



Original Research Article

AMMI and GGE biplot analysis of root yield performance of cassava genotypes in the forest and coastal ecologies

Accepted 16 February, 2015

¹Agyeman, A*, ²Parkes, E.
and
²Peprah, B. B.

¹Crops Research Institute, P.O.
Box 3785, Kumasi, Ghana.

²International Institute of
Tropical Agriculture, Ibadan, Oyo
State, Nigeria.

*Corresponding Author
E-mail: amaagyeman@gmail.com
Tel.: +233 208185929

Multiple environment trials (MET) are generally carried out by plant breeders to select and recommend high yielding and stable genotypes for a set of environments. The analysis of MET data often results in genotype-by-environment interactions which often causes difficulties in the interpretation of results and reduce efficiency in selecting the best genotypes. AMMI and GGE biplot analysis are two recent methods that are widely used to overcome these difficulties in MET data analysis. The objective of this study was to compare GGE biplot and AMMI analysis that determine the most efficient method for evaluating and describing genotype performance across environments. Ten (10) cassava (*Manihot esculenta*) genotypes including two local checks were evaluated across six (6) environments in Southern Ghana. The experimental layout was a randomized complete block design with three replications. The Additive Main Effects and Multiplicative Interaction (AMMI) analysis of variance identified highly significant effects for environment, genotype and genotype by environment interaction denoting different responses of genotypes across environments. The AMMI1 biplot identified AR14-10, CR42-4 and CR59-4 as the most stable genotypes but could not accurately display the performance of a given genotype in a given environment. However, the GGE biplot provided more information with regards to environments and genotype performance than the AMMI1 biplot analysis and was able to identify the environment PK08 as being the most representative and desirable of all.

Key words: Cassava, root yield, AMMI, GGEbiplot, Ghana

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is the most important vegetative propagated food crop in Africa. It is also the second most important food staple in terms of calories per capita. More than 800 million people depend on it for their calorie needs (Burns et al. 2010). The total cassava consumption more than doubled from 24 million tons per year in the early 1960's to 58 million tons per year in the early 2000s (FAO, 2006). Cassava has been adjudged in Africa, as a food security crop mainly because of its ability and capacity to yield well in drought-prone, marginal wastelands under poor management where other crops would fail (Akinwale et al., 2011). Despite cassava's ability to grow in marginal areas large differential genotypic

responses occur under varying environmental conditions (Mkumbira et al., 2003). This phenomenon is referred to as genotype × environment interactions (GEI), which routinely occurs in plant breeding programs (Kang, 1998).

In plant breeding programs, genotypes are evaluated in multi-environment trials (METs) by testing their performance across environments and selecting the best genotypes in specific environments. However, selection of superior genotypes in multi-environment trials usually results in genotype-by-environment interactions that often complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). This interaction is the

result of changes in genotype's relative performance across environments, due to differential responses of the genotypes to various abiotic and biotic factors (Dixon and Nukenine, 1997). Thus, a significant Genotype \times Environment (GE) interaction for a quantitative trait such as root yield can complicate the identification of superior genotypes for both improved crop development and new crop introduction.

Several statistical methods have therefore been proposed to facilitate the interpretation of GEI from MET's. The most commonly used statistical technique for analyzing GEI is the two-way cross classification analysis of variance (ANOVA). However, while this technique can adequately explain only the main effects and identify GEI as a source of variation, it fails to analyze the inherent effects of GEI. This is because the additive nature of the ordinary ANOVA model does not allow it to analyze a non-additive interaction component and other statistical techniques are therefore required to identify interaction relationships. Manrique and Hermann (2002) conducted a MET study to compare the efficiency of a number of suitable statistical techniques to classify clones based on the stability of their performances. They concluded that regression analysis did not effectively identify stable genotypes, but did provide information on genotype performance under improving environments. Gauch and Zobel (1988) also compared the performance of the ANOVA method with the regression method and found that ANOVA fails to detect a significant interaction component and the regression approach accounts for only a small portion of the interaction sum of squares only when the pattern fits a specific regression model.

The AMMI model has been reported to be an efficient method because it captures a large portion of the GE sum of squares and uniquely separates main and interaction effects as required for most agricultural research purposes (Gauch, 2006). It has proved to be a powerful tool used by researchers to evaluate a number of genotypes established in a number of environments, identify stable and adaptable genotypes and determine the magnitude of GEI (Crossa, 1990). Consequently, Gruneberg et al. (2005) suggested that the AMMI model was a highly efficient multivariate tool for the analysis of MET data. Likewise, the most well known and appealing component of AMMI analysis is the graphical display of the results in a very informative biplot (AMMI1) that shows both main and interaction effects for both genotype and environment (Zobel et al. 1988). Yet, the AMMI1 biplot does not have the most important property of a true biplot, namely the inner-product property. In addition, the AMMI1 biplot does not display the discriminating ability and representativeness view of a biplot which is effective in evaluating test environments. This has been recognized by Yan et al., (2000) who adopted the proposal of Gabriel, (1971) by using the biplot technique to display the genotype main effect plus genotype by-environment interaction (G+GE) of a MET's data, and called it the GGE biplot.

GGE biplot is a graphical tool which displays, interprets

and explores two important sources of variation, namely genotype main effect and GE interaction of MET data (Fan et al. 2007; Yan, et al. 2000). GGE biplot analysis considers that only the G and GE effects are relevant and that they need to be considered simultaneously when evaluating genotypes. The GGE biplot has therefore been used in crop variety trials to effectively identify the best-performing genotype across environments, identify the best genotypes for mega-environment delineation, whereby specific genotypes can be recommended to specific mega-environments and evaluate the yield and stability of genotypes (Yan and Kang, 2003; Yan and Tinker, 2006). The relative versatility of the GGE biplot, especially in mega-environment analysis and genotype selection, is worthy of being exploited for selection of genotypes for specific environments. More importantly, it would assist in guiding the direction of varietal development for stable ecology based selections.

The differences between the GGE biplot and AMMI methods are the following; firstly, AMMI stands for the additive main effect and multiplicative interaction (Gauch, 1992), and GGE stands for genotype main effect plus GE interaction (Ma, 2004). Secondly, the GGE biplot analysis is based on environment-centered principal component analysis (PCA), whereas AMMI analysis is established on double centered PCA (Kroonenberg, 1995). However, according to (Yan and Tinker, 2006) AMMI could be misleading if used for the purpose of "which-won-where" (i.e., identification of mega-environments as well as their winning genotypes). Also, Ding et al. (2007) asserted that the GGE biplot is superior to the AMMI, because it provides a lot more visual interpretations than the AMMI, by allowing the visualization of any crossover GE interaction which is usually essential to breeding programs.

