
RESEARCH ARTICLE

G x E interactions and stability analysis in cowpea genotypes (*Vigna unguiculata* (L.) Walp)

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Abstract

Grain yield and stability of yield performance of 26 cowpea genotypes was determined using AMMI model, GGE biplot analysis and the joint regression analysis of Eberhart and Russell for the interpretation of genotype x environment interaction. The results revealed significant ($P \leq 0.01$) genotype differences (2632.45) for all the characters evaluated suggesting genetic diversity among the cowpea genotypes studied. The AMMI and GGE-biplot analyses were found to be more efficient than the Eberhart and Russell analysis because the first two provided visual diagrams (biplots) in addition to the sum of squares. The first two interaction principal component axes of the GGE-biplot and AMMI models accounted for 79.4% and 75.1% of the total variation among the genotypes respectively. The GGE-biplot grouped the four environments into three mega-environments with Abeokuta-2 being the most representative and Igboora-2 the most discriminative environment. The GGE-biplots identified NG/SA/07/0113, NG/SA/07/0157 and NG/SA/07/0176 as the stable genotypes across the studied environments. The study concluded that NG/SA/07/0176 and NG/SA/07/0157 were stable across the environments as grouped by AMMI and GGE-biplot. These

two genotypes with high yield and stability are recommended for cultivation.

Key words: G x environment interaction, additive main effect, stability, cowpea, seed yield

Introduction

Genotype by environment interaction (GEI) is a major problem in the study of quantitative traits because it complicates the interpretation of genetical experiments and makes predictions difficult. It is particularly a problem in plant and animal breeding where genotypes have to be selected in one environment and used in another. A number of methods have been used for measuring these interactions which have practical implications for stability of performance of many crop varieties. The most commonly used is the regression technique (Eberhart and Russell, 1966; Perkins and Jinks, 1968; Ntare and Aken-Ova, 1985; Ariyo, 1987) in which variety yield is regressed on an environmental index which is the mean yield of all genotypes tested in each environment minus the grand mean. The measure of adaptability of the regression technique is based on an assumption that a variety responds linearly to environmental condition.

The Principal Components Analysis (PCA) method that shows the mean squares of the principal components axes (Gauch and Furnas, 1991) has also been employed. Francis and Kannenberg (1978) suggested a genotype grouping technique by plotting genotypes mean yield on the Y-axis against its coefficient of variation (cv) on the X-axis. Genotypes are therefore classified into four groups as high mean yield, low cv; high mean yield, high cv; low mean yield, low cv; and low mean yield, high cv. Based on this classification, a desirable variety is that which is characterized by high mean yield and low cv.

The Additive Main Effect and Multiplicative Interaction (AMMI) model (Kempton, 1984; Zobel *et al.*, 1988; Crossa *et al.*, 1990) which has proved superior and more effective in explaining the G x E interaction has been developed to take over from the traditional stability analysis (Crossa, 1990; Gauch and Furnas, 1991). AMMI analysis has been reported to have significantly improved the probability of successful selection (Gauch and Zobel, 1988). It has been used to analyze G x E interaction with greater precision in many crops (Bradu, 1984; Gauch, 1990; Crossa *et al.*, 1991 and Ariyo, 1998). Ariyo and Ayo-Vaughan (2000) reported that the least square fit to the AMMI was obtained in two steps: the main effect is the additive part of the model and was analyzed by ordinary analysis of variance (ANOVA) leading to the non-additive residual, (G x E interaction which is the multiplicative part of the model) to be analyzed by principal component analysis (PCA). However, Ariyo and Ayo-Vaughan (2000); Alake and Ariyo (2012) concluded that for any particular genotype or environment, the main effect equals the cultivar mean plus environment mean minus the grand mean while the interaction is the cultivar PCA score multiplied by the environmental score. GGE biplot is effective for identifying the best performing cultivar for a given environment

