Comparative Analysis of Genotype x Environment Interaction Techniques in West African Okra, (*Abelmoschus caillei,* A. Chev Stevels)

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Abstract

West African okra occurs in wild and unselected variants in Nigeria but farmers desire stable and high-yielding cultivars. Twenty-five West African okra genotypes from diverse geographical backgrounds were evaluated in five different environments for stability of performance. Performance was measured by number of days to 50% flowering, number of pods per plants, number of seeds per pod, plant height at maturity and seed yield per plant. A regression method, Additive main effects and Multiplicative Interaction (AMMI) and Genotype main effect and genotype x environment Interaction (GGE) were employed in the evaluation. Joint regression and AMMI analyses showed significant ($P< 0.01$) G x E interaction with respect to seed yield, and both identified NGAE-96-0060 and NGAE-96-0063 as stable genotypes. The AMMI and GGE biplot analyses are more efficient than the Eberhart and Russell analysis. The GGE biplot explains higher proportions of the sum of squares of the GxE interaction and is more informative with regards to environments and cultivar performance than the AMMI analysis. GGE-biplot models showed that the five environments used for the study belonged to three mega-environments with environment 2 (Upland, 2007) being the most representative and most desirable of all. The GGE results also confirmed NGAE-96-0063 as being stable with NGAE-96-04 as the most stable. NGAE-96-04 was identified as most superior genotype in terms of yield and stability of performance and could be recommended for cultivation.

Keywords: West African okra, Joint regression, Genotype x Environment Interaction, Stability, GGE Biplot

1. Introduction

Phenotypic variance is a composite of two variables, genetic, environment and their interaction. It is a common practice in trials involving varieties and breeding lines to grow a series of genotype in a range of different environments. If all the genotypes respond similarly to the entire environment tested, their relative performance in other environments may be predicted with some confidence. A genotype x environment interaction (GEI) exists where the relative performance of varieties changes from environment to environment (Kang, 2004). The presence of GEI is a major problem in getting a reliable estimate of heritability and it makes difficult to predict with greater accuracy the rate of genetic progress under selection for a given character.

Various techniques have been used to assist in the assessing, studying and interpreting GEI (Hussein *et al.,* 2000; Sabaghnia *et al.,* 2006). Some models are based on linear regression of a genotype means on environmental index (Eberhart and Russell 1966; Finlay and Wilkinson 1963). However, the practical utility of different statistical models to explain GEI and facilitate variety release have been extensively reviewed and published elsewhere (Becker and Leon, 1988; Crossa, 1990; Flores *et al.,* 1998; Zobel *et al.,* 1988; Lin *et al.,* 1986; Hussein *et al.,* 2000; Ferreira *et al.,* 2006). Two new methods, which helps identify important characteristics of GEI are worth mentioning; Additive Main effects and Multiplicative Interaction (AMMI) biplot model which was popularized by Gauch and Zobel (1988) and Genotype plus Genotype x Environment interaction (GGE) which was developed by Yan (2001) and thoroughly documented by Yan and Kang (2003). However not all of them are not always effective enough in analyzing the multi-environment data structure in breeding programme (Navabi *et al.,* 2006). Eberhart and Russell (1966) developed a methodology for identifying cultivars with

greater adaptability and stability that has been widely used in the identification of genotypes (Miranda *et al.* 1998, Grunvald *et al.* 2008). AMMI and GGE biplot models are defined powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programs (Zobel *et al.,* 1988; Ebdon and Gauch, 2002a; Yan *et al.,* 2000; Samonte *et al.,* 2005) with new information for cultivars, environmental stratification and cultivar x environment interaction (Miranda *et al.,* 2009). Yan *et al.,* (2007) compared the GGE biplot analysis and AMMI analysis with three aspects of genotype by-environment data (GED) analysis, namely megaenvironment analysis, genotype evaluation, and test environment evaluation. Yan *et al.* (2007) concluded that both GGE biplot analysis and AMMI analysis combine rather than separate G and GE in mega-environment analysis and genotype evaluation. The authors maintain that the GGE biplot is superior to the AMMI1 graph in mega-environment analysis and genotype evaluation because it better explains GGE and has the inner product property of the biplot. Moreover, the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible with AMMI analysis. Gauch Junior *et al.,* (2008) reviewed AMMI and GGE analyses, concluding that AMMI megaenvironment graph incorporated more of the genotype main effect and capture more of the GGE than did the GGE biplot graph, and thereby display the which-won-where pattern more accurately for complex data sets. Thus, the goal of this study was to (1) compare the AMMI and GGE multivariate methods with joint regression of Eberhart and Russell method for the interpretation of genotype x environment interaction and (2) to determine the environmental effect on the performance of 25 genotypes of West African okra.

2. Materials and Methods

Twenty-five West African okra accessions were collected from the gene bank of National Center for Genetic Resources and Biotechnology (NACGRAB), Centre for Environment, Renewable Natural Resources Management, and Development (CENRAD), both in Ibadan, Oyo-State and from several locations in Ekiti and Ondo states in the south-western part of Nigeria as listed in Table 1

All 25 genotypes were planted in two ecologies representing Upland and inland valley (Inland valley) in Derived savannah transition agro-ecological zone (Abeokuta) 7^0 29N, 3^0 30E. Busari (2011) described soil around the experimental sites as loamy sand and was classified as Arenic Plinthic Kandindalf. The study was carried out over a four-year period (2006-2009) with two planting seasons in the year 2007 (early and late plantings) and one planting in each of the year 2006, 2008 and 2009 to give a total of five plantings. In each season at each location, land preparation was done by ploughing and harrowing at the upland ecology and manually at Inland valley ecology. The experimental design in both ecologies was a Randomized Complete Block Design with three replications. A block consisted of 25 rows of all the genotypes and each row was 6m long. The rows were 1 m apart while plant-to- plant distance in each row was 0.6 m. Three seeds were sown per hole and later thinned to two plants per stand at 2 weeks after planting (WAP). Weeds were controlled manually as at when due while field insect pests were controlled using karate at 50 ml to 20L of water. Data were collected from ten plants in each row. Harvesting was done when the pods were at physiological maturity.

Regression, Additive Main and Multiplicative Interaction model (AMMI) and Genotype plus Genotype x environment interaction (GGE) methods were employed to investigate the response of the genotypes to different environments as measure by the following characters:

Number of days to 50% flowering: This was determined as the average of the number of days to flowering of ten plants in the inner rows.

Number of pods per plants: Average value of the total of pods from ten competitive plants from inner rows was obtained.

Number of seeds per pod: This was determined at maturity by counting the number of seeds in ten randomly picked pods and averaging over ten.

Plant height at maturity: This was taken by measuring the plant from the soil level to the tip of the main stem when the plants had shed their leaves and other floral parts and the shoot had dried up.

Seed yield per plant: This was determined by bulking the weight of the dry seeds of ten inner plants and dividing by ten.

In the regression method, data were subjected to combine analysis of variance and regression analysis following procedure outlined by Eberhart and Russel (1966). In this method, a genotype with average sensitivity will have a unit regression coefficient (b=1.0) while a stable genotype will have a minimum deviation from regression (S^2di).

