

Statistical analysis of cassava yield trials with the Additive Main Effects and Multiplicative Interaction (AMMI) model

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Abstract

Genotype \times environment ($G \times E$) interactions have been observed in cassava multilocal trials. There are various statistical tools for handling main effects (genotypes and environments) and $G \times E$ interaction in multilocal trials, but hardly any can handle both these main effects and interaction quite clearly and effectively. However, AMMI analysis model combines regular analysis of variance for additive main effects with principal components analysis for multiplicative structure within the interaction. AMMI is therefore effective among others for understanding $G \times E$ interactions, improving the accuracy of yield estimates and increasing the probability of successfully selecting genotypes with highest yields. The objective of this paper is to analyze yield data from six cassava multilocal trials conducted for three years in Nigeria with AMMI model. The AMMI analysis revealed that environments, genotypes and $G \times E$ interaction were highly ($p < 0.01$) significant. Within environments, AMMI1 frequently ranked genotypes differently than unadjusted means, and in nine of 18 cases AMMI1 estimates changed the top-yielding entry. AMMI1 estimation also produced sharper and stratified rankings as compared with unadjusted means. The biplot showed that the genotypes TMS 50395 and TMS 30572 were superior yielders with broad adaptation while a moderately good yielder (TME 1) was specifically adapted to Ubiaja. In addition, four groupings of genotypes were evident from the biplot: TMS 30001 and TMS 4(2)1425 generally low yielding, had high negative values for the first principal component scores of the $G \times E$ interaction (IPCA1), were early maturing and unstable; TMS 63397 and TMS 91934 were high yielding, had intermediate but negative IPCA1 scores and thus were moderately stable across environments; TMS 30572 and TMS 50395 showed negligible interactions and thus were stable across environments as well as high yielding; and U/14044 (low yielding) and TME 1 (high yielding) showed high positive IPCA1 scores, were late maturing and very unstable across environments. There were also positive and negative interaction patterns for the environments. Owerri and Onne were stable while Ubiaja was an unstable location across the three years. Superior selections with specific and broad adaptation were accurately identified by AMMI.

Key words: AMMI, biplot, cassava, genotype \times environment interaction, multilocal trials

Introduction

A priority of the cassava breeding programmes in international and national research institutions is to improve storage root yields for different agroecologies. Plant breeders use yield trials to identify promising and stable cassava genotypes. Cassava as a crop has wide adaptation and cassava scientists have long believed that cassava genotypes are adapted to a wide range of environments. However, results from multilocal trials of cassava genotypes, conducted by the International Agricultural Research Centers and National Programmes, have provided very little support for this view due to high genotype \times environment interactions ($G \times E$) observed in the trials (Dixon et al. 1994; Ngeve 1994, Makame 1995; Tan & Mark 1995).

The success of identifying high yielding genotypes from the data of yield trials depends on the effectiveness of the statistical analysis used to understand patterns in the data, estimate yields as accurately as possible and select truly superior genotypes (Gauch & Furnas 1991). There are various and earlier statistical methods for handling main effects (genotypes and environments) and the $G \times E$ interaction in multilocal yield trials, but none can handle both these main effects and interaction quite clearly and effectively in a single model or package at the same time (Gauch 1993).

The Additive Main Effects and Multiplicative Interaction (AMMI) analysis is an important statistical tool for understanding $G \times E$ interactions. It is used in field research where both the main effects and the interaction among effects are

considered important, the most common case in yield trials (Bradu & Gabriel 1978; Gauch 1988). The model partitions the treatment variation ($G \times E$ matrix) into a model and a residual. It computes the additive main effects for genotypes and environments, and then analyses the nonadditive residual (namely the interaction) by principal component analysis (PCA). The model provides a biplot using the first interaction principal component axis (IPCA1) and the mean yields. On this biplot, both genotypes and environments (location and/or year) occur, such that clearer responses of the genotypes, locations and environments as well as their interactions are obtained. AMMI analysis also increases precision of yield estimates, identifies high yielding and stable genotypes as well as assesses the underlying principles for adoption in specific agroecologies (Gauch 1993).

In this paper, we report on the AMMI analysis of yield data of nine cassava genotypes from three years of evaluation in six representative locations to show the pattern of responses of genotypes, environments and their interactions, and to identify genotypes with broad or specific adaptation to target agroecologies or environments.

