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Research Paper

Application of AMMI biplot model to evaluate some ginger (*Zingiber officinale*) genotypes for adaptation and stability

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Abstract. This research was conducted in three environments in Cross River State in 2016 and 2017 growing seasons on some ginger genotypes to determine their adaptation and stability using Additive main effects and multiplicative interaction (AMMI) biplot model. The ginger genotypes were evaluated in the field in a split-plot arrangement using the Randomized Complete Block Design (RCBD) in three replications. Results from AMMI analysis of variance for number of rhizome fingers per plant, rhizome length and rhizome yield showed that genotype and environment, as well as their interactions (GEI), were highly significant ($P < 0.001$), indicating a wide range of variation. The genotypes G4, G3 and G7 with small IPCA1 scores had wide adaptation while G14 with a large negative IPCA score of (-3.47) was better adapted to E5 (Ogoja 2016) and E6 (Ogoja 2017) respectively, this shows specific adaptation. For the number of rhizome length, the genotypes G10, G15, G13 and G3 had wide adaptation while G2 with large negative IPCA1 score (-2.28) specifically adapted to E1 and E2 (Calabar 2016 and 2017) respectively. For rhizome yield, G4 and G13 with small IPCA scores showed lesser interaction and hence greater stability. Further evaluation of these genotypes is required before their release.

Keywords: Genotype and environment interaction (GEI), interactive principal component axis, variation, specific environment, rhizome.

INTRODUCTION

Ginger (*Zingiber officinale* Roscoe) is a slender erect herbaceous plant grown for its edible rhizome. The ginger plant can grow to a height of 90 cm (Rashid *et al.*, 2013) and it is refreshingly aromatic, but it is the rhizome (raw or processed) that is valued as a spice Babu (2007). The rhizome is brownish with a corky layer and pale yellow scented center.

Ginger is used in the treatment of diarrhoea, nausea, asthma, and respiratory disorders (Medova *et al*., 2009). It has been reported to aid digestion, boost the immune system and reduce cholesterol level (Yakubu, 2007). Ground ginger is used to preserve meat, soup and beverages (Jakes and Susan, 2007).

Ginger is grown in many parts of the world (Ashraf et al., 2014). The major producing countries are Nigeria, Nepal, India, China, Indonesia, Thailand, Korea, Philippines, Australia and Malaysia. Nigeria is the largest producer and exporter in Africa and ranks 4th in the world FAO (2018). Ginger may presently be considered a minor crop because it has not received the research attention that other crops like cocoa, maize, rice, groundnut and cassava had received. However, it is a crop of great potential for the export market. The production trend of ginger in Nigeria is low when compared to other export crops due to its poor yields which can be attributed to the lack of improved varieties (Amadi, 2012).

The cultivation of ginger in Nigeria started in 1927 and since then, farmers have depended entirely on two

landraces (UG1 and UG2). UG1 is yellowish in colour and yields higher than UG2. UG2 is dull grey and is more pungent than UG1 (Chukwu and Emehuite, 2003). Recently, some ginger lines were developed through mutation breeding. These mutant lines cannot be released to farmers unless they are evaluated in different agro-ecological zones for adaptation and stability.

In plant breeding programmes, genotypes are evaluated in multi-environment trials (METs) to test their performance across environments and selecting the best genotypes in specific environments. However, the 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). Genotype by environment interaction (GEI) reflects the different responses of the genotypes to environmental conditions, e.g., the best genotypes in a specific environment may not be the best for others, this brings about the difficulty in the recommendation of genotypes by the breeder (Gauch, 1992; Falconer and Mackay,1996; Arciniegas-Alarcin *et al.*, 2010; Gauch *et al*., 2011; Gauch, 2011).

METs are the most appropriate methods used to select the best genotypes for any environment and to identify genotypes that keep their genetic potential in many different environments (Farshadfar *et al.*, 2012). METs provides an opportunity to plant breeders to identify the adaptability of a genotype to a particular environment and the stability of the genotypes over different environments. Since the data obtained from METs are quite large, it is difficult to interpret these data without graphs. Therefore, different models have been used recently by many investigators to evaluate the data obtained from studies conducted in different environments.

The additive main effects and multiplicative interaction (AMMI) model Gauch (1992) is one of the widely used statistical methods for the interpretation of METs data. The AMMI model has been reported to be an efficient method because it captures a large portion of the Genotype by Environment (GE) sum of squares and uniquely separates main and interaction effects as required for most agricultural research purposes (Gauch, 2006). AMMI analysis can help in the identification of genotypes that have high productivity and are well adapted to an agro-ecological zone, with the aim of regionalised recommendation and selection of test sites Gauch and Zobel 1996; Gauch *et al.*, 2011; Gauch, 2011). AMMI is important to analyze multi-environment trials data and it interprets the effect of the Genotype (G) and Environments (E) as additive effects and the G×E as a multiplicative component (which are the two sources of variation). This research work was therefore carried out with the following objectives:

(1) To determine the adaptation and yield stability of the ginger genotypes across the test sites in two years using the AMMI biplot model.
(2) To determine the most stable genotypes among the investigated ginger genotypes.

MATERIALS AND METHODS

This research work was conducted in three locations in Cross River State, Nigeria during the 2016 and 2017 cropping seasons (March to December). The locations were Calabar (4.9757° N, 8.3417° E); with an annual rainfall of “2915 to 3500 mm and optimum temperature of 26°C, Ikom (5.9617° N, 8.7206° E); with an annual rainfall of 2250 to 2332 mm and optimum temperature of 27°C and Ogoja (6.6548° N, 8.7977° E); with an annual rainfall of 1848 to 2200 mm and optimum temperature of 28.7°C.

Seventeen ginger genotypes consisting of fifteen (15) mutant lines (UG1-11-07, UG1-13-02, UG1-2-35, UG1-5-04, UG1,-5-18, UG1-5-22, UG1-5-31, UG1-5-35, UG1-5-38, UG1-5-48, UG1-5-49, UG1-5-52, UG1-7-24, UG2-11-03, UG2-9-01) and two local check landraces (UG1 and UG2) were sourced from National Root Crop Research Institute (NRCRI), Umudike, Nigeria. The fifteen mutant lines were derived from the existing landraces UG1 and UG2 by exposing them to different doses of gamma rays irradiation. The mutant lines derived from UG1 were exposed to 2GY, 5GY, 7GY, 11GY and 13GY doses of gamma-ray to give the following mutant lines; UG1-2-35, UG1-5-04, UG1-5-18, UG1-5-22, UG1-5-31, UG1-5-35, UG1-5-38, UG1-5-48, UG1-5-49, UG1-5-52, UG1-7-24, UG1-11-07, UG1-13-02 (Iwo *et al.*, 2013). The mutant lines derived from UG2 were exposed to 9GY and 11GY doses of gamma-ray to give the following mutant lines: UG1-9-01 and UG2-11-03 (Iwo *et al.*, 2013).

