Journal of Applied Biosciences (2008), Vol. 8 (1): 288 – 303.
ISSN 1997 – 5902: www.biosciences.elewa.org

Genotype and genotype by environment (GGE) biplot analysis of fresh fruit bunch yield and yield components of oil palm (*Elaeis guineensis* Jacq.).

Okoye M N[1*], Okwuagwu C O[1*] And Uguru M I[2]
[1]Plant Breeding Division, Nigerian Institute for Oil Palm Research (Nifor) P.M.B 1030 300001, Benin City, Edo State, Nigeria; [2]Department of Crop Science, Faculty of Agriculture, University of Nigeria, Nsukka.

*Corresponding author e-mail: Maxokoye2001@yahoo.co.uk; Telephone: +234-8035522176

ABSTRACT

Objectives: The yield of fresh fruit bunches (FFB) in oil palm (*Elaeis guineensis* Jacq.) is a function of the number of bunches produced (BN) and the average weight of the bunch (SBW). The objectives of this study were to (i) assess genotype by environment (G X E) interaction and, (ii) determine stable oil palm genotypes using genotype and genotype by environment (GGE) biplot analysis.

Methodology and results: Fifteen oil palm genotypes were evaluated for four consecutive years (1999-2002) in a randomized complete block design with six replications. Both genotype (G) and G X E interaction were considered as important parameters because environment (E) accounts for about 80% of total yield variation in multiple environment trial (MET). The GGE methodology uses a biplot to show G and G X E that are important in genotype evaluation, which are also sources of variation in G X E interaction analysis of multiple environment yield trials. Genotype main effect and year were highly significant ($P<0.001$) for all the measured traits, G X E interaction also showed highly significant differences for SBW, BN and FFB yield. Analysis of variance indicated that varieties De10 and Det2 were not different in BN while Det6 and Det5 were superior to other genotypes with respect to SBW and FFB yield, respectively. Principal component analysis (PCA) of GGE biplot analysis revealed that genotypes Det2 and De10 had high yields for BN (4.4 and 4.5 bunches/palm/year), Det6 for SBW (14.5 kg/palm/year) and Det5 for FFB (51.3 kg/palm/year) in all the four years. Results from stability analysis using GGE biplot showed that Det5 was the most stable for BN and SBW, while Det9 and De15 were considered stable for FFB yield.

Conclusion and application of findings: Cultivation of the identified genotypes is likely to give stable performance across years. Genotypes Det6 and Det5 were selected as ideal genotypes for SBW and FFB yield based both on their mean performance and stability. These genotypes could be used in a breeding program to develop new stable cultivars with high yield potential. The study environments (E99, E00, E01 and E02) were most discriminating but not representative of the test environments; and are thus useful for culling genotypes that are below average performance. This study shows that GGE biplot analysis was effective in oil palm hybrids yield trials for selecting cultivars that are stable, high yielding and responsive.

Key words: oil palm genotypes, genotype by environment interaction, GGE biplot, fresh fruit bunch yield, principal component analysis.

Citation: Okoye MN, Okwuagwu CO. and Uguru MI, 2008. Genotype and genotype by environment (GGE) biplot analysis of fresh fruit bunch yield and yield components of oil palm (*Elaeis guineensis* Jacq.). *Journal of Applied Biosciences* 8 (1): 288 – 303.

INTRODUCTION

Fresh fruit bunches (FFB) are the major economic product of oil palm (*Elaeis guineensis* Jacq.). The FFB yield is determined by two sequentially developed traits, i.e. the number of bunches produced (BN) and the average weight of the bunch (SBW). Bunches produced and SBW are influenced by environmental and edaphic factors and the genetic background of planting material.

Oil palm is extremely responsive to environmental conditions and therefore yields show great variation (Rajanaidu *et al*., 2001). These variations are the main cause of the differential performance of genotypes in different environments, thus giving rise to the concept of genotype by environment (G x E) interaction (Lee *et al*., 1988; Ataga 1993). This interaction results from the relative ranking of the genotypes or changes in the magnitudes of differences between genotypes from one environment to another (Baker, 1988). Changes in ranking make it difficult for the plant breeder to decide which genotype should be selected. Busey (1983) suggested that lack of consistency in genotype performance across locations or years validates the need for broad based testing in different environments. The degree of inconsistency could help to predict the variability expected among different plantations.

The concept of stability has been defined in several ways and many biometrical methods have been developed to assess stability (Lin *et al*., 1986; Kang & Gauch, 1993; Kang, 1998). A number of stability studies have been carried out on different crops including oil palm (Obisesan & Fatunla, 1983; Ong *et al*., 1986; Lee *et al*., 1988; Hutomo & Pamin, 1992; Ataga, 1993; Rafii *et al*., 2001). These authors adopted the traditional analysis of G X E interaction to determine the consistency of a variety's yield across years or locations of testing when G X E interaction is a significant source of variation without providing an insight into the genotypes or environments that give rise to the interaction (adaptation).

A significant G X E interaction may be either (i) a non-crossover type when the rank order of genotypes across environments remains unchanged due to changes in the magnitude of genotype performance, or (ii) a crossover type when genotype ranks change across environments. According to Baker (1990), crossover interaction is more important than non-crossover interaction. When selecting genotypes across a number of environments, plant breeders look for a non-crossover type of G X E interaction for general adaptation (Matus-Cadiz *et al*., 2003), and a crossover type of G X E interaction for specific adaptation.