Materials and Methods

The experiment was carried out in three years (1989, 1990 and 1991) at six locations in Nigeria. The locations included Ibadan, Ilorin, Mokwa, Onne, Owerri and Ubiaja. The agroecological characteristics of the locations, which represent major cassava growing areas in Nigeria, are shown in

Table 1. Eight improved (U/41044, TMS 4(2)1425, TMS 30001, TMS 30555, TMS 30572, TMS 50395, TMS 63397 and TMS 91934) and one local (TME 1) cassava genotypes were used in the study. At each of the locations, the genotypes were grown under rainfed conditions in a randomized complete block design with four replications. Planting was done at the beginning of the rains (May–June) at each location for the three years. Each plot consisted of 40 plants in four rows (ridges of height 30 cm and 10 m in length) spaced 1 m apart. Plant spacing was 1 m × 1 m giving a plant population of 10 000 plants per hectare. No fertilizer or herbicides were applied during the course of the experiment, and hand weeding was done when necessary.

Data obtained from each plot included reactions to diseases such as African cassava mosaic disease (ACMD), cassava bacterial blight (CBB), cassava anthracnose disease (CAD) and the arthropod pest, cassava green mite (CGM) by scoring for their symptom expressions using a scale of 1 to 5 (1: no symptoms; 5: severe damage) (IITA 1990). The severity of disease symptoms were recorded at 1, 3 and 6 months after planting (MAP) for ACMD; at 3 and 6 MAP for CBB; and at 6 and 9 MAP for CAD. CGM damage severity was assessed during the dry season (6–7 MAP) (December–January). The middle two rows of a plot were harvested at 12 MAP and the fresh storage roots were weighed.

Data on diseases and pest damage scores were subjected to analysis of variance using SAS package (SAS 1991). The AMMI statistical model (MATMODEL 2.0; Gauch 1993) was then used to analyze the yield data. The AMMI model is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

where Y_{ger} : yield of genotype g in environment e for replicate r ; μ : grand mean; α_g : mean deviation of the genotype g (genotype mean minus grand mean); β_e : mean deviation of the environment mean e ; λ_n : the singular value for IPCA axis n ; γ_{gn} : the genotype g eigen-vector value for IPCA axis n ; δ_{en} : the environment e eigen-vector value for IPCA axis n ; ρ_{ge} : the residual; and E_{ger} : the error.

Results and Discussion

Environments (E) obtained as location × year combination, genotypes (G) and G × E interaction were highly significant ($P < 0.01$) and accounted for 42.5, 22.5 and 35.1% of the treatment (G × E combination) sum of squares, respectively (Table 2). The postdictive success for AMMI using all data (all four replications) and F-test at the 0.05 probability level involve the inclusion of the first three interaction PCA axes in the model. In this study, AMMI1, AMMI2 and AMMI3 mod-

els accounted for 78.19, 86.22 and 91.37% of the treatment sum of squares, respectively. A significant feature of multivariate models, including AMMI analysis, is that they account for a large proportion of pattern in the first few dimensions, with subsequent dimensions accounting for diminishing percentage of pattern and increasing percentage of noise (Gauch 1982, 1988). Thus, since AMMI1 captured a large (78.19%) proportion of the pattern in the data presented herein, it should be accurate enough postdictively. Although, AMMI2 showed a highly significant F-test like AMMI1 and explained a greater pattern than AMMI1, genotypes and environments were grouped similarly by AMMI1 and AMMI2.

Within environments, AMMI1 frequently ranked genotypes differently than unadjusted means. In nine out of 18 cases, AMMI1 estimation changed the top-yielding entry (Table 3). Thus, AMMI1 and unadjusted means selected the same winner in 9 out of 18 environments, but selected different winners in the remaining 9 environments. For the unadjusted means, each of the genotypes, except two (TMS 30001 and TMS 30555) featured among the best yielders in at least one out of the 18 environments. With AMMI1 estimates, only three (TME 1, TMS 91934 and TMS 50395) among the nine genotypes featured among the best in at least one environment, suggesting that the noise in unadjusted means elevated some genotypes (U/41044, TMS 4(2)1425, TMS 63397 and TMS 91934) to the top position. Studies in maize (Crossa et al. 1990) and soybean yield trials (Gauch & Zobel 1989) also showed that AMMI1 estimates differentially ranked top performing entries in over half the environments when compared with the unadjusted means. Consequently, AMMI1 estimation was recommended, since ranking discrepancies between AMMI1 estimates and unadjusted means were attributed to random statistical variation.

