



## Research article

## Genotype × environment interaction and adaptation of cowpea genotypes across six planting seasons

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### Abstract

Cowpea exhibits significantly inconsistent performances across different environments, and hence demands performance evaluation of genotypes prior release or cultivation in every breeding program. Hence, the goal of this study was to compare 16 cowpea genotypes over six planting seasons (2014-2019) in Akungba-Akoko, Nigeria for their stability and adaptation through Finlay and Wilkinson (FW), Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype × Environment (GGE) analyses. ANOVA revealed high significant genotype (15.33%), environment (14.71%) and GEI (64.34%) effects for seed yield among genotypes. All analyses were able to pinpoint stable high-yielding genotypes including G14 and G9. Genotypes G14, G3, G4, G5, G6 and G9 were high yielding and stable according to FW; AMMI showed G10, G9, G16, G14 and G13 stable high-yielding while GGE showed G14, G16, G9 and G13 as stable high-yielding. As analyses explored the variation in the data due to GEI, they also complemented one another, in that where one erroneously included a wrong genotype as stable; the other excluded such genotype, making recommendation possible on the basis of consistency to gain reliability.

**Keywords:** *Adaptation; cowpea; g × e interaction; stability; yield*

### 1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp], one of Nigeria's most popular grain legumes, and in all the tropical and subtropical countries (Ajayi and Gbadamosi, 2020). This legume is vital for its contribution to the nutrition of people and livestock. Its high plasticity nature allows it to adapt to wide range of environmental conditions. Its inherent ability at fixing atmospheric nitrogen in soil with consequent soil enhancement (Olayiwola et al., 2015; Gomes et al., 2019; Aliyu et al., 2019) and being a source of income to millions of people of these regions (Kebede and Bekeko, 2020) make it a choice crop for cultivation. Cowpea seeds are rich in protein and minerals

(Gerrano et al., 2015). Its capacity in biological nitrogen fixation ranges between 70 and 350 kg of nitrogen per hectare with its impact projected to reach 77, 320 tons in 2020. Presently, Africa accounts for 94.9 percent of the total worldwide cowpea production (7.23 MT/annum) and harvested area of land (12.59M ha), with more than 36 percent of the total production accounted for by Nigeria (at 2.61 MT/annum) as the largest world's producer (FAOSTAT, 2020). In spite of this, grain yield of cowpea in Nigeria has been seriously compromised by inappropriate cultural practices, abiotic and biotic factors (Ajayi and Gbadamosi, 2020) making its productivity grossly inadequate to cater for the protein needs of the ever-increasing population of the country.

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According to the United Nations (UN), the current world population explosion is predicted to be increased from Africa; with an expected addition of 1.2 billion people of the projected 1.9 billion increase between 2020 and 2050. Also, the Nigerian population is expected to surpass that of the United States during the same period (UN, 2019) demanding an accelerated food production to meet the Nigerian growing population. In the same vein, climate change is expected to aggravate rising temperature and free CO<sub>2</sub>, disorganize rainfall patterns and soil salinity thereby, making occurrence of drought highly unpredictable; when combined with population growth, their impacts on food and nutritional security would be devastating (Gomes et al., 2019; Ajayi et al., 2020). Therefore, in line with the present reality, there is need for quick and sustainable increase in domestic cowpea production in Nigeria. However, the biggest challenge associated with the improvement of yield is the complexity of the trait, in that it is polygenic in nature with strong environmental influences.

Cowpea genotypes have been found to exhibit significantly inconsistent performances across different environments (Ajayi and Gbadamosi, 2020), which is regarded as genotype-by-environment interaction (GEI /  $G \times E$ ). Before the release of novel genotypes or varieties, their GEI must be evaluated to pinpoint individuals that show both superior performances (in terms of mean yield) coupled with extraordinary stability across multiple environment trials (MET) (Agahi et al., 2020; Pour-Aboughadareh et al., 2022).

Innumerable multivariate techniques have previously been employed to assess the existence of yield stability and  $G \times E$  in crop species (Bocianowski and Prazak, 2022; Pour-Aboughadareh et al., 2022). Among them, the Finlay and Wilkinson analysis (FW), Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype and Genotype  $\times$  Environment (GGE) Biplot analysis are the most commonly used ones in plant breeding research, recently. These three analyses have been proven to be highly effective, sophisticated and efficient (Olayiwola et al., 2015). FW relies on the regression of the performance of each genotype on environmental means in two-step procedure; step one computes environmental sample means, while the second step deals with the estimation of intercepts and slopes of each line, by regressing within line the performance of each line on estimated environmental means (Olayiwola et al., 2015; Lian and Campos, 2016).

AMMI pools Principal Component Analysis (PCA) and Analysis of Variance (ANOVA) for effective interpretation of GEI (Aremu et al., 2020) whereas the GGE analysis uses the Sites Regression (SREG) model with emphasis on the importance of genotype main effects and effects of GEI. While both AMMI and GGE combine  $G$  and  $GE$  in mega environment study and assessment, the GGE superiority over AMMI lies in the fact that it elucidates more of the  $G+GE$  plus possession of inner product property of the biplot, and has higher discerning and representative power which is effective for test environment evaluation (Yan et al., 2007; Neisse et al., 2018; Maniruzzaman et al., 2019; Kebede and Bekeko, 2020). To improve and sustain yield, it is imperative to identify cowpea genotypes suitable for specific regions in Nigeria because of its diverse agro-ecological zones.

The goal of this study was therefore to evaluate, through FW, GGE and AMMI analysis, sixteen cowpea genotypes over six years in Akungba-Akoko, to identify stable high-yielding genotypes that are appropriate for cultivation in tropical regions.