Yan (2000) proposed that when a significant G X E interaction is detected in yield trials, selection should be based on both G and G X E interaction rather than on one of them. The GGE is a contraction of G + G X E interaction. The GGE biplot methodology recently developed by Yan *et al*., (2000) is an addition to the tools available for analyzing multi-environment trials (MET). This methodology facilitates visual examination of the G X E interaction pattern of MET data and clearly shows which genotype won in which environments. This is useful for cultivar recommendation and identification of superior genotypes. The effectiveness of this method in analyzing MET data has been well documented (Yan *et al*., 2001; Yan & Hunt, 2002; Yan & Kang, 2003; Yan & Tinker, 2005, Bhan *et al*., 2005; Nwachukwu *et al*., 2006). This methodology uses a biplot to show the factors (G and G X E) that are important in genotype evaluation as well as sources of variation in G X E interaction (Yan *et al.,* 2000, 2001). The GGE biplot shows the first 2 principal components (PC1 and PC2) also referred to as primary and secondary effects, respectively, derived from subjecting environment-centered yield data (yield variation due to GGE) to singular value decomposition (Yan *et al.,* 2000).

These considerations have led to the initiation of this present study in oil palm to (i) assess BN, SBW and FFB yield performance, (ii) determine the nature of G X E interaction, and (iii) estimate the stability of 15 hybrids of Deli *dura* x *Tenera* across four years using GGE biplot analysis.

Materials and methods

A total of 14 oil palm crosses (Deli X *Tenera*) from the Nigerian Institute for Oil Palm Research (NIFOR), second cycle modified reciprocal recurrent selection (RRS) breeding program was used for this study. The breeding material involved 4 Deli *Dura* and 10 *Tenera* parents of different origins which included introductions from South East Asia, Republic of Benin, and Nigeria. Extension work seeds (EWS) was used as a control in the trial. The parents were selected based on their high general combining ability for the two FFB yield components with respect to their individual and family performance. The test cross population was a 5 X 5 Complete Factorial Mating Scheme with a total of 3 crossing groups. Each Deli was crossed to 3-4 *Tenera* parents as recommended by United Kingdom Technical Assistance Team (UKTAT) report (West, 1976). The pedigree of each progeny is given in Table 1.

The experiment was arranged in a randomized complete block design (RCBD) of 6 replicates with 12 palms per progeny plot. A spacing of 9 meters triangular was adopted and planting was done in 1987 at the Main Station of NIFOR, Benin City, Nigeria (6° 31' N and 5° 40' E).

Table 1: Pedigrees of 15 hybrids of Deli x Tenera oil palm progenies.

Progeny	Parentage	Genotype
1	(NIFOR ex Serdang x IRHO) x (Ogba ex Calabar)	Det1
2	(NIFOR ex Serdang) x (Umuabi)	Det2
3	(Ufuma x Aba) x (NIFOR ex Serdang x IRHO)	Det3
4	(Sabah ex Bantig) x (Serdang x Aba)	Det4
5	(NIFOR ex Serdang) x (Aba x Calabar)	Det5
6	(NIFOR ex Serdang x IRHO) x (Aba x Calabar	Det6
7	(Sabah ex Bantig) x (Ufuma)	Det7
8	(NIFOR ex Serdang x IRHO) x (Umuabi)	Det8
9	(Aba x Calabar) x (Sabah ex Bantig)	Det9
	(NIFOR ex Serdang) x (Calabar)	De10
11	(Igala) x (NIFOR ex Serdang)	De11
12	(Igala) x (Sabah ex Bantig)	De12
13	(Ulu Remis x Aba) x (NIFOR ex Serdang x IRHO)	De13
14	(Ulu Remis x Aba) x (NIFOR ex Serdang x IRHO)	De14
15	EWS (control)	De15

Clean weeding of palm circle was carried out to prevent competition from weeds and to facilitate loose fruit collection while strip weeding was performed to provide access for harvesting and other field operations. Fertilizer was applied at the rate of 0.5 kg N, 0.25 kg P, 0.75 kg K and 0.2 kg Mg per palm from compound NPKMg fertilizer (12:12:17:2) after transplanting in the field. Empty fruit bunches; pruned fronds and palm trunks and fronds were subsequently applied to the field as a substitute to the inorganic fertilizers.

Data were collected for four consecutive years (1999-2002) on BN, SBW, and FFB yield on progeny mean basis. Each palm was inspected every 10 days and any ripe fruit bunch present was harvested and weighed using a simple spring balance. The weight of bunch (es) and the number of bunches were recorded for each palm. The SBW was derived as the ratio of FFB yield to BN. The data were pooled for four years and statistical analyses were performed according to Obi (2002). The progeny means for BN, SBW and FFB yield by year were computed and analyzed using the GGE biplot software (Yan, 2001; Yan & Kang, 2003). The basic model for the GGE biplot is

$$Y_{ij} - \tilde{Y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where Y_{ij} is the average yield of genotype i in environment j; $\tilde{Y}_j$ is the average yield of all genotypes in environment j; λ_1 and λ_2 are singular values for PC1 and PC2, respectively; ξ_{i1} and ξ_{j2} are the PC1 and PC2 scores, respectively, for genotype i; η_{j1} and η_{j2} are the PC1 and PC2 scores, respectively, for environment j; ε_{ij} is the residual of the model associated with the genotype I in environment j. To display PC1 and PC2 in a biplot, the equation is rewritten as

$$Y_{ij} - \tilde{Y}_j = \xi_{i1}^* \eta_{j1}^* + \xi_{i2}^* \eta_{j2}^* + \varepsilon_{ij}$$

where $\xi_{j1}^* = \lambda_n^{1/2} \xi_{in}$ and $\eta_{jn}^* = \lambda_n^{1/2} \eta_{jn}$, with n =1, 2. This scaling method has the advantage that PC1 and PC2 have the same unit.

Evaluation of environments was also carried out using the GGE biplot analysis. The four consecutive years 1999, 2000, 2001 and 2002 are designated as E99, E00, E01 and E02, respectively.