A number of multi-environment trial studies have compared the AMMI and GGE biplot analyses to obtain an effective tool for analyzing GEI and have come out with differing results. Kandus et al. (2010) found the AMMI model was the best model to describe the GEI in maize. Stojaković et al. (2010) and Mitrovic et al. (2012) also found out that the models provided similar results. Moreover, (Rad et al., 2013) indicated that both models performed equally using data on bread wheat while, Samonte et al (2005) found the AMMI and GGE biplot analyses complemented one another. Contrary to these findings, Yan et al. (2007) compared the GGE biplot and AMMI analyses and concluded that the GGE biplot was superior to the AMMI biplot in mega-environment analysis and genotype evaluation.

OBJECTIVES

The main objectives of this study were (1) to determine the magnitude and patterns of G \times E interaction effects in cassava using the AMMI and GGE biplot methods of analysis (2) to display graphically the mean performance and stability of 10 cassava genotypes and (3) to compare GGE

biplot and AMMI analysis that determine the most suitable method for evaluating and describing cassava genotype performance in the forest and coastal ecologies of Ghana.

MATERIALS AND METHODS

The study was conducted in two cropping seasons (2007-2008 and 2008-2009) at three experimental sites: Fumesua (with annual rainfall of 1500-1750 mm; altitude 277 m; mean annual temperature of 20 to 34°C; coordinates 6° 41' N; 1° 28' W; Ferric Acrisol soils, Bomso series; forest); Ohawu (with annual rainfall of 1000-1500 mm; altitude 24 m; mean annual temperature of 24 to 34°C; coordinates 6°8' N 0°54' E ; Dystric Luvisol soils, Toje Alajo series; coastal savanna); and Pokuase (with annual rainfall of 800-1000 mm; altitude 65 m; mean annual temperature of 21 to 30°C; coordinates 5° 41'N; 0° 17' W; Chromic Lixisol soils, Adams series; coastal savanna) in Ghana. Total rainfall, mean maximum and minimum temperatures during the experimental period was presented in Table 1.

Ten genotypes were tested on experimental sites at Fumesua, Ohawu and Pokuase in this study. Out of the 10 advanced lines assessed, 8 elite inter-specific hybrid cassava genotypes were introduced from International Center for Tropical Agriculture (CIAT) through National Root Crops Research Institute (NRCRI), Umudike: AR14-10, AR15-5, CR41-10, CR42-4, CR52A-25, CR52A-31, CR52A-4 and CR59-4. The other two genotypes used as checks, comprised of Afisiafi, an improved cultivar and a land race called Sisipe166, extensively grown in Ghana because of their outstanding agronomic performance and moderate resistance to major pests and diseases. The experimental design was a randomized complete block design with three replications at each site under rain fed conditions. Planting dates at Fumesua, Ohawu and Pokuase were on the 10th, 13th and 15th day of July respectively for the two cropping seasons. The plot size was 4 × 10 m and a spacing of 1 × 1 m was used. Hand weeding was done as and when necessary. At harvest (12 months after planting (MAP)) data were collected for fresh root yield and converted into (kg ha⁻¹). Data was collected from the inner plants within a plot.

AMMI method of analysis

AMMI analysis was carried out for root yield of ten cassava genotypes obtained per plot across environments using the Genstat software Release 7.22 DE, 2008. The AMMI model combines the analysis of variance for main effects of G and E with principal components analysis of GEI. It has proven useful in understanding complex GEI. Stable genotypes for each environment were selected by AMMI and principal component axes (PCAs) were extracted and statistically tested by Gollob's (1968) F-test procedure (Vargas and Crossa, 2000). These components from AMMI analysis were used to obtain a biplot of the main effect of means versus the first Interaction Principal Component Analysis Axis (IPCA1). IPCA1 The pattern of response of G, E, and GEI

were then identified.

The AMMI model equation according to Gauch and Zobel (1996) for T genotypes and S environments is

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

$$\theta_{ij} \sim N(0, \sigma^2); i = 1, 2, \dots, T; j = 1, 2, \dots, S.$$

Where, Y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment; μ is the general mean g_i is the i^{th} genotypic effect; e_j is the j^{th} location effect; λ_n is the eigen value of the PCA axis n ; α_{in} and γ_{jn} are the i^{th} genotype j^{th} environment PCA scores for the PCA axis n ; θ_{ij} is the residual; n' is the number of PCA axis retained in the model.

The genotype x environment interaction effects were calculated using the formula $(GxE)_{ij} = \bar{y}_{ij} - \bar{y}_i - \bar{y}_j + \bar{y}..$ (where y_{ij} is the mean of the i^{th} genotype on the j^{th} environment and y_i , y_j , and $y..$ are the mean of the i^{th} genotype, the mean of the j^{th} environment, and the overall mean, respectively (Vargas et al., 1999).

GGE biplot method of analysis

The GGE biplot method outlined by Yan, (2002) was used to display the G and GE interaction patterns in the data in a biplot. The which-won-where pattern (which is an intrinsic property of the GGE biplot rendered by the inner-product property of the biplot, of the cassava Genotype Environment Data (GED) set was also visually presented. In addition, the GGE biplot was used to identify high yielding and adapted cassava genotypes as well as suitable test environments. The best cassava genotypes were represented by large principal component scores (PCA 1, high root yield) and small principal component scores (PCA 2, high stability) (Yan, 2001). Genotypes that had PCA 1 scores >0 were identified as higher yielding and those that had PCA 1 scores <0 were identified as lower yielding. PCA 1 scores >0 detected the genotypes of interest (i.e. adaptable or higher yielding), while PCA 1 scores <0 discriminated the non-adaptable ones (Zerihun, 2011). PCA 2, which was related to genotypic stability or instability, divided the genotypes of interest based on their scores. The model for the GGE biplot based on singular value decomposition (SVD) of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is the measured mean of genotype i in environment j , μ is the grand mean, β_j is the main effect of environment j , $\mu + \beta_j$ being the mean yield across all genotypes in environment j , λ_1 and λ_2 are the singular values (SV) for the first and second principal component (PCA 1 and PCA 2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PCA 1 and PCA 2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j