## 2. Materials and methods

### 2.1. Collection procedure of materials

The 16 selected cowpea genotypes came from a germplasm of 25 genotypes collected from the International Institute of Tropical Agriculture (IITA), Nigeria. The selection was based on their consistency in both germination rate and vigorous growth pattern at the same field across 6 years survey spanning 2014 through 2019 at Adekunle Ajasin University, Plant Breeding Unit Experimental Field, Department of Plant Science and Biotechnology. The Latitude, Longitude and Altitude of the site lie between 7.2° N, 5.44' E and 423 m above the sea level, respectively. The planting season of 2014 fell between March and June, while that of 2015 through 2019 fell between May and October; all of which fell within the raining seasons.

The site of the study is characterized with tropical climate located within the southwestern Nigeria. It has variable rainy and dry seasons, with rainy season lasting from March to November accompanied by an August break which is an interruption of rains leading to a short dry season. The region has a mean annual rainfall ranging between 800 mm and 1,500 mm with about 85% of the rains falling from June to September. The average air temperature of the location is 24.7°C, and the type of soil is sandy loam ultisol (Salami and Sangoyomi, 2013; Oladele et al., 2019; Akinde et al., 2020). Besides, the initial physico-chemical properties of the experimental site were done in 2014 according to procedures cited in Oladele et al. (2019; 2022). The soil initial pH was 6.50, total organic matter (TOM) of 2.60, total nitrogen, TN (%) of 0.70, available phosphorus, (P) of 2.20 cmol kg<sup>-1</sup>, cation exchange capacity (CEC) of 11.74 cmol kg<sup>-1</sup>, and texture class of sandy loam.

The selected genotypes, their origins, biological status and identification codes are provided in Table 1. In each year, plant materials were sown in randomized complete block design (RCBD) with three replications.

**Table 1**

List of cowpea genotypes used in  $G \times E$  analysis with their origin.

S/N	Genotype ID	Biological Status	Origin	Code
1	TVu-7362	Landrace	Ghana	G1
2	TVu-199	Breeding material	USA	G2
3	TVu-207	Breeding material	USA	G3
4	TVu-224	Breeding material	USA	G4
5	TVu-235	Breeding material	Ghana	G5
6	TVu-236	Breeding material	Ghana	G6
7	Tvu-239	Breeding material	South Africa	G7
8	TVu-241	Breeding material	USA	G8
9	IT98K-205-8	Unknown	Nigeria	G9
10	IT98K-555-1	Unknown	Nigeria	G10
11	TVu-4886	Landrace	Niger	G11
12	TVu-4866	Landrace	Niger	G12
13	TVu-9225	Landrace	Tanzania	G13
14	TVu-9256	Landrace	Burkina Faso	G14
15	TVu-9252	Landrace	Burkina Faso	G15
16	TVu-11979	Landrace	Sudan	G16

Two rows within plots were utilized; spacing within and between rows were 30 cm and 50 cm, respectively. Each plot was 5 m x 1 m in dimension. Each plot was separated from the other by 1 m, while each replicate was separated from the other by 2 m. No fertilizer application was performed during the seasons in order to access the natural genetic potentials of the genotypes. Hand weeding of the field was done when required. During the flowering and podding phases, 10% EC Cypermethrin was applied to control insect pest. Determination

of the yield (in grams) for data analyses was performed on a plant basis in each season.

**2.2. Data analysis**

ANOVA was adopted for determining the effect of genotype, environments, and their interaction across the years using the version 20 of the SPSS Program (SPSS, 2017). Significant differences of the means were performed at  $P \leq 0.05$  level of probability by DMRT. The AMMI and GGE analyses were performed by using the version 1.4 of the Plant Breeding Tools (PBTools, 2014).

The AMMI model was determined in line with Agahi et al. (2020) as:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \delta_{gn} \delta_{en} + \rho_{ge} ;$$

Where,  $Y_{ge}$  = mean yield of genotype  $g$  in environment  $e$ ;  $\mu$  = grand mean;  $\alpha_g$  = genotype deviation from the grand mean;  $\beta_e$  = environmental deviation;  $\lambda_n$  = the singular value for principal component (PC)  $n$ ;  $\delta_{gn}$  = eigenvector value for genotype  $g$  and component  $n$ ;  $\delta_{en}$  = eigenvector value for environment  $e$  and component  $n$ ;  $\rho_{ge}$  = residual.

The GGE biplot was determined in line with Das et al. (2019) as:

$$Y_{ij} = \mu + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \epsilon_{ij} ;$$

Where,  $Y_{ij}$  = mean response of  $i$ th genotype in the  $j$ th environment;  $\mu$  = grand mean;  $e_j$  = environment deviations from the grand mean;  $\lambda_n$  = the eigen value of PC analysis axis;  $\delta_{in}$  and  $\delta_{jn}$  = genotype and environment PCs scores for axis  $n$ ;  $N$  = number of PCs retained in the model;  $\epsilon_{ij}$  = residual effect.

**3. Results and discussion**

The focus of plant breeding programs is principally on yield as it relates to stability and adaptability of genotypes. Ability of a genotype to utilize the environmental stimuli and show a highly predictable behavior is referred to as stability (Almeida et al., 2012). ANOVA revealed noteworthy differences amongst the 16 genotypes (15.33%) of cowpea for seed yield. Highly significant environment (14.71%), replication (0.05%) and genotype x environment (64.34%) effects were observed (Table 2).

**Table 2**

Analysis of variance and degree of freedom (DF) for seed yield (g plant<sup>-1</sup>) measured among 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).

