Yield performance of cassava genotypes in the forest and coastal ecologies of Southern Ghana

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ABSTRACT

Root yield performances of 10 cassava genotypes were assessed across six environments to determine stable cassava (*Manihot esculenta*) cultivar(s) for root yield in southern Ghana. The assessments were carried out in the forest zone (Fumesua), coastal savanna zone (Ohawu) and coastal savanna zone (Pokuase) in the 2007-2008 and 2008-2009 growing seasons. The experimental layout was a randomized complete block design with three replications. Additive main effects and multiplicative interactions analysis (AMMI) indicated that genotype by environment interactions were significant. Genotype 6 (CR52A-25) was the highest yielding genotype with a root yield of 60.33 kg ha^{-1}, while Genotype 9 (CR59-4) had the lowest root yield of 26.86 kg ha^{-1}. Root yield was significantly lower ($P = 0.001$) at the forest zone compared to the coastal savanna zones.

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Introduction

In Africa cassava (*Manihot esculenta* Crantz) is the most important vegetatively propagated food crop, and the second most important staple food in terms of calories per capita, consumed regularly by more than 200 million people (Nweke, Spencer & Lynam, 2002). Total world cassava use is expected to increase from 172.7 million ton to 275 million ton in the period 1993-2020 using the International Food Policy Research Institute's (IFPRI) base line data. Cassava contributes about 22 per cent of Ghana's Agricultural GDP and has assumed industrial and cash crop status in the country (SRID, 2009). The success of cassava in Africa, as a food security crop, is largely because of its ability and capacity to yield well in drought-prone, marginal wastelands under poor management where other crops would fail.

Despite cassava's ability to grow in marginal areas (Mkumbira, Mahungu & Gullberg, 2003), large differential genotypic responses occur under varying environmental conditions. That is, genotypes of differing genetic composition may respond differently when placed in varied growing conditions. This phenomenon is referred to as genotype × environment interactions (GEI), which is a routine occurrence in plant breeding programmes (Kang, 1998). Such interactions may confound the effect of genotypes with that of environments. Hence, selection of superior genotypes for both improved crop development, and new crop introduction can be difficult in the presence of a significant GEI (Shafii & Price, 1998). For this reason, Akinwale *et al*. (2011) determined the effects of genotypic and environmental differences in root yield of cassava. Aina *et al*. (2009) investigated GEI effects of cassava genotypes in Nigeria and Kvitschal *et al*. (2006) evaluated the effect of GE interactions for cassava root yield.

The additive main and multiplicative interaction (AMMI) model suggested by Zobel, Wright & Ganch (1988), Gauch (1992) and Shafti *et al.* (1997) is considered to be a better model for analysis of G × E interaction in yield data of multilocation varietal trials. Moreover, the AMMI model does not only estimate total G × E interaction effect of each genotype, but also further partitions it into interaction effects due to individual environments.

Additionally, two types of biplots, the AMMI biplot (Gauch, 1988; Gauch & Zobel, 1997) and the genotype main effects and genotype × environment interaction (GGE) biplot (Yan *et al.*, 2000) have been used widely to visually examine the genotype × environment interaction (GEI) pattern of yield data. The GGE biplot is an effective tool for multi-environment analysis (e.g. "which-won-where" pattern), whereby specific genotypes can be recommended for specific environments (Yan & Kang, 2003; Yan, & Tinker, 2006), and is based on G and GEI parts of the analysis. The AMMI biplot also provides a means of visualising the mean performance (G) and the stability (IPC1) of the genotypes simultaneously. The GGE biplot is superior to AMMI biplot, in that it particularly allows visualisation of any crossover G × E interaction.

Yan *et al*. (2007) compared the GGE biplot and AMMI graph and concluded that the GGE biplot was superior to the AMMI graph in mega-environment analysis and genotype evaluation, because it explained G + G × E more effectively and had the inner-product property of the biplot. That is, the GGE biplot shows not only the mean performance and stability of each genotype, but also the relative performance of each genotype in each environment. Kang *et al*. (2006) used GGE biplot methods and concluded that the analysis helped identify cultivars that were adapted across locations, or whose stability was influenced by a linear effect of an environmental index. Dehghani, Ebadi & Yousefi, (2006) evaluated the effects of genotype and genotype × environment interaction on grain yield of 19 barley (*Hordeum vulgare* L.) genotypes *via* the GGE biplot method and identified three barley mega-environments, as well as the best cultivar for the mega-environments.

The objectives of the paper were to (1) assess the effect of genotype (G), environment (E), and G × E (GE) interaction on root yield of cassava, and (2) identify stable cassava genotypes adapted to the forest and coastal ecologies of Ghana by applying the GGE biplot and AMMI analysis.

