

**ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTIONS
ANALYSIS OF HARVEST INDEX PERFORMANCES IN CASSAVA
(*Manihot esculenta*, Crantz) GENOTYPES ACROSS 4 ENVIRONMENTS**

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ABSTRACT: Eight cassava genotypes were evaluated for harvest index performance across four environments. Data analysis was performed using MATMODEL and GGEbiplot. AMMI analysis of variance showed that 10.02% of the total sum of squares was attributable to environmental effects, 3.99% to genotypic effects and 50.13% to GEI effects. The GEI sum of squares contained approximately 76.52% (0.30709) pattern and 23.48% (0.09442) noise of the total GEI. The mean squares for IPCA 1 and IPCA 2 were significant at $P = 0.000$ and 0.002 respectively; all together they contributed 94.18% of the total GEI. Therefore, the post-dictive evaluation using an F-test at 0.000 and 0.002 suggested that two principal axes of the interaction were significant for the model with 16 degrees of freedom. The predictive assessment measured by the average root mean square predictive difference (RMS PD), selected AMMI1 with the first interaction PCA axis as the most predictively accurate. The AMMI1 model had the lowest average RMS PD (9.996). Mean performance and stability of the genotypes assessed by biplot analysis showed that the most stable genotypes were G2, G1 and G7. However G5 was highly unstable followed by G8 and G3. Two mega-environments were defined namely: G5-winning niche and G3-winning niche. The current study has demonstrated that the GGE biplot is a useful tool for the analysis of multi-environment trial (MET) data.

Key Words: AMMI, GGEbiplot, stability, harvest index, mega-environment

INTRODUCTION

Yield performance of a number of genotypes evaluated across a number of environments is always affected by genotype x environment interaction (GEI). Difference in genotype ranking across environments may depend on the magnitude of the interactions or the differential responses to environments. Interaction effect can be quantified by using a combined analysis of variance. However analysis of variance is not informative for explaining GEI.

The additive main effect and multiplicative interaction (AMMI) model is a useful model for understanding GEI. The model integrates additive main effects and multiplicative components, extracting first the additive main effects and then using principal components analysis to investigate the GEI. Accuracy of estimates of genotypic yields in multi-location trials is the main focus of plant

breeding. This method has been referred to as yield prediction assessment and functions by splitting the data into modelling and validation data, with the values expected by the model compared with the validation data (Gauch and Zobel 1988).

Visual examination of GEI can be done by a biplot where both genotypes and locations occur on the same scattergram. It clearly shows which genotype won in which environment and therefore facilitates mega-environment identification (Mohammadi and Haghparast 2007).

MATERIALS AND METHODS

This study was carried out to determine the harvest index performance of 8 cassava genotypes across four environments in the 2004-2005 growing season. Environments comprised two locations and two different harvest times. The two locations were Bunso and Legon.

