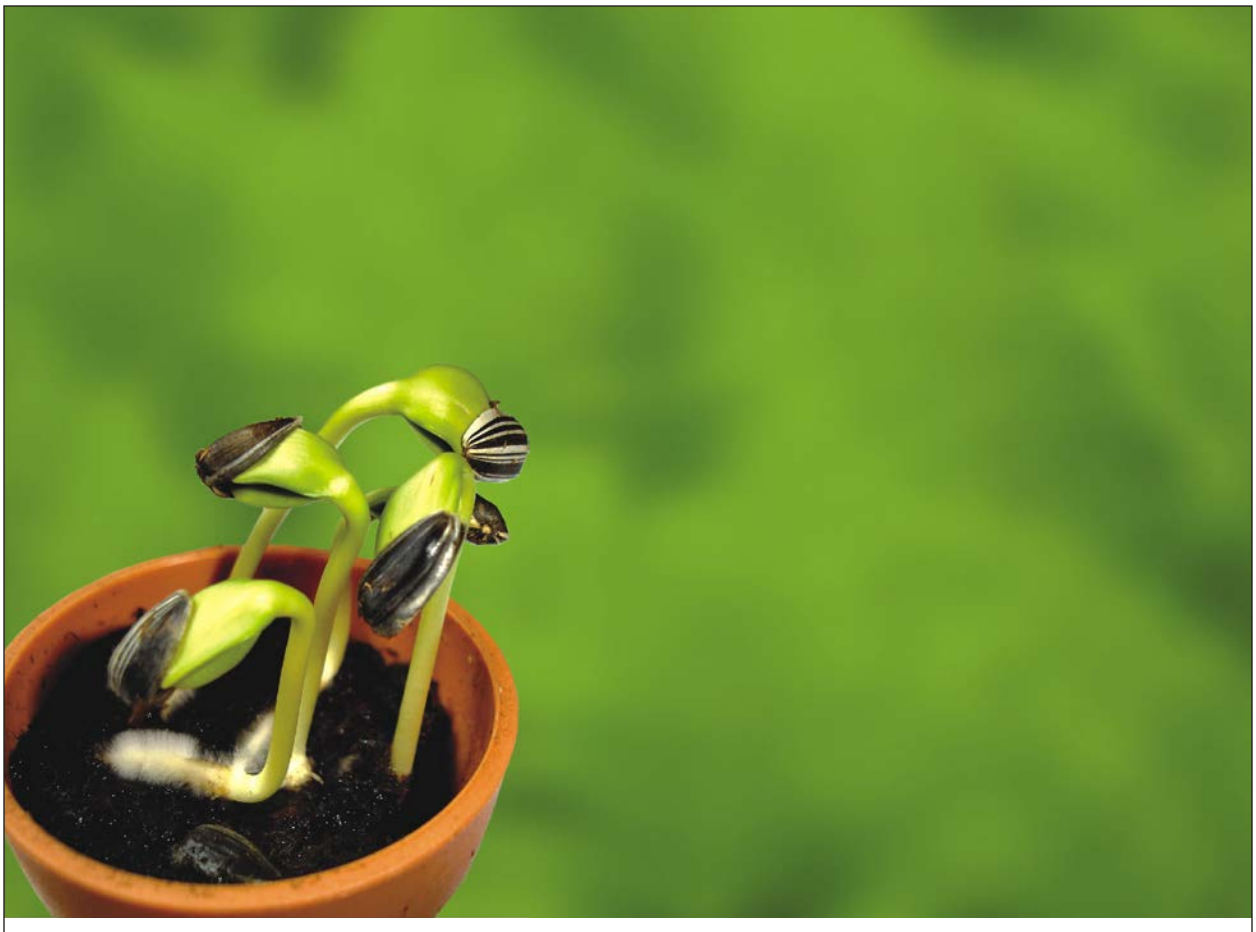

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Modelling Fresh Fruit Bunch Yield Stability in Oil Palm using Different Stability Statistics

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ABSTRACT

Several biometrical methods available for the analysis of g×e interaction and yield stability, often fail to provide an accurate picture of complete response pattern of the genotypes because the stability indices are usually univariate. The objective of this study was to examine the various statistical methods for stability analysis of bunch yield in order to determine their congruence in identification of stable oil palm genotype. Fifteen *dura*×*tenera* oil palm genotypes were evaluated for genotype by environment interaction (g×e) and yield stability across four environments. The five statistical methods examined are Eberhart and Russell joint linear regression (ER), Shukla's Stability index (SH), Francis and Kanennberg genotype-grouping technique (FK), Lin and Binn's cultivar superiority values (LB) and Yan's Genotype and Genotype by Environment interaction model (GGE). Significant crossover g×e interaction was observed, suggesting specific adaptation. Spearman's rank correlation coefficient between the stability parameters and environments indicated a weak relationship. However, SH was significantly correlated with ER and LB. The level of convergence between any two methods ranged from 25 to 67% while that among three, four or the five methods were between 29 to 57%. Two genotypes, DT7 and DT11 were identified as high yielding and stable by all methods. These genotypes would be reliable for future breeding programme to develop high yielding planting materials with stable performance. Furthermore, farmers will be assured of the yield from season to season. In most cases, genotypes selected by GGE were also classified as stable by the other four methods. Thus, simultaneous use of stability statistics would protect the breeder from making wrong selections.