The AMMI model analysis combines additive components in a single model for the main effects of genotypes and environments, as well as multiplicative components for the interaction effect. For any particular genotype-environment, the main effect equals the cultivar mean plus the environment mean minus the grand mean. The interaction is the cultivar principal component axis (PCA) score multiply by the environment score. When a cultivar and the environment have the same sign on their respective principal component axes, their interaction is positive, if different, their interaction is negative. Cultivars or environments with large Interaction principal component axis (1PCA) scores, either positive or negative had large interactions whereas cultivar with IPCA score of zero or near zero had small interaction (Crossa, 1990). The AMMI model does not make provision for a specific stability measure to be determined and such a measure is essential in this study in order to rank genotypes in terms of stability. Because the IPCA 1 score contributes more to G x E sum of squares, a weighted value is needed. This weight is calculated according to the relative contribution of IPCA1 and IPCA2 to the interaction mean squares. Purchase (1997) proposed the formula to calculate AMMI's stability value (ASV) as follows:

$$ASV= \{[(SS_{pca1}/SS_{pca2}) (GPCA1 score)]^2 + (GCPA2 scores)\}^{½}$$

Where:

ASV = the distance from zero in a two dimensional scattergram of IPCA 1 (Interaction Principal Components Analysis) scores against IPCA 2 scores.

SSpca1/SSpca2 = the weight given to the PCA1 value by dividing the PCA1 sum of squares by the PCA2 sum of squares.

GPCA1 score = the PCA1 score for that specific genotype, and

GPCA2 = the PCA 2 score for that specific genotype.

The third analysis was genotype main effects and genotype x environment interaction (GGE) methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and GGE concept (Gauch and Zobel, 1996; Yan *et al*., 2000) was also used to visually analyze the results of site regression analysis (SREG) analysis of multi-environmental trial (MET) data. This methodology uses a biplot to show the two factors (G plus GE) that are important in cultivar evaluation and that are also sources of variation in SREG model analysis of MET data (Yan *et al.,* 2000). The GGE biplot show the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment–centred yield data (the yield variation due to GGE) to singular value decomposition (Yan *et al.*, 2000). In this study, GGE biplot was used to compare the performance of different genotypes at five environments, identify the highest yielding genotype(s) at the different mega-environments, and identify ideal genotypes and test location(s)

A comparison of the three procedures was made with respect to which genotypes were considered stable using any of the procedures.

3. Results

The analysis of variance for stability of performance as measured by seed yield per plant, days to flowering, plant height at maturity, number of pods per plant and number of seeds per pod using Eberhart and Russell (1966) procedure showed significant difference among the West African okra genotypes (Table 2). The seasonal variation in these characters may be due to climatic or soil factor differences among environments especially during pod formation. Additive environmental effects were significant for all the characters evaluated, and genotypes x environment linear mean square (MS) were not significant with respect to plant height at maturity. The pooled deviations for all the characters were significant indicating a non linear response to environment.

The average seed yield per plant, regression coefficients and deviation mean squares of each genotype are presented in Table 3. Since regression coefficients measure response of genotypes to an increment in improving environment genotypes NGAE-96-0061, NGAE-96-0060, NGAE-96-0065 and Oja-Oba-2 with regression coefficients (b) significantly greater than 1.0 had above average responses and was consistently high yielders in all above average environments. Furthermore, except for genotypes CEN 010, NGAE-96-04, CEN 015, AGA 79/066-5780, ADO-EKITI-1, CEN 001, CEN 009 and NGAE-96-0067 all genotype had deviation MS greater than zero. Only these eight genotypes can be considered to stable with respect to seed yield by this regression technique. The regression coefficients and MS of other characters evaluated are presented in Table 4 and 5. It is noteworthy that most characters responded to environmental changes. Genotypes CEN 007, CEN 015, OAA96/175-5328, Ado-Ekiti-1 and CEN001 produced higher pod number under more favourable environment. None of these genotypes were stable with respect to pod number by having non-significant deviation MS.

The AMMI analysis is showed in Table 6. Differences between environments accounted for 4.6% while G x E interaction captured 18.1% of the total sum of squares. The first interaction PCA accounted for 68.9%. The four interaction PCA axes were significant and cumulatively contributed 100% of the total GEI. In the joint regression analysis, G x E interaction mean square was only about two and half times the error mean square. The AMMI model demonstrated the presence of G x E interaction and this has been partitioned among the first four IPCA 1 axes and this is about 55 times the MS of the error.

Table 7 presents the genotype and environment means as well as their respective first PCA axes from the AMMI analysis. Seed yield per plant ranged from as low as 9.47g in in 2007 inland valley to 32.63g for inland valley 2006, with an average seed yield of 16.5g. Cen- 016 had the lowest mean seed yield of 12.23g while ngae-96-0060 had the highest mean of 28.64g over the five environments.

Table 8 shows the AMMI model IPCA1 and IPCA2 scores of seed yield for each genotype and the AMMI stability value (ASV) for 25 West African okra genotypes. According to ASV ranking, NGAE-96 0060(G17) had the least value and the most stable genotype while Ado- Ekiti-3 (G24), NGAE-96-012-2 (G2) and NGAE-96-012-3 (G3) were unstable.

Figure 1 presents the AMMI plot for okra yield grown in five environments. By plotting both genotypes and environments on the same graph, the association between the genotypes and the environments became more obvious. Displacement along the abscissa reflected differences in main effect, in this case, the yield of okra seeds. Whereas, displacement along the ordinate exhibited differences in the first PCA. The biplot accounted for 94.37% of the treatment sum of squares leaving 5.63 in the residual. The additive part of the AMMI equals the G mean plus the E mean minus the grand mean and the multiplicative part i.e interaction effect, is the product of G and E. The main effect of G1 grown in Inland valley 2006 (E1) was 16.67 + 17.37 – 16.59 = 17.45g/plant. The interaction effect was 0.42 x 0.89 = 0.37. Therefore AMMI model gave a yield estimation of 17.82g/plant instead of 17.37g/plant. Similarly, G24 in E3 gave the yield of 11.25g/plant instead of 12.5g/plant while G3 in E5 gave the yield of 22.23g/plant instead of 12.60g/plant. The genotypes CEN 010 (G1), CEN 012 (G5), AGA79/066-5780 (G10), NGAE-96-0067 (G25), NGAE-96-0063 (G19), NGAE-96-04(G7) and NGAE-96-0060 (G17) were generally high yielding since AMMI placed them on the right hand side of the midpoint of the axis.

The GGE Biplot analysis of the twenty-five West African okra accessions evaluated in five environments with respect to seed yield per plant is presented in Fig 2. The first two principal components explained 76.9% of the total variation. This figure explicitly displays the polygon view of a GGE- biplot with which-won-where pattern. The convex hull in this graph is drawn on genotypes relatively remote from the biplot origin so that all other genotypes are contained within the convex hull. The biplot also contains a set of lines perpendicular to each side of the convex hull. These perpendiculars divide the biplot into several sectors. There are six sectors and the environments fall into three of them. The environment group within each sector and the cultivar at the polygon's extremity characterized the mega-environment (Yan and Rajcan, 2002). Thus, three mega-environments were characterized, one with Inland valley'06 (E1) and Inland valley'07 (E3), Environment 2 (Upland '07) is alone grouped as another mega environment, while environment 4(Upland '08) and 5 (Upland '09) were grouped as another mega environment.