and the most suitable environment for each cultivar. It compares pairs of cultivars in individual environment, identifies the best cultivar for each environment. Better still, the AMMI model determines the discriminating abilities and representativeness of given environments (Yan and Kang 2003; Yan and Tinker 2006; Yan *et al.*, 2007). The decision as to whether location groups could be considered as mega-environments is based on the consistency of location groupings and of the winning genotypes in the individual location-groups across years (Yan *et al.*, 2000, 2007, 2010). Therefore, the objectives of this study were: to determine the effectiveness of the AMMI model, GGE and biplot analysis and the joint regression analysis of Eberhart and Russell in the interpretation of genotype x environment interaction, and to determine the effect of different environments on the seed yield performance of 26 cowpea genotypes tested.

Materials and methods

Seeds of twenty-six (26) cowpea genotypes used for this study were sourced from the International Institute of Tropical Agriculture (IITA) and National Center for Genetic Resources and Biotechnology (NACGRAB), both in Ibadan, Oyo state (Table1). The experiments were conducted at the Teaching and Research Farm of Federal University of Agriculture, Abeokuta, Ogun State (7°16'N, 3°34'E, 67m above sea level) and the Research Farm of Oyo State College of Agriculture, Igboora, (7°3'N, 2°47'E, 140m above sea level) Oyo State. The study was carried out over a period of two years planting seasons of 2013 and 2014 in four growing environments namely: Abeokuta 1 (September-December 2013); Abeokuta 2 (June-August, 2014); Igboora 1 (September-December 2013); Igboora 2 (August-November, 2014).

Table 1: Cowpea genotypes used in this study and their sources

S. No.	Genotype	Source
1	IT04K-332-1	International Institute of Tropical Agriculture
2	IT04K-333-2	International Institute of Tropical Agriculture
3	IT98K-573-1-1	International Institute of Tropical Agriculture
4	IT98K-573-2-1	International Institute of Tropical Agriculture
5	IT06K-134	International Institute of Tropical Agriculture
6	IT99K-529-2	International Institute of Tropical Agriculture
7	IT99K-494-6	International Institute of Tropical Agriculture
8	IT06K-242-3	International Institute of Tropical Agriculture
9	IT07K-303-1	International Institute of Tropical Agriculture
10	IT07K-243-1-2	International Institute of Tropical Agriculture
11	IT07K-243-1-10	International Institute of Tropical Agriculture
12	IT07K-298-15	International Institute of Tropical Agriculture
13	IT07K-299-6	International Institute of Tropical Agriculture
14	IT07K-210-1-1	International Institute of Tropical Agriculture
15	UAM1055-6	International Institute of Tropical Agriculture
16	UAM1056-2	International Institute of Tropical Agriculture
17	NG/SA/07/0157	National Center for Genetic Resources and Biotechnology
18	NG/SA/07/0176	National Center for Genetic Resources and Biotechnology
19	NG/SA/07/0042	National Center for Genetic Resources and Biotechnology
20	NG/SA/07/0306	National Center for Genetic Resources and Biotechnology
21	NG/SA/07/0008	National Center for Genetic Resources and Biotechnology
22	NG/SA/07/1066-2	National Center for Genetic Resources and Biotechnology
23	NG/SA/07/0128	National Center for Genetic Resources and Biotechnology
24	NG/SA/07/0063	National Center for Genetic Resources and Biotechnology
25	NG/SA/07/0113	National Center for Genetic Resources and Biotechnology
26	NG/SA/07/0086	National Center for Genetic Resources and Biotechnology

The study was carried out over a period of two years planting seasons of 2013 and 2014 in four growing environments namely: Abeokuta 1 (September-December 2013); Abeokuta 2 (June-August, 2014); Igboora 1 (September-December 2013); Igboora 2 (August-November, 2014).

The field was laid out in a randomized complete block design (RCBD) with 3 replications. The size of each plot was 3m X 0.6m with 45cm spacing between plants to give a total of 28 plant stands per plot. Each genotype was randomly allocated to a plot. Field pests were controlled using Cypermethrin at the rate of 40 ml to 15 litres of water and weeding was done manually as at when necessary. Seeds were harvested at physiological maturity and data were collected on following observations.