A chart showing how the names of the mutant lines were derived is given in Table 1.

This experiment was a split-plot laid out in a Randomized Complete Block Design (RCBD) with three (3) replications. Location served as whole plot treatment while the ginger lines served as the sub-plot treatment. An experimental plot measuring 26 m × 8 m (208 m^2) was used for this research in each of the locations. The land was manually cleared, ploughed and seedbeds prepared. Each rhizome was planted 4 to 5 cm beneath the soil with the growth buds facing up so that the shoots can grow towards the surface. Mulching was carried out immediately after planting using *Chromolaena odorata* (L.) R.M.King & H.Rob. (Commonly called siam weed). Manual hoe weeding was carried out at 5, 10, 16 and 24 WAP (weeks after planting). The genotype by environment (GE) interactions and stability parameters of the ginger genotypes across the three locations in two years were evaluated using The Additive main effect and multiplicative interaction (AMMI) model according to Gauch (1992) as follows:

$Y_{ij} - \mu - \beta_j - \alpha_j = j_{ij}$ i

Table 1. Provide legend.

S/N	Wild types or landraces	Doses of gamma rays	Mutant lines derived
35	UG1	2GY	UG1-2-35
04		5GY	UG1-5-04
18			UG1-5-18
22			UG1-5-22
31			UG1-5-31
35			UG1-5-35
38			UG1-5-38
48			UG1-5-48
49			UG1-5-49
52			UG1-5-52
24		7GY	UG1-7-24
07		11GY	UG1-11-07
02		13GY	UG1-13-02
01	UG2	9GY	UG2-9-01
03		11GY	UG2-11-03

Table 2. AMMI ANOVA for number of rhizome fingers/plant.

Source	df	SS	MS	%Treatment SS	%Interaction SS
Total	305	9141	29.97		
Treatments	101	7734	76.57***		
Genotypes	16	2160	135.00***	27.93%	
Environments	5	2671	534.25***	34.54%	
Block	12	47	3.89		
Interactions	80	2902	36.28***	37.52%	
IPCA1	20	1416	70.81***		48.79%
IPCA2	18	736	40.88***		25.36%
Residuals	42	750	17.86		
Error	192	1361	7.09		

*** indicates highly significant , P < 0.001

Where Y_{ij} is the measure of the *i*th genotype in the *j*th environment; u is the grand mean; α_i is the main effect of the *i*th genotype; β_j is the main effect of the *j*th environment; j_{ij} is the interaction between the *i*th genotype and *j*th environment The seventeen ginger genotypes served as the genotype while the three locations and the two years formed a combination of six (6) environments. The characters analysed were the number of rhizome fingers per plant, rhizome length and rhizome yield.

RESULTS

AMMI analysis for the number of rhizome fingers/plant

The AMMI analysis of variance for the number of rhizome fingers/plant in 17 ginger genotypes tested in three environments is displayed in Table 2. AMMI analysis of variance showed that the number of rhizome fingers/plant, genotype and environment, as well as their interactions (GEI), were highly significant (P < 0.001), indicating a wide range of variations. Genotype and environment accounted for 27.93 and 34.54% of the treatment sum of squares (treatment SS) respectively while their interaction (GEI) accounted for 37.52% of the treatment SS. The interaction sum of squares (interaction SS) was partitioned into interaction principal component axis 1 (IPCA1), and interaction principal component axis 2 (IPCA2) and the residuals. IPCA1 and IPCA2 were both highly significant (P < 0.001) and jointly accounted for 74.15% of the total variation due to interaction; with IPCA1 explaining 48.79% and IPCA2 explaining 25.36% of the variations. The genotype and environment mean for the number of rhizome fingers/plant as well as their

Table 3. AMMI analysis showing genotype and environment mean scores for the number of rhizome fingers per plant together with their IPCA1 and IPCA2 scores.

Genotype	Calabar 2016 (E1)	Calabar 2017 (E2)	Ikom 2016 (E3)	Ikom 2017 (E4)	Ogoja 2016 (E5)	Ogoja 2017 (E6)	Mean	IPCA(g)1	IPCA(g)2
UG1	10.76	19.99	14.57	14.38	13.80	14.50	14.67	1.28	2.14
UG1-11-07	6.21	9.00	11.90	12.27	11.54	11.74	10.44	0.61	0.37
UG1-13-02	10.61	12.11	15.48	15.58	18.00	19.22	15.17	-0.27	0.34
UG1-2-35	8.82	7.98	15.40	16.03	15.69	15.77	13.28	0.12	-0.58
UG1-5-04	11.08	9.15	16.56	16.82	20.21	21.52	15.89	-0.87	-0.49
UG1-5-18	8.79	13.07	14.11	14.37	13.53	13.80	12.94	0.80	0.76
UG1-5-22	6.27	10.53	10.90	10.94	11.87	12.76	10.56	0.39	0.96
UG1-5-31	9.21	10.12	16.20	16.97	14.24	13.60	13.39	0.88	-0.35
UG1-5-35	10.49	12.36	14.56	14.40	18.65	20.53	15.17	-0.65	0.63
UG1-5-38	10.20	11.87	16.45	16.99	15.63	15.53	14.44	0.63	0.001
UG1-5-48	14.11	9.43	20.42	20.94	24.18	25.25	19.06	-1.14	-1.26
UG1-5-49	9.91	12.09	16.39	17.01	14.67	14.27	14.06	0.91	0.04
UG1-5-52	10.87	11.13	18.23	19.12	15.91	15.07	15.06	0.90	-0.57
UG1-7-24	11.21	9.32	12.40	11.29	25.92	31.19	16.89	-3.47	0.67
UG2	10.05	9.76	14.78	14.82	18.95	20.64	14.83	-0.86	0.03
UG2-11-03	12.91	12.68	18.79	19.19	20.25	20.86	17.44	-0.14	-0.27
UG2-9-01	17.17	11.69	27.19	28.89	22.97	20.76	21.44	0.90	-2.41
Mean	10.51	11.31	16.14	16.40	17.41	18.06			
IPCA(e)1	0.36	1.73	1.36	1.69	-1.97	-3.16			
IPCA(e)2	0.05	3.17	-1.40	-1.84	-0.36	0.38			

Key: IPCA(g)1=Interaction principal component axis (genotype)1, IPCA(e) = Interaction principal component axis (environment)1

IPCA1 and IPCA2 scores are presented in Table 3. Genotype means ranged from 10.44 in (UG1-11-01) to 21.44 in (UG2-9-01) which also had the largest IPCAg2 score (-2.41). UG1-7-24 with a mean of 16.86 had the largest IPCAg1score (-3.49). While (UG1-2-35) with a mean of 13.28 had the smallest IPCAg1 score (0.11). Across the six environments, E6 (Ogoja 2017) had the highest mean of 18.06 and the second largest IPCAe1 score (-3.163) while E1 (Calabar 2016) had the lowest mean of 10.51 also had the smallest IPCAe1 and IPCAe2 scores (0.36 and 0.05 respectively). E2 (Calabar 2017) which had the second-lowest mean of 11.31 had the largest IPCAe2 score (3.18)

In the AMMI estimates for each environment, UG2-9-01 ranked top in three of the six environments (Calabar, 2016; Ikom, 2016, 2017); UG1-7-24 topped in two environments (Ogoja, 2016, 2017) while UG1 ranked top in one environment (Calabar, 2017). UG2-11-03 was among the first four AMMI selections in each of the six environments while UG1-5-48 was among the first four in five environments.