Table 1. Average maximum and minimum temperature and total rainfall during the experimental period at Fumesua, Ohawu and Pokuase

Location	Season 1 (2007-2008)			Season 2 (2008-2009)		
	Rainfall (mm)	Temperature (°C)		Rainfall (mm)	Temperature (°C)	
		Min.	Max.		Min.	Max.
FUMESUA	2011.0	22.06	31.47	1839.2	22.54	31.38
OHAWU	923.4	23.18	32.95	1092.9	22.53	33.58
POKUASE	830.1	23.07	32.35	1174.0	22.56	32.85

Source: Ministry of Food and Agriculture (MOFA)

Table 2. Mean yield (kg ha⁻¹) of 10 cassava genotypes under 6 environments

Genotype	FM08	FM09	OH08	OH09	PK08	PK09	Mean
AFISIAFI	46.33	37.12	68.57	44.93	67.83	41.13	50.99
AR14-10	36.50	2.63	52.00	20.63	40.17	34.93	31.14
AR15-5	36.50	1.40	46.00	34.10	40.97	40.40	33.23
CR41-10	46.00	11.87	65.33	13.00	56.33	24.77	36.22
CR42-4	45.67	10.63	54.67	28.27	49.83	36.83	37.65
CR52A-25	85.67	24.70	97.33	26.87	99.50	27.90	60.33
CR52A-31	48.00	33.20	58.33	61.43	54.17	50.03	50.86
CR52A-4	35.17	34.60	71.60	65.83	68.50	51.60	54.55
CR59-4	26.33	8.73	43.67	9.13	42.17	31.10	26.86
Sisipe166	52.33	49.07	69.33	54.00	63.83	47.27	55.97
Mean	45.85	21.40	62.68	35.82	58.33	38.60	43.78
SED	14.19	7.30	6.84	13.32	7.52	6.08	
CV%	37.90	41.8	13.40	45.50	15.8	19.30	
P<(0.05)	0.044	<0.001	<0.001	0.003	<0.001	0.003	

for PCA 1 and PC2, respectively, ε_{ij} is the residual associated with genotype *i* in environment *j*.

RESULTS

Descriptive analysis

The mean yields of the ten genotypes grown in six environments were presented in Table 2. Mean yields ranged from 26.86 kg ha⁻¹ for 'CR59-4' to 60.33 kg ha⁻¹ for 'CR52A-25'. Five of the genotypes (50%) had above the mean average yields. Among the environments, FM09, OH09 and PK09 had below the mean average yields. The highest yields were recorded in environments OH08 followed by PK08 with mean yields of 62.68 and 58.33 t ha⁻¹, respectively.

AMMI analysis

The AMMI analysis of variance for root yield (kg ha⁻¹) of ten cassava genotypes tested in six environments showed that 33.14% of the total sum of squares was attributable to environmental effects, 22.02% to genotypic effects, and 18.35% to G x E interaction as shown in Table 3. The analysis revealed that variances due to environments,

genotypes and G x E interactions were highly significant (P<0.01). The large sum of squares for environments indicated that the environments were diverse, with differences among environmental means causing about a third of the variation in root yield. This might probably be due to differences in growing season rainfall which has been known to have positive impacts on cassava yield. Generally, total monthly rainfall at Fumesua for both seasons were higher than that of Ohawu and Pokuase, while mean temperatures ranged between 22.06°C and 33.58°C, as shown in Table 1. Moreover, the highly significant (P<0.01) GE interaction for cassava root yield is an indication of different performance of genotypes across environments and this necessitates the investigation of the nature of different response of the genotypes to environments. In spite of this high significance, the magnitude of the GEI sum of squares was smaller than that of genotypes, indicating the presence of moderate variation among the genotypes over environments.

The GEI was partitioned into three interaction principal component analysis axis (IPCA). This implied that the interaction of the cassava genotypes with six environments was predicted by the first three components of genotypes and environments. The results further indicated that the first two interaction principal components (IPCA 1 and IPCA 2) were extremely important in explaining the interactions while the rest IPCA's were not significant and thus

Table 3. Additive main effect and multiplicative interactions (AMMI) analysis of variance for cassava root yield (kg ha⁻¹) across environments

Source	DF	Sum of Squares (SS)	Mean of Squares (MS)	Variation Explained (%)
Total	179	105401		
Environment (E)	5	34932	6986***	33.14
Genotype (G)	9	23272	2586***	22.08
G x E	45	19345	430***	18.35
IPCA 1	13	14415	1109***	13.68
IPCA 2	11	2664	242*	2.53
IPCA 3	9	1299	144	1.23
Residual	12	967	81	0.92

***, *: significant at the 0.01 and 0.1 probability level respectively

Table 4. AMMI selections of stable genotypes per environment

Environment No.	Environment	Mean	Score	First four AMMI selections
4	Ohawu-09	35.82	4.802	CR52A-4 CR52A-31 Sisipe166 Afisiafi
6	Pokuase-09	38.60	3.226	CR52A-31 Sisipe166 CR52A-4 Afisiafi
2	Fumesua-09	21.40	1.809	Sisipe166 Afisiafi CR52A-4 CR52A-31
3	Ohawu-08	62.68	-2.875	CR52A-25 Sisipe166 Afisiafi CR52A-4
5	Pokuase-08	58.33	-3.286	CR52A-25 Sisipe166 Afisiafi CR52A-4
1	Fumesua-08	45.85	-3.676	CR52A-25 Sisipe166 CR41-10 Afisiafi

constituted a residual noise component. IPCA 1 explained 74.52 % of the variability relating to GEI and 28.89% of the interaction degrees of freedom. Similarly, the second principal component axis (IPCA 2) accounted for 13.77% of the variability of the GEI sum of squares as shown in Table 3. The first two IPCA axes jointly accounted for 88.29% of the GE interaction sum of squares, leaving 11.71% of the variation in the GE interaction (within 26.67% of the interaction df) in the residual. The residual in fact accounted for only 0.92% of total sum of squares. The mean squares for the first PCA is more than four times that of the residual whose mean squares was indeed not significant. This showed that there were differences in yield performance among the cassava genotypes across the six test environments due to the presence of significant G × E interaction effects.