Materials and methods

Experimental site and materials

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 21 – 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 23 to 33 °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 23 to 33 °C; coordinates 5° 41′ N; 0° 17′ W; Chromic Lixisol soils, Adams series; coastal savanna) in Ghana. These sites represent the major cassava-growing agro-ecological zones in the country.

Ten genotypes were tested at experimental sites of CRI-Crops Research Institute in the study. Out of the 10 advanced lines assessed, eight elite inter-specific hybrid cassava genotypes were introduced from CIAT through 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 rainfed conditions. Planting dates at Fumesua, Ohawu and Pokuase were on the 10th, 13th and 15th of July, respectively, for the two cropping seasons. The plot size was 4 m × 10 m and a spacing of 1 m × 1 m was used. Hand weeding was done as and when necessary. At harvest (12 MAP), data collected for fresh root yield per plot were weighed and converted into kilograms per hectare in line with standard unit of measuring root yield.

Data analysis

AMMI and GGE biplots analysis was carried out for root yield of 10 cassava genotypes across six environments to identify high yielding genotypes best suited for the forest and coastal savanna agro-ecological zones of Ghana. The meta analysis procedure for AMMI analysis available in Genstat software release 14.1, 2011 was used to partition cassava root yield variation into environments (E), genotypes (G), and genotypes × environment (GE) interaction and estimated according to Gauch & Zobel (1996);

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

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

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} geneotypic 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 and n′ is the number of PCA axis retained in the model.

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 & Crossa, 2000). The AMMI biplot was obtained from the graphical ordination of mean cassava yield and the interaction principal component axes (Kempton, 1984). The pattern of response of G, E, and GEI were then identified using the AMMI biplot.

The GGE biplot was estimated by the method suggested by Yan (2002);

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

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 (PC1 and PC2), respectively, and ξ_{i1} are ξ_{i2} eigenvectors of genotype i for PC1 and PC2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j for PC1 and PC2, respectively and ε_{ij} is the residual associated with genotype i in environment j.

The GGE biplot was constructed from the environment centered cassava yield data following the method described by Yan (2001) and Yan *et al.* (2007). The "which-won-where" pattern was represented in the form of a polygon. The best cassava genotypes were represented by large principal component scores (PC1, high root yield) and small principal component scores (PC2, high stability) (Yan, 2001). Genotypes that had PC1 scores > 0 were identified as higher yielding and those that had PC1 scores < 0 were identified as lower yielding. PC1 scores > 0 detected the genotypes of interest (adaptable or higher yielding), whilst PC1 scores < 0 discriminated the non-adaptable ones (Zerihun, 2011). PC2, which was related to genotypic stability or instability, divided the genotypes of interest based on their scores.

Results

The mean yields of the 10 genotypes grown in six environments are shown in Table 1. Mean yields ranged from 26.86 t ha^{-1} for 'CR59-4' to 60.33 t ha^{-1} for 'CR52A-25'. Five of the genotypes (50%) had above the mean average yields (Table 1). 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 model combines the analysis of variance for main effects of genotypes (G) and environment (E) with principal components analysis of genotype × environ-

TABLE 1

Mean Yield (kg ha $^{-1}$) of 10 Cassava Genotypes Under Six 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

ment interaction (GEI). The AMMI analysis of variance of root yield (kg ha^{-1}) of the 10 genotypes tested in six environments showed that 33.14 per cent of the total sum of squares was attributable to environmental effects and 22.02 per cent to genotypic effects (Table 2). Environment had a significant ($P \leq 0.001$) effect on root yield, and this was probably attributable to differences in rainfall.

Generally, total monthly rainfall at Fumesua for both seasons was higher than that at Ohawu and Pokuase, whilst mean temperatures ranged between 21 °C and 34 °C. A large SS for environments indicated that the environments were diverse, with differences among environmental means causing about a third of the variation in root yield. The mean squares from AMMI analysis of variance (Table 2) indicated significant variations among the genotypes, the environments and their interaction for root yield. The GEI is highly significant ($P < 0.01$) accounting for 18.35 per cent (Table 2) of the SS, and this implies the need for investigating the nature of differential response of the genotypes to environments. Inspite of this high significance, the magnitude of the GEI SS was smaller than that of genotypes, indicating that there were no substantial differences in genotypic response across environments. The GEI was partitioned into three interaction principal component analysis axis (IPCA) (Table 2).