Source of Variation	DF	SS	MS	%TSS
Environment (E)	5	32124.35	6424.87**	14.71
Genotype (G)	15	33461.55	2230.77**	15.33
Replicate	2	114.56	57.28**	0.05
G×E	75	140467.42	1871.57**	64.34
Residual	190	12149.23	63.94	5.56
Total	287	218317.11	10648.43	

In literature, large magnitude of  $G \times E$  interactions have been observed in cowpea (Olayiwola et al., 2015; Tariku et al., 2018; Horn et al., 2018; Odeseye et al., 2018; Sousa et al., 2018; Owusu et al., 2020) and other crop species (Baraki et al., 2020; Verma et al., 2020). The variations among the present genotypes may be due to genotype and environment factors because in

most cases, different genotypes won in different environments. This level of variation indicates the importance of multi-environment evaluation of genotypes since the aim is to pinpoint genotypes possessing predictable characters across diverse environments to guide against errors afflicting recommendation of genotypes (Almeida et al., 2012; Aremu et al., 2020). The level of diversity displayed among the genotypes in the present study would be useful for selection of parents for breeding programs and also for exploiting heterosis in the development of hybrids (Gerrano et al., 2020).

Yield for the genotypes studied across the six (6) environments are shown in Table 3. G14 won in E1 (134.97 g), G16 won in E2 (54.09 g) with G2 producing no seeds (0.00 g), G6 won in E3 (98.67 g), G3 consistently won in E4 (57.56 g) and E6 (63.88 g), whereas the performance of G15 was consistently the poorest in five of the six environments (E1, E2, E4, E5 and E6). The poor performance of G15 in terms of yield was due to the fact that it was unable to flower in most of the environments included in the study, which indicated low adaptability of the genotype to these environments (Oliveira et al., 2020). The overall best across the six environments was G10 (49.05 g), followed by G16 (45.08 g), while G14 fell in the third position with mean yield of 43.85 g per plant. The best environment for the genotypes was E1 with pooled mean yield of 47.75 g per plant, followed by E3 (44.23 g), and E6 (32.84 g) taking the third position. According to Aremu et al. (2020), differences in weather across years (environments) cause differential responses of genotypes indicating the presence of  $G \times E$ , hence justifying the adoption of stability, AMMI and GGE for further analysis of the performance of the crop as also opined by others (Olayiwola et al., 2015; Das et al., 2019).

FW utilizes regression coefficient as a measure of stability, and it states that regression coefficients approaching 1.0 is an indication of average stability and in turn must be linked and inferred with the mean of genotype yield to confirm adaptability (Lian and de lo Campos, 2016; Osekita, 2019). From the present FW stability analysis and ranking of seed yield across test environments (Table 4), nine out of the sixteen genotypes showed average stability with high mean yield. Genotypes 10, 16, 13 and 8 which had very high mean yield were found unstable due to the low slope of regression. The first two genotypes with the highest mean yield (G10 and G16), were unstable whereas, from the rear genotypes 12 and 2 with very low mean yields were stable judging from the slope of regression in Table 4. At the same time, selecting on the basis of stability and average yield identified the following genotypes; 2, 3, 4, 5, 6, 7, 9, 12 and 14 as the best stable genotypes out of the sixteen genotypes evaluated across the test environments. These findings indicate that genotypes identified as the most stable by FW may not necessarily be the most productive as established in the present study (Padi, 2007; Almeida et al., 2012).

AMMI and GGE concepts are useful methodologies in genotype evaluation. AMMI combines ANOVA and PCA into a unified approach (Agahi et al., 2020; Verma et al., 2020), while GGE visually analyzes the results of site regression analysis for multi-environment trial data (Osekita, 2019; Tena et al., 2019). Comparison of the two analytical techniques is presented in Table 5. IPCs 1 to 3 jointly accounted for 94.7% of the entire variation among the genotypes in AMMI analysis, whereas in GGE analysis, same IPCs (1 to 3) jointly accounted for 94.1% of the entire variation. These are higher than the contributions of three PCs reported by Tariku et al. (2018) among sixteen accessions of cowpea, but similar to the findings of Baraki et al.