In addition, the AMMI analysis selected Sisipe199 and Afisiafi with average yields of 55.97 and 50.99 kg ha⁻¹ respectively as the most stable genotypes across all the environments followed closely by CR52A-4 with a mean yield of 54.55 kg ha⁻¹ in five environments (Table 4). Overall CR52A-31, CR52A-4, Afisiafi and Sisipe166 were identified as being good performing genotypes when under fairly good seasons represented by year 2009 (Table 4).

AMMI biplot analysis

The AMMI biplot analysis for cassava root yield grown in six environments was presented in Figure 1. The x-axis shows the main effects while the y-axis shows the first PCA axis. The biplot accounted for 75.1% of the total treatment SS leaving a sizable 24.9% in the residual and revealed

differential responses of genotypes to the study environments. The results showed that genotypes AR14-10, CR42-4 and CR59-4 were least interactive with the environment (low IPCA-1 scores) and also had low yields. However, these three genotypes showed little variation in main effect with each other. They were considered as average and stable genotypes being the ones closest to the midpoint of the biplot. CR52A-31 had the largest positive interaction scores while CR52A-25 had the largest negative interaction (-6.5) but a high mean yield of 60.33 kg ha⁻¹. CR52A-31, Sisipe166 and Afisiafi are similar in main effects but vary appreciably in interaction. The environments were also variable in both main effects and interaction.

Season 2 environments (FM09, OH09 and PK09) were positively related to the interaction, whilst season 1 environments (FM08, OH08 and PK08) were negatively related. The first season sites were classified as poor environments and appeared not to give any unique information among the genotypes.

GGE biplot analysis

The partitioning of GGE through GGE biplot analysis showed that PCA 1 and PCA 2 accounted for 60.0% and 33.0% of GGE sum of squares respectively for root yield, explaining a total of 93.0% variation as shown in Figure 2. The GGE biplot revealed the best genotypes under different environments and accurately identified the best genotype with respect to site FM08, PK08 and OH08 as genotype CR52A-25. Genotypes Afisiafi, Sisipe166, CR52A-31 and CR52A-4 were best for environment FM09, PK09 and OH09. Genotype CR52A-25 gave the highest average yield (largest

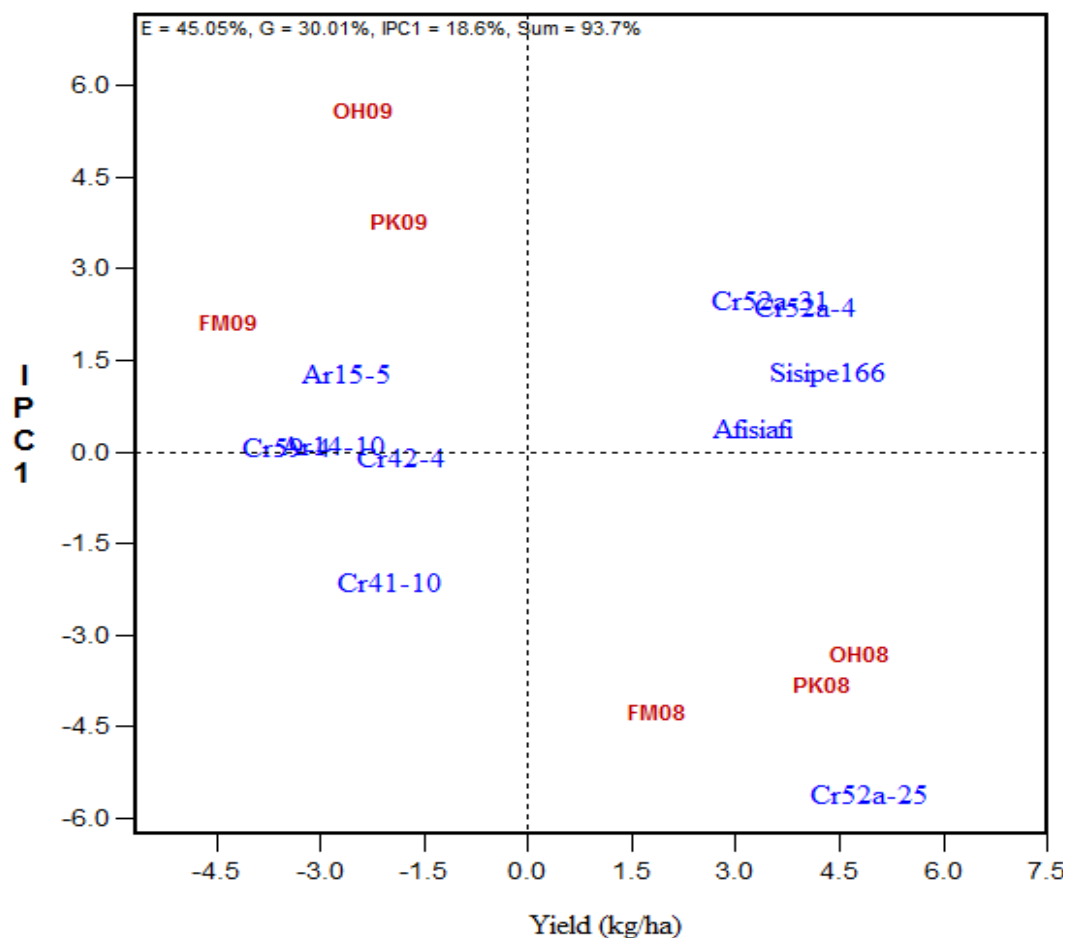


Figure 1: AMMI1 biplot for Root yield of 10 Cassava Genotypes in 6 Environment

PCA 1 scores), but was unstable over the environments, due to its high absolute PCA 2 scores. In contrast, CR42-4 yielded poorly in all environments, as indicated by its small PCA 1 scores (low yielding) and relatively small PCA 2 scores (relatively stable). The average yield of genotypes CR41-10, CR59-4, AR14-10, AR15-5 and CR42-4 were below the mean average (PCA 1 scores < 0), as shown in Figure 2, and were thus classified as the non-adaptable genotypes. On the other hand, genotypes (CR52A-25, Afisiafi, Sisipe166, CR52A-31 and CR52A-4) with PCA 1 scores > 0 were detected as the genotypes of interest (i.e. adaptable or higher yielding). The locations in two different years of the study were clearly separated in the which-won-where graph denoting the winning genotypes as CR52A-4 and CR52A-31 in one the first year (FM08, PK08 and OH08) and genotype CR52A-25 in the second year (FM09, PK09 and OH09).