Figure 1 displays IPCA1 vs mean (AMMI-1 biplot) showing the relative mean performance of the genotypes and environments for the number of rhizome fingers/plant. The biplot indicated G17 (UG2-9-02) and G11 (UG1-5-48) as the best performing genotypes for this character while G2 (UG1-11-07) and G7 (UG1-5-22) were the poorest performers. E6 (Ogoja, 2017) and E5 (Ogoja, 2016) were indicated as the best environment for this trait while E1 (Calabar, 2016) and E2 (Calabar, 2017) were the worst.

Figure 2 displays the IPCA1 vs IPCA2 (AMMI-2 biplot) for rhizome fingers/plant. The biplot explained 74.2% of the variation due to interaction and indicates the stability of the genotypes and environment. G16 (UG2-11-03), G4 (UG1-2-35), G3 (UG1-13-02), G10 (UG1-5-38) and G2 (UG1-11-07) were indicated as the most stable genotypes for the number of rhizome fingers/plant as they exhibited very little interaction and were closest to the origin of the biplot. G14 (UG1-7-24), G1 (UG1) and G17 (UG2-9-02) had high interactions and were furthest from the origin; indicating low stability. E2 (Calabar, 2017) and E6 (Ogoja, 2017) were furthest from the biplot origin thus were the most unstable environments. E2 (Calabar, 2017) interacted positively with G1 (UG1) while E6 (Ogoja, 2017) interacted positively with G14 (UG1-7-24).

AMMI analysis for rhizome length (cm)

The additive main effects and multiplicative interaction ANOVA for rhizome length are presented in Table 4. The model showed that genotype, environment and their

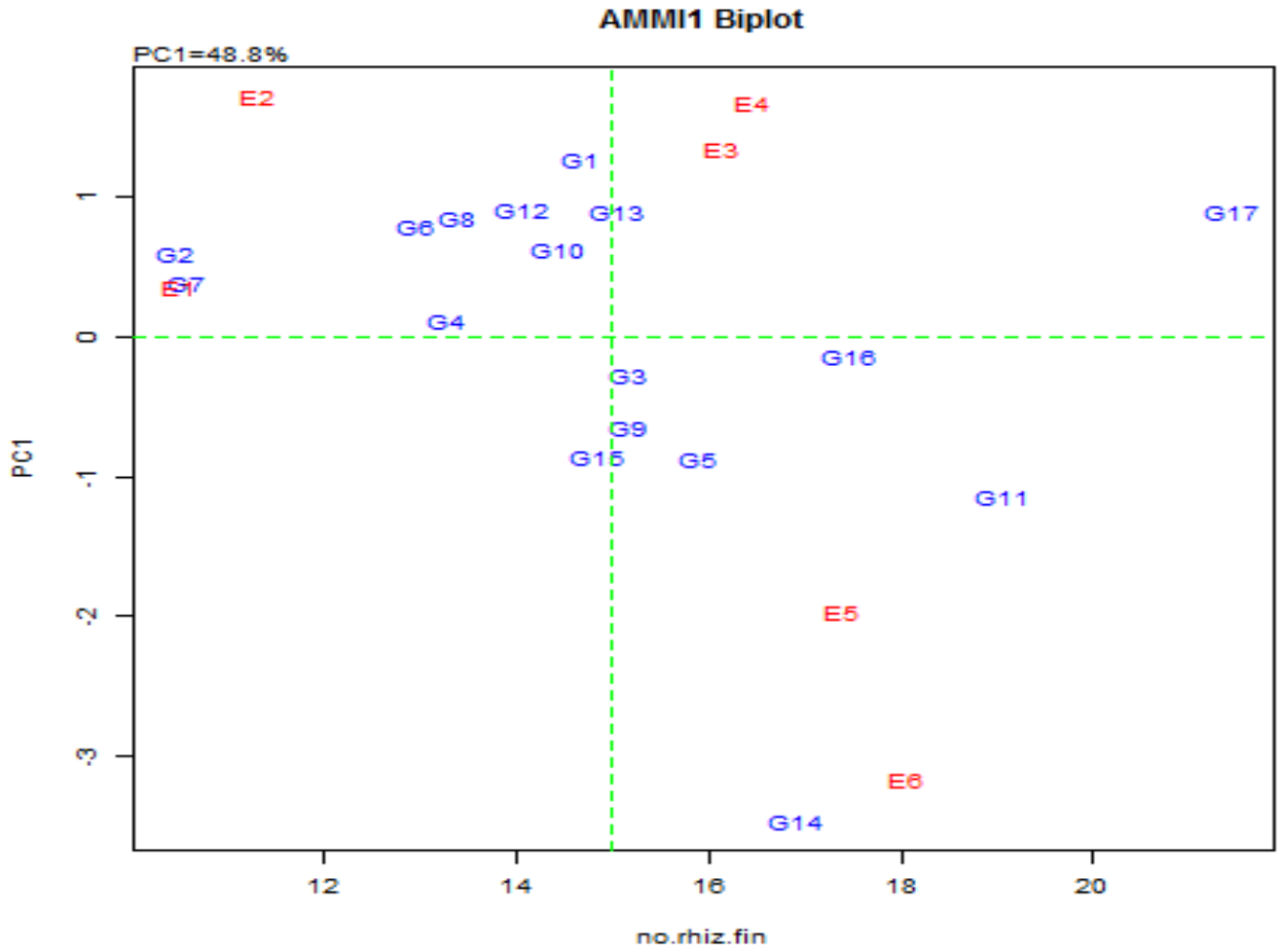

Figure 1. IPCA1 vs mean (AMMI-1 biplot) showing the relative mean performance of the genotypes and environments for the number of rhizome fingers/plant. G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017

interaction (G×E) were highly significant (P < 0.001) for the trait. Genotype accounted for 26.75% of the treatment SS while environment accounted for 44.85% showing that wide differences existed among the environments causing most of the variations in rhizome length. Genotype x environment (interaction accounted for 28.41% of the treatment SS. The total variation due to interaction was partitioned into IPCA1 and IPCA2 and both were highly significant (P < 0.001). IPCA1 captured 50.59% of the interaction SS while IPCA2 Captured 25.46%. The remaining fraction of the interaction SS was captured as the residual.