**Table 3**Mean yield (g plant<sup>-1</sup>) of 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).

Genotype	E1 (2014)	E2 (2015)	E3 (2016)	E4 (2017)	E5 (2018)	E6 (2019)	Genotype Mean
G1	12.59 <sup>ab</sup>	27.07 <sup>bcd</sup>	30.11 <sup>b</sup>	23.66 <sup>fg</sup>	21.57 <sup>bcd</sup>	28.47 <sup>c</sup>	23.91 <sup>bc</sup>
G2	12.04 <sup>ab</sup>	50.83 <sup>de</sup>	0.00 <sup>a</sup>	28.94 <sup>h</sup>	35.20 <sup>ef</sup>	14.33 <sup>b</sup>	23.56 <sup>b</sup>
G3	15.75 <sup>ab</sup>	34.38 <sup>cde</sup>	38.34 <sup>bc</sup>	<b>57.56<sup>i</sup></b>	44.33 <sup>fg</sup>	<b>63.88<sup>g</sup></b>	42.38 <sup>f</sup>
G4	16.12 <sup>ab</sup>	27.71 <sup>bcd</sup>	84.13 <sup>fg</sup>	18.81 <sup>d</sup>	20.1 <sup>bc</sup>	46.35 <sup>d</sup>	35.54 <sup>e</sup>
G5	14.50 <sup>ab</sup>	27.40 <sup>bcd</sup>	69.01 <sup>ef</sup>	25.27 <sup>gh</sup>	<b>53.3<sup>g</sup></b>	27.45 <sup>c</sup>	36.16 <sup>e</sup>
G6	22.71 <sup>b</sup>	28.43 <sup>bcd</sup>	<b>98.67<sup>g</sup></b>	15.45 <sup>cd</sup>	33.37 <sup>def</sup>	53.48 <sup>ef</sup>	42.02 <sup>f</sup>
G7	8.39 <sup>ab</sup>	28.19 <sup>bcd</sup>	57.65 <sup>de</sup>	20.74 <sup>ef</sup>	40.57 <sup>ef</sup>	30.21 <sup>c</sup>	30.96 <sup>de</sup>
G8	10.24 <sup>ab</sup>	32.78 <sup>b-e</sup>	51.81 <sup>cd</sup>	19.55 <sup>e</sup>	28.8 <sup>cde</sup>	31.78 <sup>c</sup>	29.16 <sup>cd</sup>
G9	98.43 <sup>d</sup>	15.49 <sup>abc</sup>	31.74 <sup>b</sup>	12.92 <sup>bc</sup>	22.17 <sup>bcd</sup>	31.89 <sup>c</sup>	35.44 <sup>e</sup>
G10	98.45 <sup>d</sup>	52.91 <sup>e</sup>	35.06 <sup>bc</sup>	18.26 <sup>de</sup>	33.53 <sup>def</sup>	56.07 <sup>f</sup>	<b>49.05<sup>g</sup></b>
G11	50.81 <sup>c</sup>	34.68 <sup>cde</sup>	40.57 <sup>bc</sup>	11.29 <sup>b</sup>	0.44 <sup>a</sup>	1.26 <sup>a</sup>	23.18 <sup>b</sup>
G12	37.39 <sup>c</sup>	8.315 <sup>ab</sup>	43.85 <sup>bcd</sup>	12.65 <sup>de</sup>	0.52 <sup>a</sup>	18.92 <sup>b</sup>	20.27 <sup>b</sup>
G13	123.99 <sup>e</sup>	16.23 <sup>abc</sup>	30.51 <sup>b</sup>	8.93 <sup>ab</sup>	3.27 <sup>a</sup>	19.95 <sup>b</sup>	33.81 <sup>de</sup>
G14	<b>134.97<sup>e</sup></b>	31.62 <sup>bcd</sup>	31.37 <sup>b</sup>	9.09 <sup>ab</sup>	3.05 <sup>a</sup>	53.04 <sup>def</sup>	43.85 <sup>fg</sup>
G15	0.00 <sup>a</sup>	0.00 <sup>a</sup>	33.84 <sup>b</sup>	5.46 <sup>a</sup>	0.00 <sup>a</sup>	6.55 <sup>a</sup>	6.55 <sup>a</sup>
G16	107.68 <sup>e</sup>	<b>54.09<sup>e</sup></b>	31.09 <sup>b</sup>	17.13 <sup>de</sup>	12.23 <sup>ab</sup>	48.25 <sup>de</sup>	45.08 <sup>fg</sup>
Env. Mean	47.75	29.38	44.23	19.11	22.03	32.84	<b>32.56</b>

**Table 4**Finlay-Wilkinson stability analysis and ranking for seed yield (g plant<sup>-1</sup>) of 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).

Code	Slope	Standard Error	Mean Yield	Yield Rank	Stable Genotype
G1	-0.12	0.27	23.91	5	
G2	2.12	0.88	23.56	4	+
G3	1.73	0.84	42.38	13	+
G4	1.46	0.58	35.54	10	+
G5	1.32	0.32	36.16	11	+
G6	3.05	1.21	42.02	12	+
G7	3.25	1.29	30.96	7	+
G8	0.48	0.53	29.16	6	
G9	0.21	1.02	35.44	9	+
G10	-1.1	0.57	49.05	16	
G11	-0.96	0.57	23.18	3	
G12	1.03	1.01	20.27	2	+
G13	0.07	0.89	33.81	8	
G14	1.29	1.15	43.85	14	+
G15	0.02	0.02	6.55	1	
G16	0.15	0.15	45.08	15	

Note: + stable genotypes across environments

(2020) among six genotypes of mung bean. At the fifth PC, AMMI analysis accounted for 100% of the total variation, while 100% variation was accounted for at PC6 in GGE analysis indicating that wide differences was quickly achieved in AMMI compared to GGE analysis among genotypes tested in various test environments. The complete AMMI model showed the presence of significance of the G × E interactions partitioned among the five IPCAs (100%) without residuals in line with Osekita et al. (2019), and the six IPCAs for the GGE analysis. However, only the IPCA1 was significant among cowpea genotypes evaluated in South Africa (Gerrano et al., 2020) due to GEI. The observed interaction captured in a diatonic sequence among the IPCAs has been reported among many workers

**Table 5**AMMI and GGE analyses for seed yield (g plant<sup>-1</sup>) of 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).

