia, the Caribbean, and Latin America. They are a versatile ingredient and can be prepared in various ways, including boiling, frying, roasting, or mashing. The taste and texture of yams can be starchy and sweet, making them suitable for both savory and sweet dishes. Yams are a rich source of carbohydrates, providing energy to those who consume them. They also contain essential vitamins and minerals such as vitamin C, vitamin B6, potassium, and fiber. Additionally, yams have been associated with various health benefits, including improved digestion and immune system support. One of the aims of yam (*Dioscorea* spp.) improvement programmes is to improve fresh tuber yields. Yams are

grown in many agroecologies and it is important to assess adaptation and yield stability of promising genotypes across environments (Egesi and Asiedu, 2002).

High yields of yam depend on good planting material and husbandry, particularly weed control to establish a reasonable crop leaf area, adequate water and near optimum temperatures (25-30°C) during the period of maximum potential growth at 14-20 weeks after planting (Norman *et al*, 1995). Success of any genotype depends not only on its good performance with respect to yield and pest and disease tolerance but also its consistency in an ever-changing environment. A genotype by environment (G x E) interaction is said to exist if changes are observed in relative performance of genotypes across environments. Genotype by environment interactions are of great interest when evaluating the stability of breeding clones under different environmental conditions. Several methods have been proposed for statistical analysis of G x E and to predict the phenotypic response to changes in the environment (Van Eeuwijk, 1995). The success of identifying high yielding genotypes from yield trials depends on the effectiveness of the statistical analysis used to evaluate patterns in the data and estimated yields (Gauch and Furnas, 1991). A significant G x E interaction for a quantitative trait reduces the usefulness of the genotype means over all locations or

environments for selecting and advancing superior genotypes to the next stage of selection (Pham and Kang, 1988). This implies that a significant G x E interaction reduces the correlation between phenotypic and genotypic values and confounds yield evaluations of clones (Mariani and Manmana, 1986). Very little work has been done in yams except 1 with respect to identifying means of selecting stable and high yielding yam clones. Environmental conditions strongly influence agricultural production, leading to considerable variations in yield. Such influence is discriminated when yield experiments are performed in various locations and in different years (Pacheco et al., 2005; Akbarpour et al., 2014). Such influence is termed genotype-environment interaction (GEI). In the case of multi-environment trial (MET) data, GEI is frequently present. Due to the nature of this kind of data, it is often represented in two-way tables containing genotype means across all of the environments in the study (Rodrigues et al., 2014; Hongyu et al., 2014). Identifying high-yielding genotypes from trials relies on robust statistical analyses that effectively evaluate patterns in data and estimated yields. A significant G x E interaction, however, poses challenges to the correlation between phenotypic and genotypic values, confounding yield evaluations of clones (Emmanuel et al. 2006).

Despite the importance of yams, minimal research has been conducted on the selection of stable and high-yielding yam clones. This study addresses this gap by employing the GGE procedure to analyze the yield data of sixteen yam (*D. rotundata*) genotypes in four environments (Anderson, et al. 2018). The objective is to determine the level of adaptation (broad or specific) of IITA/Umudike-developed hybrid yams to the agroecological zones in southeast Nigeria.

Methodology

Study Area

The trial was planted in NRCRI, Umudike: Humid Rain Forest (05°28'09.1N, 007°45'4.61E), in Ikwano LGA, Abia State, Akwa Ibom State University, Obioakpa: Humid Rain Forest in Oruk Anam LGA of Akwaibom state, (007°54'47.07E, 05°2'15.86'N). Anambra State University, Igbariam: Humid Rain Forest in Anambra East LGA of Anambra state (007°33'29.6E, 06°213'19.22'N,) and Ebonyi state university: Derived Savanna/ Humid Rain Forest 6.3852° N, 8.0111° Ebonyi state

Plant materials

A multi-locational trial was conducted across four different environments, evaluating the performance of Sixteen *D. rotundata* genotypes (refer to Table 1). These genotypes included fourteen hybrid yam genotypes were sourced from IITA Ibadan alongside two checks (One

National landrace and one National check as standard check). Table 1

Field experimental design

The four multiple environment trials were set up using a randomized complete block design (RCBD) with three replications. In each replication, there were 16 plots with each measuring 10m x 1m with 1m between plot and 1m within reps 24 m x 32 m = (768m²). Each plot comprised 10 stands/plot giving a total of 30 setts/genotype. The furrow spacing between each ridge was 0.5m. Yam setts weighing 150g each, were cut and planted in ridges with a spacing of 1m x 1m apart and individually staked with bamboo poles measuring 2-3 m in height. Planting took place at the onset of rains across the locations (March-April). During the growing season, all the recommended agricultural practices were carried out, and trials were carried out under rain-fed conditions across the locations following Good Agronomical Practices (GAP).