The result indicated that the first interaction principal component (IPCA 1) was highly important in explaining the interactions, whilst the remaining IPCA's were not significant and, thus, constituted a residual noise component. IPCA 1 explained 74.52 per cent of the variability relating to GEI and 28.89 per cent of the interaction degrees of freedom. Similarly, the second principal component axis (IPCA 2) accounted for 13.77 per cent of the variability of the GEI SS. The first two IPCA axes jointly accounted for 88.29 per cent of the G × E interaction SS, leaving 11.71 per cent of the variation in the G × E interaction (within 26.67 per cent of the interaction df) in the residual. The residual accounted for only 0.92 per cent of total SS. The mean squares for the first PCA

TABLE 2

Additive Main Effect and Multiplicative Interactions (AMMI) Analysis of Variance for Cassava Root Yield (kg ha^{-1}) across Six 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 × 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 levels, respectively.

is more than four times that of the residual whose mean squares were indeed not significant. The other two IPCAs captured insignificant portion of variability which could be regarded as noise.

On the basis of selection of stable genotypes per environment by AMMI, Sisipe 166 and 'Afisiafi' ranked among the top four genotypes in all the six environments followed by CR52A-4 in five environments. CR52A-31 and CR52A-25 also ranked among the top four genotypes in three environments, while CR41-10 ranked among the top four genotypes in only one environment. Thus, CR52A-31, CR52A-4, 'Afisiafi' and Sisipe166 were identified as being good performing genotypes when under fairly good seasons represented by OH09, PK09 and FM09 (Table 3). The first season (2007/2008) was a poor environment and appeared not to give any useful discrimination among the genotypes with the exception of CR52A-25, which performed very well under the environments in the season. Sisipe199 and 'Afisiafi', with average yields of 55.97 and 50.99 kg ha^{-1}, respectively (Table 1), were stable in all the environments.

The biplot of the AMMI-1 model result is shown in Fig. 1. The x-axis shows the main effects while the y-axis shows the first PCA axis. The biplot accounted for 75.3 per cent of the total treatment SS leaving a sizable 24.7 per cent in the residual. The biplot further revealed differential responses of genotypes to the study environment. 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, therefore, considered as average and stable genotypes being the ones closest to the midpoint of the biplot. CR52A-31 had the largest positive interaction scores, whilst CR52A-25 had the largest negative interaction (-6.5) but a high yield of 60.33 kg ha^{-1}. CR52A-31 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.

GGE biplot analysis

The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 60.0 per cent and 33.0 per

TABLE 3

AMMI Selections of Stable Genotypes per Environment

Env. No	*Env.*	*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

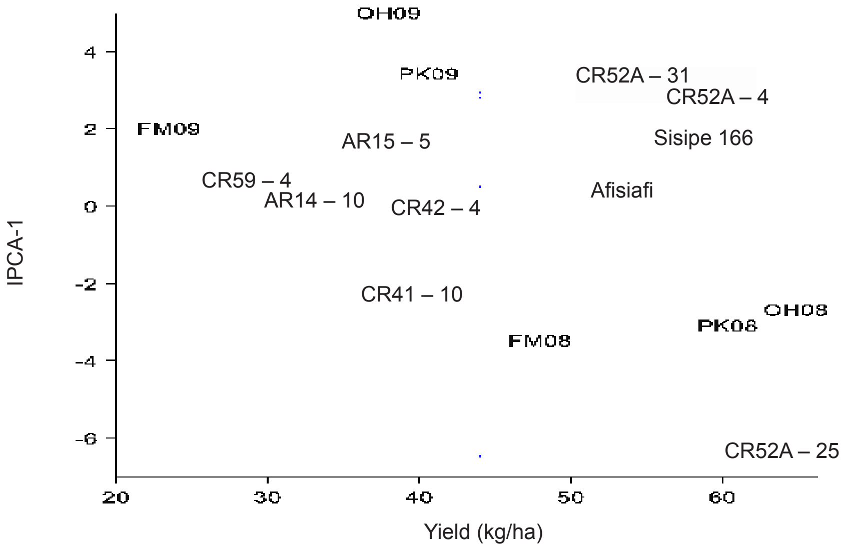

Fig. 1. AMMI - 1 model biplot for root yield (kg ha^{-1}) of the 10 cassava genotypes in six environments

cent of GGE SS, respectively, for root yield, explaining a total of 93.0 per cent variation (Fig. 2). The GGE biplot (Fig. 2) revealed the best genotypes under different environments. The biplot 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 PCA 1 scores), but was unstable over the environments, because it did not give small 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 average (PCA 1 scores < 0) (Fig 2). PC1 scores > 0 detected the genotypes of interest (i.e. adaptable or higher yielding), whilst PC1 scores < 0 discriminated the non-adaptable ones.