Key words: Genotype x environment interaction, stability statistics, concordance, Spearman's correlation coefficient, climate change

INTRODUCTION

The inherent global climatic change has resulted in significant annual variation in yield performance of most agricultural species including oil palm. Consequently, genotype by environment interaction (g×e) is an important issue facing plant breeders and agronomist. Breeders therefore search for consistently high yielding and profitable cultivars for sustainable production in target areas while adapting to changing climatic conditions (Kevin *et al*., 2000; Okoye, 2010).

Different concepts and definition of stability have been described over the years and several biometric methods have been proposed for analysis of g×e interaction and stability of crops grown over a range of environments (Truberg and Huhn, 2000; Crossa, 1990; Hohls, 1995; Kang and Gauch, 1996). The most widely adopted method is the regression coefficient model, for example Finlay and Wilkinson (1963) and Eberhart and Russell (1966) proposed the linear regression coefficient and the deviations from linear regression as a stability parameter for each genotype. Other conventional models such as Shukla (1972) stability variance model considered the contribution of each genotype to g×e interaction and concluded that the variance of a genotype across environments is the stability measure (Adugna and Labuschagne, 2003; Martin, 2004). In addition the cultivar performance measure of Lin and Binns (1988) assumes the genotype with the lowest cultivar performance value as the most stable. The cluster analysis of Francis and Kannenberg (1978) is based on phenotypic coefficients of variation of each genotype as a stability measure. According to Hohls (1995), these stability indices are univariate and as a result, lack the ability to provide accurate picture of the complete response pattern of a genotype because genotype's response to varying environments is multivariate. More recently, the principal component analysis model of Yan (1999, 2001) provided a GGE- biplot methodology that permits visual examination of the g×e interaction pattern of Multiple Environment Yield Trial (MEYT) data. This model is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al*., 2000). The GGE biplot has been shown to effectively identify the g×e interaction pattern and clearly show which genotype won in which environment, thus facilitating mega environment identification (Yan *et al*., 2000; Yan and Hunt, 2002; Yan and Kang, 2003; Okoye, 2008; Okoye *et al*., 2008, 2011).

Stability analysis has been applied to multi-environment evaluation of oil palm using predominantly the linear regression models and the cluster analysis methods (Ataga, 1993; Rafii *et al*., 2001). According to DeLacy *et al*. (1996), the choice of a particular method for measuring genotype stability should consider the breeding and agronomic implication of the method.

There is a general consensus among plant breeders on the importance of g×e interaction in the characterization of cultivars adaptation or stability and determination of appropriate breeding programme. However, the lack of agreement on the definition of "stability", the best method to quantify and improve yield stability has to be reviewed especially with the ongoing climate change scenario. It is therefore critical to assess and determine which method best meets producers, processors and consumers need for stability assessment of new varieties.

It is therefore, the objective of this study to examine the various statistical methods for stability analysis of bunch yield in order to determine their congruence in identification of stable oil palm genotype.

MATERIALS AND METHODS

Fifteen oil palm genotypes from the Nigerian Institute for Oil Palm Research (NIFOR) Main Breeding Programme were evaluated over a period of four years (1999-2002) in a tropical rainforest zone of Benin City, Edo State, Nigeria (6° 31'N and 5° 40'E). The experimental layout was a Randomized Complete Block Design (RCBD) with six replications. A spacing of 9 meters triangular was adopted while fertilizer application and other cultural practices were as recommended by NIFOR. Fresh Fruit Bunch (FFB) yield (kg palm^{-1}) was recorded *in-situ* in the field for four years for each progeny.

Progeny means were subjected to pooled analysis of variance. Genotypes were assumed to be fixed while year and replicate effects were random. Stability analysis was performed using the joint linear regression method of (Eberhart and Russell, 1966) (ER), the stability index of Shukla (1972) (SH), the Coefficient of Variation (CV) of Francis and Kannenberg (1978) (FK), the cultivar performance measure (P_i) of Lin and Binns (1988) (LB) and the relative adaptation technique in the GGE biplot of Yan (1999) and Yan *et al.* (2000) (GGE). The GGE biplot was facilitated by the GGE software (Yan, 2001).