Table 2. AMMI analysis for yield of nine selected cassava genotypes grown in 18 environments (6 locations over 3 years)

Source	df	SS	MS	P level
Total	647	33470.36	51.73	
Treatment	161	21044.45	130.71	***
Genotype (G)	8	4709.59	588.70	***
Environment (E)	17	8950.13	526.48	***
G × E	136	7384.73	54.30	***
IPCA1	24	2794.82	116.45	***
IPCA2	22	1689.97	76.82	***
IPCA3	20	1084.74	54.24	**
Residual	70	1815.19	25.93	ns
Error	486	12425.91	25.57	

Grand mean of fresh storage root yield = 18.24 t/ha

** , *** Significant at $p < 0.01$, $p < 0.00$,

ns: not significant at $p > 0.05$

Table 1. Agroecological characteristics of the trial locations

Location	Agroecological zone	Soil type	Coordinates	Altitude (m)	Rainfall (mm)	Wet season	Min/max temperature (°C)
Onne	Humid forest (HF)	Thionic Fluvisols	7° 10' E; 4° 46' N	30	2501.6	Feb-Dec	12-23/28-32
Owerri	Humid forest	Eutric Gleysols	4° 21' E; 3° 31' N	67	2385.0	Mar-Dec	20-22/27-32
Ubiaja	Humid forest	Dystric Nitosols	6° 25' E; 6° 40' N	210	1943.5	Mar-Dec	12-22/27-32
Ibadan	HF-savanna transition	Ferric Luvisols	3° 54' E; 7° 26' N	210	1252.8	Mar-Aug, Aug-Nov	12-23/28-34
Ilorin	S. Guinea savanna	Ferric Luvisols	2° 75' E; 5° 11' N	304	1283.5	Apr-Nov	19-12/28-36
Mokwa	S. Guinea savanna	Ferric Luvisols	5° 40' E; 9° 18' N	210	1235.2	Apr-Nov	13-24/28-36

Source: Jagtap (1993); S.: Southern.

Table 3. Ranking of the genotypes following AMMI1 estimates and unadjusted means (in parenthesis) for fresh root yield (t/ha) of 9 cassava genotypes grown in 6 locations over 3 years (18 environments) (AMMI and unadjusted means picked the same winner in 9 environments (50%) but picked different winners in 9 other environments (50%))

Environment	TME 1	U/41044	TMS 4(2)1425	TMS 30001	TMS 30555	TMS 30572	TMS 50395	TMS 63397	TMS 91934
Ibadan, 1989	2 (4)	6 (5)	8 (8)	9 (9)	7 (7)	4 (3)	1 (1)	5 (6)	3 (2)
Ilorin, 1989	5 (6)	8 (8)	6 (7)	9 (9)	7 (5)	4 (3)	1 (1)	3 (2)	2 (4)
Mokwa, 1989	6 (6)	9 (8)	4 (4)	8 (5)	7 (9)	5 (7)	1 (3)	3 (1)	2 (2)
Onne, 1989	9 (4)	9 (9)	4 (8)	8 (5)	7 (7)	5 (3)	1 (2)	3 (6)	2 (1)
Owerri, 1989	6 (8)	9 (7)	4 (3)	8 (9)	7 (4)	5 (6)	1 (1)	3 (2)	2 (5)
Ubiaja, 1989	1 (2)	3 (1)	8 (8)	9 (9)	6 (6)	4 (5)	2 (4)	7 (3)	5 (7)
Ibadan, 1990	8 (8)	9 (9)	2 (5)	6 (4)	7 (7)	5 (6)	3 (2)	4 (3)	1 (1)
Ilorin, 1990	1 (1)	3 (5)	8 (8)	9 (9)	6 (4)	4 (2)	2 (3)	7 (7)	5 (6)
Mokwa, 1990	6 (4)	8 (5)	4 (1)	9 (9)	7 (7)	5 (3)	1 (6)	3 (8)	2 (2)
Onne, 1990	3 (2)	7 (6)	6 (4)	9 (9)	8 (3)	4 (5)	1 (7)	5 (5)	2 (8)
Owerri, 1990	2 (2)	5 (4)	8 (8)	9 (9)	7 (6)	3 (7)	1 (1)	6 (5)	4 (3)
Ubiaja, 1990	1 (1)	3 (4)	8 (6)	9 (9)	6 (8)	4 (2)	2 (3)	7 (6)	5 (5)
Ibadan, 1991	8 (5)	9 (9)	3 (1)	7 (8)	6 (7)	5 (6)	2 (3)	4 (4)	1 (2)
Ilorin, 1991	5 (5)	8 (4)	6 (2)	9 (9)	7 (8)	4 (3)	1 (1)	3 (6)	2 (7)
Mokwa, 1991	6 (4)	9 (8)	4 (1)	8 (9)	7 (7)	5 (6)	1 (5)	3 (2)	2 (3)
Onne, 1991	2 (6)	5 (3)	8 (8)	9 (9)	7 (7)	4 (4)	1 (1)	6 (5)	3 (2)
Owerri, 1991	6 (7)	9 (9)	4 (3)	8 (6)	7 (8)	5 (1)	1 (4)	3 (2)	2 (5)
Ubiaja, 1991	1 (2)	3 (3)	8 (8)	9 (9)	6 (6)	4 (5)	2 (1)	7 (7)	5 (4)