In Figure 3 the mean root yield and stability performance of the cassava genotypes were shown. The genotypes were ranked along the average environment co-ordinate (average environment axis (AEC x-axis) with an arrow indicating the highest value based on their mean performance across all environments. Thus genotype

CR52A-25 which was closer to the AEC x-axis arrow had the highest mean yield whilst genotypes CR59-4, AR14-10, AR15-5, CR41-10 and CR42-4 which were further away from the AEC x-axis arrow had the poorest mean yields. However, CR52A-25 with the longest projection from the AEC x-axis was adjudged as a highly unstable genotype whereas CR59-4, AR14-10 and CR42-4 with barely visible projections from the AEC x-axis were very stable genotypes. The double arrowed line also separated the above average mean yield genotypes (CR52A-25, Sisipe166, CR52A-4, Afisiafi and CR52A-31) from the below average mean yield genotypes (CR59-4, AR14-10, AR15-5, CR41-10 and CR42-4).

The discriminating power vs. representativeness view of the GGE biplot as shown in Figure 4 showed that test environments OH09 and PK08 with the longest projection from the biplot origin were found more discriminating of the genotypes (i.e., they provided much information about the differences among genotypes). On the other hand, PK09, with its shortest vector from the biplot origin, was found less discriminating of the test genotypes. Test environments FM09, OH08 and PK08 were found to be more representative of other test environments due to the

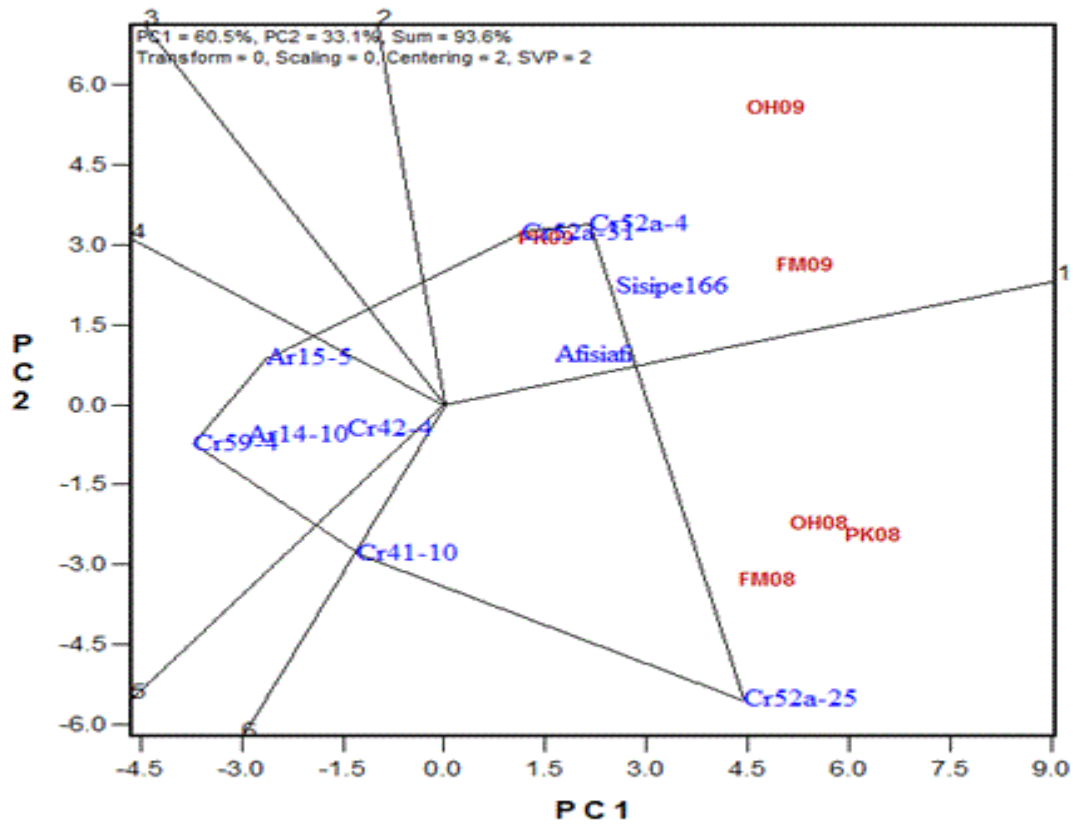


Figure 2: GGE Biplot Analyses(which wins where and which is best for what)