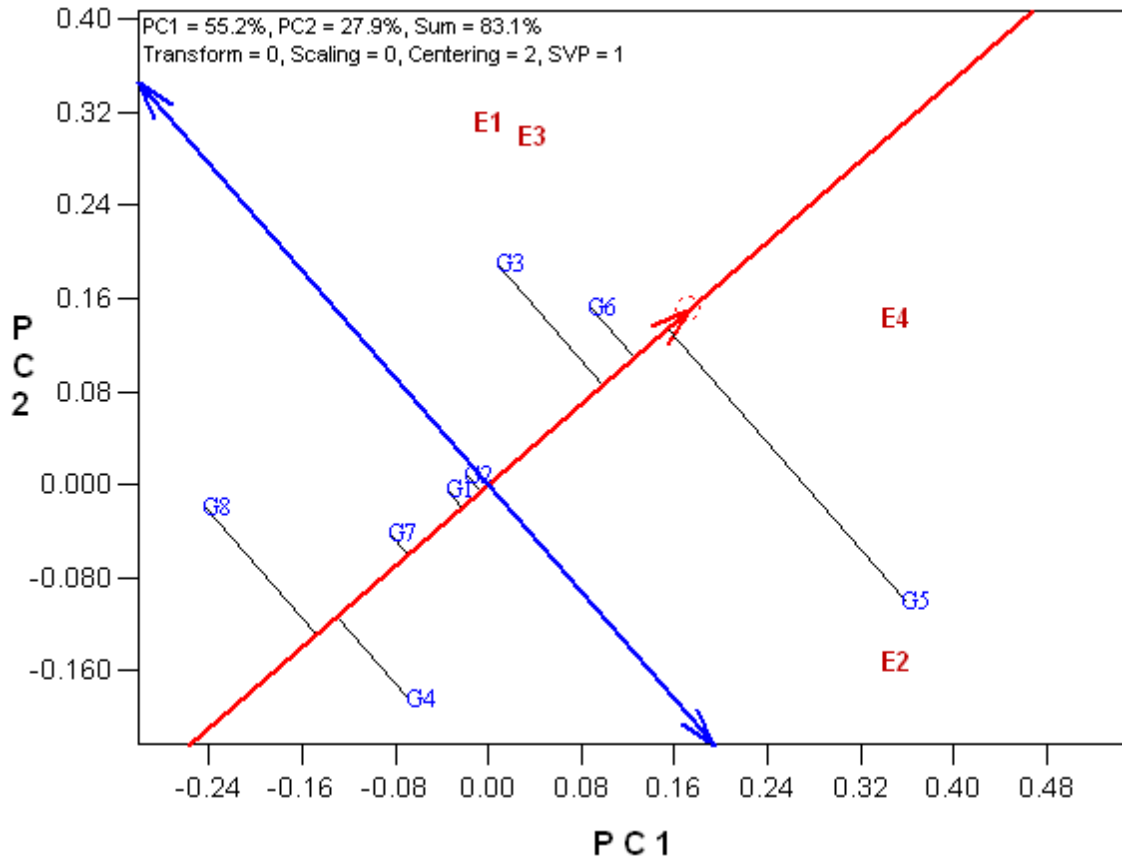


Figure1. Mean performance and stability of 8 cassava genotypes for harvest index

Table 1. Origin, code and source of cassava genotypes

Cassava genotype	Genotype Code	Origin
Afisia fi	G1	Released variety
HO001	G2	Volta Region
Bosome Nsia	G3	Local material
UCC90	G4	Western Region
DMA030	G5	Dormaa Ahenkro
UG126	G6	University of Ghana
HO015	G7	Volta Region
HO008	G8	Volta Region

Bunso is located in the semi-deciduous agroecological zone in the Eastern region of Ghana and Legon is located in the coastal savannah agroecological zone in the Greater Accra region of Ghana. Description and designations of the four environments are shown in Table 2. The experimental materials (Table 1) were the top 8 genotypes of 32 early bulking cassava genotypes stored at the research farm of the Department of Crop Science University of Ghana Legon. The experimental layout was a randomized complete block design with three replications. The experimental area was divided into three blocks with inter-block distance of 2 m. Each block measured 23 m long and 11 m wide. Each block was further divided into eight 5 m by 5 m plots with 1 m spacing between plots. Harvest index was calculated as weight of cassava storage roots divided by sum of top weight and storage root weight.

The MATMODEL (Version 3.0, Gauch, 2007) was used to perform analysis of AMMI on the data. Biplot analysis was carried out by using the GGEbiplot (version 4.1)

RESULTS AND DISCUSSION

The AMMI analysis of variance of cassava harvest index of the 8 cassava genotypes tested in the four environments showed that 10.02% of the total sum of squares was attributable to environmental effects, 3.99% to genotypic effects and 50.13% to GEI effects (Table 2). The magnitude of the GEI sum of squares was 2.5 times larger than that for genotypes, indicating that there were

some levels of differences in genotypic response across environments. The noise sum of squares in the interaction can be estimated as GEI degrees of freedom multiplied by the Error MS. Accordingly, the GEI sum of squares contains approximately 76.52% (0.30709) pattern and 23.48% (0.09442) noise of the total GEI.