Discussion

The study demonstrated the importance of applying AMMI analysis to investigate the main effects of genotypes and environment, and the complex patterns of their interaction. Subsequently, two types of biplots were obtained to explore the effects of the G × E interaction (AMMI biplot), and to observe also the genotypes which were superior or had adapted well in each environment (GGE biplot). The high variability observed among genotypes as indicated by the range of their mean performance, indicates the presence of sufficient genetic variability for root yield. The significant interaction between genotype and environment (G×E) for root yield also indicated that there is the need for multi-locational testing to identify superior genotypes for specific locations. The highly significant mean squares effects for both genotypes and environments revealed

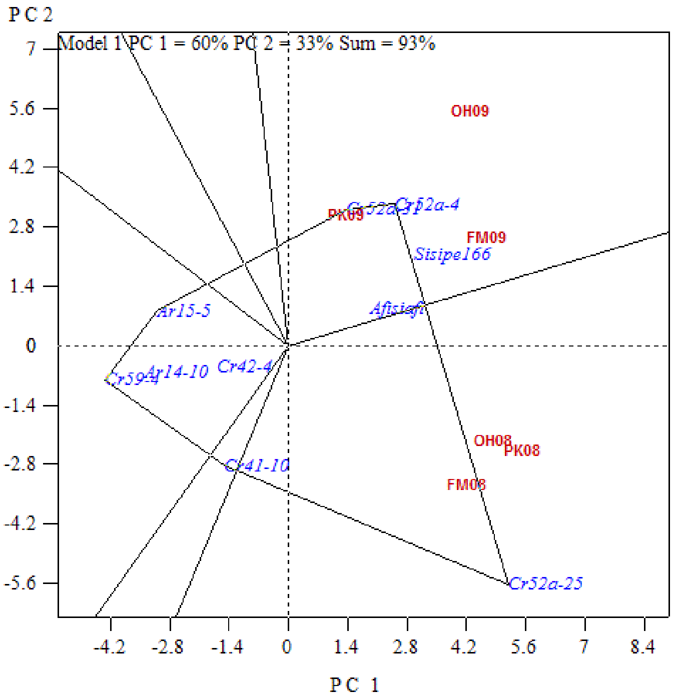

Fig. 2. GGE biplot based on the yield data for 10 cassava genotypes in six environments.

genotypic differences towards adaptation to different environments. This suggested that specific genotypes are adapted to specific environments. Aina *et al*. (2009) observed similar result when he evaluated 18 cassava genotypes across four locations in Nigeria.

Although the GEI SS accounted for a sizable and significant portion of variability in root yield of cassava, it was smaller than that of the genotypes, indicating differences in genotypic response across environments, though not substantial. Furthermore, the significant G × E interaction indicates existence of crossover interactions which suggested that genotypes that are superior in one environment do not maintain their superiority in other environments (Baker, 1990; Cornelius, Ceccarell & Grands, 1996; Singh, Crosser & Seyedsadr, 1999). Consequently, using the AMMI model in the study, the variability relating to GEI has been partitioned into pattern rich model represented by IPCA 1 and IPCA 2 (accounted for 88.3% of the variation caused by GEI) and noise rich residual (IPCA 3 and IPCA 4). The AMMI analysis in the study left a non-significant 0.92 per cent of the total variation in the residual and identified ‘CR59-4’ as having a combination of low G × E interaction and average yield, making it the most suitable for cultivation across seasons in terms of stability. As identified by both AMMI and GGE, however, its low root yield even under fairly good season makes it less attractive.

The AMMI analysis in the study identified CR52A-25 as the highest yielding genotype and CR42-4 as the most stable genotype though not high yielding. The interaction of the 10 cassava genotypes with six environments was best predicted by the first principal component of genotypes and environments as the F-test at $P < 0.001$ for the model with 13 df suggested. Further interaction principal component axes captured mostly noise and, therefore, did not help to predict validation observations. However, Gauch & Zobel (1996) and Yan *et al*. (2002) advocates that the most accurate model for AMMI can be predicted by using the first two PCAs. Conversely, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four PCAs.

CR41-10 had an overall negative but low interaction with the environments. The variety, however, recorded above average yields in the first season and would, therefore, be suitable for cultivation in the environment and similar ones. Due to the limited number of environments being tackled, the study may not provide the ideal framework for identifying target testing environments for cassava breeding in Ghana. However, it does provide some initial information on the studied environments. CR52A-4 and CR52A-31 had positive interactions with four environments and were also selected by AMMI as stable genotypes. This means that they were specifically adapted to those environments evaluated and produced the highest levels of yield. Though AR14-10 also recorded little interaction, it had a very low yield.