GGE biplot methodology, which is composed of 2 concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.,* 2000), was used to visually analyze the FFB yield data. Genotypic scaling was used in visualizing for genotypic comparison, with environment-focused scaling for environmental comparison according to Yan (2002). In addition, symmetric scaling was adopted in visualizing the which-won-where pattern of the MET data. Five different views of data were generated through the GGE biplot analyses:

1. A data based GGE biplot showing the model and the percentages of GGE explained by the two axis (PC1 and PC2).
2. The principle of genotype evaluation was based on the mean performance and stability of the genotype. The lines parallel to the average tester co-ordinate (ATC) y-axis help rank the genotypes in terms of average yield. The stability of the cultivars is measured by their projection to the ATC y-axis. The greater the absolute length of the projection of a genotype, the less the stability.
3. A comparison of all genotypes with the "ideal" genotype; the closer a genotype is located relative to the "ideal" genotype, the more desirable it is in terms of both mean performance and stability.
4. The "which won where" pattern shows the best genotype(s) for each environment. The vertex genotype in each sector is the winner (i.e. has the largest value) in all environments falling within that sector.
5. The principle of test environment evaluation was based on the discriminating ability and representativeness of the environment. The vector length of an environment represents its discriminating ability: the longer the vector, the more discriminating the environment, while the projection of the vector length of an environment onto the ATC y-axis is a measure of its representativeness: the longer the projection, the less representative the environment.

RESULTS

The analyses of variance for BN, SBW and FFB yield showed that genotype main effect, year, genotype by year effects were highly significant (Table 2). The coefficient of variation ranged from 10.2 to 20.6% for the three bunch yield traits.

Table 2: Mean squares for bunch number, average weight of bunches and fresh fruit bunch yield of oil palm progenies grown at Benin for four consecutive years.

Sources of variation	d.f.	MEAN Bunch number	SQUARES Single bunch weight	Fresh fruit bunch yield
Replicate	5	3.2***	13.8***	633.3***
Genotype	14	7.6***	59.8***	920.1***
Gen. x Rep.	70	0.7***	3.5***	122.8***
Year	3	106.3***	46.8***	13445.8***
Rep. x Year	15	5.0***	4.3***	709.8***
Gen. x Year	42	1.2***	2.1**	148.1***
Rep. x Gen. x Year	210	0.4	1.4	66.8
C.V. (%)		18.7	10.2	20.6

,* Significant at P= 1% and 0.1% respectively; d.f. = degrees of freedom

Evaluation of genotypes based on GGE biplot analysis: Genotypes Det2 and Det5 had the highest BN in environments E99 (1999) and E01 (2001), respectively (Table 3). Genotypes De12 and De10 showed the highest FFB yield in environments E99 and E02 (2002) respectively (Table 5), while genotype Det6 exhibited the highest SBW yield in environments E99, E00 and E02 (Table 4). Although De10 had the highest BN yield in environments E00 and E02, Det5 had the highest FFB yield in environments E00 and E01 (Tables 3 & 5).Upon examination of these progeny means using GGE biplot analyses, the first two principal components (PC1 andPC2) explained 89.8, 98.1, and 87.4% of the variations for BN, SBW, and FFB yield, respectively (Figures.1a, b and c).

The average yield of the 15 genotypes was approximated by the projection of their markers to the ATC x-axis. Genotype Det2 had the highest average BN production, and Det1 had the lowest (Fig.2a). The lines parallel to the ATC y-axis rank the cultivars in terms of average yield. A double arrowed line divides the biplot into two thus separating genotypes with below-average means from those with above-average means, showing that genotypes Det1, De13, Det7, Det6, Det4 and Det8 performed below the average (Fig.2a). The biplot revealed Det8 as the least stable genotype, while Det5, De11, and De13 were the most stable (Fig.2a). With respect to SBW, Det6 had the highest average yield while genotypes De11, De15, Det4, De13, Det8, Det2, De10 and De14 performed below the average (Fig.2b). Genotypes Det5, Det1, Det7, Det3, De10, and Det8 were very stable across the environments. The highest mean FFB yield performance was by genotype Det5 while Det9, De15, and De13 were the most stable for FFB yield (Fig.2c).

The results of comparison of the genotypes with an “ideal” genotype based on mean BN, SBW, and FFB yield performance and stability across environments showed that genotypes Det2 and De10 were close to the center of the concentric circles where the ideal genotype should be located. The smaller the distance from a genotype to such a virtual genotype, the more ideal the genotype is (Fig.3a). However, genotypes Det5, De11 and De15 appear to be similar although other genotypes (Det8, De14, Det6, Det7, De13 and

Det1) were apparently inferior. Genotypes Det6 and Det5 were the most ideal for SBW and FFB yield, respectively (Figs. 3b and 3c).

Table 3: Mean number of bunches produced by 15 oil palm genotypes between 1999 and 2002.

Genotype	1999 (E99)	2000 (E00)	2001 (E01)	2002 (E02)	Mean
Det1	2.70	2.03	3.12	1.90	2.45
Det2	5.97	2.65	5.57	3.57	4.44
Det3	4.98	2.47	4.43	2.58	3.62
Det4	3.60	2.35	4.87	2.37	3.30
Det5	4.43	2.62	5.67	2.58	3.83
Det6	3.68	2.27	4.53	2.32	3.20
Det7	3.98	2.27	3.83	2.53	3.15
Det8	3.07	2.40	4.53	3.50	3.38
Det9	4.43	2.90	4.37	2.90	3.65
De10	4.52	3.37	5.65	4.27	4.45
De11	4.53	2.35	4.93	2.97	3.70
De12	5.03	2.69	4.44	2.45	3.65
De13	3.08	2.05	3.62	1.68	2.61
De14	3.80	2.57	5.33	2.65	3.59
De15	5.13	2.92	4.86	2.72	3.91
LSD (5%)	0.83	0.72	1.05	0.66	0.48

LSD (5%) = 0.48.

Table 4: Means of single bunch weight (Kg) of 15 oil palm genotypes between 1999 and 2002.