Table 5 shows the AMMI estimate of the genotype and environment means together with their respective IPCA1 and IPCA2 scores for rhizome length. G17 (UG2-9-01) had the longest rhizomes with a mean of 20.46cm. G17 had an IPCA1 score of 1.65 and an IPCA2 score of 0.67. G11 (UG1-5-48) and G14 (UG1-7-24) were next with mean rhizome lengths of 18.91 and 18.84 cm, respectively. The AMMI estimates of mean performance showed G2 (UG1-11-03) and G7 (UG1-5-22) as the genotypes with the shortest rhizomes with mean rhizome lengths of 11.06 cm and 11.83 cm. G2 (UG1-11-07) also had the largest IPCA1 score (-2.28). G10 (UG1-5-38) with a mean of 16.81 cm had the smallest IPCA1 score (0.03) while G16 (UG2-11-03) with the fourth-highest mean of 18.09 cm had the smallest IPCA2 score (0.01). G16 had an IPCA1 score of (-0.47). Among the environments, E5 (Ogoja, 2016) and E6 (Ogoja, 2017) gave the highest mean rhizome length with 19.57 and 18.84 cm, respectively. E1 (Calabar, 2016) gave the shortest rhizomes (10.21 cm) and had the largest IPCA1 score (-3.05). E3 (Ikom, 2016) had the smallest IPCA1 score (0.90). Across the six environments, G17 (UG2-9-01) was ranked top for rhizome length in three (3) environments while G16 (UG2-11-03), G14 (UG1-7-24) and G9 (UG1-5-35) were top in one environment each.

Figure 3 displays the IPCA vs mean (AMMI-1 biplot) for rhizome length. The biplot gives a visual representation of the relative performance of the genotypes and

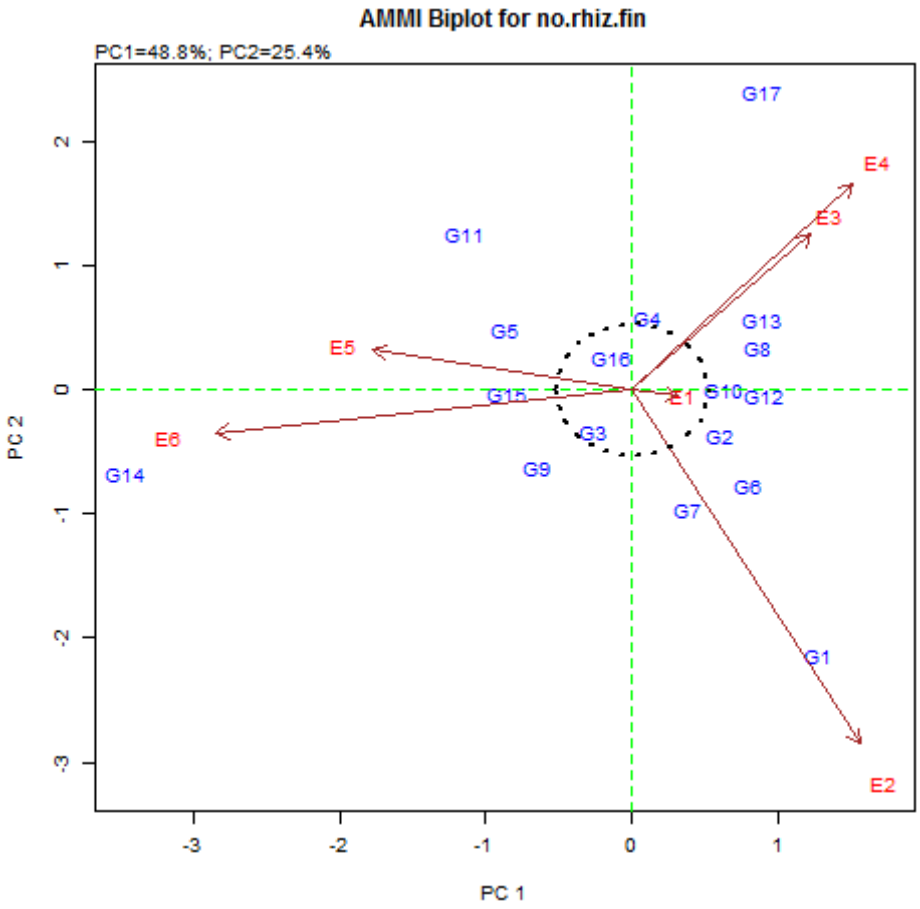

Figure 2. IPCA1 vs IPCA2 (AMMI-2 biplot) showing the interaction of the genotypes and environments for the number of rhizome fingers/plant. G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017

Table 4. AMMI ANOVA for rhizome length (cm).

Source	Df	SS	MS	%Treatment SS	%Interaction SS
Total	305	7178	23.54		
Treatments	101	6262	62.00***		
Genotypes	16	1675	104.66***	26.75%	
Environments	5	2809	561.72***	44.85%	
Block	12	73	6.06		
Interactions	80	1779	22.23***	28.41%	
IPCA1	20	900	44.99***		50.59%
IPCA2	18	453	25.18***		25.46%
Residuals	42	426	10.13		
Error	192	844	4.39		

*** indicates highly significant , P < 0.001.

environments for rhizome length. The biplot indicated G17 (UG2-9-01), G14 (UG1-7-24) and G11 (UG1-5-48) as the best performing genotypes while G2 (UG1-11-07) and G7 (UG1-5-22) were the poorest performing genotypes for the trait. E5 (Ogoja, 2016) and E6 (Ogoja, 2017) were the best-performing environments with

Table 5. AMMI analysis showing genotype and environment means for rhizome length (cm) together with their IPCA1 and IPCA2 scores.