Data collection

At harvest, yield and yield components were collected. All harvest data were done based on the standard operating protocol for the yam varietal performance evaluation trial and the trait ontology dictionary described in YamBase (<https://yambase.org/>)

Statistical analysis

All of the analyses in this study concern only the yield weight, which was the only measured trait with replicates. Replication is a key characteristic for the AMMI model, making it possible to perform analysis of variance (ANOVA). The yield weight (t/ha) was primarily analyzed with simple ANOVA and conjoint analysis to assess the genotypic and environmental main effects as well as the GEI effects. Once GEI was evaluated as a significant effect present in the data, adaptability and phenotypic stability analyses were performed using the GGE models. All statistical

analyses were performed in an open-source R environment version 4.3.1. Multiple comparisons of agronomic characters were used with the help of the “Agricolae” and “Metan” packages Introduced by Gauch (1992), the additive main effects (G and E) and multiplicative interaction (GE) model, or AMMI model, combines ANOVA and PCA in a single model. The ANOVA is based on the AMMI model

$$Y_{ijr} = \mu + g_i + e_j + b_r(e_j) + \sum \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} + \varepsilon_{ijr}$$

where Y_{ijr} is the phenotypic trait (e.g. yield) of genotype i in environment j for replicate r , μ is the grand mean, g_i are the genotype main effects as deviations from μ , e_j are the environment main effects as deviations from μ , λ_k is the eigenvalue for the interaction Principal Component (PC) axis k , α_{ik} and γ_{jk} are the genotype and enviro

onment PC scores (i.e. the left and right eigenvectors) for axis k, $b_r(e_j)$ is the effect of the replication r within the environment j, r is the number of replications, ρ_{ij} is the residual containing AMMI and GGE Biplot for genotype \times environment interaction 103 all multiplicative terms not included in the model (1), n is the number of axes or principal components (PC) retained by the model, and ε_{ijr} are the experimental errors, assumed independent with identical distribution, $\varepsilon_{ijr} \sim N(0, \sigma^2_r)$ (Gauch, 1992; Hongyu et al., 2014).

The GGE Biplot model (Yan et. al., 2000) was introduced based on biplots, which are an effective tool for visualizing two-way data, and are frequently used for the analysis of MET data. A GGE biplot is able to simultaneously display genotype main effects (G) and genotype \times environment effects (GE) from a two-way data table (Yan et. al., 2000). Its first component, when highly correlated

with genotype main effect (G), represents the proportion of production solely attributed to the genotype. The second represents the proportion explained by GEI. For the GGE Biplot to be generated, the mean matrix must be environment-centered and then decomposed into principal components by SVD; the first two PCs are then used to generate the graphic (Yan and Tinker, 2005). The GGE biplot is based on the model:

$$Y_{ij} - \bar{Y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where Y_{ij} is the mean across replications for genotype i ($i = 1, \dots, g$) in environment j ($j = 1, \dots, e$); \bar{Y}_j is the mean of environment j across all genotypes and replications; $\lambda_1 \xi_{i1} \eta_{j1}$ and $\lambda_2 \xi_{i2} \eta_{j2}$ are PC1 and PC2 respectively; λ_1 and λ_2 are the eigenvalues associated with each PC; ξ_{i1} and ξ_{i2} are the PC's scores in the ith genotype; η_{j1} and η_{j2} are the scores for each PC in the jth environment, and ε_{ij} is the error associated with the model (Yan et. al., 2000; Miranda et al., 2009).