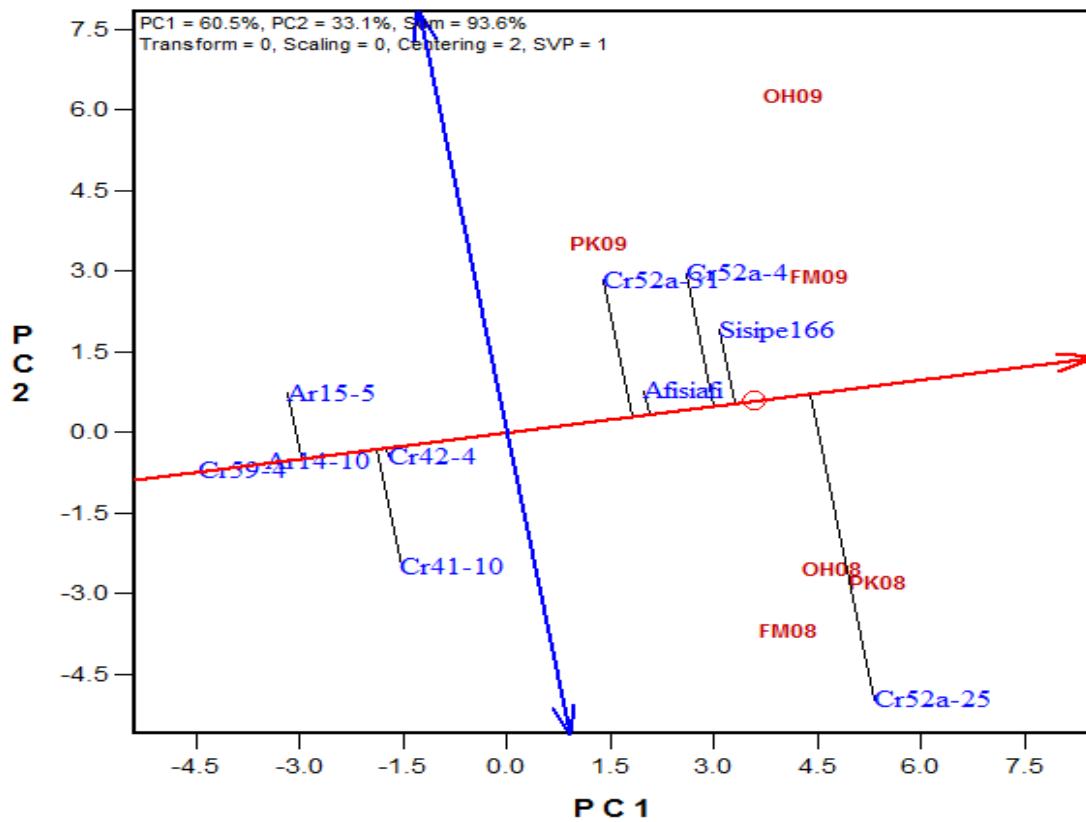


Figure 3: Mean Performance and Stability of 10 Cassava Genotypes

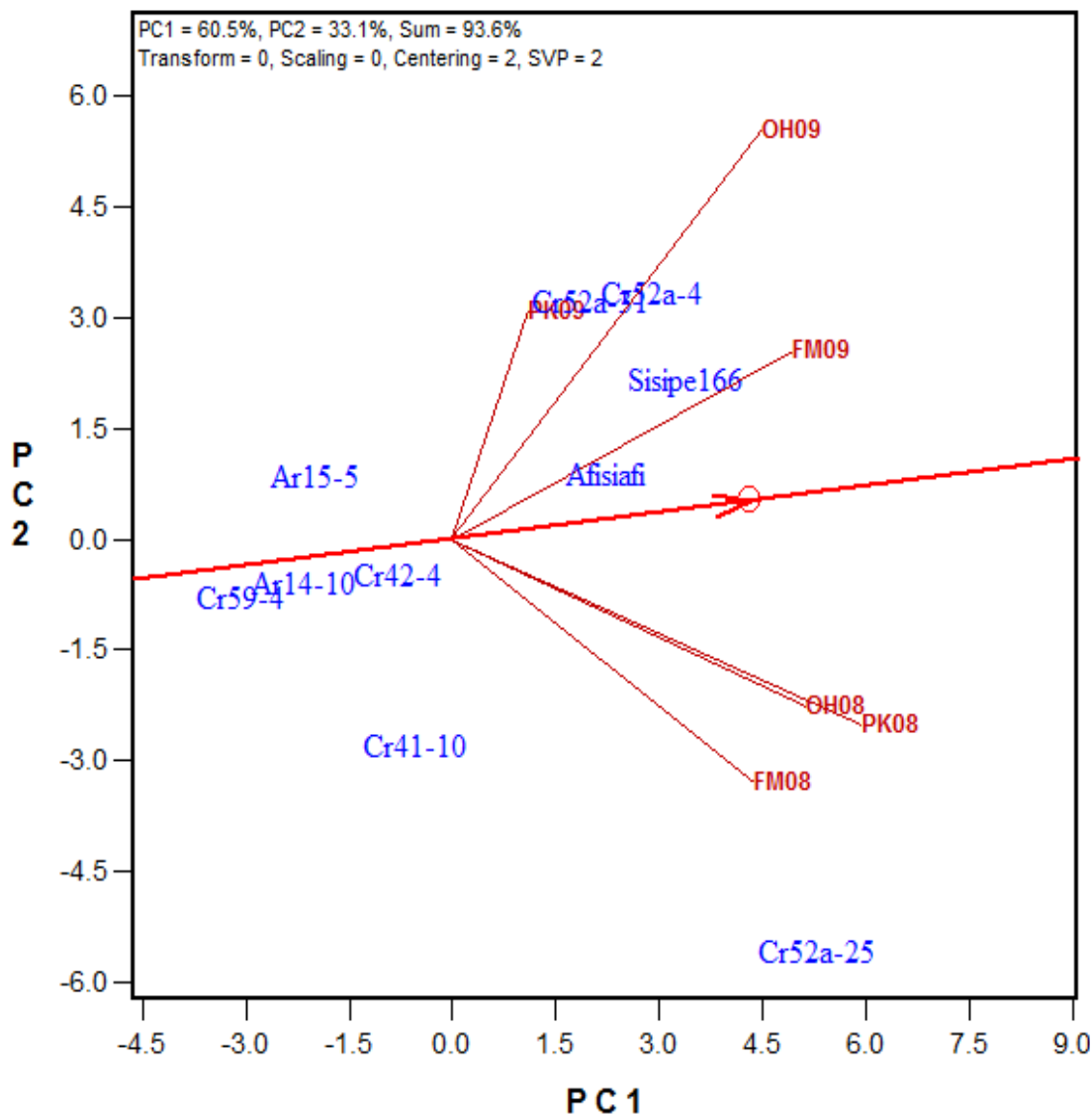


Figure 4: Discriminating power and representativeness of the six environments

fact that they have smaller angles with the AEAs. PK08 was therefore identified as an ideal environment that has both discriminating ability of the genotypes and representativeness of the other test environments. Therefore, environment PK08 can be used to effectively select superior cassava genotypes that can perform consistently across environments.

DISCUSSION

The results from this study indicate that GE interaction is a significant source of variation in the cassava MET data. This observed pattern of GE interaction for root yield of cassava suggests that genotypes respond differently in different environments, hence the need for biplot analysis which

allows visual interpretation of GE interaction and facilitate genotype recommendations in MET. Subsequently, two types of biplots (AMMI1 and GGE) were used to graphically display, interpret and explore important sources of variation, namely genotype main effect and GE interaction of MET data, to identify the genotypes which were superior or had adapted well in each environment based on their mean performance and stability and to also evaluate test environments for effective genotype evaluation based on their discriminating ability and representativeness.