Genotype	Calabar 2016 (E1)	Calabar 2017 (E2)	Ikom 2016 (E3)	Ikom 2017 (E4)	Ogoja 2016 (E5)	Ogoja 2017 (E6)	Mean	IPCA(g)1	IPCA(g)2
UG1	10.52	19.43	14.96	13.97	21.46	19.91	16.71	-0.36	-1.33
UG1-11-07	12.30	13.63	11.02	10.17	10.00	9.21	11.06	-2.28	0.81
UG1-13-02	10.16	17.53	17.72	17.03	20.93	20.10	17.24	0.19	-0.26
UG1-2-35	10.89	14.58	17.17	16.64	16.13	15.86	15.21	-0.42	1.00
UG1-5-04	11.39	15.84	20.68	20.30	19.35	19.34	17.81	0.30	1.16
UG1-5-18	7.12	16.39	18.68	18.12	22.73	22.05	17.52	1.24	-0.41
UG1-5-22	9.23	14.41	19.99	10.07	13.73	12.50	11.83	-1.28	-0.26
UG1-5-31	10.69	18.64	20.73	20.35	19.78	19.76	17.82	0.52	1.06
UG1-5-35	11.54	21.10	14.14	12.99	22.24	20.32	17.06	-0.70	-1.87
UG1-5-38	9.78	18.24	16.16	15.33	21.28	20.08	16.81	0.03	-0.87
UG1-5-48	9.04	16.40	21.56	21.18	22.73	22.55	18.91	1.27	0.48
UG1-5-49	12.17	16.06	15.72	15.00	16.05	15.39	15.07	-1.00	0.52
UG1-5-52	9.22	15.65	15.84	15.15	18.21	17.45	15.26	-0.10	-0.03
UG1-7-24	7.36	18.08	19.42	18.80	25.16	24.25	18.84	1.47	-0.92
UG2	9.37	15.29	16.39	15.76	17.93	17.32	15.34	-0.06	0.23
UG2-11-03	13.23	19.01	18.40	17.67	20.53	19.73	18.09	-0.47	0.01
UG2-9-01	9.57	17.08	23.75	23.47	24.44	24.45	20.46	1.65	0.67
Mean	10.21	16.73	17.25	16.59	19.57	18.84			
IPCA(e)1	-3.06	-1.57	0.90	1.05	1.22	1.45			
IPCA(e)2	0.72	-1.48	1.61	1.81		-1.05			

respect to mean rhizome length while E1 (Calabar, 2016) was the worst-performing environment for this trait.

Figure 4 displays the IPCA1 vs IPCA2 (AMMI-2 biplot) for rhizome length showing the interaction of the genotypes and environments. The biplot captured 76.1% of the total variation in rhizome length that is due to G×E interaction. G13 (UG1-5-52), G15 (UG2), G3 (UG1-13-02) and G16 (UG2-11-03) were indicated as the most stable genotypes for this trait as they fell closer to the origin of the biplot. G2 (UG1-11-07) and G9 (UG1-5-35) exhibited high interactions and were furthest away from the origin. Among the environments, E6 (Ogoja, 2017) had the smallest interactions while E1 (Calabar, 2016) exhibited the highest interaction. The environments fell into four groups with E5 (Ogoja, 2016) and E6 (Ogoja, 2017) having similar interaction pattern; both had positive interactions with G14 (UG1-7-24) and G6 (UG1-5-18) while E3 (Ikom, 2016) and E4 (Ikom, 2017) had similar pattern having positive interactions with G8 (UG1-5-31), G5 (UG1-5-04), G11 (UG1-5-48) and G17 (UG2-9-01). E1 (Calabar, 2016) had positive interactions with G2 (UG1-11-03),G12 (UG1-5-49) and G4 (UG1-2-35) . E2 (Calabar, 2017) had positive interactions with G7 (UG1-5-22), G1 (UG1) and G9 (UG1-5-35).

AMMI analysis for rhizome yield (t/ha)

Table 6 shows the AMMI analysis of variance model for rhizome yield of seventeen (17) ginger genotypes across six (6) environments. The model indicated that the Genotype, environment, as well as their interaction (G × E), were highly significant ($P < 0.001$). Genotype and environment accounted for 37.61 and 9.43% of the treatment SS respectively while the G×E interaction accounted for 52.95% of the treatment SS. The first two IPCA of the interaction SS were highly significant ($P < 0.001$) and both accounted for 69.94% of the total variations due to the G×E interactions. The first IPCA (IPCA1) captured 41.53% of the G×E interaction sum of squares while the second IPCA (IPCA2) captured 28.41% of the interaction sum of squares.

Table 7 shows the AMMI estimates of means of genotypes and environments for rhizome yield (t/ha) together with their respective IPCA1 and IPCA2 scores. G5 (UG1-5-04) had the highest mean rhizome yield of 22.06 t/ha followed by G9 (UG1-5-35) with a mean yield of 21.06t/ha and G17 (UG2-9-01) with a mean of 20.06 t/ha. G2 (UG1-11-07) and G7 (UG1-5-22) had the lowest mean yield with 6.44 and 7.67 t/ha respectively. G7 had the largest IPCAg1score of -2.54 while G2 had the largest IPCAg2 score of -2.72. AMMI estimated E3 (Ikom, 2016) as the environment with the highest mean for rhizome yield (18.88 t/ha) followed by E5 (Ogoja, 2016) with a mean of 17.92 t/ha while E1 (Calabar, 2016) had the lowest mean yield of 12.71 t/ha. E1 (Calabar, 2016) had the largest IPCAe1 score (-3.85) and largest IPCAe2 score (-3.35). E2 (Calabar, 2017) had the smallest

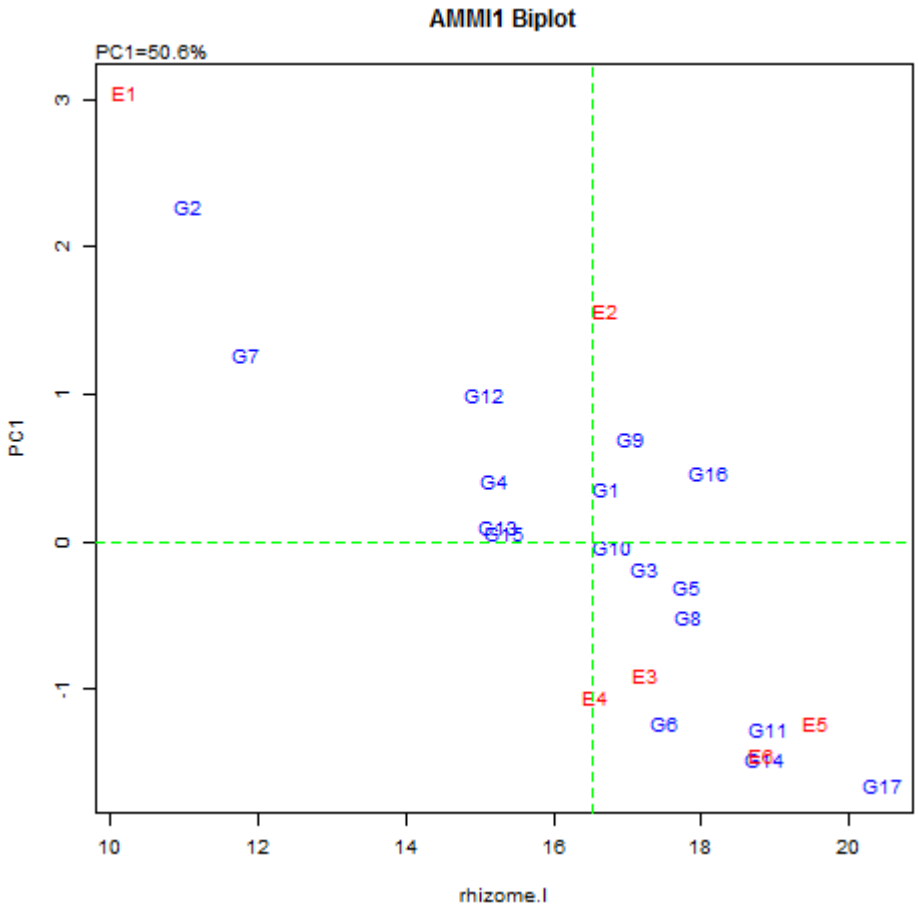

Figure 3. IPCA1 vs mean (AMMI-1 biplot) for rhizome length showing the mean performance of the genotypes and environments. G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017.