Figure 1 presents three contrasting genotypes showing stratified ranking patterns based on their unadjusted means and AMMI1 estimates. With the unadjusted means, the genotype TMS 50395 was generally in the top position (rankings

from 1–6), but also occurred four times in the middle (rankings from 7–12) and only once towards the bottom (rankings from 13–18). With AMMI1 estimates, it was always in the top third and never in the middle or bottom. Similarly with the unadjusted means, TMS 30572 was equally always in the top as in the middle, and was also two times in the lower positions. However, AMMI1 estimates generally placed this genotype in the middle. Using unadjusted means, U/41044 was often in the bottom (8 times) than in the middle (7 times) and the top (3 times). The pattern for U/41044 using AMMI1 estimates had 11, 3 and 4 occurrences in the bottom, middle and top groupings, respectively. AMMI1 estimation had a profound effect in producing a sharper and stratified ranking patterns and on this basis TMS 50395 would be considered more adapted to a wide range of environments than TMS 30572. Crossa et al. (1991) obtained a similar stratification of wheat genotypes using unadjusted means and AMMI1 estimates and noted that without AMMI1 estimation, noise in the data blurred adaptation patterns of genotypes to the extent that relatively well adapted genotypes were grouped by chance in the middle and bottom positions. A relatively poorly adapted line sometimes occurred at the top for the same reason. AMMI analysis provides a graph or biplot (Figure 2) to summarize information on the main effects and the first principal component scores of the interactions (IPCA1) of both genotypes and environments simultaneously (Kempton 1984). Displacement along the x-axis reflected differences in main effects, whereas displacement along the y-axis exhibited differences in interaction effects. Zobel et al. (1988) pointed that the AMMI1 expected yield for any genotype and environment combination can be calculated from Figure 2. The additive AMMI0 part of the AMMI model is the sum of genotype and environment means minus the grand mean, while interaction part is the genotype PCA score times the environment PCA score. These two parts are added to produce the expected value of AMMI1 model. The biplot captured 78.19% of the treatment sum of squares.

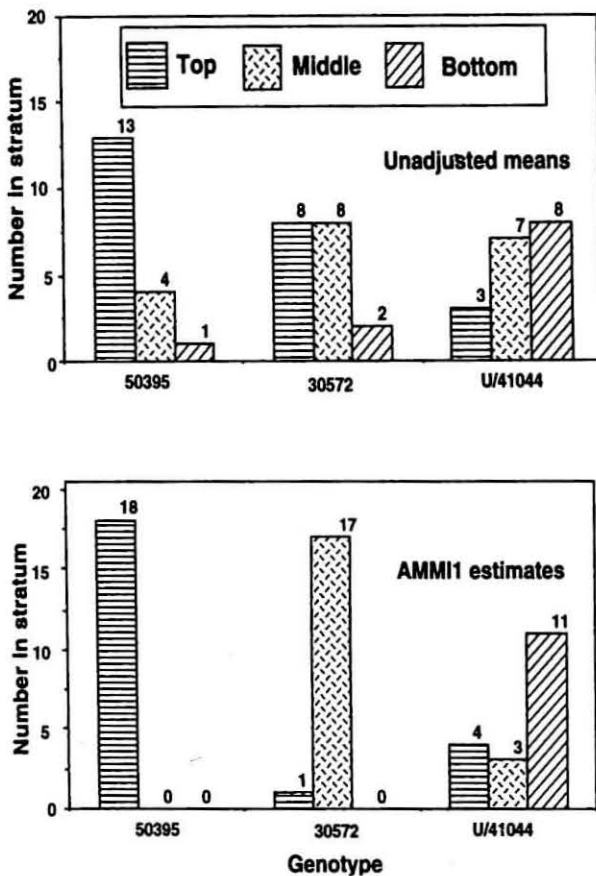


Figure 1. Stratified ranking of the three selected genotypes by unadjusted means and AMMI1 estimates over all environments, giving number of locations for which a genotype occurred in the top, middle and bottom groupings of the entries for fresh yield.