The genotypes located at the sector's vertex had optimum performance in their respective mega-environment. Thus, CEN 001(G12) and AGA 79/066-5780 (G10) had the best performance in environment denoted by E1 and E3. Similarly, genotype NGAE-96-0060 (G17) exhibited the best performance in environments E4 and E5.

Figure 3 presents the biplot of stability and mean performance. The small circle near environment 2 indicates average environment which is defined by the intercept of PC1 and PC2 scores of the environment. According to this figure, the line that passes through the biplot origin and the average environment with single arrow is called the average environment axis (the ordinate). 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 NGAE-96-0060 (G17) was clearly the highest yielding genotype on average while OAA96/175-5328 (G9) was the lowest yielding genotype.

The AEC ordinate is the double arrowed line that passes through the biplot origin and is perpendicular to the AEC abscissa. The AEC ordinate approximates the GxE interaction associated with each genotype and this is a measure of variability or instability of the genotypes. Greater projection onto AEC ordinate, regardless of the direction means greater instability. Therefore, genotypes CEN001 (G12), NGAE-96-0060 (G17) and AGA79/066-5780 (G10) are unstable. NGAE-96-0066 (G15), CEN-012 (G5) and NGAE-96-04 (G7) with shorter projections were relatively stable over the environments. The genotypes that combined good performance

with stability include NGAE-96-04 (G7), NGAE-96-0063 (G19) and NGAE-96-0067(G25) because of their closeness to the mean yield and short projection of the genotype marker lines.

Figure 4 shows 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). This is also a measure of their discriminating ability. The centre of concentric circles is where an ideal environment should be located, Inland valley'06 (E1), UPL'07 (E3), UPL'08 (E4) and UPL'09 (E5) are the most discriminating while Inland valley'07 (E2) is the least discriminating. The biplot way of measuring representativeness of an environment is to define an average environment and use it as a reference or benchmark (Yan and Kang, 2003). The average environment is indicated by the small circle in Fig 4. The line that passes 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, UPL'07 (E2) was found to be nearer to the small circle and therefore, the most representative while Inland valley'06 (E1) and UPL'09 (E5) are the least representative of the environment.

4. Discussion

In this study, the joint regression analysis indicated that the performance of the cultivars could not be predicted in a linear manner. Although both joint regression analysis and AMMI had 250 degrees of freedom for residual, the residual mean square of 3.50 for joint regression analysis versus the AMMI residual of 0.39 demonstrated a greater accuracy of the latter (Tables 2 and 6). That AMMI and GGE biplot accounted for a substantial part of total sum of square suggested that the models were more appropriate in explaining GxE interaction

G1 and G3 at one extreme on the PCA scores flowered fairly late whereas G7 at the other extreme of the PCA scores flowered relatively early. G2, G9, G11, G18 and G23 had large yield responses and positive interaction with the largest interaction produced by G2 and G24 had low mean yield and a similar large negative interactions. G3, G5, G7, G13, G16 and G17 had low mean yield but with different negative interactions. Based on AMMI stability values, G17, G12 and G13 could be considered fairly stable. The upland environment 2009 (E5) had the largest interaction while Inland valley 2007 (E3) had the least. From GGE point of view, the five environments used were grouped into three mega environments, one represented Inland valley environments (Inland valley 2006 and 2007), another represented the upland environments (Upland 2008 and 2009), while the last was represented by the Upland 2007. Also, the grouping of the environments met the two criteria for the existence of different mega environments. G12 and G10 were the winning genotypes for the Inland valley mega environments while G17 was the winning genotype for the upland mega environment.

According to GGE interpretation, an ideal test environment should be both discriminating and representative. An 'ideal' environment probably does not exist in reality but can be used as a reference point. From this study, it can be seen that E2 (Upland, 2007) is the closest to the ideal environment, and therefore, is the most desirable of the five environments. The AMMI and GGE biplot analyses are more efficient than the Eberhart and Russell analysis. The GGE biplot explains higher proportions of the sum of squares of the GxE interaction and is more informative with regards to environments and cultivar performance than the AMMI analysis.

By using Eberhart and Russell (1966) model, the genotype's performance is generally expressed in terms of three parameters, mean yield (x), regression coefficient (b) and deviation (S^2d) from regression (Table 3). The b-value is a measure of genotype's response, and S^2d a measure of stability. According to this model, a desirable genotype should have a high mean yield, b=1.0 and S^2d =0. Only genotype NGAE-96-0060 (G17) with regression coefficient values of 1.27, non-significant deviations from regression and highest seed yield (28.46g) could be considered the most widely adapted genotype (Table 3). This was closely followed by NGAE-96-0063 (G19) and NGAE-96-0060 (G18). Adaptability of cultivars to environments was determined by the direction and size of the perpendicular projection of the genotype point onto the environment line in a Biplot (Kempton, 1984). If the projection falls far out from the origin on the location line then the genotype is well adapted to the environment. If the line has to be extended backwards through the origin to meet the projection, the entry is poorly adapted to the environment. Thus lack of adaptation was observed for NGAE-96-04 (G7) in E3, NGAE-96-0066 in E5 and NGAE-96-012-3 in E1.

In terms of stability, the GGE Biplot identified NGAE-96-0066 (G15) and NGAE-96-04 (G7), which were collections from NACGRAB, Ibadan, as stable varieties. CEN 001 (G12), NGAE-96-012-2 (G2), AGA79/066-5780 (G10), CEN 005 (G8) and OAA96/175-5328 (G9) were the most unstable of all the genotypes tested (Fig. 3). This contradicts the result got from AMMI and regression analyses which classified NGAE-96-0060 (G17) has been stable (Table 8). In crop improvement programmes, genotypes are tested in

different seasons and locations to determine performance and adaptation of genotypes. Thus evaluation based on several seasons and locations is best strategy. Farmers in developing countries, who use no or limted imputs, or under unpredicted environments will prefer yield stability than increment. However, stability is useful only when considered jointly with the mean performance of genotypes (Yan and Kang, 2002). Based on the above information, NGAE-96-00060 (G17), NGAE-96-0063 (G19) and NGAE-96-04 (G7) which have above average mean performance and fairly stable of all the genotypes were the most desirable. There is, in any case, a need to test these genotypes in a more diverse and wider range of locations to assure more reliable recommendations.

In conclusion, the results revealed that the GEI was an important source of West African okra yield variation and its biplots were effective enough for visualizing the response patterns of genotypes and environments. AMMI and GGE methods are adequate to explain the genotype x environment interactions, providing results that are consisitent with the classic method of regression of Eberhart and Russell. The AMMI and GGE biplot analyses are more efficient than the Eberhart and Russell analysis. The discriminating power x representativeness view of the GGE Biplot was effective in evaluating test environment, which was not possible with AMMI analysis. However, if one is interested in stability i.e ability of genotypes to have the same relative performance in different environments, there is no need to go via the GGE plot. This can be computed from genotype's contribution to the interaction sum of square directly (ASV).