IPCAe2 score (0.80) while E5 (Ogoja, 2016) had the smallest IPCAe1 score (0.69). In the first four AMMI selections per environment, G5 (UG1-5-04) was among the first four genotypes in five of the six environments and ranked first in three environments. G14 (UG1-7-24) was among the first four in three environments but ranked first in one. G11 (UG1-5-48) and G9 (UG1-5-35) ranked first in one environment each.

The AMMI-1 biplot (IPCA1 vs mean) for rhizome yield is displayed in Figure 5. The biplot showed G5 (UG1-5-04) as the highest yielding genotype, followed by G9 (UG1-5-31) and G17 (UG2-9-01). The poorest yielding genotype was G2 (UG1-11-07) followed by G7 (UG1-5-22) and G12 (UG1-5-49). E3 (Ikom 2016) was selected as the environment with the highest yield followed by E5 (Ogoja, 2016) and E6 (Ogoja, 2017). E1 (Calabar, 2016) and E2 (Calabar, 2017) were the lowest yielding environments.

Figure 6 displays the AMMI-2 biplot showing the interactions of the genotypes and environments for rhizome yield. Among the genotypes, G13 (UG1-5-52), G12 (UG1-5-49), G16 (UG2-11-03) and G4 (UG1-2-35) showed the greatest stability for yield while G2 (UG1-11-07), G8 (UG1-5-31), G11 (UG1-5-48), G7 (UG1-5-22) and G1 (UG1) exhibited high interactions and therefore unstable. E2 (Calabar, 2017) and E5 (Ogoja, 2016) were the most stable environment for yield while E1 (Calabar, 2016) and E6 (Ogoja, 2017) were the environments with high interactions. G11 (UG1-5-48) and G14 (UG1-7-24) interacted positively with E5 (Ogoja, 2016) and E6 (Ogoja, 2017) while G2 (UG1-11-07) had a positive interaction with E1 (Calabar, 2016).

DISCUSSION

Multi-location trials are necessary to confirm the differences, uniformityand stability of newly developed crop varieties in readiness for recommendation to farmers.The interaction that exists between genotypes

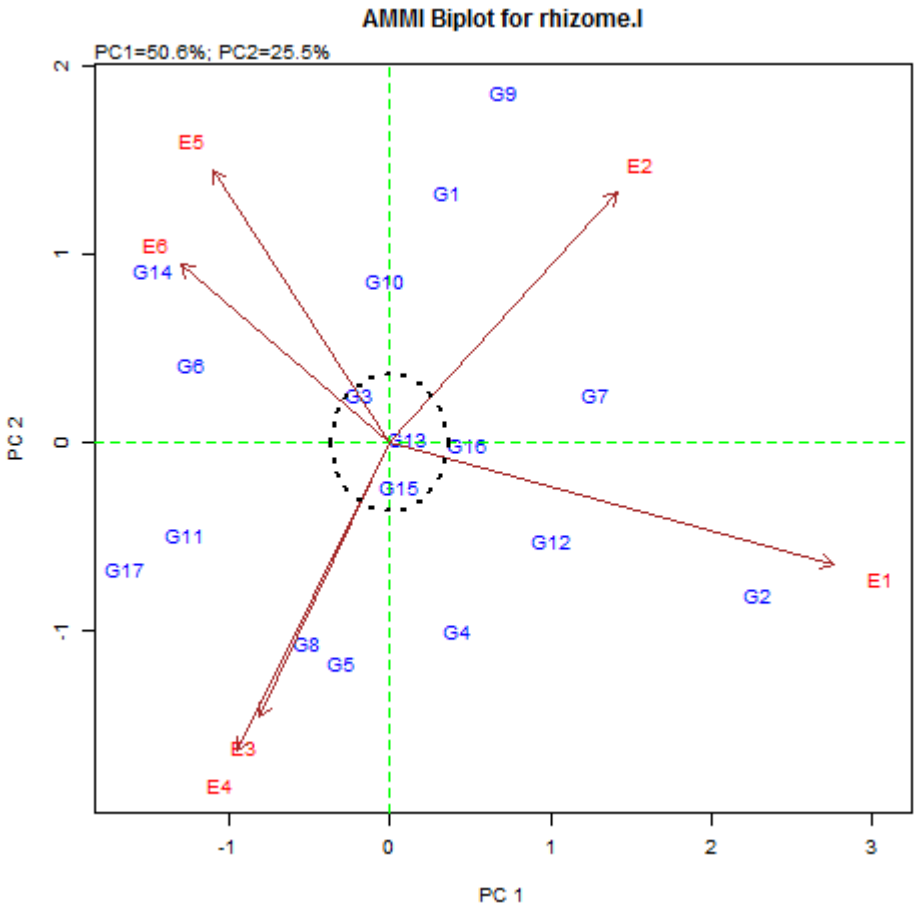

Figure 4: IPCA1 vs IPCA2 (AMMI-2 biplot) showing the interaction of the genotypes and environments for rhizome length (cm). G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017

Table 6. AMMI ANOVA for rhizome yield (t/ha).

Source	Df	SS	MS	%Treatment SS	%Interaction SS
Total	305	20690	67.8		
Treatments	101	16558	163.9***		
Genotypes	16	6228	389.3***	37.61%	
Environments	5	1562	312.3***	9.43%	
Block	12	445	37.1		
Interactions	80	8768	109.6***	52.95%	
IPCA1	20	3641	182.1***		41.53%
IPCA2	18	2491	138.4***		28.41%
Residuals	42	2636	62.8		
Error	192	3687	19.2		

*** indicates highly significant , P < 0.001.

and environment in different environments makes selection of any genotype for recommendation challenging for breeders. Hence, there is a need to select for distinctiveness, uniformity and stability whenever such interactions become of practical value in a testing programme (Funnah and Mark, 1980).

Table 7. AMMI analysis showing genotype and environment means for rhizome yield (t/ha) together with their IPCA1 and IPCA2 scores.