Results and Discussion

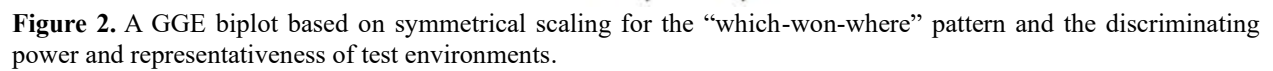
Table 1: The accessions of *D.rotundata* and their collection sites

Sn	Accessions	Description	Origin
1	TDr1302032	Test Clone	IITA
2	TDr1302035	Test Clone	IITA
3	TDr1302039	Test Clone	IITA
4	TDr1302042	Test Clone	IITA
5	TDr1302043	Test Clone	IITA
6	TDr1302051	Test Clone	IITA
7	TDr1302052	Test Clone	IITA
8	TDr1302054	Test Clone	IITA
9	TDr1302096	Test Clone	IITA
10	TDr1302100	Test Clone	IITA
11	TDr1302101	Test Clone	IITA
12	TDr1302116	Test Clone	IITA
13	TDr1302128	Test Clone	IITA
14	TDr8902665	Standard check	IITA
15	TDr9501924	Test Clone	IITA
16	TDrOjuiyawo	Local check	IITA

Table 2: Combined analysis of variance for yield

Source	Df	SumSq	MeanSq	F	Pr(>F)	Proportion(%)
ENV	3	1325.2	441.7	104.2	0.0***	
REP(ENV)	8	33.9	4.2	0.4	0.9	
GEN	15	1174.9	78.3	8.2	0.0***	
GEN:ENV	45	701.1	15.6	1.6	0.0***	
PC1	17	261.7	15.4	1.6	0.1	74.7
PC2	15	64.4	4.3	0.5	1.0	18.4
PC3	13	24.5	1.9	0.2	1.0	7
Residuals	312	2969.0	9.5			
Total	428	6554.6	15.3			

The combined analysis of variance is a useful statistical model that helps express the main effect and estimate the interactions among and within the source of variations as shown in Table 2. Significance differences were observed for genotype-by-environment interactions (GEN:ENV) ($p < 0.001$), illustrating the differences in performances of accessions from one location to another, and the agro-pedology of the environments impacted the agronomic characteristics of accessions tested. Highly significant ($P < 0.001$) genotype (GEN) and environment (ENV) effects were also observed on yield of the tested genotypes. Genotype accounted for 19.05%, environment 21.4% and G x E 11.36% of the total sum of squares (Table 2).