This study revealed that the GGE biplot and the AMMI1 graph explained 93 and 75% of the total G+GE, respectively. The GGE biplot thus explained more G+GE than the AMMI1 graph and was, therefore, a more accurate presentation of the GGE of the cassava root yield data. This might probably be due to the fact that although, the AMMI1 biplot (Zobel et

al., 1988) has been proven to be very efficient in detecting important sources of variation of GE interaction effects and has also been adjudged as either superior or equal to GGE biplot analysis, (Gauch, 2006), it is not able to effectively display the relative performance of each genotype in each environment (i.e., does not have the most important property of a true biplot, namely the inner-product property). As a result, the performance of a given genotype in a given environment cannot be accurately visualized even if it fully displays the data. Similarly, Yan et al, (2007) concluded that the GGE biplot is superior to the AMMI1 biplot in mega-environment analysis and genotype evaluation because it explains more G+GE and pinpointed that, the AMMI1 biplot is better viewed as a tool for presenting conclusions rather than as a tool for discovering which-won-where patterns. On the contrary, the GGE biplot was criticized by Ebdon and Gauch (2002) and Gauch (2006) for not being able to reveal which-won-where patterns if more than two PCs are required to approximate the data.

With regards to visualizing the mean performance and the stability of the genotypes simultaneously, both the GGE and AMMI1 biplots identified CR52A-25 as the highest yielding genotype showing high absolute interaction with all the first season environments. In addition, CR42-4 was adjudged the most stable genotype though not high yielding by both biplots. Moreover, Sisipe166 and Afisiafi genotypes which are among the most recently recommended genotypes for Ghana, (RTIP Factsheet, 2002), were also found to be stable for cultivation across seasons. It also supports the fact that, Afisiafi is a released variety and has been tested across locations in Ghana. Although, CR59-4 was found to have a combination of low GE interaction and average yield, making it the most suitable for cultivation across seasons in terms of stability, its low root yield even under fairly good seasons makes it a less attractive genotype for selection and recommendation. Similarly, Hagos and Abay, (2013), suggested that both GGE and AMMI biplots were important for evaluating stable and adaptable genotypes in MET. Similar outcomes have also been reported by Stojaković et al, (2010) and Mitrovic et al, (2012) and likewise, Rad et al, (2013) indicated that he AMMI biplot performed equally well as the GGE biplot.

Evaluating test environments for effective selection of superior genotypes is one of the most important features of GED and biplot analysis. Yet, the AMMI1 biplot (Zobel et al., 1988) displays the test environments by their main effects E and IPC1 scores, but provides no information on the environment's ability in identifying superior genotypes, only the GGE biplot is able to optimize genotype selection based on its discriminating ability and representativeness view (Yan et al., 2007). Thus, the GGE biplot was able to identify PK08 as the ideal environment having a long vector length (discriminating ability) and a small angle (representativeness) to the average environment axis (AEA) and selecting CR52A-25 as a superior genotype that can perform consistently across good environments. Similarly, Khalil et al., (2011) identified environment

Nowshera as discriminating as well as most representative, as it was far away from the plot origin and had a shortest projection onto average tester coordinate (ATC) Y-axis, respectively in a maize study using GGE biplot analysis. Likewise, Noerwijati et al, (2014) also identified Kediri as the ideal environment for the selection of superior cassava genotypes based on the discriminating and representativeness view of the GGE biplot having small absolute PCA2 scores and large PCA1 scores.

Conclusions

This study indicates that the GGE and AMMI1 biplots are useful techniques that were able to effectively detect the existence of a significant amount of GE interaction between ten cassava genotypes across six environments. Both models revealed that CR52A-25 outperformed the checks Afisiafi (an IITA released variety in Ghana) and Sisipe166 (a landrace) indicating that it has the potential to increase cassava productivity in Ghana and should therefore be recommended for further breeding and subsequently its release to cassava farmers. In addition, the GGE biplot analysis found two distinct mega-environments for major cassava-growing agro-ecological zones in Ghana and helped the cassava plant breeding program to identify high yielding and stable genotypes. CR52A-4 and CR52A-31 which are new genotypes also showed high mean yields and were more stable and better adapted to the second season mega-environment.

The performance of a given genotype in a given environment was more accurately displayed by the GGE biplot compared to the AMMI1 biplot. The reason for this assertion is that, the which-won-where view of the GGE biplot proved to be a more effective visual tool in the mega-environment analysis and genotype evaluation, because it explained more G+GE and depicted the inner product property of a biplot. Whereas, the AMMI1 biplot provides no information on the environment's ability in identifying superior genotypes, only the GGE biplot is able to optimize genotype selection based on its discriminating ability and representativeness view. Although, both methods have proved to be important tools that can be used to effectively analyze and interpret GE interactions, the GGE biplot analysis provides a better innovative approach to the interpretation of genotype \times environment interactions and this will enable breeders to effectively design the dissemination strategy for new cassava genotypes.

REFERENCES

- Akinwale MG, Akinyele BO, Odiyil AC, Dixon AGO (2011). Genotype X Environment Interaction and yield performance of 43 improved cassava (*Manihot esculenta* Crantz) genotypes at three agro-climatic zones in Nigeria. Bri. Biotechnol. J., 1(3): 68-84. [Crossref](#)
- Annicchiarico P, Perenzin M (1994). Adaptation patterns