Genotype	Calabar 2016 (E1)	Calabar 2017 (E2)	Ikom 2016 (E3)	Ikom 2017 (E4)	Ogoja 2016 (E5)	Ogoja 2017 (E6)	Mean	IPCA(g)1	IPCA(g)2
UG1	21.01	9.04	9.35	8.87	17.87	20.17	14.39	-2.53	-0.07
UG1-11-07	20.05	-0.48	5.44	6.03	5.20	2.43	6.44	-2.04	-2.72
UG1-13-02	10.37	18.72	27.56	23.36	20.24	17.41	19.61	1.61	-0.09
UG1-2-35	10.69	14.19	18.62	15.43	19.37	19.33	16.22	0.04	0.61
UG1-5-04	9.84	21.92	30.39	25.61	23.41	21.16	22.06	1.90	0.46
UG1-5-18	4.66	17.44	27.19	22.22	18.02	14.81	17.39	2.28	0.18
UG1-5-22	13.96	2.40	2.51	1.98	11.33	13.82	7.67	-2.54	0.04
UG1-5-31	21.37	14.65	26.05	24.13	15.57	19.55	18.56	0.70	-2.65
UG1-5-35	21.65	17.54	24.49	22.39	21.28	18.97	21.06	-0.12	-1.04
UG1-5-38	10.38	17.44	24.01	20.14	20.59	19.44	18.67	0.93	0.41
UG1-5-48	8.14	12.02	8.88	6.04	22.00	28.25	14.22	-1.76	2.85
UG1-5-49	7.59	5.69	10.17	7.85	10.95	10.75	8.83	-0.49	-0.06
UG1-5-52	10.26	12.79	17.89	14.82	17.29	16.95	15.00	0.11	-0.29
UG1-7-24	9.96	18.39	20.06	16.23	24.77	27.58	19.50	-0.13	2.00
UG2	10.91	12.33	18.78	15.81	16.02	14.51	14.72	0.32	-0.23
UG2-11-03	12.31	16.72	24.86	21.33	19.02	16.43	18.44	1.04	-0.35
UG2-9-01	12.81	18.54	24.74	21.10	22.05	21.09	20.06	0.70	0.36
Mean	12.71	13.49	18.88	16.08	17.92	17.22			
IPCA(e)1	-3.85	1.08	3.13	2.23	-0.68	-1.91			
IPCA(e)2	-3.35	0.79	-0.93	-1.50	1.65	3.33			

Key: IPCA (g)1= Interaction principal component axis (genotype)1,IPCA(e) = Interaction principal component axis(environment)1

AMMI analysis is a valuable tool for identifying genotypes with either specific or wide adaptation. The potential of AMMI analysis for describing G×E interactions in different crops has been proven (Nachit *et al.*, 1992; Yan *et al.*, 1995) on wheat, (Fox *et al*., 1990) on triticale, Adugna (2008) on sorghum. In this study, the AMMI analysis of variance for the number of rhizome fingers per plant, rhizome length and rhizome yield indicated a wide range of variation in genotypes (G), environment (E), as well as their interactions (GEI) (Tables 2, 4 and 6). The genotypes with Interaction Principal Component Axis (IPCA) scores close to zero expressed general adaptation whereas the larger scores depicted more specific adaptation to certain environments, this agrees with Ebdon and Gauch (2002). The IPCA scores of genotypes in the AMMI analysis are an indication of the stability or adaptation of the genotypes and environments (Steyn *et al.*, 1993). The greater the IPCA scores, either negative or positive, the more specifically adapted a genotype is to certain environments. The closer the IPCA scores to zero, the more stable or adapted the genotype is in all the environments (Gauch and Zobel, 1996). Large IPCA scores is an indication of high interaction; hence less stability. Conversely, small IPCA scores is an indication of low interaction; hence higher stability. Genotypes with IPC1 scores near zero expressed general adaptation whereas those with larger IPC1 scores showed more specific adaptation to certain environments or locations Ebdon and Gauch (2002). In contrast to this, the genotypes with smaller IPCA scores have lower interaction and are considered as widely adapted genotypes. Therefore, for rhizome fingers per plant, the genotypes G4, G3 and G7 with small IPCA1 scores had wide adaptation while G14 with a large negative IPCA score of (-3.47) was better adapted to E (5) and E (6) respectively, this shows specific adaptation (Table 2). For the number of rhizome lengths, the genotypes G10, G15, G13 and G3 had wide adaptation while G2 with a large negative IPCA1 score (2.28) specifically adapted to E1 and E2 respectively (Table 4). For rhizome yield, G4 and G13 with small IPCA scores showed lesser interaction and hence greater stability.

The specific adaptation indicates the high mean productivity of a genotype in selected environments therefore, the identification of varieties with specific adaptations can be extremely useful for more regionalized varietal recommendations. According to Najafian *et al.* (2010), specific adaptation is the key point for yield improvement. Wide adaptation shows high mean productivity and stability across several environments. Figure 1, 3 and 5 shows the relative mean performance of the genotypes and environments for the number of rhizome fingers, rhizome length and rhizome yield. The genotypes with the highest mean performance for these traits could be termed superior genotypes as regards these traits. The best genotypes should combine high