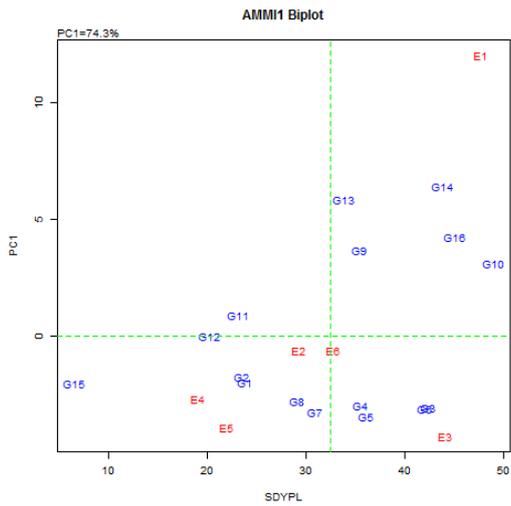
Source	DF	AMMI Analysis				GGE Analysis			
		Variance (%)	Acum Variance (%)	SS	MS	Variance (%)	Acum Variance (%)	SS	MS
IPC1	19	74.30	74.30	104238.35	5486.23**	63.20	63.20	109840.89	5781.09**
IPC2	17	15.90	90.20	22327.29	1313.37**	18.30	81.50	31776.18	1869.18**
IPC3	15	4.50	94.70	6326.71	421.78**	12.60	94.10	21902.75	1460.18**
IPC4	13	3.10	97.80	4403.80	338.75**	2.90	97.00	5053.56	388.74**
IPC5	11	2.20	100.00	3071.27	279.21**	2.40	99.40	4120.47	374.59**
IPC6	9	0.00	100.00	0.00	0.00 <sup>ns</sup>	0.70	100.00	1135.12	126.12**

\*\* : Highly significant; ns: Not significant.

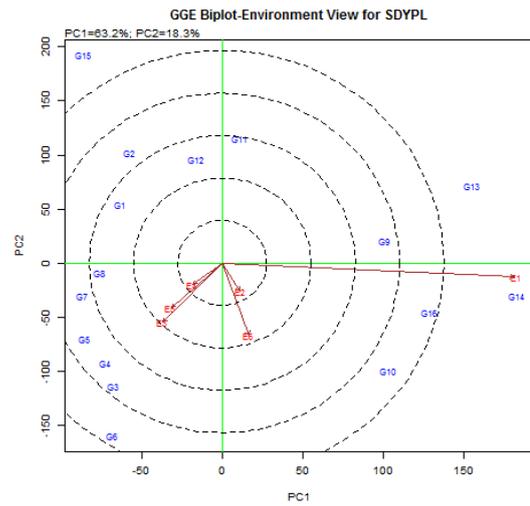
DF: Degree of freedom; SS: Sum of squares; MS: Mean squares

(Aremu et al., 2020).

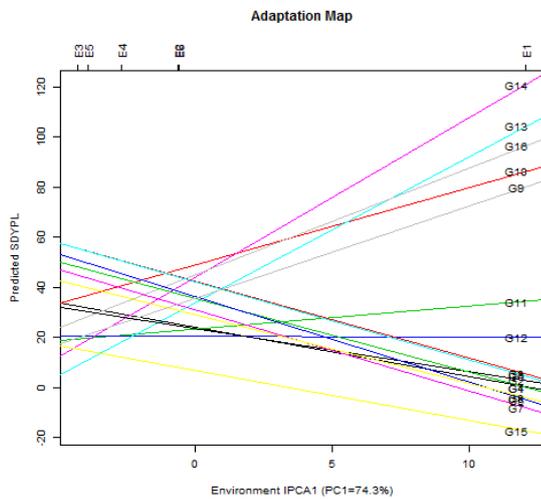
Fig. 1 presents the AMMI biplot of the first PC for yield stability among sixteen genotypes evaluated in six environments. The biplot is often used to investigate the response pattern of G, E, and their interaction (GEI) (Verma et al., 2020) utilizing means' main effect versus the first interaction principal component axis (IPCA1) (Yan et al., 2007). It is also used to discover genotypes for seed yield that have broad and particular adaptation to target conditions. By graphically combining genotypes and environments on a graph, the link between genotypes and environments became clearer. In the case of seed yield, displacement along the horizontal axis revealed variations in the main effect, but displacement along the vertical axis revealed differences in the first PCA. Furthermore, the biplot accounted for 90.2% of the treatment sum of squares, whereas the residual accounted for 9.8%. This indicates sufficient variability as 70% is the minimal amount of variability required for the AMMI to be reasonably trustworthy (Neisse et al., 2018). In addition, Tariku et al. (2018) suggested that the first three multiplicative component axes are adequate for the authentication of variation explained by GEI. This value is higher than the values reported by many workers, especially in cowpea (Tariku et al., 2018) and sugarcane (Tena et al., 2019). G11 and G12 were considered the most stable genotypes, with suitable adaptation to test environments (Fig. 2) and being the genotypes closest to zero. Since AMMI positioned them on the right-hand side of the biplot, genotypes G9, G10, G13, G14, and G16 were significantly greater yielding (Fig. 1). Likewise, in terms of both major effects and interaction, the environments were heterogeneous. Nonetheless, E2, E3, E4, E5 and E6 exhibited consistency in their responses to genotypes, and while E1 was significantly different from other environments, it was shown that E2 and E6 had relatively similar mean yield.



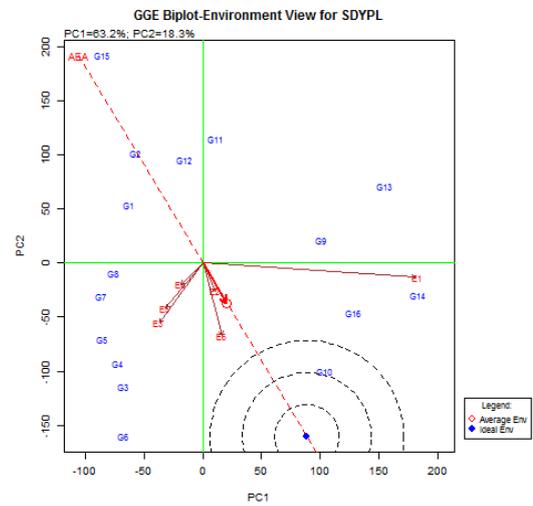
**Fig. 1.** AMMI Biplot showing yield ( $\text{g plant}^{-1}$ ) stability on axis 1 of the Principal Component for 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).