Number of branches per plant: Average number of branches from selected 10 plants shall be counted and recorded at flowering.

Plant height at flowering: Plant height measured from the ground level to the tip of the highest point recorded at flowering.

Number of peduncles per plant: By counting the number of peduncles and averaging over ten randomly selected plants in a plot.

Peduncle length: Taken as the length of peduncles averaged over 10 plants in a plot measured.

Days to 50% flowering: Number of days from sowing to first flower opening on 50% of plants per plot estimated using a calendar.

Number of pods per plant: Total number of pods per plant, averaged over 10 selected plants per plot.

Pod length: Measured as the length of pods averaged over 10 plants in a plot.

Days to 95% maturity: Number of days from sowing to when 95% of the plants reach physiological maturity.

Weight of 100 seeds: Weight of 100 seeds from 10 selected plants harvested per plot.

Seed yield per plant: Weight of total seeds harvested per plant, averaged over 10 selected plants.

Data collected were subjected to analysis of variance (ANOVA). Stability and response of the 26 genotypes over four environments for yield and its components was estimated using the coefficient regression b and deviation from regression S^2_{di} according to Eberhart and Russell (1966). Additive main effect and multiplicative interaction (AMMI) model and GGE biplot were also used to determine the stability of the genotypes across environments.

Results and discussion

The pooled analysis of variance for seed yield per plant for the 26 cowpea genotypes in four environments using Eberhart and Russell (1966) model is presented in Table 2. It indicated that genotypes, environment and

their interaction were highly significant. The model partitions the sum of squares due to environment and genotype x environment interaction into environment (E) linear, genotype x environment (g x e) linear and non-linear (pooled deviation) components. The G x E as well as pooled deviation mean squares were found to be significant indicating the presence of both predictive and non-predictive components. The mean seed yield per plant, regression coefficients and deviation mean squares are presented in table 3. The highest mean seed yield (69.11g plant⁻¹) over the environments was recorded for genotype NG/SA/07/0086 followed by NG/SA/07/0063 (51.34 g plant⁻¹) and genotype NG/SA/07/1066-2 (45.78g plant⁻¹). Genotype IT06K-134 had the lowest mean seed yield per plant of 7.15g over the four environments.

Table 2: Mean squares from the analysis of for seed yield of cowpea genotypes

Source of variation	DF	Seed yield per plant (g plant ⁻¹)
Environment	3	3208.00**
Genotype x Environment	75	656666**
Genotype	25	888.13**
Env. + (Genotype x Env.)	78	228.13ns
Environment (linear)	1	1156.87**
Genotype x Env. (linear)	25	32.65ns
Pooled deviation	52	335.65**
Pooled error	208	3.73

**, * significant at 0.01 and 0.05 level of probability respectively; ns = Non significant

The significant genotype x environment indicate that the regression coefficients were different. The variation observed in the regression coefficients indicates that genotypes respond differently to environmental changes. Genotypes IT98K-573-2-1, IT06K-134, IT99K-494-6, IT06K-242-3, IT07K-243-1-2, IT07K-243-1-10, IT07K-210-1-1, UAM1055-6, UAM1056-2, NG/SA/07/0157 and NG/SA/07/0086 had regression coefficients (b) significantly greater than 1.0. Whereas the remaining fifteen genotypes had regression coefficients (b) less than 1.0, suggesting that the fifteen are adapted to below average environments. The most desirable genotypes are the ones whose value of S^2_{di} tends towards 0 and $b = 1.0$. Such genotypes measured by the

seed yield were NG/SA/07/0008, NG/SA/07/0042, IT07K-303-1, and IT99K-529-2. The AMMI analysis of variance for seed yield in four environments is presented in Table 4. It was revealed that highly significant ($P \leq 0.01$) values were obtained for the genotypes and their interactions. About 21% of the total sum of squares was accounted for by the genotypic effects, the environmental effects accounted for 3.04% while genotype by environment interaction (GEI) effects captured 27.87%. The first interaction principal components (IPCA1) accounted for 80.18% of the interaction sum of square, while the second interaction principal components (IPCA2) accounted for 10.44%, leaving only 9.38 % in the residual GEI.