Results of the AMMI analysis (Table 3) further showed that the first principal component axis (PCA 1) of the interaction captured 66.53% of the interaction sum of squares in 42.86% of the interaction degrees of freedom. Similarly, the second principal component axis (PCA 2) explained a further 27.65% of the GEI sum of squares. Furthermore, the sums of squares for PCA 1 and PCA 2 were greater than that of genotypes. The mean squares for PCA 1 and PCA 2 were significant at $P = 0.000$ and 0.002 respectively; cumulatively they contributed to 94.18% of the total GEI. Therefore, the post-dictive evaluation using an F-test at 0.000 and 0.002 suggested that two principal axes of the interaction were significant for the model with 16 degrees of freedom.

The most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1996; Yan et al., 2002). Predictive PCA axis cannot be specified a priori without AMMI model-validation for predictive assessment (Gauch, 2007). In the current study, predictive assessment measured by the average root mean square predictive difference (RMS PD), selected AMMI1 with the first interaction PCA axis as the most predictively accurate. The AMMI1 model had the lowest average RMS

Table 2. Designation of the environments

Environment	Environment code	Location	Harvesting period
1	E1	Bunso	12MAP
2	E2	Legon	12MAP
3	E3	Bunso	8MAP
4	E4	Legon	8MAP

Table 3. Additive main effects and multiplicative interaction analysis of variance for harvest index including the first three interaction principal component analysis (PCA) axes.

Source of variation	df	Sum of squares	Mean squares	Explained %
Treatment combination	31	0.5135	0.0166***	
Genotype (G)	7	0.032	0.0046	
Environment (E)	3	0.0802	0.0267***	
G-E	21	0.4013	0.0191***	
Interaction PCA 1	9	0.267	0.0297***	66.53
Interaction PCA 2	7	0.111	0.0159**	27.65
Interaction PCA 3	5	0.0234	0.0047	5.83
Residual	64	0.2671	0.0045	
Total	95	0.8006	0.0084	

PD (9.996) (Table 4) based on 1000 runs having 32000 validations with actual treatment data. This model has 19 df (3 for environments plus 7 for genotypes plus 9 for interaction PCA axis 1) and is 1.4 times parsimonious (few df) as AMMI2, which was selected for postdictive success (i.e., AMMI2 contains 1.4 times as many df as AMMI1).

Table 4. Average root mean square predictive difference (RMS PD) for four models constructed based on harvest index from the cassava trial.

Model	df	RMS PD
AMMI0	10	0.0921
AMMI1	19	0.0839
AMMI2	26	0.0812*
AMMI3	31	0.0824

Mean performance and stability of the genotypes were assessed by biplot analysis (Fig. 1). On the biplot the single-arrowed line, the average-environment coordination (AEC) abscissa points to higher mean harvest index across

environments. The double-arrowed line is the AEC ordinate and it points to greater variability (poor stability) in either direction. Genotype G5 had the highest value of harvest index followed by G6 and G3. Genotype G8 had the lowest value. The most stable genotypes were G2, G1 and G7. However G5 was highly unstable followed by G8 and G3.

A biplot was generated using genotypic and environmental sources of the first two AMMI components (Vargas and Crossa, 2000). The biplot was used to identify winning genotypes and mega-environments (Fig. 2). On the biplot, some corner or vertex genotypes, which are the most responsive ones, can be visually identified. These are either the best or the poorest genotypes at some or all environment (Weikai *et al.*, 2006). The vertex genotypes for the present work were G1, G4, G8, G3 and G6 (Fig. 2). Genotypes G1, G2, and G7 were located within the polygon and were found less responsive (Weikai *et al.*, 2006). Two mega-environments were defined namely: G5-winning niche and G3-winning