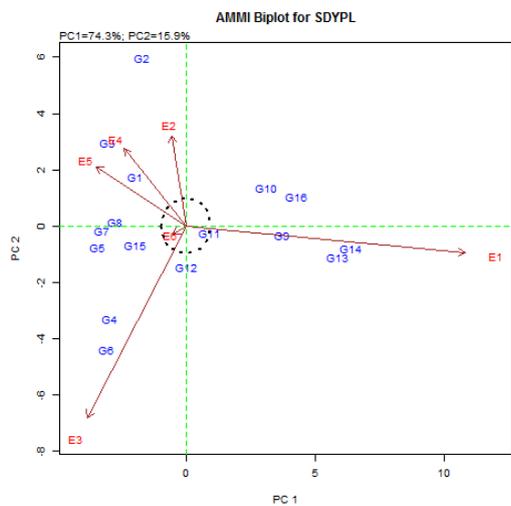
**Fig. 4.** Environment-vector view of the GGE biplot to show similarity among test environments in discriminating the 16 cowpea genotypes.



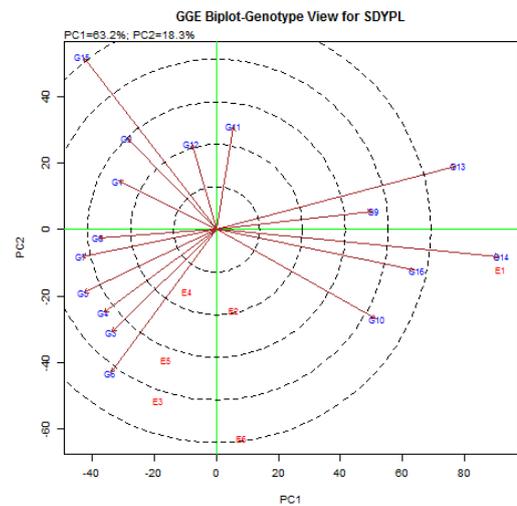
**Fig. 2.** Adaptation map showing stability of genotype interaction with the first Principal Component for seed yield ( $\text{g plant}^{-1}$ ) of 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).



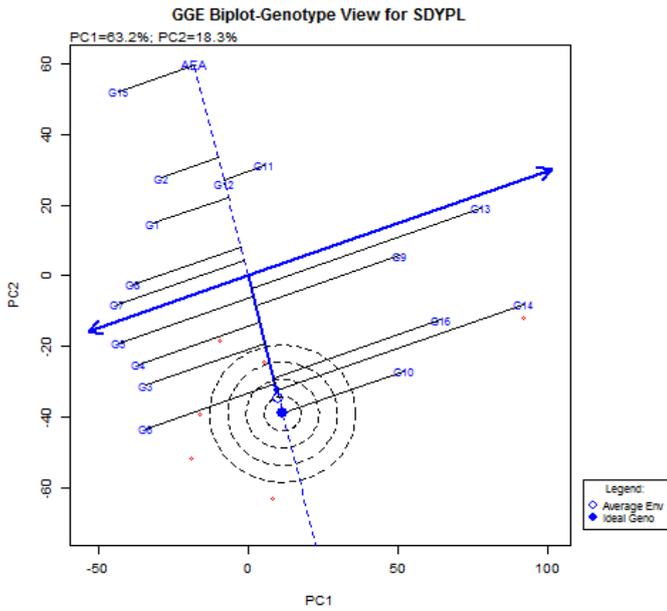
**Fig. 5.** The discrimination and representativeness view of the GGE biplot to rank test genotypes relative to an ideal test environment (season).



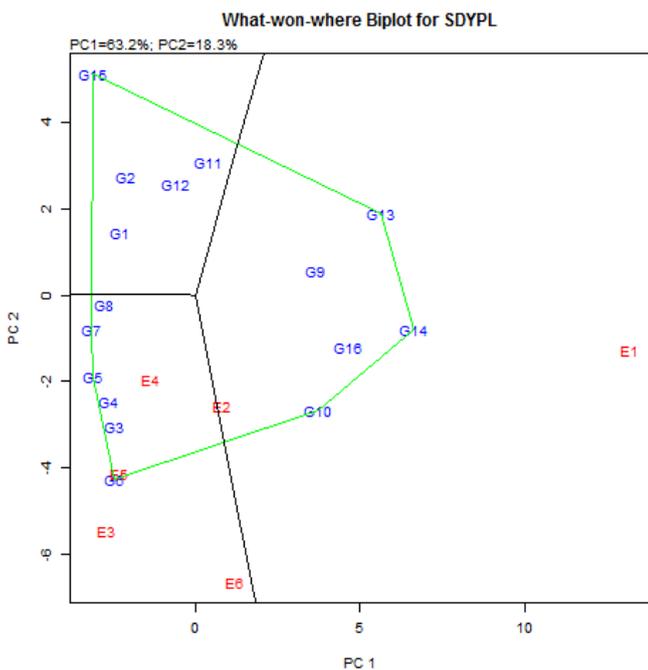
**Fig. 3.** AMMI Biplot for Axis 1 and 2 of the Principal Component for seed yield ( $\text{g plant}^{-1}$ ) of 16 cowpea genotypes evaluated in Akungba-Akoko, Nigeria across 6 seasons (2014-2019).



**Fig. 6.** The Genotype-vector view of the GGE biplot showing the performance of 16 cowpea genotypes in test environments (6 seasons).



**Fig. 7.** Ranking of 16 cowpea genotypes based on mean yield (g plant<sup>-1</sup>) and stability relative to an ideal genotype.