Table 3: Mean seed yield per plant, regression coefficients and deviation mean squares of cowpea genotypes

Genotype	Mean seed yield /plant	Regression coefficient $\pm$ SE	Deviation mean square
IT04K-332-1	20.82	0.12 ± 0.47^b	203.86
IT04K-333-2	24.37	0.02 ± 0.70^b	464.38*
IT98K-573-1-1	23.26	0.10 ± 0.66^b	406.15
IT98K-573-2-1	24.98	0.04 ± 0.42^a	165.61
IT06K-134	7.15	0.07 ± 0.29^a	79.81
IT99K-529-2	27.27	0.15 ± 0.73^b	501.08*
IT99K-494-6	20.52	0.06 ± 0.38^a	134.84
IT06K-242-3	19.57	0.01 ± 0.35^a	118.06
IT07K-303-1	26.02	0.17 ± 0.67^b	416.05
IT07K-243-1-2	15.42	0.10 ± 0.36^a	121.59
IT07K-243-1-10	18.02	0.03 ± 0.30^a	86.87
IT07K-298-15	19.45	0.09 ± 0.60^b	338.01
IT07K-299-6	21.56	0.11 ± 0.48^b	216.33
IT07K-210-1-1	31.84	0.05 ± 0.27^a	69.47
UAM1055-6	25.84	0.07 ± 0.30^a	83.96
UAM1056-2	24.59	0.01 ± 0.32^a	97.00
NG/SA/07/0157	41.53	0.05 ± 0.34^a	108.223
NG/SA/07/0176	53.78	0.09 ± 0.55^b	28.76
NG/SA/07/0042	36.24	0.03 ± 0.69^b	442.31*
NG/SA/07/0306	45.02	0.24 ± 1.06^b	1050.06*
NG/SA/07/0008	36.25	0.01 ± 0.49^b	225.96
NG/SA/07/1066-2	45.78	0.17 ± 0.66^b	412.55
NG/SA/07/0128	34.60	0.17 ± 0.95^b	884.90*
NG/SA/07/0063	51.34	0.18 ± 0.57^b	305.06
NG/SA/07/0113	35.71	0.28 ± 1.25^b	1466.34*
NG/SA/07/0086	69.11	0.06 ± 0.30^a	86.66
Total	800.04		
Mean	30.77		

* Deviation Mean Square (S_{2di}), significantly greater than 0; a = Regression coefficient (b) significantly greater than 1.0; b = Regression coefficient (b) significantly less than 1.0

Table 4: AMMI analysis of variance for cowpea genotypes over four environments

Source	Df	SS	MS	TRT SS (%)	GXE (%)
Genotypes	25	65811.00	2632.00**	20.78	
Environments	3	9624.00	3208.00	3.04	
Block	8	9970.00	1246.00		
Interactions	75	88278.00	1177.00**	27.87	
IPCA 1	27	70781.00	2622.00**		80.18
IPCA 2	25	9212.00	368.00		10.44
Residuals	23	8285.00	360.00		9.38
Error	200	143096.00	715.00		
Total	311	316778.00	1019.00		

% TRT SS= Treatment Sum of Squares ** Significant at P = 0.01

Table 5 showed the mean yield of 26 cowpea genotypes grown in four environments and the value of their first PCA scores. Genotype mean yield ranged from 7.15g plant⁻¹ to 69.11g plant⁻¹ for genotypes IT06K-134 and NG/SA/07/0086, respectively. The environmental means ranged from 26.15 for Igboora 1 to 36.28 for Abeokuta 2. Genotype IT98K-573-2-1 had the largest PCA score

(10.10) and genotype IT07K-299-6 had the smallest PCA score (0.00). On the other hand, environment 4 had the largest PCA score (-10.55) and Abeokuta 2 had the smallest PCA score of (2.01). Thus, when a cultivar and an environment have the same sign on their respective first PCA axes, their interaction is positive; if the sign is different, their interaction is negative.