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Table 1. 25 West African okra genotypes collected in Nigeria and their morphological traits

Genotype Code names	Source	Stem colour	Stem pubescence	Pod colour	Pod pubescence	Pod position
CEN 010 (G1)	CENRAD	LP	Glabrous	DG	Downy	Erect
NGAE-96-012-2 (G2)	NACGRAB	Purple	Conspicuous	LG	Pricky	SE
NGAE-96-012-3 (G3)	NACGRAB	Green	Glabrous	GwR	Downy	SE
CEN 016 (G4)	CENRAD	Purple	SP	DG	Prickly	SE
CEN 012 (G5)	CENRAD	Purple	Conspicuous	Green	Prickly	Horizontal
CEN 007 (G6)	CENRAD	Green	Glabrous	YwG	Downy	SE
NGAE-96-04 (G7)	NACGRAB	Green	Glabrous	Green	SP	SE
CEN 015 (G8)	CENRAD	LP	Glabrous	DG	Downy	SE
OAA96/175-5328 (G9)	NACGRAB	Green	SP	DG	Prickly	Horizontal
AGA79/066-5780(G10)	NACGRAB	Purple	Glabrous	DG	Downy	Horizontal
ADO-EKITI-1 (G11)	Ekiti state	Green	Glabrous	DG	Prickly	Horizontal
CEN 001 (G12)	CENRAD	Purple	Glabrous	GwY	Prickly	Horizontal
CEN 009 (G13)	CENRAD	LP	Glabrous	Green	Downy	Horizontal
NGAE-96-0062-2 (G14)	NACGRAB	Purple	Glabrous	Green	Downy	Horizontal
NGAE-96-0066 (G15)	NACGRAB	Purple	Glabrous	Green	SP	Horizontal
NGAE-96-0061(G16)	NACGRAB	LP	Glabrous	GwR	SP	SE
NGAE-96-0060 (G17)	NACGRAB	Purple	Glabrous	Green	Downy	Horizontal
NGAE-96-0064 (G18)	NACGRAB	PwG	SP	GwR	Prickly	Horizontal
NGAE-96-0063 (G19)	NACGRAB	DR	SP	Green	Prickly	Erect
CEN 005 (G20)	CENRAD	GwP	Glabrous	YG	SP	Horizontal
NGAE-96-0065 (G21)	NACGRAB	PwG	Glabrous	Green	Downy	Horizontal
OJA OBA-2 (G22)	Ondo state	Green	Glabrous	YG	SP	Horizontal
OJA OBA-3 (G23)	Ondo state	Green	Glabrous	Green	SP	Erect
ADO-EKITI-3 (G24)	Ekiti state	Purple	Glabrous	Green	Downy	ST
NGAE-96-0067(G25)	NACGRAB	GwP	Glabrous	GwR	SP	Horizontal

LG-Light Green, ***GwP***-Green with Purple, ***PwG***- Purple with Green, ***DG***- Dark Green, ***LP***- Light Purple, ***GwR***-Green with Red, ***YG***-Yellowish Green, ***GwY***-Green with Yellow, ***DGwR***-Dark Green with Red, ***SP***- Slightly prickly, ***SE***-Semi-Erect

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Table 2. Mean squares from the analysis of variance for seed yield (g/plant) and four agronomic traits of 25 genotypes of *Abelmoschus caillei* in five environments using Eberhart and Russell, 1966

Source of variation	DF	Days to 50% flowering	Plant height at maturity	Number of pods per plant	Number of seeds per pod	Seed yield/ plant
Environment (Env)	4	1926.68**	7700.64**	67.44**	2187.40**	44.16
Genotype (Acc)	24	47.75**	800.23**	14.43**	461.91**	367.26**
Acc x Env	96	11.58**	315.65**	4.09**	83.81**	7.20**
Env. + (Acc x Env.)	100	88.19**	611.05**	6.63**	167.95**	8.67**
Env. (linear)	1	7706**	30802.54**	269.76**	8749.61**	176.66**
Acc x Env. (linear)	24	16.44*	359.68	5.79*	133.19**	1.99**
Pooled deviation	75	9.57**	288.93**	3.39**	64.66**	8.57**
Pooled error	250	3.58	10.91	0.21	3.50	0.84

** Significant at P=0.01

* Significant at P=0.05

Note: Genotype x Environment (linear) indicates the linear portion of the G x E Interaction

Pooled deviation is the non linear portion of the G x E Interaction

Table 3. Mean seed yield per plant, regression coefficients, b, and deviation mean squares for 25 West African okra genotypes

Genotype Code names	Mean seed weight per plant (g)	Regression coefficient (b± SE)	Deviation Mean square (S^2di)
CEN 010 (G1)	17.86	1.55 ± 1.13^{b}	8.97^{*}
NGAE-96-012-2 (G2)	13.29	0.84 ± 0.18	0.23
NGAE-96-012-3 (G3)	12.41	0.63 ± 0.45^{b}	1.43
CEN 016 (G4)	12.23	0.95 ± 0.68^{b}	3.28
CEN 012 (G5)	19.15	0.88 ± 0.45^{b}	1.44
CEN 007 (G6)	13.16	0.80 ± 0.23	0.38
NGAE-96-04 (G7)	27.89	1.02 ± 1.15^{b}	9.38^{*}
CEN 015 (G8)	14.85	2.05 ± 2.37^{b}	46.62^{*}
OAA96/175-5328 (G9)	12.73	0.39 ± 0.71^{b}	3.55
AGA79/066-5780(G10)	22.14	-0.03 ± 2.25^{b}	35.75^{*}
ADO-EKITI-1 (G11)	15.93	2.24 ± 2.21^{b}	34.58^{*}
CEN 001 (G12)	13.93	1.20 ± 1.06^{b}	7.98^{*}
CEN 009 (G13)	14.83	1.69 ± 1.90^{b}	25.53^{*}
NGAE-96-0062-2(G14)	13.09	0.35 ± 0.51^{b}	1.82
NGAE-96-0066 (G15)	14.05	0.30 ± 0.80^{b}	4.52
NGAE-96-0061(G16)	13.34	1.29 ± 0.57^{a}	2.31
NGAE-96-0060 (G17)	28.46	1.27 ± 0.66^{a}	3.12
NGAE-96-0064 (G18)	15.25	1.35 ± 0.69	3.40
NGAE-96-0063 (G19)	25.87	1.27 ± 0.89^{b}	5.59
CEN 005 (G20)	15.91	1.02 ± 0.31^{b}	0.68
NGAE-96-0065 (G21)	13.43	0.71 ± 0.16^{a}	0.18
OJA OBA-2 (G22)	12.72	1.12 ± 0.25^{a}	0.45
OJA OBA-3 (G23)	13.48	0.70 ± 0.72^{b}	3.73
ADO-EKITI-3 (G24)	13.84	0.64 ± 0.33	0.77
NGAE-96-0067 (G25)	23.04	0.76 ± 1.11^{b}	8.69^{*}
Total	412.25		
Mean	16.49		

* Deviation Mean Square (S2di), significantly greater than 0

a= Regression coefficient (b) significantly greater than 1.0

b= Regression coefficient (b) significantly less than 1.0

Table 4. Regression coefficients b, for four characters of 25 West African okra genotypes