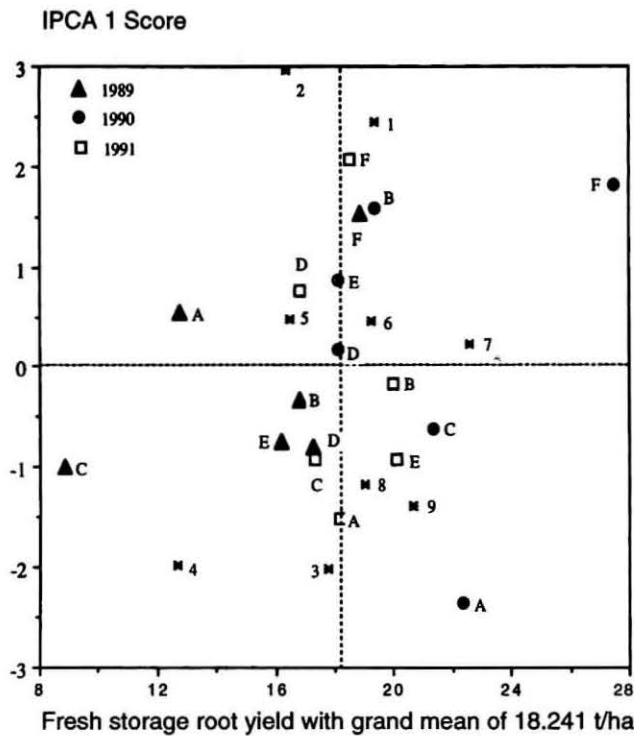


Figure 2. Biplot of the first AMMI interaction (IPCA1) scores (Y-axis) plotted against mean fresh storage root yield (X-axis) for 9 genotype grown in 6 locations for 3 years (18 environments). Location: A: Ibadan, B: Ilorin, C: Mokwa, D: Onne, E: Owerri, F: Ubiaja. Genotype: 1: TME 1; 2: U/41044; and TMS series—3: 4(2)1425; 4: 30001; 5: 30555; 6: 30572; 7: 50395; 8: 63397; and 9: 91934.

Genotypes or environments on the same parallel line relative to the y-axis have similar yields (Figure 2), and a genotype or environment on the right side of the midpoint of this axis has higher yields than those on the left hand side. Consequently, the genotypes TMS 50395, TMS 91934, TMS 30572, TME1 and TMS 63397 were generally high yielding with 50395 being the overall best. In contrast, U/41044, TMS 4(2)1425, TMS 30555 and TMS 30001 were generally low yielding genotypes with TMS 30001 being the least yielder. Generally, 1990 was the most productive year for the genotypes in terms of fresh yield, while 1989 was the least. In 1991, the locations of Ubiaja, Ilorin and Owerri were more favorable for the genotypes, Ibadan was moderate and Mokwa and Onne were least favorable. Ubiaja which was always on the right hand side of the midpoint of the main effect axis, seemed to be a favorable environment for the genotypes while Onne which was always on the left hand side of the axis, was less favorable for them. Owerri was specifically favorable to genotypes TMS 63397 and TMS 91934 in 1991.

Genotypes with IPCA1 scores near zero had little interaction across environments and, vice versa for environments (Cossa et al. 1991). For such genotypes, overall mean ranking will be reliable. Genotype and environment combinations with IPCA1 scores of the same sign produced positive specific interaction effects, whereas combinations of opposite signs had negative specific interactions. Three genotypes (TMS 50395, TMS 30572 and TMS 30555) had negligible interactions with the environments indicating their broad adaptations while 50395 was the most stable genotype across environments. Although TMS 30555 was quite stable, it was

not very productive. U/14044, TME 1, TMS 30001 and TMS 4(2)1425 were highly unstable genotypes. TME 1 was specifically adapted to Ubiaja while TMS 4(2)1425 was somehow adapted to Ibadan. Genotypes TMS 30001 and U/14044, were poorly adapted to all the environments.