Genotype	1999 (E99)	2000 (E00)	2001 (E01)	2002 (E02)	Mean
Det1	13.65	11.97	11.93	14.68	13.06
Det2	10.37	10.167	9.02	9.92	9.87
Det3	13.48	10.95	11.48	13.62	12.38
Det4	11.00	10.20	9.65	10.75	10.40
Det5	13.78	12.73	12.95	13.32	13.20
Det6	15.97	14.32	12.77	14.80	14.46
Det7	14.00	12.03	12.95	13.70	13.17
Det8	10.28	9.55	9.47	10.38	9.92
Det9	12.58	11.37	12.15	12.82	12.23
De10	10.07	9.00	9.37	9.72	9.54
De11	11.90	9.92	10.97	11.87	11.16
De12	14.38	11.95	11.27	12.47	12.52
De13	11.97	8.93	9.75	10.35	10.25
De14	9.92	8.72	9.27	10.10	9.50
De15	10.45	9.77	11.49	11.85	10.89
LSD (5%)	1.44	1.93	1.27	1.65	0.84

The polygon views of the bunch yield traits are shown in Figs. 4a-c. The perpendicular line divides the biplot into several sectors, and the environments inevitably fall into the sectors. There are six sectors in Fig.4a, with genotypes De10, Det2, Det12, De13, Det1, and Det8 as the corner or vertex genotypes. Environments E02, E01, and E00 fell in the sector in which De10 was the vertex genotype, suggesting that De10 is suitable for the 3 environments. The other environment E99 fell in the sector in which Det2 was the vertex genotype. No environment fell into the sector with Det12, De13, Det1, and Det8 as the vertices, indicating that none of these genotypes are suitable for the test environments. For SBW, all the environments fell in the sector with Det6 and Det12 as the vertex genotypes (Fig.4b), while Det5 had the largest value in environments E01, E00, and E02. E99 fell in the sector with Det12 as the vertex genotype (Fig.4c).

Table 5: Mean fresh fruit bunch (FFB) yield (Kg/palm/year) of 14 oil palm genotypes measured between 1999 and 2002.

Genotype	1999 (E99)	2000 (E00)	2001 (E01)	2002 (E02)	Mean
Det1	34.62	22.73	38.03	26.47	30.46
Det2	60.18	27.18	49.70	36.38	43.36
Det3	61.68	25.40	50.23	35.57	43.22
Det4	37.90	22.18	45.85	24.93	32.72
Det5	61.73	33.02	74.13	36.35	51.31
Det6	52.72	31.13	58.20	32.98	43.76
Det7	50.88	27.05	48.63	33.33	39.98
Det8	48.88	22.43	44.37	36.93	38.15
Det9	53.18	32.10	52.82	36.97	43.77
De10	44.78	31.22	53.07	42.93	43.00
De11	51.73	22.00	50.32	34.53	39.65
De12	62.00	31.28	48.68	30.42	43.10
De13	36.35	19.65	35.85	17.15	27.25
De14	38.93	20.85	48.23	28.53	34.14
De15	53.40	28.83	53.93	28.25	41.10
LSD (5%)	10.61	8.30	12.70	9.28	5.85

Evaluation of environments based on GGE biplot analysis: Figures 5 a, b, and c (vector views) represents vectors of years for BN, SBW, and FFB yield, respectively. Fig. 5a shows that the year 1999 was the most discriminating environment (longest vector) for genotypes. The years 2000 and 2001 were very similar as shown by the very small angle between their vectors since the cosine of the angle between vectors of two years approximate correlation coefficient between them. Year 2000 was the least discriminating but highly representative (near zero projection on the y-axis) of all years. Three years (2000, 2001, and 2002) were very similar but year 2001 was better than the other two because of its longer vector. Figure 5b revealed that all the environments (years) were discriminating and not representative of the average environment for SBW. For FFB yield, year 2000 was least discriminating while year 2002 was most representative of all years. Years 1999 and 2001 were highly discriminating but not representative of the years (Fig.5c). Years 2000 and 2002 were very similar because of the small angle between their vectors.

DISCUSSION

The significant G X E interaction showed the amount of variability that existed among environments and the presence of genetic variability among the three bunch yield traits. The large (>75%) variation explained by the GGE biplots is an indication that GGE pattern can be successfully utilized in developing bunch yield selection strategies specific to each environment. However, this variation should not be confused with the total yield variation, which includes the environment (E) as well as the genotype (G) and G X E (Yan, 2001). Evidence of significant GE interaction was further emphasized by the large (>50%)

PC1 score. The patterns observed in a GGE biplot have been referred to as GGE pattern (Yan & Tinker, 2005) consisting of the genotypic, environmental and the genotype and environmental patterns.

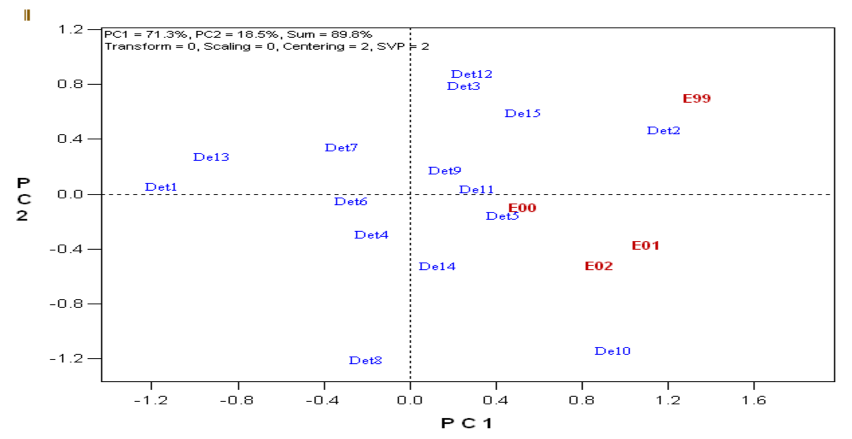
Simultaneous selection for yield and stability of performance is most desirable in plant breeding programmes especially when G X E interaction is significant (Yan, 1999). In our study, the high yielding BN genotypes were not the best for SBW.