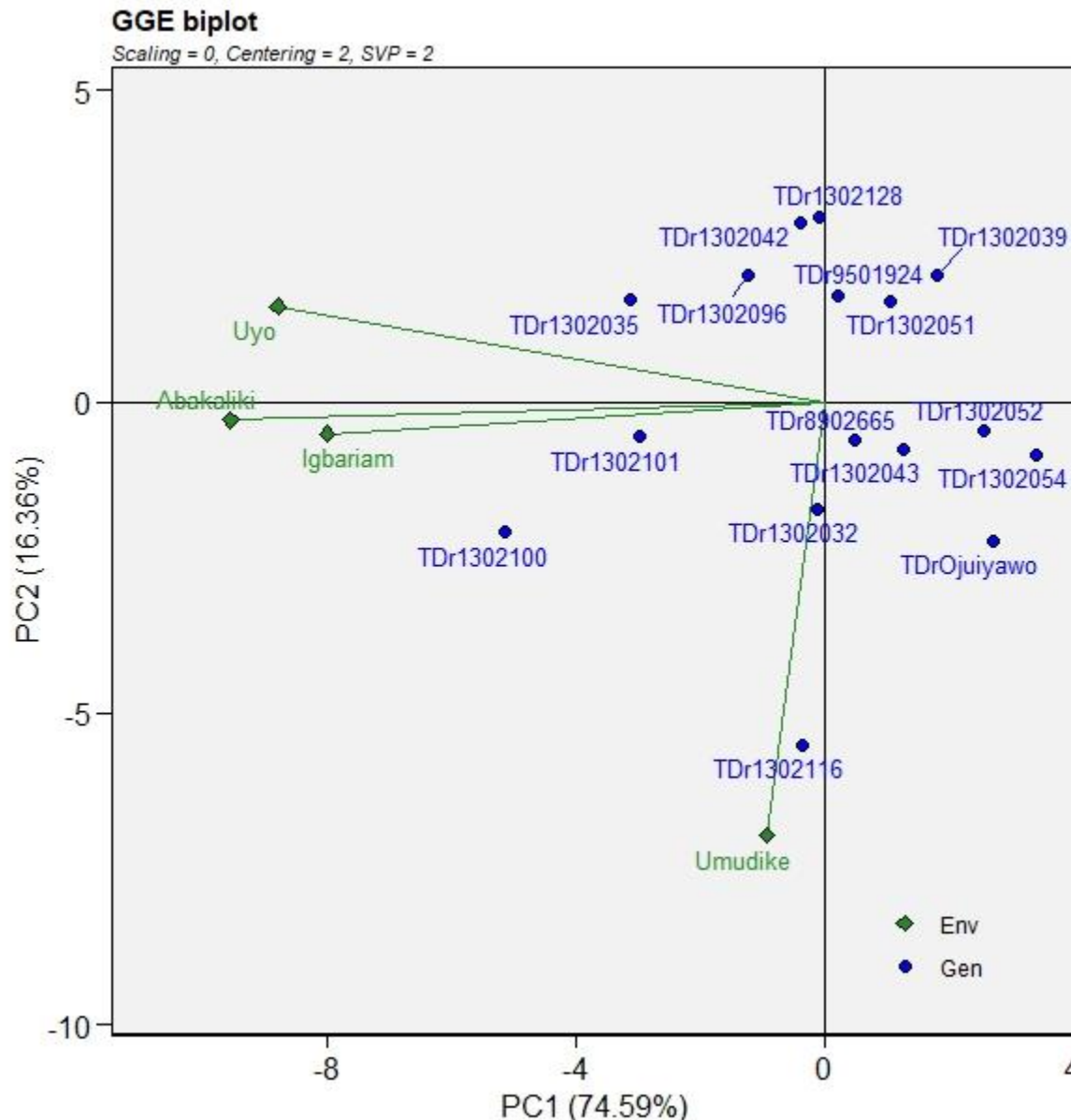


Figure 3. A GGE biplot based on symmetrical scaling involving 16 yam genotypes for total yield of yams (t/ha) evaluated in four environments based on scaling =0, centering = 2 and singular value partitioning (SVP) =2

The GGE biplot is a model that allows us to understand the GEI effects and to detect genotypes targeted for specific environments for their adaptability, as genotypes cannot always win in all environments. Figure 1 show the mean vs. stability of the genotypes evaluated. The abscissa and the ordinate of the average environment coordinate (AEC) are the two lines passing through the origin of the biplot on the basis of singular value partitioning (SVP = 1). The average environment coordination abscissa showed a single direction arrow indicating the ideal genotype main effect. The following are the genotypes toward the arrow that yielded above the average means: TDr1302096, TDr1302032,

TDr1302035, TDr1302101, TDr1302116 and TDr1302100. The projection on the abscissa toward the ordinate of the AEC is a measure of stability, so a genotype with zero projection or very short direction from the ordinate is considered the most stable, while a genotype with the longest projection from the abscissa is unstable. Genotype TDr1302100 and TDr8902665 had the shortest projection and are considered the most stable genotypes across all environment under the study while TDr1302116 had the longest. The GGE polygon plot gave a visual assessment of the GEI. The GGE biplots explained 92.9% of the total variations, with 74.6% and 18.3% for PC1 and PC2 (Figure 3). The

mega-environments were identified for the trait. There were three mega-environments for the total yield of yams (t/ha). The first mega environment included Umudike with the vertex genotypes as TDr1302116 and TDrOjuiyawo. The second mega environment included only one environment which was Abakaliki with vertex genotypes TDr1302096, TDr1302035 and TDr1302101 as the best performer for the environment. The third mega environment consisted of two major environments which are Uyo, and Igbariam. The mega environment has these vertex genotypes TDr1302100 and TDr9501924 as the best performer (Figure 2). The GGE biplot showed that Igbariam was the most discriminating environment as was revealed by the long environmental vector (Figure 3).