Genotypes	**Days to flowering**	**Plant height at maturity(cm)**	**Number of pods per plant**	**Number of seeds per pod**
CEN 010 (G1)	0.79± 0.22	0.73±0.28	1.94±0.32[a]	1.45±0.37
NGAE-96-012-2 (G2)	1.13 ±0.17	1.79±0.40[a]	0.17±0.61	0.33±0.36 [a]
NGAE-96-012-3 (G3)	0.42±0.18[a]	1.17±0.37[b]	0.53±0.19[a]	0.17±0.31 [a]
CEN 016 (G4)	1.04±0.09[b]	1.17±0.28[b]	2.01±0.42[a]	0.28±0.25
CEN 012 (G5)	1.43±0.13[b]	1.11±0.23[b]	1.66±0.80	1.46±0.80[b]
CEN 007 (G6)	0.84±0.03a	0.91±0.24[b]	0.75±0.90 [b]	1.37±0.33
NGAE-96-04 (G7)	1.12±0.25[b]	0.82±0.31[b]	1.29±0.53	0.98±0.19[b]
CEN 015 (G8)	1.13±0.14	0.35±0.85	0.86±0.98 [b]	1.00±0.12
OAA96/175-5328 (G9)	0.89±0.06[a]	1.61±0.52	1.19±1.17 [b]	0.49±0.49
AGA79/066-5780(G10)	1.35±0.22[a]	0.65±0.23	0.26±0.83	0.67±0.26
ADO-EKITI-1 (G11)	1.14±0.20	0.08±0.58	0.53±0.73 [b]	1.42±0.39
CEN 001 (G12)	0.94±0.11[b]	0.12±0.53	-1.1±0.34[b]	0.92±0.10
CEN 009 (G13)	0.68±0.12[a]	1.68±0.50	1.62±0.28[a]	1.50±0.16[a]
NGAE-96-0062-2(G14)	0.95±0.09[b]	0.25±0.94	1.31±0.19	0.20±0.23 [a]
NGAE-96-0066 (G15)	0.90±0.19[b]	0.87±0.34[b]	1.09±0.11	0.57±0.57
NGAE-96-0061(G16)	0.66±0.16[a]	2.14±0.37[a]	1.36±0.49	0.42±0.73
NGAE-96-0060 (G17)	1.09±0.32[b]	0.96±0.19[b]	1.76±0.84	2.15±0.77
NGAE-96-0064 (G18)	0.90±0.13	1.53±0.22[a]	1.84±0.23[a]	0.88±0.23[b]
NGAE-96-0063 (G19)	0.88±0.16	0.71±0.21	1.53±0.29	2.05±0.62
CEN 005 (G20)	1.35±0.22[a]	1.37±0.34	1.91±0.32[a]	0.94±0.12[b]
NGAE-96-0065 (G21)	1.03±0.14[b]	0.43±0.40	0.46±0.33	0.55±0.24a
OJA OBA-2 (G22)	1.03±0.12[b]	1.26±0.92 [b]	0.53±0.10[a]	0.71±0.39
OJA OBA-3 (G23)	0.97±0.12[b]	0.58±0.31	0.44±0.17[a]	0.42±0.67
ADO-EKITI-3 (G24)	1.29±0.33	1.37±0.83	0.49±0.39	1.78±0.36[a]
NGAE-96-0067 (G25)	1.05±0.16[b]	1.34±0.31	0.57±0.35 [a]	2.17 ±0.38[a]

a= Regression coefficient (b) significantly greater than 1.0

b= Regression coefficient (b) significantly less than 1.0

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Table 5. Deviation mean squares (S^2di) of four characters of 25 West African okra genotypes

Genotypes	Days to flowering	Plant height at maturity(cm)	Number of pods per plant	Number of seeds per pod
CEN 010 (G1)	15.31 [b]	96.52 [b]	1.07 [b]	47.85 [b]
NGAE-96-012-2 (G2)	8.68	191.83 [b]	4.00 [b]	45.08 [b]
NGAE-96-012-3 (G3)	9.45 [b]	167.36 [b]	0.37	33.58 [b]
CEN 016 (G4)	2.32	98.37 [b]	1.94 [b]	22.32 [b]
CEN 012 (G5)	5.01	65.27 [b]	6.97 [b]	221.97 [b]
CEN 007 (G6)	0.24	71.91 [b]	8.68 [b]	37.97 [b]
NGAE-96-04 (G7)	19.06 [b]	117.10 [b]	3.01 [b]	12.81 [b]
CEN 015 (G8)	6.30	886.54 [b]	10.45 [b]	5.16
OAA96/175-5328 (G9)	1.26	335.04 [b]	14.80 [b]	83.46 [b]
AGA79/066-5780(G10)	15.38 [b]	64.38 [b]	7.50 [b]	24.00 [b]
ADO-EKITI-1 (G11)	12.76 [b]	415.12 [b]	5.79 [b]	53.85 [b]
CEN 001 (G12)	3.50	349.66 [b]	1.47 [b]	3.23
CEN 009 (G13)	4.46	301.41 [b]	0.84 [b]	8.44
NGAE-96-0062-2(G14)	2.33	1097.15 [b]	0.39	18.60 [b]
NGAE-96-0066 (G15)	11.03 [b]	144.72 [b]	0.13	114.75 [b]
NGAE-96-0061(G16)	7.89	171.92 [b]	2.59 [b]	188.75 [b]
NGAE-96-0060 (G17)	30.63	46.41 [b]	7.56 [b]	207.62 [b]
NGAE-96-0064 (G18)	4.83 [b]	61.08 [b]	0.56 [b]	19.19 [b]
NGAE-96-0063 (G19)	8.11	56.04 [b]	0.88 [b]	135.40 [b]
CEN 005 (G20)	14.39 [b]	143.98 [b]	1.12 [b]	5.05
NGAE-96-0065 (G21)	5.66	202.12 [b]	1.16 [b]	19.42 [b]
OJA OBA-2 (G22)	4.32	1059.92 [b]	0.11	53.70 [b]
OJA OBA-3 (G23)	4.71	115.83 [b]	0.31	157.26 [b]
ADO-EKITI-3 (G24)	33.82 [b]	848.09 [b]	1.65 [b]	46.07 [b]
NGAE-96-0067 (G25)	7.69	115.52 [b]	1.30 [b]	50.94 [b]

[b] Deviation Mean Squares (S^2di) significantly greater than 0

Table 6. AMMI analysis of variance for 25 genotypes of West African okra seed yield tested over five environments

Source	Df	Sum of square	Mean Square	% Total SS	%TRT	% G X E
Treatment	124	11426.52	92.15***	99.1		
Genotype(G)	24	8824.34	367.68***		77.2	
Environment(E)	4	529.99	132.50***		4.6	
G X E	96	2072.19	21.59***		18.1	
IPCA 1	27	1428.48	52.91***			68.9
IPCA 2	25	312.73	12.51***			15.1
IPCA 3	23	312.02	13.57***			15.1
IPCA 4	21	18.97	0.90**			0.9
Error	250	98.11	0.39	0.9		
Total	374	11524.63	30.81			