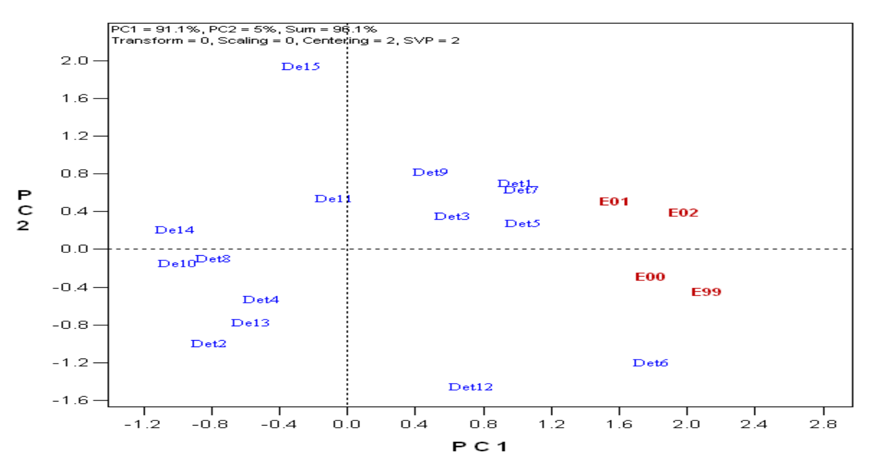
This occurrence strengthens the strong negative relationship between the two traits as was reported by other researchers (Okwuagwu & Tai, 1995; Kushairi *et al*., 1999; Okoye *et al*., 2007). This trend was however different in FFB yield. The best yielding FFB genotypes was as a result of the multiplicative relationship between the two traits (BN and SBW). This relationship shows the effectiveness of selecting parents whose yield components will complement each other in their offspring to produce higher FFB yield (Okwuagwu *et al*., 2006).

Of all the average genotypes, only two genotypes (Det5 and De11) were considered highly stable for BN. With respect to SBW, Det5, Det1, Det7, and De15 were most stable while Det9 and De15 were identified as stable FFB yield genotypes. Farmers would desire highly stable genotypes because they are more reliable with consistent performance (Kang *et al*., 1991). The highest yielding genotypes (Det2 for BN, Det6 for SBW, and Det5 for FFB yield) were not stable across the environments. This result supports the earlier report of Rafii *et al*., (2001) that some of the average genotypes may not necessarily be highly stable across the environments. An ideal genotype has the highest mean yield and identical yield in all environments (Yan & Kang, 2003). Based on this thesis, Det6 and Det5 were considered as ideal genotypes for SBW and FFB yield, respectively. This contradicts the earlier reports (Obisesan & Fatunla, 1983; Ataga, 1993; Rafii *et al*., 2001) on the absence of suitable genotypes among oil palm genotypes. The suitable genotypes identified in this study would make good sources for developing high yielding stable oil palm cultivars. For BN, Det2 and De10 were the closest genotypes to the ideal BN genotype.

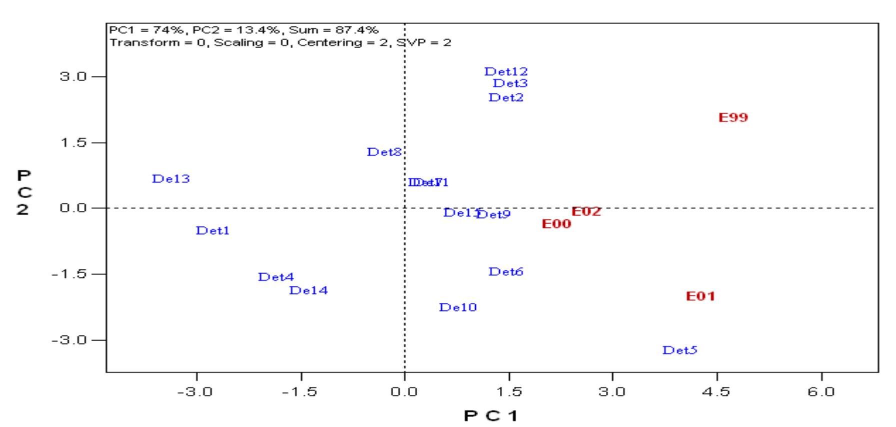
A comparison of the four years with the ideal environment revealed the differences in environments with respect to their discriminating ability and representativeness. An ideal environment is one that is most discriminating of genotypes and is most representative of all environments (Yan & Kang, 2003). Highly discriminating but less representative environments observed in this study are of secondary importance to the plant breeder for culling genotypes that are below average performance. The most sought environment is one that is highly discriminating and representative for selecting genotypes with average performance. This kind of ideal environment was not depicted in the present study although E00 and E02 were very close to the ideal environment for SBW.

The presence of crossover and non-crossover types of G X E interaction is very common in MET data. The change in rank order of genotypes Det2 and Det5 (BN) and De12 and De10 (FFB yield) across the test environments revealed that there exists possible crossover G X E interaction. This inconsistency in the rank order of these high yielding genotypes across the environments complicates the identification and selection of superior genotypes. Differences in environmental factors particularly rainfall intensity and soil fertility, genetic differences and G X E interaction could be implicated for the lack of consistency of performance across environments (Lee *et al*., 1987; Ataga, 1993; Rafii *et al*., 2001). Busey (1983) suggested that a lack of consistency in genotype performance across locations or years validates the need for broad based testing in different environments. Those genotypes at the vertices with no environment in their sector suggest that they were the poorest in some or all of the environments because the vertex genotype in each sector is the winner in all environments falling within that sector.