**Fig. 8.** Polygon view of the GGE biplot based on symmetrical scaling for the which-won-where pattern for genotypes and environments (seasons).

Fig. 3 illustrates AMMI biplot for cowpea seed yield indicating the pattern of reflection of the six environments from the biplot origin. Six rays originated from the biplot origin to show the extent of variation across the test environments. E1 had the longest ray and make an obtuse angle with the biplot origin. E2, E4 and E5 were on the same quadrant with almost equal rays making an acute angle with the biplot origin in the anti-clockwise direction. E6 had the shortest ray from the biplot origin. All the six environments make an obtuse angle with E1 in reference to the biplot origin which is an indication that differences exist between the test environment and the genotypes. G11 that falls within the circle towards the biplot

origin was considered the most stable genotype across the environment; whereas, G9, G10, G13, G14, and G16 did not differ in terms of yield, because AMMI model retained them on the right-hand side of the biplot. The present observation indicates the appropriateness of AMMI in agricultural analyses for the effective separation of G and E from GE interaction (Neisse et al., 2018). These are comparable to the outcomes of Aremu et al. (2020) in African yam bean.

Fig. 4 shows the environment-vector perception of the GGE biplot; it is predicated on an environment-centered (centering = 2) G by E table with no scaling (i.e. zero), is environment-metric preserving (SVP=2), and its axes are scaled (Yan et al., 2007; Neisse et al., 2018). This biplot described 81.5% of the overall variation in the environment-centered G × E (PC1 = 63.2 percent, PC2 = 18.3 percent). This is similar to the value reported by Gerrano et al. (2020) in cowpea genotypes. Vectors are the lines that connect the test environments to the biplot origin. The cosine of angle between two vectors approximates the correlation between them (Yan and Tinker, 2006; Maniruzzaman et al., 2019; Baraki et al., 2020). In this figure, E1, E2 and E6 are positively correlated (acute angle). Similarly, E3, E4 and E5 are positively correlated. The gap between adjacent environments indicates their disparity in respect of genotype classification. As a result, the consistency (covariance) of two environments is dictated by the length of respective vectors as well as the cosine of the angle between them. The biplot's concentric circles aid in visualizing the extent of the environment vectors, which is equal to the standard deviation inside the distinct environments and is a gauge of discriminating power (Yan and Tinker, 2006; Neisse et al., 2018). Hence, E1, E5 and E6 were the most discriminating whereas E2 and E3 the least discriminating (non-informative). Test environments found continuously non-discriminatory yield minimal information on genotypes and should thus not be used as test environments.

Fig. 5 shows the discriminatory plus representativeness perspective of the GGE biplot to classify test environments compared to an ideal test environment. The optimum test environment inside a single mega environment should be the most discriminating (informative) as well as the most reflective of the target environment (Yan and Tinker, 2006; Tariku et al., 2018; Tena et al., 2019; Gerrano et al., 2020). As a result, the center of the concentric circles in this figure represents an “ideal test environment”. It is a positive point on the Average Environment Axis (AEA) (most informative) (Sharma et al., 2016; Maniruzzaman et al., 2019; Baraki et al., 2020); E2 in addition to E6 with the smallest angle to AEA are the most representative. However, E1 with longer vector length is considered as the unsurpassed environment for choosing far and wide adapted genotypes, whereas E5 is a little bit farther and may not be adequate for choosing genotype adapted to the test environment although extra years may be necessary to ratify that an exact test environment is “ideal”. This is corroborated by the reports of Yan et al. (2007). Because E6 is both discriminating and representative, it can be an excellent test environment for choosing genotypes with broad adaptation, however E2 (most representative and least discriminative) is less useful with no appreciable information as suggested by Yan and Tinker (2006). Fig. 6 portrays the genotype-vector view of the GGE biplot depicting genotype performance in test environments. The genotype and environment vectors are both drawn here in order to visualize the specific interactions between a genotype and an environment. A genotype's productivity in an environment is

better than average if the angle between its vector and the vector of the environment is less than 90°, worse than average if the angle is greater than 90°, and near average if the angle is approximately 90° (Baraki et al., 2020). Based on the above, genotypes G9, G10, G11, G13, G14 and G16 were greater than average in E1 forming acute angles, whereas, other genotypes were below average indicating that they made obtuse angles with E1 which is the ideal environment. Fayeun et al. (2016) and Osekita et al. (2019) obtained similar results.

Fig. 7 displays the classification of genotypes founded on mean yield and stability comparative to an ideal genotype. Properties of an ideal genotype are high mean productivity and stability across environments (Maniruzzaman et al., 2019). This figure defines an ideal genotype as a positive point on the AEA with a vector length equal to the longest vectors of the genotypes along AEA positive side (highest mean performance). Consequently, genotypes positioned closer to the 'ideal genotype' are superior to others (Yan et al., 2007; Tena et al., 2019; Gerrano et al., 2020). Thus, G14 was superior to G10, despite the fact that G10 had higher average yield showing that it had high yield and stability. Other genotypes next to G14 with high stability and yield that could be selected for breeding programs include G16, G9 and G13. G15 was the poorest genotype for the reason that it was consistent the lowest in terms of average yield. This figure also depicts the concept of stability; the term "high stability" is only relevant when combined with "average performance". G15 was highly unstable and poor yielding whereas others were unstable and low yielding except G2, G7, and G12 which had yield below average and highly stable. Similar results were obtained by Yan and Kang (2003), Tena et al. (2019) and Gerrano et al. (2020).