Table 5: Means and the first PCA scores from AMMI analysis of seed yield performance the cowpea genotypes studied in four environments

Genotype	Environment				Mean (g)	First PCA scores
	1	2	3	4		
IT04K-332-1	8.53	35.92	14.99	23.83	20.82	-0.07
IT04K-333-2	9.83	21.52	16.34	49.77	24.37	-2.10
IT98K-573-1-1	4.98	32.16	14.44	41.44	23.26	-1.49
IT98K-573-2-1	9.96	29.66	26.17	34.12	24.98	-10.10
IT06K-134	4.30	4.32	15.65	4.33	7.15	-0.33
IT99K-529-2	9.90	41.23	12.83	45.11	27.27	-1.40
IT99K-494-6	9.10	26.27	16.51	30.18	20.52	-0.68
IT06K-242-3	10.00	18.74	18.06	31.47	19.57	-0.88
IT07K-303-1	7.63	48.55	22.59	25.30	26.02	0.17
IT07K-243-1-2	7.50	28.66	12.58	12.93	15.42	0.76
IT07K-243-1-10	9.60	25.40	23.48	13.59	18.02	0.51
IT07K-298-15	7.53	37.15	26.86	6.26	19.45	1.28
IT07K-299-6	6.76	36.40	20.02	23.04	21.56	0.00
IT07K-210-1-1	28.21	34.89	24.43	39.82	31.84	-0.40
UAM1055-6	30.13	15.48	25.13	32.60	25.84	-0.25
UAM1056-2	36.50	21.82	21.25	18.80	24.59	1.00
NG/SA/07/0157	41.84	43.13	30.23	50.93	41.53	-0.51
NG/SA/07/0176	66.76	59.06	34.45	54.86	53.78	0.53
NG/SA/07/0042	55.40	42.06	33.03	14.46	36.24	2.54
NG/SA/07/0306	48.83	46.24	43.66	41.34	45.02	0.59
NG/SA/07/0008	52.25	36.12	34.22	22.40	36.25	2.12
NG/SA/07/1066-2	37.00	54.04	31.03	61.04	45.78	-0.83
NG/SA/07/0128	49.64	38.04	26.44	24.28	34.60	1.59
NG/SA/07/0063	54.96	54.97	41.33	54.10	51.34	1.53
NG/SA/07/0113	62.50	53.23	12.96	14.15	35.71	3.21
NG/SA/07/0086	76.60	58.30	81.19	60.33	69.11	3.19
Mean	28.70	36.28	26.15	31.94	30.77	
First PCA scores	5.23	3.31	2.01	-10.55		

Fig 1 presents the AMMI biplot. The abscissa reflected the differences in main effect and the displacement along the ordinate showed the differences in the first PCA. 75.10% of the treatment sum of squares is accounted for by the biplot while the remaining 24.99% remained in the residual. Genotypes NG/SA/07/0086, NG/SA/07/0003, NG/SA/07/0042, NG/SA/07/0113, NG/SA/

07/176, NG/SA/07/157, NG/SA/07/1066-2 and IT07K-210-1-1 were generally high yielding because the AMMI analysis placed them on the right hand side of the midpoint of the axis. On the other hand, genotypes IT07K-243-1, IT07K-243-1-2, IT07K-299-6, IT98K-573-1-1, and UAM1055-6 were generally low yielding and were placed on the left hand side of the midpoint on the biplot.