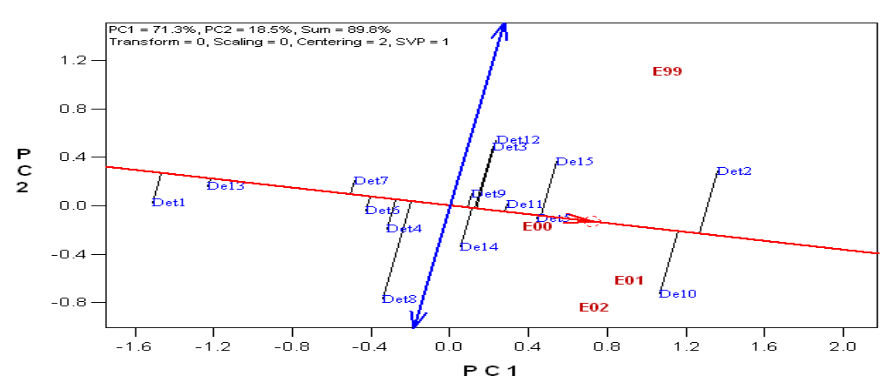


(B) GGE biplot for SBW.

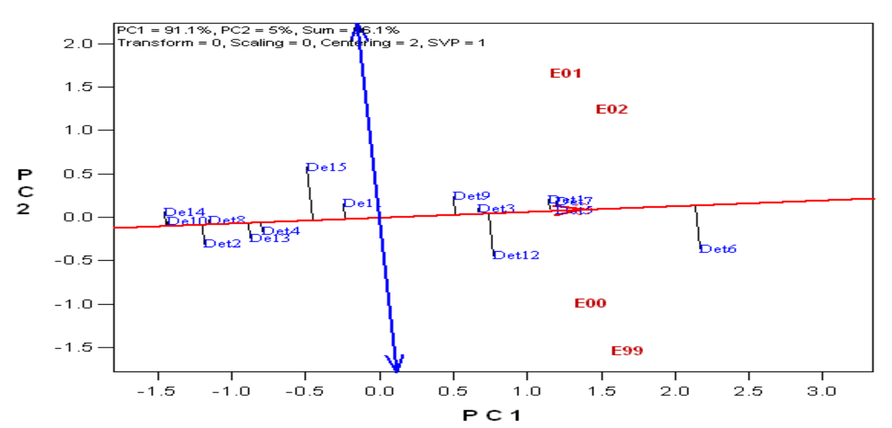


(C) GGE biplot for FFB.

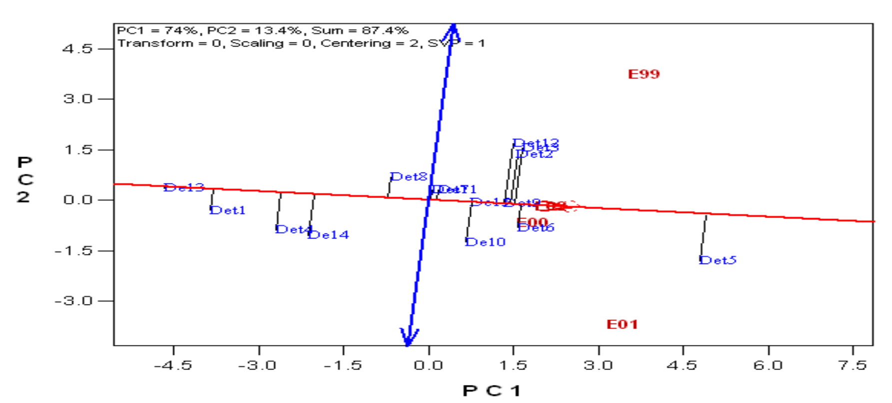
Figure 1: GGE biplot analyses of bunch yield traits of Deli x *Tenera* genotypes.



(A) Mean BN performance and stability of the genotypes.

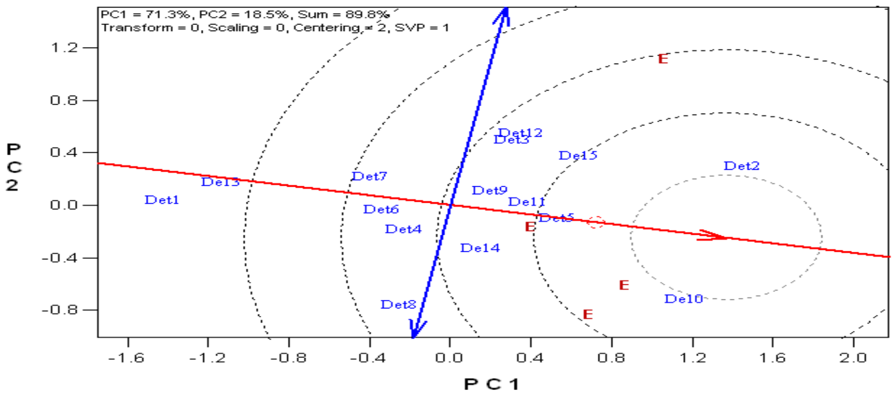


(B) Mean SBW performance and stability of genotypes.

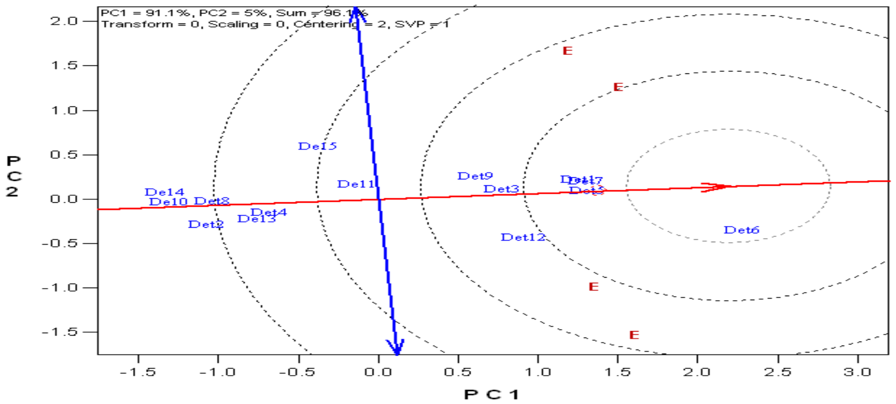


(C) Mean FFB yield performance of genotypes.