In 1989 the $G \times E$ interaction was generally low compared to 1990 and 1991. Overall, Onne and Owerri had lower IPCA1 scores than the other locations. On the average, Mokwa and Ilorin had moderate interaction (average IPCA1 scores) while Ubiaja and Ibadan had the highest IPCA1 values and were the most unstable locations over time. The latter two locations would be good selection sites for cassava improvement when targeting a wide range of environments. Ilorin was stable in 1989 and 1991 but less so in 1990 and its average yield over the years was moderate. Mokwa, a low yielding location, was a moderately stable environment when its IPCA scores for the 3 years are considered. Ibadan was variable for the 3 years.

Four groupings of genotypes were evident from the biplot (Figure 2): TMS 30001 and TMS 4(2)1425 generally low yielding, had high negative IPCA1 scores, were early maturing and unstable; TMS 63397 and TMS 91934 were high yielding but had intermediate and negative IPCA1 scores, and thus were moderately stable across environments; TMS 30572 and TMS 50395 showed negligible interactions and thus were stable across environments and were equally high yielding. U/14044 (low yielding) and TME1 (high yielding) showed high positive IPCA1 scores, were late maturing and very unstable across environments.

Stability of a genotype is enhanced by its ability to withstand prevailing stresses. Thus, resistance to biotic stresses in addition to tolerance of common abiotic factors in the environments would ensure good genotypic performance. As observed in this study and elsewhere (Cock 1985), low levels of disease and insect resistance in addition to other abiotic stresses would render a genotype/location unstable. Consequently, the most stable genotypes (TMS 50395 and TMS 30572) generally had moderate disease ratings. U/14044 (the most unstable genotype) and TMS 91934 (a moderately unstable genotype) had the highest scores for ACMD (Table 4). Except for CGM scores, the stable location especially Onne, generally had lower disease pressure when compared with the unstable locations of Ubiaja and Ibadan. The long growing period and diverse agroecologies in which the crop is cultivated expose cultivars to a lot of biotic stresses, some of which are very devastating especially when acting synergistically with other stresses. During the rainy season, diseases such as ACMD, CBB and CAD can be serious and during the dry season, arthropod pests such as the CGM can be prevalent on cassava. Any of these can cause serious yield losses of cassava. A solution to a single disease or single mite pest can not lead to increased production of cassava. Solutions should be simultaneously sought for all these major economic diseases and pest. Thus multiple disease and pest resistance will ensure stability of crop performance.

Interestingly, stable locations in general had similarities of agroecological characteristics of zone, altitude and rainfall. For example, both Onne and Owerri are in the humid forest, have low altitude (30 and 67 m, respectively), and have high annual rainfall (2501.6 and 2385 mm, respectively). With the exception of Ubiaja, the other locations are in different

Table 4. Mean disease ((African cassava mosaic disease (ACMD), cassava bacterial blight (CBB) and cassava anthracnose disease (CAD) and cassava green mite (CGM)) severity ratings (1: no symptoms and 5: maximum damage) of 9 cassava genotypes evaluated at 6 locations for 3 years

Main effect	ACMD	CBB	CAD	CGM
Genotype				
50395	2.2	2.3	2.2	2.5
91934	2.8	2.0	1.7	1.9
TME 1	1.8	2.8	2.5	1.5
30572	2.0	2.3	2.0	2.5
63397	1.9	2.2	1.8	2.4
4(2)1425	2.2	2.1	1.6	2.4
30555	2.4	2.2	1.9	2.4
U/14044	3.1	2.1	1.5	2.1
30001	1.6	2.2	1.9	2.7
Mean	2.2	2.2	1.9	2.3
CV (%)	23.37	27.49	39.78	48.43
LSD (0.05)	0.2	0.2	0.3	0.4
F-test (p < 0.01)	**	**	**	**
Location				
Ibadan	2.5	2.8	2.5	2.2
Ilorin	2.1	2.4	1.5	3.1
Mokwa	2.0	2.3	1.1	2.4
Onne	2.2	1.7	1.9	1.8
Owerri	2.1	1.8	2.2	2.4
Ubiaja	2.5	2.6	2.3	1.8
Mean	2.2	2.3	1.9	2.3
CV (%)	27.86	22.95	33.97	46.42
LSD (0.05)	0.17	0.2	0.2	0.3
F-test (p < 0.01)	**	**	**	**

agroecologies, are higher than 200 m above sea level, and have rainfall lower than 1500 mm as well as shorter rainfall duration and higher mean maximum temperature.

In conclusion, AMMI statistical model has been used successfully to diagnose G × E interaction pattern of fresh storage root yield of cassava. TMS 50395 and TMS 30572 were hardly affected by the G × E interaction and thus will perform well across a wide range of environments. Stable locations that could be regarded as good selection sites for cassava improvement were also identified.

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