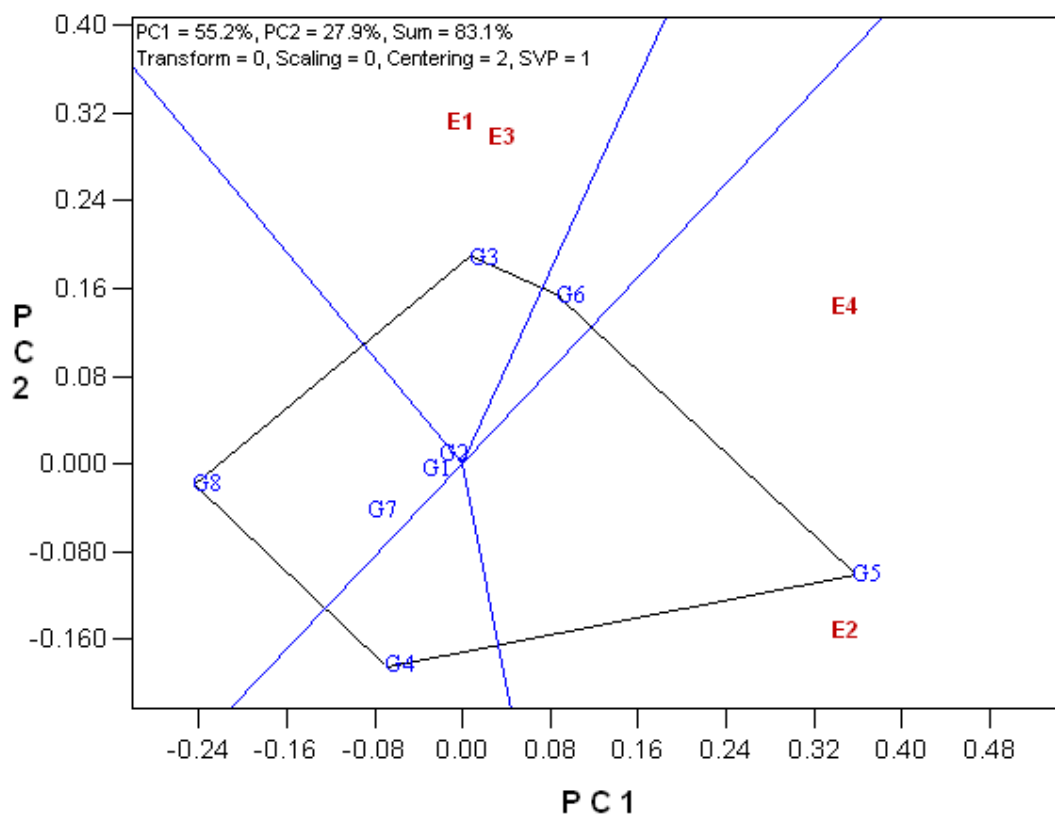


Figure 2. Mega-environment defined by different winning cassava genotypes for harvest index

niche. No environments fell in the sectors with G4, G6 and G8 as vertex genotypes. This indicates that these vertex genotypes were not the best in any of the test environments, but the poorest in some or all of the environments.

The current study has shown that the GGE biplot is a useful tool for the analysis of multi-environment trial (MET) data. On the basis of a drawn-to-scale, two-dimensional GGE biplot, the similarities and differences among environments in their discrimination and genotypes, the similarities and differences among the genotypes in their response to the environments and the nature and magnitude of interaction between any genotype and any environment can be readily visualized (Yan *et al*, 2000). Year-to-year variation may limit the value of a single year data, however biplot analysis of single year MET data is worthwhile and its reasons have been described in detail by Yan *et al* (2001). Although conclusions from a single year MET may not be conclusive, they may be valuable suggestions (Yan *et al*,

2001). Even if the which-won-where pattern is proven to be unrepeatable over years, the researcher would still want to know the average yield and the stability of the cultivars based on each year's MET.

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