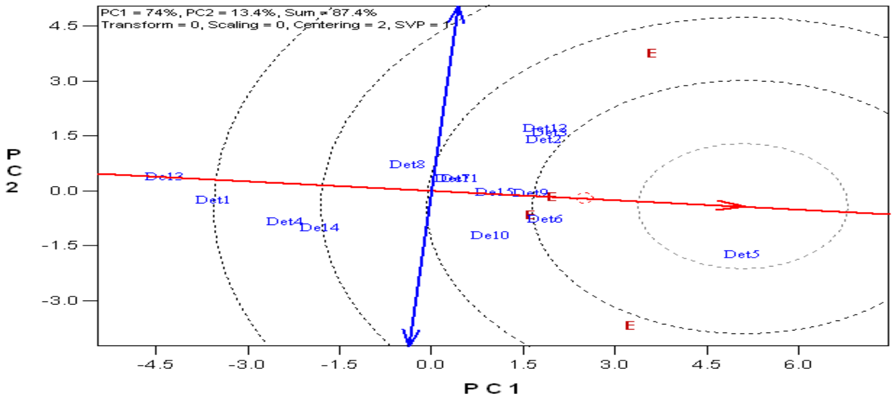
Figure 2: ATC axis views of the GGE biplot for bunch yield traits.



(A) Ranking genotypes based on both mean BN performance and stability.

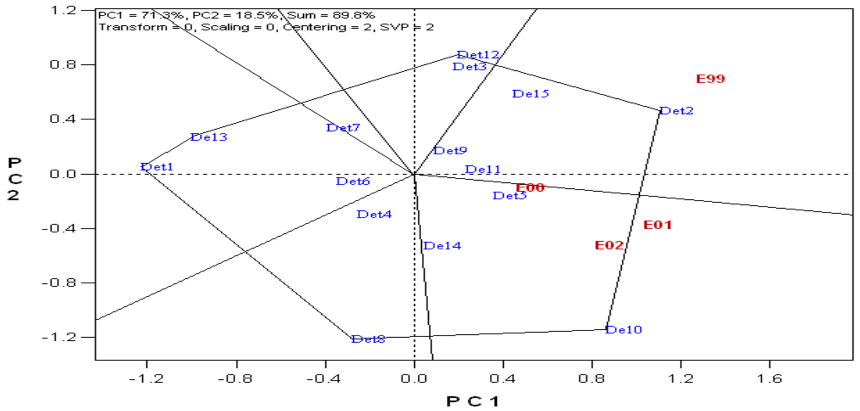


(B) Ranking genotype based on both mean SBW performance and stability.

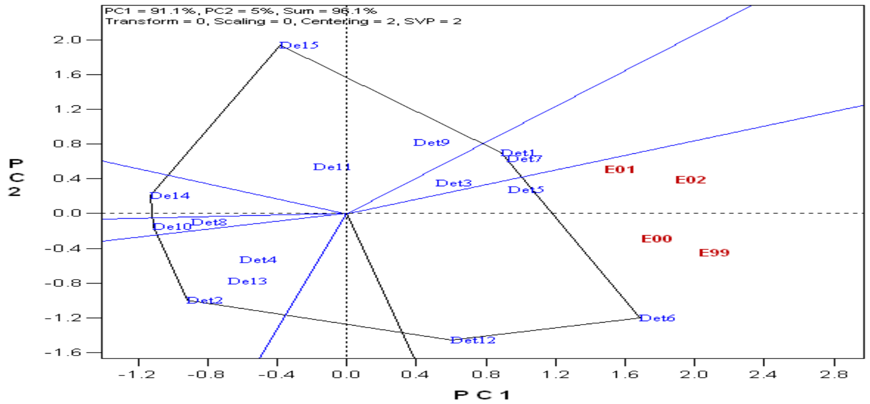


(C) Ranking genotypes based on both mean FFB yield performancee and stability.

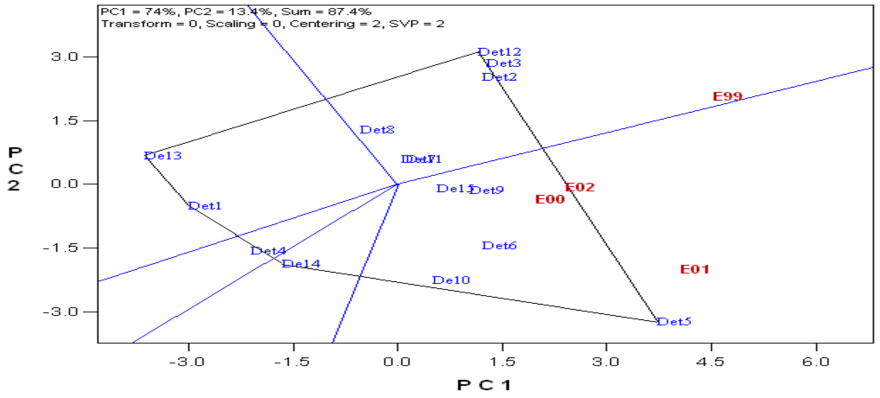
Figure 3: Comparison of oil palm Deli x *Tenera* genotypes against the 'ideal' genotype for bunch yield traits