%TRT= Treatment Total

*** Significant at P=0.001

* *Significant at P=0.01

Table 7. Means and the first PCA scores from AMMI analysis of seed yield for 25 West African okra genotypes studied in five environments

Genotype	Environment Inland valley 06 (E1)	Environment Upl 07(E2)	Environment Inland valley 07(E3)	Environment Upl 08 (E4)	Environment Upl 09 (E5)	Mean	GIPCA-1
CEN 010 (G1)	17.37	23.43	14.70	17.50	16.30	17.86	0.42
NGAE-96-012-2 (G2)	13.43	13.47	11.37	14.63	13.53	13.29	2.21
NGAE-96-012-3 (G3)	13.80	11.50	10.63	13.50	12.60	12.41	-2.20
CEN 016 (G4)	14.50	13.83	9.73	12.37	10.73	12.23	0.50
CEN 012 (G5)	17.43	20.43	17.57	20.73	19.57	19.15	-1.90
CEN 007 (G6)	12.57	14.27	11.53	14.37	13.07	13.16	0.29
NGAE-96-04 (G7)	32.63	28.20	24.60	27.50	26.50	27.89	-0.11
CEN 015 (G8)	12.50	13.57	9.47	12.53	26.17	14.85	0.25
OAA96/175-5328 (G9)	14.67	11.37	11.53	14.53	11.53	12.73	0.39
AGA79/066-5780(G10)	21.63	25.57	23.40	26.57	13.53	22.14	0.25
ADO-EKITI-1 (G11)	12.80	17.53	10.53	13.33	25.47	15.93	0.49
CEN 001 (G12)	11.70	14.63	12.00	18.73	12.57	13.93	0.07
CEN 009 (G13)	13.73	13.27	10.30	13.60	23.27	14.83	-0.01
NGAE-96-0062-2(G14)	12.50	12.50	12.53	15.33	12.57	13.09	0.12
NGAE-96-0066 (G15)	13.43	11.63	13.40	16.50	15.30	14.05	0.09
NGAE-96-0061(G16)	13.53	16.50	10.50	13.57	12.60	13.34	-0.03
NGAE-96-0060 (G17)	29.57	31.47	25.50	28.63	27.13	28.46	-0.01
NGAE-96-0064 (G18)	14.67	19.03	12.47	15.53	14.53	15.25	0.27
NGAE-96-0063 (G19)	28.40	28.67	22.63	25.63	24.03	25.87	0.08
CEN 005 (G20)	16.50	15.63	13.43	17.47	16.53	15.91	0.43
NGAE-96-0065 (G21)	13.67	13.67	11.80	14.57	13.43	13.43	0.03
OJA OBA-2 (G22)	12.53	14.63	10.27	13.43	12.73	12.72	0.14
OJA OBA-3 (G23)	12.63	16.43	14.53	17.50	16.30	13.48	0.39
ADO-EKITI-3 (G24)	13.20	13.57	12.50	15.40	14.53	13.84	-2.60
NGAE-96-0067 (G25)	27.47	21.47	20.33	23.60	22.33	23.04	0.43
Mean	**16.67**	**14.29**	**17.45**	**17.48**	**17.07**	**16.59**	
EIPCA-1	0.89	1.20	0.81	1.29	-4.16		

E1 = INLAND VALLEY 2006 E2 =UPLAND 2007 E3 = INLAND VALLEY 2007

E4 =UPLAND 2008 E5 = UPLAND 2009

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Table 8. IPCA scores for genotypes, AMMI stability value (ASV), Rank and mean performance for seed yield (g plant^{-1}) of 25 West African okra genotypes grown at five environments

Genotype	IPCA 1 scores	IPCA 2 scores	Mean Yield	Yield based Rank	ASV	ASV based Rank
CEN 010 (G1)	0.42	1.32	17.86	7	2.33	21
NGAE-96-012-2 (G2)	2.21	0.64	13.29	19	10.12	24
NGAE-96-012-3 (G3)	-2.20	0.88	12.41	24	10.09	23
CEN 016 (G4)	0.50	0.33	12.23	25	2.31	20
CEN 012 (G5)	-1.90	-0.31	19.15	6	8.69	22
CEN 007 (G6)	0.29	-0.29	13.16	20	1.36	11
NGAE-96-04 (G7)	-0.11	-0.74	27.89	2	0.89	9
CEN 015 (G8)	0.25	0.57	14.85	12	1.28	10
OAA96/175-5328 (G9)	0.39	0.36	12.73	22	1.82	13
AGA79/066-5780(G10)	0.25	0.87	22.14	5	1.44	12
ADO-EKITI-1 (G11)	0.49	0.06	15.93	9	2.24	19
CEN 001 (G12)	0.07	-0.19	13.93	15	0.37	2
CEN 009 (G13)	-0.01	-0.38	14.83	13	0.38	3
NGAE-96-0062-2(G14)	0.12	-2.00	13.09	21	2.07	17
NGAE-96-0066 (G15)	0.09	0.32	14.05	14	0.52	5
NGAE-96-0061(G16)	-0.03	0.53	13.34	18	0.55	6
NGAE-96-0060 (G17)	-0.01	-0.17	28.46	1	0.18	1
NGAE-96-0064 (G18)	0.27	-1.41	15.25	11	1.87	14
NGAE-96-0063 (G19)	0.08	-0.70	25.87	3	0.79	8
CEN 005 (G20)	0.43	-0.21	15.91	8	1.98	15
NGAE-96-0065 (G21)	0.03	0.42	13.43	17	0.44	4
OJA OBA-2 (G22)	0.14	0.17	12.72	23	0.66	7
OJA OBA-3 (G23)	0.39	-0.97	15.48	10	2.03	16
ADO-EKITI-3 (G24)	-2.60	0.01	13.84	16	11.88	25
NGAE-96-0067 (G25)	0.43	-0.93	23.04	4	2.17	18