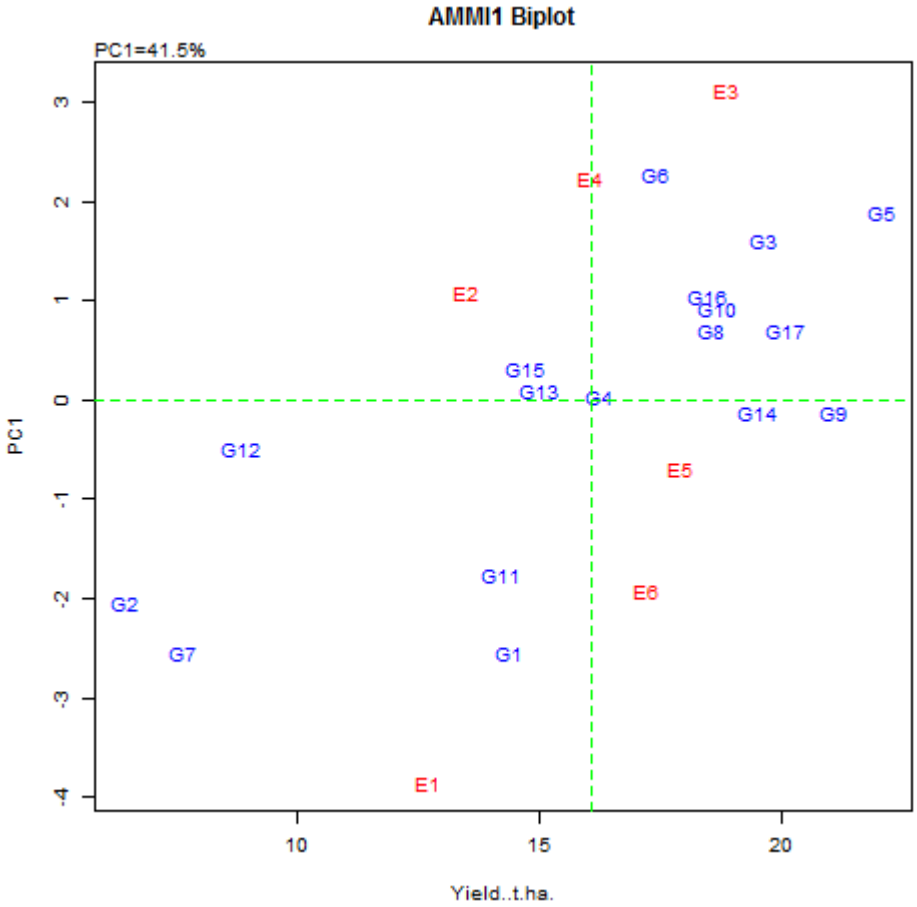

Figure 5. IPCA1 vs mean AMMI-1 biplot showing the relative mean performance of the genotypes and environments for rhizome yield (t/ha). G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017.

yield and stable performance across a range of production environments (Yan and Tinker, 2006). As regards the environments, the best performing environments could be considered favourable for the cultivation of ginger because they have little interaction with the genotypes, while the poor performing environments are considered unfavourable environments. The AMMI analysis can be used efficiently in the identification of superior environmental conditions for agricultural exploitation (selection of growing locations) and superior mean performance of genotypes (Gauch *et al.*, 2008; Yan, 2010).

The AMMI-2 biplot for the number of rhizome fingers, rhizome length and rhizome yield is presented in figures 2, 4 and 6 respectively. AMMI-2 biplot positioned the genotypes in different locations, indicating the adaptation pattern of the genotypes. The similarity in the performance of the genotypes was observed because most of them were close to one another. Genotypes and environments positioned close to each other in the biplot have positive associations, this allows the creation of agronomic zones with relative ease. The genotypes near the origin of the biplot were less sensitive to environmental interaction thus more stable while those far away from the origin of the biplot were more sensitive and had large interaction hence unstable (Figure 2, 4 and 6) this agrees with (De Vita *et al.*, 2010). AMMI-2 biplot for rhizome yield showed that (E3 and E4) were the most stable environments for this trait (Figure 6). Environmental stability is important for demonstrating the performance of a genotype in a given environment (Rocha *et al.*, 2007).

RECOMMENDATIONS /CONCLUSION

The genotypes G5, G9, G17, G3 and G14 were the highest yielding genotypes, while G4, G13, G12 and G16 were identified as the most stable, these genotypes exhibit higher adaptability and stability, therefore, they

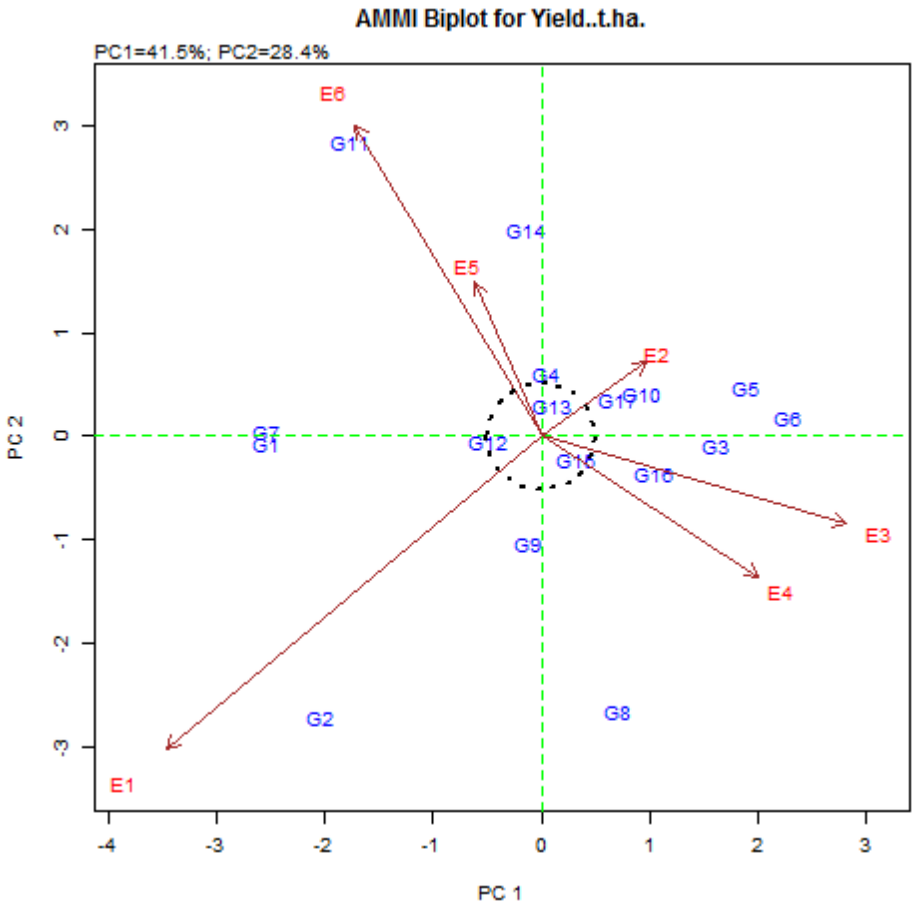

Figure 6. IPCA1 vs IPCA2 AMMI-2 biplot showing the interaction of the genotypes and environments for rhizome yield (t/ha). G1=UG1; G2=UG1-11-07; G3=UG1-13-02; G4=UG1-2-35; G5=UG1-5-04; G6=UG1-5-18; G7=UG1-5-22; G8=UG1-5-31; G9=UG1-5-35; G10=UG1-5-38; G11=UG1-5-48; G12=UG1-5-49; G13=UG1-5-52; G14=UG1-7-24; G15=UG2; G16=UG2-11-03; G17=UG2-9-01; E1=Calabar 2016; E2=Calabar 2017; E3=Ikom 2016; E4=Ikom 2017; E5=Ogoja 2016; E6=Ogoja 2017

are recommended for cultivation across all the environments in this study. In other words, these genotypes are recommended for further evaluation and subsequently release for wide cultivation. The genotypes G14 with large IPCA scores show specific adaptation to E5 and E6. G2 with a large negative IPCA1 score (-2.28) specifically adapted to E1 and E2 respectively, these genotypes are therefore recommended for cultivation in these environments. The low-yielding and stable genotypes in this study should further be evaluated and tested in these environments before recommendations are made on them.

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