Cooper, Delacy & Basford (1996) and Fox, Crossa & Ramagossa (1997) are of the view that when the IPCA-1 values of genotypes and environments are close to zero, the genotype that has a small interaction effect has a general stability. Genotypes with large positive or negative IPCA-1 scores are largely responsible for G × E interactions and reflect more specific response (Ntawuruhunga *et al.,* 2001). The IPCA scores of a genotype in the AMMI analysis are an indication of the stability of a genotype over environments. The greater the IPCA scores, either negative or positive, as it is a relative value, the more specifically adapted a genotype is to a certain environment. The more IPCA scores approximate to zero, the more stable the genotype is over the sampled environments (Shaffi *et al.*, 1997).

The non selection of genotypes AR14-10, AR15-5, CR41-10, CR42-4 and CR59-4 in all the environments by the GGE biplot was due to their very poor performance in the second season. Consequently, the genotypes would be suitable for cultivation in environments with adequate soil nutrients. CR52A-25 recorded the highest yields and showed high absolute interaction with all the first season environments except the second season environments. This explains its identification with good E × GGE. It is worth noting that CR52A-25 outperformed the checks 'Afisiafi; (an IITA released variety in Ghana) and Sisipe166 (a landrace), and should be recommended for further breeding and subsequently its release. Sisipe166 and 'Afisiafi', which are among the most recently recommended genotypes for Ghana, (RTIP Factsheet, 2002), were adjudged stable for cultivation across all six environments.

The GGE biplot analysis further showed that the first two principal components of the GGE biplot explained 93 per cent of the total variance, within the limit recommended by Cruz & Regazzi (1997) of at least 80 per cent. CR52A-25 was identified by the GGE biplot as the highest yielding genotype with the highest PCA1 scores of 5.5, and 'Afisiafi' was identified as the most stable genotype in the study as its PCA2 score was closest to zero. This is in conformity with Yan *et al*. (2000), who states that in the graphic analysis, the first principal component (PCA1) represents cultivar productivity, and the second principal component (PCA2), cultivar stability.

GGE biplot versus AMMI biplot

Although the AMMI1 biplot has been

proven to be very efficient in detecting important sources of variation of G × E interaction effects and has also been adjudged as either superior or equal to GGE biplot analysis (Gauch, 2006), the study found contrary results. The AMMI1 biplot in the study recovered about 75 per cent of the variation in the total treatment SS, and the GGE biplot, on the other hand, explained about 93 per cent of the variation in the total treatment SS. 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.

This might probably be because the AMMI1 biplot (Zobel *et al.*, 1988) is the most well known and appealing component of AMMI analysis, and provides a means of visualising the mean performance (G) and the stability (IPC1) of the genotypes simultaneously. The AMMI1 biplot does not have the most important property of a true biplot, namely the inner-product property (shows not only the mean performance and stability of each genotype, but also the relative performance of each genotype in each environment). As a result, the performance of a given genotype in a given environment cannot be accurately visualised even if it fully displays the data. This is why a different AMMI1 biplot (Yan, 2000) is needed for visualising the which-won-where pattern.

Conclusion and recommendation

The AMMI model provides a useful technique in diagnosing GE interaction patterns. The high yielding genotypes (CR52A-25, CR52A-4, CR52A-31 'Afisiafi' and Sisipe166) in the study have the potential to increase cassava productivity in Ghana. The interaction of the 10 genotypes with six environments was best predicted by the first two principal components of genotypes and environments. Consequently, biplots generated using genotypic and environmental scores of the first two AMMI components can help breeders have an overall picture of the behavior of the genotypes, the environments and GEIs.

The GGE biplot enabled visual comparison of the locations and genotypes studied and their interrelationships. This result revealed that there was a differential yield performance among cassava genotypes across testing environments which was due to the presence of GEI. The which-won-where view of the GGE biplot is superior to the AMMI1 graph for multi-environment analysis in that it explains more G + GE, it is easier to construct, and it is easier to visualise the which-won-where patterns.

The AMMI and the GGE biplot analysis selected CR52A-4, 'Afisiafi' and Sisipe166 as the most stable genotypes (these genotypes are broadly adapted for different environments and can perform well under variable conditions), whilst CR52A-25 was identified as high yielding and stable in marginal environments (the genotype can be successfully grown only in environments characteristic of favourable growing conditions).

The study, therefore, recommends that CR52A-4 and CR52A-25 should be selected for further breeding work and release to farmers.

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