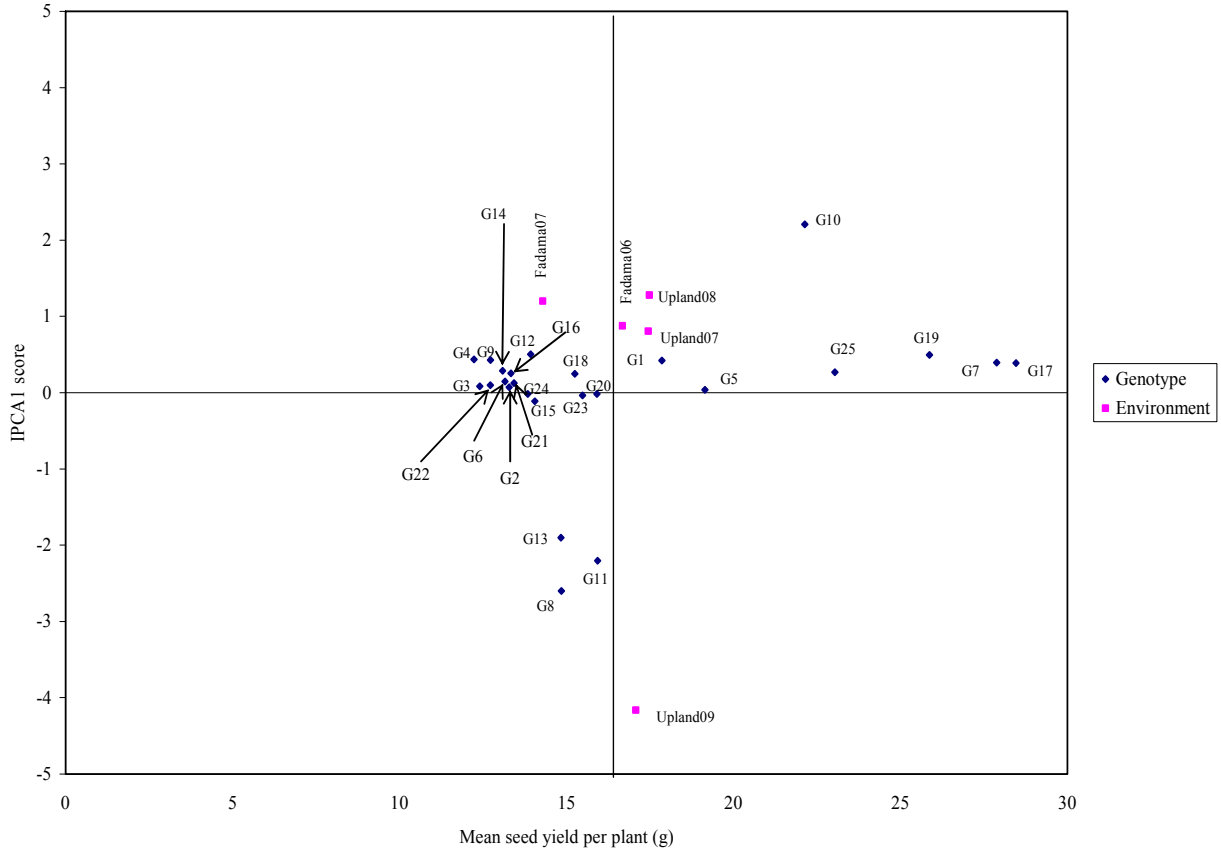

Figure 1. AMMI plot for okra seed yield trials with 25 genotypes grown in five environments

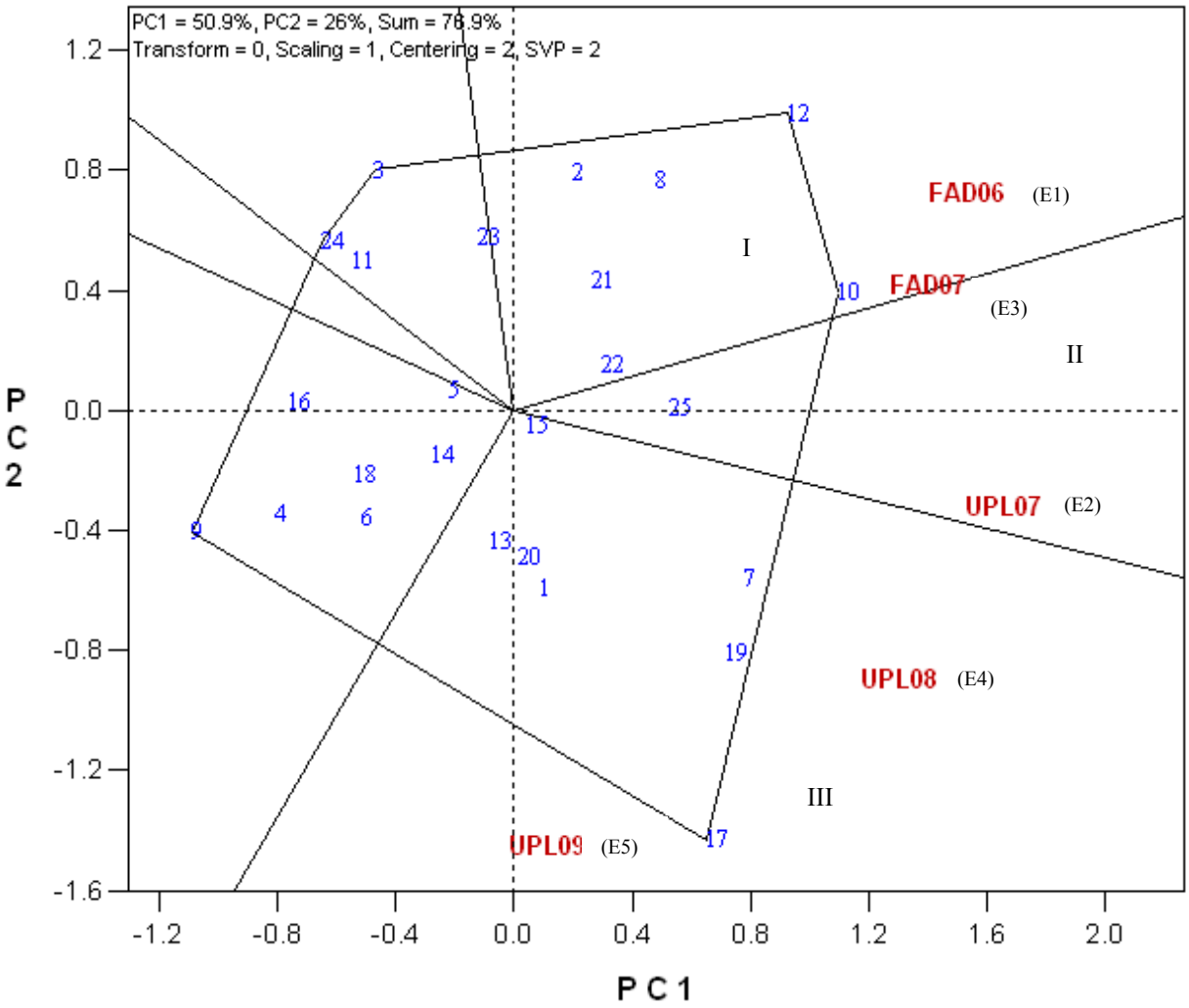

Figure 2. Polygon view of the GGE biplot of seed yield per plant of 25 okra genotypes evaluated over five environments

FAD = Inland Valley; UPL= Upland

Inland valley '06=E1, Inland valley '07=E3, Upland '07=E3, Upland '08=E4 and Upland '09=E5