Fig. 1: AMMI biplot for cowpea seed yield trials for 26 genotypes tested across four environments

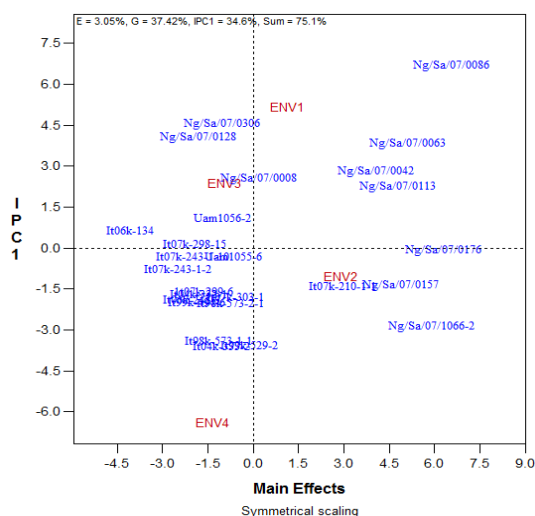
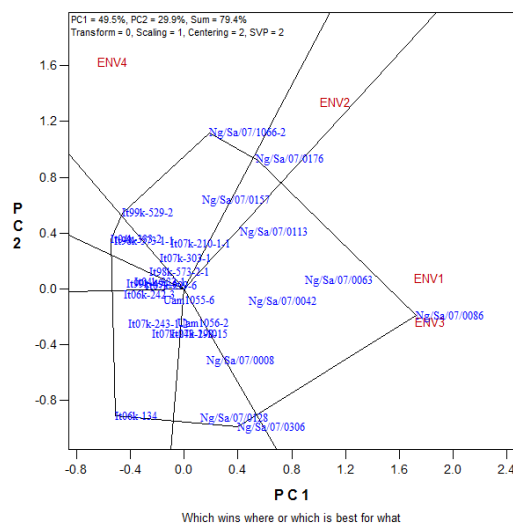


Fig. 2: Which genotype won where or best for which location



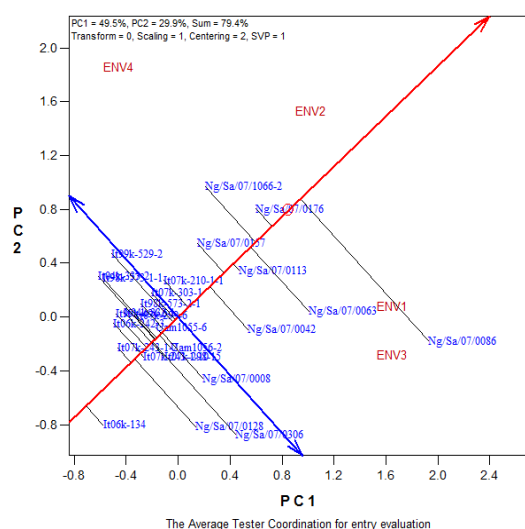
Where ENV 1 = Abeokuta 1; ENV 2 = Abeokuta 2; ENV 3 = Igboora 1; ENV 4 = Igboora 2

The poplygon view of a GGE- biplot which displays the won where pattern from the twenty-six cowpea genotypes evaluated in four environments with respect to seed yield is presented in Fig 2. The convex hull in graph is drawn on genotypes relative position from the biplot origin in order that all other genotypes are contained within the convex hull. Also, the biplot contains a set of lines perpendicular to each sides of the convex hull. These lines divide the biplot into seven sectors and the environments fall into three of them. Thus, environment 1 and environment 3 fell into the same sector and the only vertex genotype for this sector was genotype NG/SA/07/0086. Likewise, environment 4 fell into another sector with the vertex genotype NG/SA/07/1066-2. Genotypes IT06K-134, NG/SA/07/0128, and NG/SA/07/0306 were highly poor yielding genotypes and so they were not captured in any of the four environments. The biplot also divides the environments into three maga environments. The poplygon view of a GGE- biplot which displays the which won where pattern from the twenty-six cowpea genotypes evaluated in four