(A) Winning BN genotype for each environment

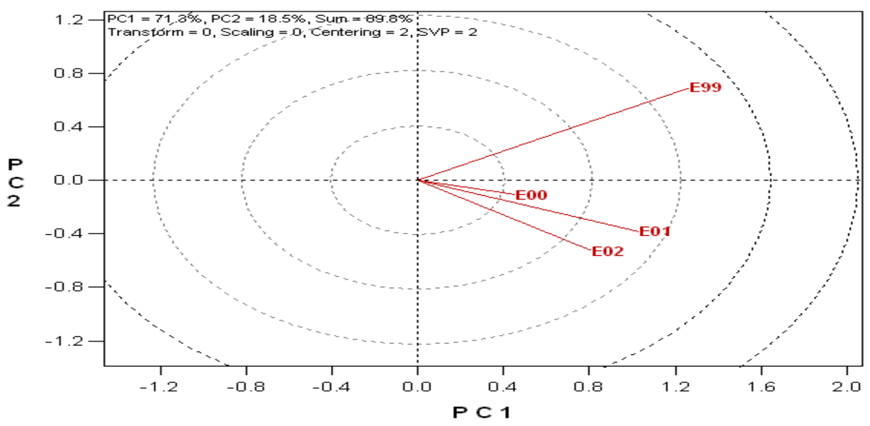


(B) Winning SBW genotype for each environment.

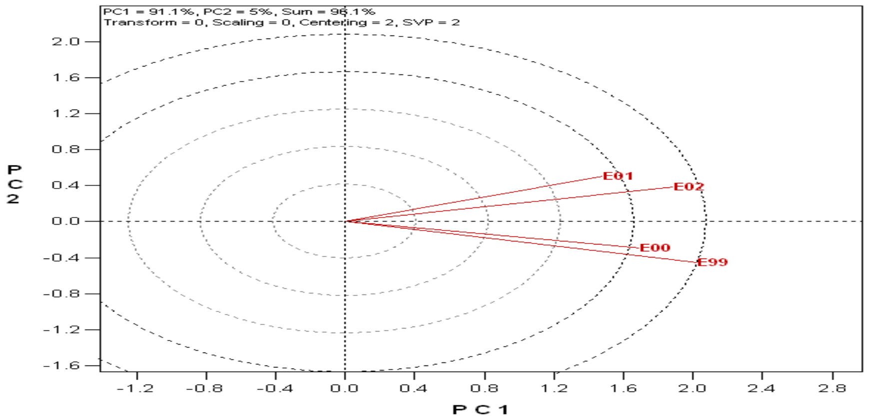


(C) Winning FFB genotype for each environment.

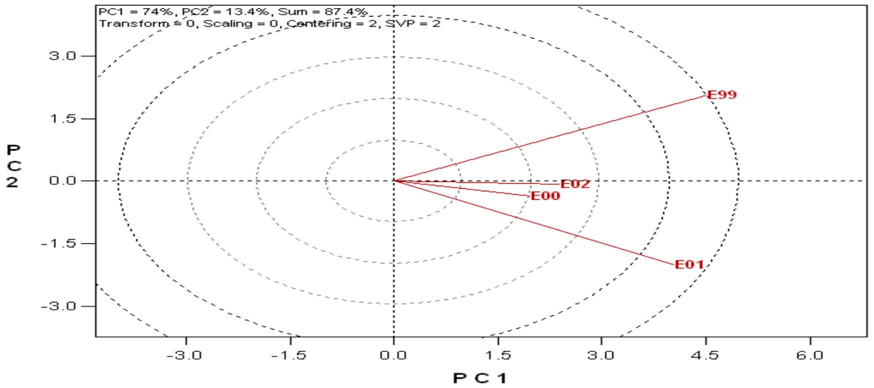
Figure 4: Polygon view of GGE biplot indicating performance of Deli x *Tenera* genotypes across environments.



(A) Relationship among BN environments.



(B) Relationship among SBW environments.



(C) Relationship among FFB yield environments.

Figure 5: Vector views of GGE biplot, showing relationships among test environments (E99-E00) for the bunch yield traits.

The G X E interactions become important when the rank of genotypes changes in different environments (Baker, 1988). The polygon view of the GGE biplot highlighted the presence of crossover interactions involving the most responsive genotypes. Environments within the same sector share the same winning genotype and environments in different sectors share different winning genotypes (Yan, 1999; Yan *et al*., 2000, 2001; Yan & Rajcan, 2002). The "which-won-where" pattern facilitates the identification of superior genotypes and test environments that permit detection of such genotype; a necessary condition for specific adaptation (Baker, 1988; Yan & Rajcan, 2002). Therefore, selection of superior genotypes for each environment ensures the effective exploitation of both G and G X E interaction. Breeding for specific adaptation offers a sustainable solution on how to improve agricultural production in marginal areas. The differential change of mean yield but not ranking of genotypes De10, Det6, and Det5 for BN, SBW, and FFB yield respectively showed that G X E interaction may also have a non-crossover nature.

The results obtained in this study demonstrated the efficiency of GGE biplot technique for selecting cultivars that are stable, high yielding, and responsive. Both the standard analysis of variance and the GGE biplot analysis identified genotypes De10, Det6, and Det5 as superior for BN, SBW, and FFB yield, respectively. The most stable genotypes were Det5, De11, and De13 for BN; Det5, Det7, Det1, Det3, Det8, and De10 for SBW, and Det9, De15 and De13 for FFB yield. The use of these genotypes by farmers would result in stable performance over the years. Genotypes Det6 and Det5 were identified as suitable genotypes for SBW and FFB yield, respectively. These genotypes could also be used in breeding programmes to develop new cultivars with consistent performance. The significant genotype by year interactions in FFB yield and its components implies that more environments may be needed for reliable genotype evaluation.

ACKNOWLEDGEMENTS: The authors would like to thank Dr D. A. Okiy, the Executive Director of Nigerian Institute for Oil Palm Research (NIFOR) for support and Mr. Sam Ofodile of the biometric unit of IITA Ibadan for provision of the GGE biplot software and assistance with statistical analysis.

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