Fig. 8 displays a polygon view of the which-won-where trend of cowpea genotypes tested in six environments. The GGE biplot's polygon view reveals which genotype achieved the best performance in which environment (Yan and Tinker, 2006; Horn et al., 2018; Das et al., 2019; Maniruzzaman et al., 2019; Tena et al., 2019; Baraki et al., 2020; De Melo et al., 2020). A polygon is constructed on genotypes farthest from the biplot origin so that all other genotypes are confined inside the polygon, and then perpendicular lines are drawn beginning from the biplot origin on each side of the polygon (Yan et al., 2007). In this figure a pentagon was drawn with genotypes G13, G14, G10, G6 and G15 at the vertex of the pentagon. Perpendicular lines drawn from the biplot's origin divide the pentagon into three sectors. The equality between G13 and G14 indicates that G13 and G14 were better in all the environments, it is also noted that G9 falls within the line that connects G13 and G14, also G16 falls within the line which connects G14 and G10, by ranking it means that G13>G9>G14>G16>G10 through the environments. The equality lines that partition the biplot into sectors, with the winning genotype located on the respective vertex, which are G13, G14, G10, G6 and G15. The following genotypes; G9, G10, G13, G14 and G16 fell into sector 1 and perform best in environments E1 and E2, while G3, G4, G5, G6, G7 and G8 fell into sector 2 having environments E3, E4, E5 and E6 in common, G1, G2, G11, G12 and G15 fell into the third sector. G15 located on the vertex of the polygon without any corresponding environment is considered as low yielder as reported by Baraki et al. (2020), hence cannot be recommended for breeding programs as described by Gerrano et al. (2020).

Fig. 9 indicates the outlook of the genotypes in response to the sixteen cowpea genotypes. The performance of the genotypes varied widely in environment 1. The extent of

variation in environment 4 is convergent except for G3 that separated widely. In other environments the dispersibility of the genotypes followed a unique pattern and better response of the cowpea genotypes in terms of mean yield.

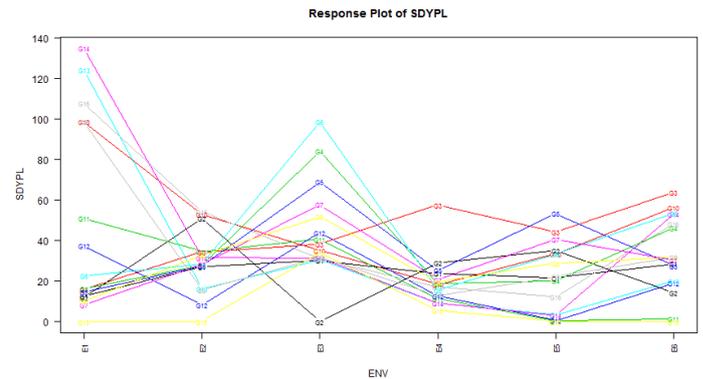


Fig. 9. Environment (season) response view of the GGE Biplot among the 16 cowpea genotypes.

Fig. 10 displays the environment view based on the cowpea genotypes, environment 4 and 6 were consistently the poorest for evaluation of the sixteen cowpea genotypes according to the graphical representation of the environment view, while others show diversity in performance in the remaining four environments. Similar results were reported by Osekita (2018).

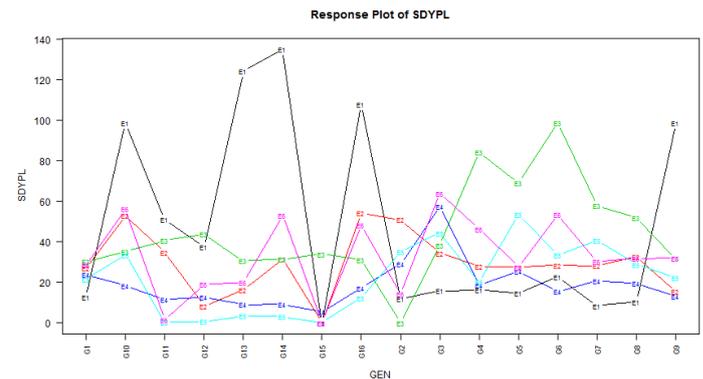


Fig. 10. Genotype response view of the GGE Biplot across test environments (seasons).

The outcomes of the current study indicate that the existing genotypes of cowpea in Nigeria and other tropical countries of the world have high stability and yield potential that could be exploited in breeding programs of the crop. For instance, G14 and G9 which were the most stable genotypes were respectively, from Burkina Faso and Nigeria in West Africa, these genotypes outperformed others which are all of tropical origins. Adoption of these genotypes in tropical countries of the world will contribute positively to the productivity of cowpea in those regions. Regions of the world where the present information could be useful include Central America, Mexico, the Caribbean islands, all of Africa excluding Tunisia, Lesotho and Swaziland. Others include part of Middle East, part of India and all countries in the South East Asia. Countries situated within the tropic are known as Tropical countries (Morgan, 2011).

#### 4. Conclusion

In the present evaluation, seed yield was highly influenced by genotype effect, environment, and GEI. All analyses were able to pinpoint high yielding and stable genotypes in Akungba-

Akoko environment; and these included G14 and G9 as the consistent high yielding stable genotypes adopted by FW, GGE and AMMI. G14, G3, G4, G5, G6 and G9 were high yielding and stable according to FW; AMMI showed G10, G9, G16, G14 and G13 as high yielding and stable, while GGE showed G14, G16, G9 and G13 as high yielding and stable. However, consistencies of G14 and G9 with the three methods make them the candidates of choice for Akungba-Akoko environment, other parts of south west Nigeria, and are hence recommended for cultivation.

These genotypes may also exhibit similar stability and yield performances in other tropical regions of similar characteristics in Africa, Asia, America, and hence could be

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