environments with respect to seed yield is presented in Figure 2. The convex hull in graph is drawn on genotypes relative position from the biplot origin in order that all other genotypes are contained within the convex hull. Also, the biplot contains a set of lines perpendicular to each sides of the convex hull. These lines divide the biplot into seven sectors and the environments fall into three of them. Thus, environment 1 and environment 3 fell into the same sector and the only vertex genotype for this sector was genotype NG/SA/07/0086. Likewise, environment 4 fell into another sector with the vertex genotype NG/SA/07/1066-2. The biplot also divides the environments into three maga environments. Environment 1 and 3 were grouped together as one mega environment. Environment 2 was grouped alone as another mega environment, and lastly, only environment 4 formed one mega environment. The implication of this grouping was that environments 1 and 3 are similar and the experiments conducted in these environments will likely produce the same results and similar to Dudhe *et al.*, (2019). The biplot of stability and mean performance cowpea genotypes presented in Fig 3.

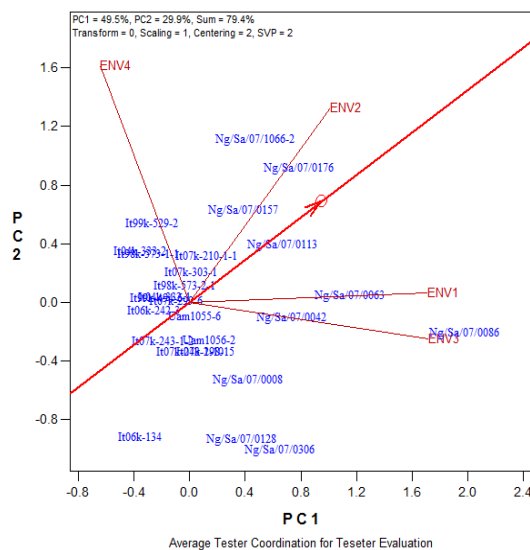
The small circle near environment 2 indicates the average environment which is defined by the intercept of PC1 and PC2 scores of the environment. The line that passed through the biplot origin and the average environment with single arrow is the average environment axis. The line with double arrow heads is called the abscissa. Projections of genotype markers onto the average environment axis approximate the mean yield of genotypes. Thus, the genotypes are ranked along the ordinate. Genotype NG/SA/07/0086 was the highest yielding genotype. The AEC ordinate is the double arrowed line that passed through the biplot origin and is perpendicular to the average environment coordinates (AEC) abscissa. The AEC ordinate approximates the G x E interaction associated with each genotype and this is a measure of variability or instability of the genotypes. Greater projection onto AEC ordinate, regardless of direction means greater instability. So, genotypes NG/SA/07/0086, NG/SA/07/0063, NG/SA/07/1066-2, and NG/SA/07/0042 were considered unstable. Genotypes NG/SA/07/0176, NG/SA/07/0157, IT07K-210-1-1 with shorter projections were relatively stable over the environments. The

Fig. 3: The mean performance and stability of genotypes evaluated across four environments



genotypes that combined good performance with stability include NG/SA/07/0176, NG/SA/07/0157, and IT07K-210-1-1. Fig. 4 displays the representativeness and discriminating ability of the genotypes and the environments. From the vector view of the biplot, the length of the environment vectors approximates the standard deviation within each environment (Yan and Kang, 2003). It is also the measure of their discriminating ability. The centre of concentric circles is where an ideal environment should be located, and thus, environments 1, 3 and 4 are the most discriminating while 2 is the least discriminating. The average environment is indicated by the small circle in fig. 4. The line that passed through the biplot origin and the average environment is the average environment coordinates (AEC). The angle between the vector of an environment and AEC axis is a measure of the representativeness of the environment thus, environment 2 is the most representative while 3 and 4 are the least representative of the environments. Our results are similar to Yan *et al.*, (2010) and Alake *et al.* (2012).

Fig.4: Discriminating ability versus representativeness of the environments



Where ENV 1 = Abeokuta 1; ENV 2 = Abeokuta 2; ENV 3 = Igboora 1; ENV 4 = Igboora

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