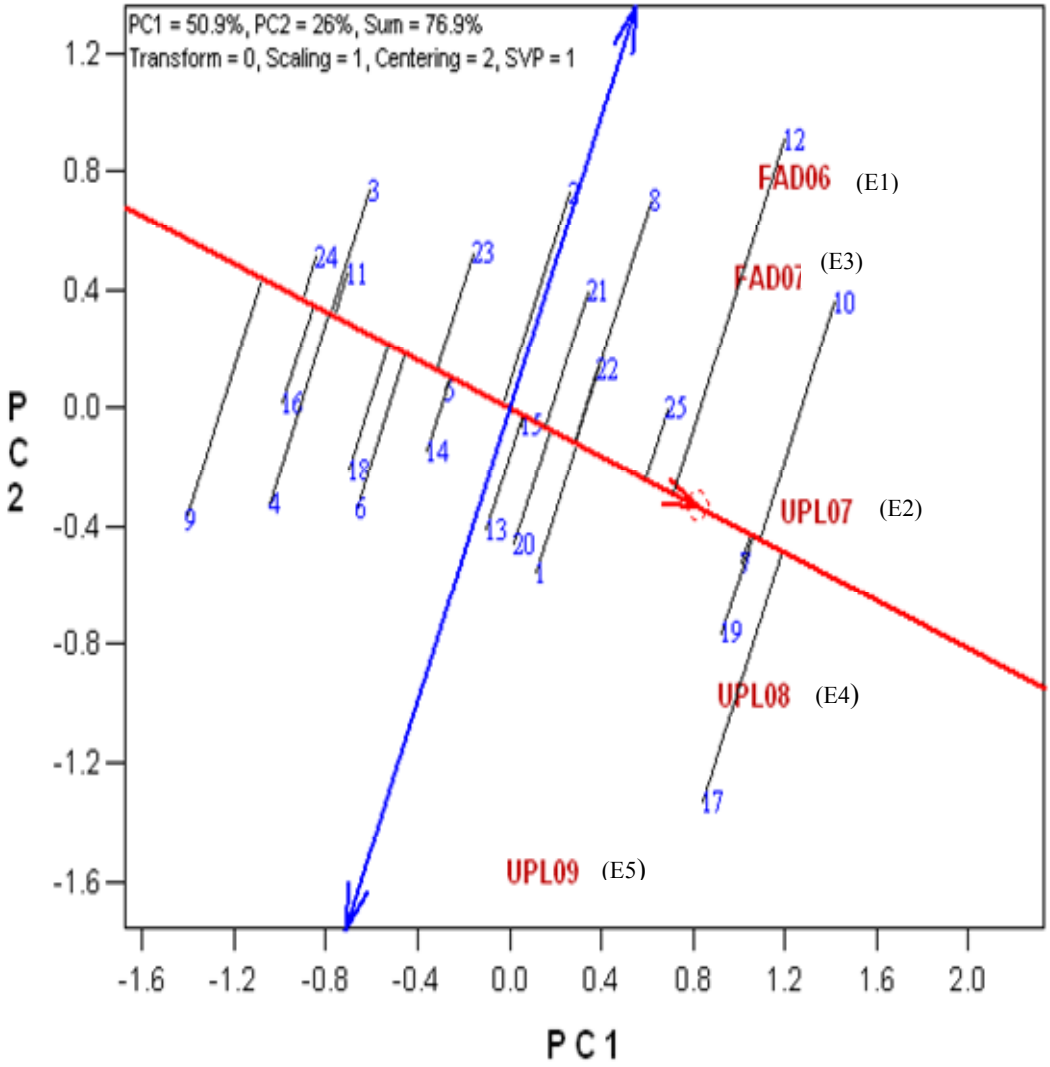

Figure 3. Biplot of stability and mean performance of seed yield of 25West African okra genotypes evaluated in five environments

FAD = Inland Valley; UPL= Upland
Inland valley '06=E1, Inland valley '07=E3, Upland '07=E3, Upland '08=E4 and Upland '09=E5

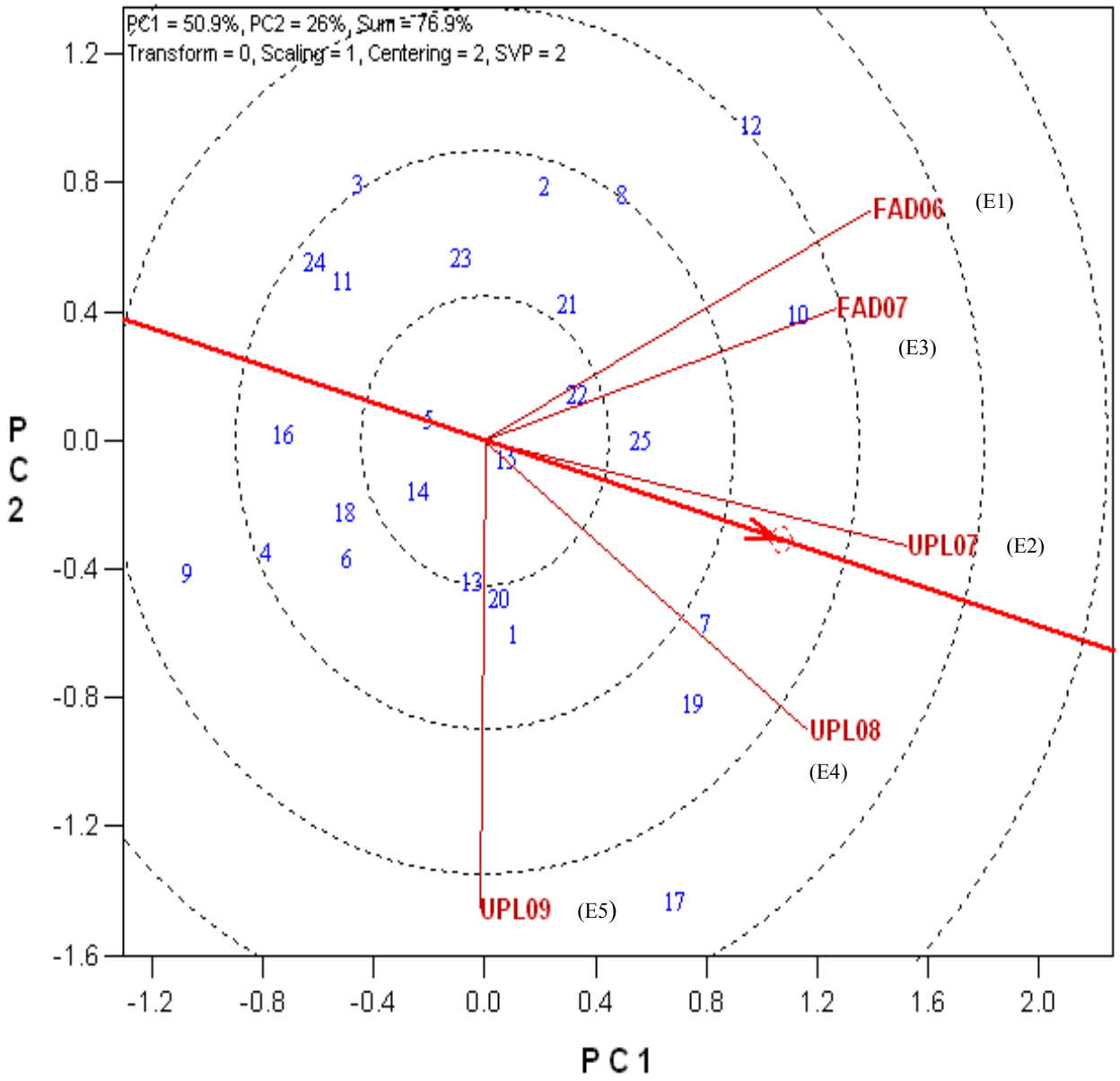

Figure 4. Biplot showing discriminativeness and representativeness of the environhments and the genotypes
FAD = Inland Valley; UPL= Upland