Conclusion

The 16 yam accessions used in the current investigation showed different variations in their responses to the three test environments due to the effects of GEI and different expressions of genes that regulate the agronomic traits. TDr1302100 was the top most-yielding genotype and the most stable across the environments among the 16 genotypes. TDr1302096, TDr1302032, TDr1302035, TDr1302101, TDr1302116 and TDr1302100 have above-average yields. Abakaliki was discriminating and representative and is classified as the superior environment. This study identified the genotypes that adapted well and uniquely to each environment. TDr1302096, TDr1302035 and TDr1302101 recorded the highest yields in Abakaliki. TDr1302100 and TDr9501924 were the best in Uyo and Igbariam and TDr1302116 and TDrOjuiyawo outperformed in Umudike.

Reference

- Akbarpour O., Dehghani H., Sorkhi B., Gauch Jr. H.G. (2014): Evaluation of Genotype \times Environment Interaction in Barley (*Hordeum Vulgare* L.) Based on AMMI model Using Developed SAS Program. *J. Agr. Sci. Tech.* 16: 909-920.
- Anderson, C. N., Jhessica L. K., Kuang H. (2018). AMMI and GGE Biplot for genotype \times environment interaction: a medoid-based hierarchical cluster analysis approach for high dimensional data. *Biometrical Letters* Vol. 55, No. 2, 97-121. DOI: 10.2478/bile.2018-0008.
- Coursey, D. G. (1967). Yams: An Account of the Nature, Origins, Cultivation, and Utilization of the Useful Members of the Dioscoreaceae. *Longmans*.
- Egesi, C.N and Asiedu, R. (2002). Analysis of yam yields using the additive main effects and multiplicative interaction (AMMI) model. *African Crop Science Journal* 10(3):195-201.
- Emmanuel, O., Christian C. O., Robert A. (2006). Stability studies of hybrid yam (*Dioscorea rotundata* Poir.) genotypes in Ghana. *Journal of Food, Agriculture & Environment* Vol.4 (1): 234-238.
- Gauch H.G. (1992): Statistical analysis of regional yield trials: AMMI analysis of factorial designs. *Elsevier, Amsterdam*.
- Gauch, H.G. and Furnas, R.E. (1991). Statistical analysis of yield trials with MATMODEL. *Agron. J.* 83:916-920.
- Hongyu K., Peña M.G., Araújo L.B., Dias C.T.S. (2014): Statistical analysis of yield trials by AMMI analysis of genotype \times environment interaction. *Biometrical Letters* 51(2): 89-102.
- Mariani, B.M. and Manmana, P.N. (1986). Combination of results of several data sets: Some possibilities for a better understanding of the genotype-environment interaction. *Genetica Agraria* 40:83-96.
- Miranda G.V., Souza L.V., Guimarães L.J.M., Namorato H., Oliveira L.R., Soares M.O. (2009): Multivariate analyses of genotype \times environment interaction of popcorn. *Pesq. agropec. bras., Brasília* 44(1): 45-50.
- National Research Council. (2009). Lost Crops of Africa: Volume II: Vegetables. *National Academies Press*.
- Norman, M.J.T., Pearson, C.J. and Searle, P.G.E. (1995). Yams. Tropical Food Crops in Their Environment. 2ed. *Cambridge University Press, Cambridge*.
- Pacheco R.M., Duarte J.B., Vencovsky R., Pinheiro J.B., Oliveira A.B. (2005): Use of supplementary genotypes in AMMI analysis. *Theor Appl Genet* 110: 812-818.
- Pham HN and Kang MS (1988) Interrelationships among respectability of several stability statistics estimated from international maize trials. *Crop Sci* 28:925-928.
- Rodrigues P.C., Malosetti M., Gauch H. G., Van Eeuwijk F.A. (2014): A weighted AMMI algorithm to study genotype-by-environment interaction and QTL by environment interaction. *Crop Science* 54(4): 1555-1570.
- Van Eeuwijk, F.A. (1995). Linear and Bilinear Models for the Analysis of Multi-Environment Trials: I. An Inventory of Models. *Euphytica*, 84, 1-7. <http://dx.doi.org/10.1007/BF01677551>
- Yan W., Hunt L.A., Sheng Q., Szlavnick Z. (2000): Cultivar evaluation and mega environment

investigation based on the GGE biplot.
Crop Science 40(3) : 597-605.

Yan W., Tinker N.A. (2005): An Integrated Biplot Analysis System for Display ing, Interpreting, and Exploring Genotype \times Environment Interaction. *Crop Science* 45 : 1004-1016.