- and definition of macro environment for selection and recommendation of common wheat in Italy. *Plant Breed.* 113:197-225.[Crossref](#)
- Burns A, Gleadow R, Cliff J, Zacarias A, Cavagnaro T (2010). Cassava: the drought, war and famine crop in a changing world. *Sustainability*, 2(11): 3572-3607.[Crossref](#)
- Crossa J (1990). Statistical analysis of multilocation trials. *Adv. Agron.* 44: 55-85.[Crossref](#)
- Ding M, Tier B, Yan W (2007). Application of GGE biplot analysis to evaluate Genotype (G), Environment (E) and G × E interaction on *P. radiata*: a case study. Paper presented to Australasian Forest Genetics Conference Breeding for Wood Quality, 1114 April 2007, Hobart, Tasmania, Australia.
- Dixon AGO, Nukenine, EN (1997). Statistical analysis of cassava yield trials with additive main effects and multiplicative interaction (AMMI) model. *Afr. J. Root Tuber Crops*, 3: 46-5.
- Ebdon JS, Gauch HG Jr. (2002). Additive Main Effect and Multiplicative Interaction Analysis of national turfgrass performance Trials: II. Cultivar recommendations. *Crop Sci.*42: 497-506.[Crossref](#)
- Fan XM, Kang MS, Chen H, Zhang YT, Xu JC (2007). Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. *Agron. J.* 99: 220-228.[Crossref](#)
- FAO (2006). Statistical database of the Food and Agricultural Organisation of the United Nations. Available at <http://faostat.fao.org/>accessed
- Gabriel K (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58: 453-467.[Crossref](#)
- Gauch HG (1992). Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, The Netherlands pp. 53-110.
- Gauch HG (2006). Statistical analysis of yield trials by AMMI and GGE. *Crop Science*, 46: 1488-1500.[Crossref](#)
- Gauch HG, Zobel RW (1988). Predictive and postdictive success of statistical analyses of yield trials. *Ther. Appl. Genet.* 76: 1-10.[Crossref](#)
- Gauch HG, Zobel RW (1996). AMMI analysis of yield trials. In Kang MS, Gauch HG (Eds.) *Genotype-by-environment interaction* (pp. 85-122). Boca Raton, FL, CRC Press.[Crossref](#)
- GenStat for Windows (2008). 9th Edn. VSN International Ltd., Hemel Hempstead, UK."
- Gollob HF (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, 33: 73-115.[Crossref](#)
- Gruneberg WJ, Manrique K, Zhang D and Hermann M (2005). Genotype x environment interactions for a diverse set of sweet potato clones evaluated across varying ecographic conditions in Peru. *Crop Sci.* 45: 2160-2171.[Crossref](#)
- Hagos HG, Abay F (2013). AMMI AND GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia. *J. Plant Breed. Genet.*, 1(1): 12-18.
- Kandus M, Almorza D, Boggio Ronceros R, Salerno JC (2010). Statistical methods for evaluating the genotype-environment interaction in maize (*Zea mays* L.). *Phy.Yld.* 39-46.
- Kang MS (1998). Using Genotype-by-Environment Interaction for Crop Cultivar Development. *Adv. Agron.* 62: 199-252.[Crossref](#)
- Khalili IA, Rahman H, Rehman NU, Arif M, Khalili, IH, Iqbal M, Ullah H, Afridi K, Sajjad M, Ishaq M (2011). Evaluation of maize hybrids for grain yield stability in north-west Pakistan. "Sarhad J. Agric. 27(2): 213-218.
- Kroonenberg PM (1995). Introduction to biplots for G × E Tables. Dep. of Mathematics, Res. Rep. 51. Univ. of Queensland, Australia.
- Ma BL, Yan W, Dwyer LM, Frégeau-Reid J, Voldeng HD, Dion Y, Nass H (2004). Graphic analysis of genotype, environment, Nitrogen fertilizer, and their interaction on Spring Wheat yield. *Agron. J.* 96: 169-180.
- Mandel J (1971). A New Analysis of Variance Model for Non-Additive Data. *Technometrics* 13: 1-8.[Crossref](#)
- Manrique K, Hermann M (2002). Comparative study to determine stable performance in sweetpotato (*Ipomoea batatas* [L.] Lam.) Regional Trials. *Acta Hort.* 583: 87-94.
- Mitrovic B, Stanisavljevi D, Treski S, Stojakovic M, Ivanovic M, Bekavac G, Rajkovic M (2012). Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE biplot analyses. *Turkish J. Field Crops*, 17: 35-40.
- Mkumbira J, Mahungu N M, Gullberg U (2003). Grouping locations for Efficient Cassava Evaluation in Malawi. *Experimental Agriculture*, 39:167-179.[Crossref](#)
- Noerwijati K, Prajitno D (2014). Fresh Tuber Yield Stability of Fifteen Cassava Genotypes across Five Environments in East Java (Indonesia) using GGE Biplot. *Energy Procedia*, 47: 156-165.[Crossref](#)
- Rad NM, Kadir MA, Rafii MY, Jaafar HZ, Naghavi MR, Ahmadi F (2013). Genotype x environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. *Aust. J. Crop Sci.*, 7: 956-961.
- RTIP Fact sheet No. 1, Rev. June 2002.
- Samonte, SOP, Wilson LT, McClung AM, Medley JC (2005). Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analyses. *Crop Science*, 45(6): 2414-2424.[Crossref](#)
- Stojaković M, Ivanović M, Jocković Đ, Bekavac G, Purar B, Nastasić A, Stanisavljević D, Mitrović B, Treskić S, Laišić R (2010). NS maize hybrids in production regions of Serbia. *Field and Vegetable Crops Research*, 47: 93-02.
- Vargas M, Crossa J (2000). The AMMI analysis and graphing the biplot. Biometrics and Statistics Unit, CIMMYT.
- Vargas VJ, Crossa J, van Eeuwijk FA, Rami ME, Sayre K (1999). Using partial least squares regression, factorial regression, and AMMI models for interpreting genotype & times; environment interaction. *Crop Science*, 39, 955-967. Gauch HG Jr. (Eds.). *Genotype-by-Environment Interaction*. CRC Press, Boca Raton, FL.[Crossref](#)
- Yan W (2001). GGE biplot – A Windows Application for Graphical Analysis of Multi-environment trial data and

- other types of two-way data. *Agron. J.* 93: 1111–1118.[Crossref](#)
- Yan W (2002). Singular-value partitioning in biplot analysis of multi-environment trial data. *Agron. J.*, 94: 990–996.[Crossref](#)
- Yan W, Hunt LA, Sheng Q, Szlavnic Z (2000). Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Science*, 40: 596–605.[Crossref](#)
- Yan W, Kang MS (2003). 'GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists.' (CRC Press: Boca Raton, FL).
- Yan W, Kang MS, Ma B, Woods S, Cornelius PL (2007). GGE Biplot vs. AMMI Analysis of Genotype-by-Environment Data. *Crop Science*, 47: 641–653.[Crossref](#)
- Yan W, Tinker (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.* 86: 623–645.[Crossref](#)
- Zerihun J (2011). GGE-biplot Analysis of Multi-environment Yield Trials of Barley (*Hordeium vulgare* L.) Genotypes in South-eastern Ethiopia Highlands. *Int. J. Plant Breed. Genet.*, 5: 59-75.[Crossref](#)
- Zobel RW, Wright MJ, Gauch HG (1988). Statistical analysis of a yield trial. *Agron. J.* 80: 388–393.[Crossref](#)