Stability of genotypes were defined as regression coefficient of $b_i = 1$ and deviation from the regression as small as possible ($S^2d_i = 0$) for ER method, high mean yield and consistent low CV for FK method, low stability variance for SH method, low cultivar performance for LB method and a lower absolute value for GGE method.

To statistically compare the above stability procedures, Spearman's coefficient of rank correlation (r_s) was determined (Steel and Torrie, 1980). All the genotypes were ranked according to the assigned values for each procedure's analyses and definitions. Concordance analysis was carried out to determine the proportion of genotypes that were jointly selected as stable by two or more analytical methods. The concordance coefficient (CC_{ij}) for any two methods was calculated as follows:

$$CC_{ij} = 100 \times N_{ij} / (N_{ii} + N_{ij})$$

Where:
N_{ii} = No. of genotypes selected by the ith but not the jth method
N_{jj} = No. of genotypes selected by the jth but not the ith metho,
N_{ij} = No. of genotypes selected simultaneously by the ith and jth methods

A concordance coefficient approaching zero would indicate complete divergence of analytical methods while a coefficient near unity would suggest a high level of convergence of the methods.

RESULTS AND DISCUSSION

The analysis of variance table for the 15 oil palm genotypes showed significant differences among genotypes, environment and genotype x environment interaction (Table 1). The significant g×e suggests wide adaptation of the genotypes. The large proportion of environmental variance indicates the enormous influence of environment on yield performance of oil palm hybrids in Nigeria. This result is in tandem with the earlier reports of Asfaw *et al.* (2008) in small red beans and Jalata (2011) in barely.

According to ER method, it is specifically the deviation from the regression (S^2di) which is used as a measure of genotype's stability across environments. The most stable genotypes with the lowest S^2d_i values were DT 9, DT 7, DT 1, DT 11, DT 6, DT 13 and DT 15 (Table 2). The most unstable genotypes with the highest S^2d_i values were DT 12, DT 5, DT 3, DT 10 and DT 8.

If the mean bunch yield, regression coefficient value and the deviation from the regression (S^2d_i) are considered together, then the most widely adapted would be DT 7 and DT 9 because their regression coefficients were close to unity ($b_i = 1$), $S^2d_i = 0$ and high bunch yield (Fig. 1). The genotype, DT 10 had high bunch yield and the regression coefficient was nearly equal to one. It was however considered unstable because $S^2d_i > 1$ (Table 2, Fig. 1). These present findings were in agreement with earlier investigations of Sreedhar *et al.* (2011) on yield stability in hybrid rice.

Table 1: Analysis of variance of fresh fruit bunch yield of 15 oil palm genotypes grown in 4 environments

Source of variation	df	SS	MS	F	p-value
Replicate	5	3106.765	621.353	9.4780	<0.0000
Genotype	14	12970.395	926.457	13.7717	<0.0000
Gen×Rep.	70	8625.912	123.227	1.8382	<0.0005
Env	3	40164.102	13388.034	201.2439	<0.0000
Rep.×Env	15	10631.675	708.778	10.6238	<0.0000
Gen×Env	42	6294.000	149.857	2.2160	<0.0000
Rep.×Gen x Env	210	14022.678	66.775	0.0000	

Table 2: Fresh Fruit Bunch (FFB) yield and associated stability parameters of 15 oil palm genotypes grown in four environments

Genotypes	FFB	ER	FK	SH	LB	GGE
DT1	30.5	-10.689	22.0806	32.9	53.354	-0.629
DT2	43.4	2.278	17.3056	35.3	15.50	1.495
DT3	43.2	23.273	25.1201	41.0	18.89	1.68
DT4	32.7	2.831	10.02355	38.5	29.13	-1.101
DT5	51.3	30.898	58.3696	45.4	97.00	-1.375
DT6	43.8	-1.636	7.0543	39.9	11.91	-0.678
DT7	39.9	-11.772	1.14918	37.4	0.623	0.306
DT8	38.1	15.719	16.2328	33.9	9.26	0.627
DT9	43.8	-13.403	1.9986	38.3	9.10	0.021
DT10	43.0	20.518	32.5858	28.5	21.80	-1.196
DT11	39.6	-3.134	7.263	37.7	3.63	0.319
DT12	43.1	46.091	31.6744	39.2	21.73	1.805
DT13	27.3	-0.452	10.6798	42.6	82.37	-0.045
DT14	34.1	8.822	10.02355	45.7	21.12	-1.222
DT15	41.1	-0.331	9.6286	37.4	5.83	-0.007

S^2d_i is represented in column 3 as ER

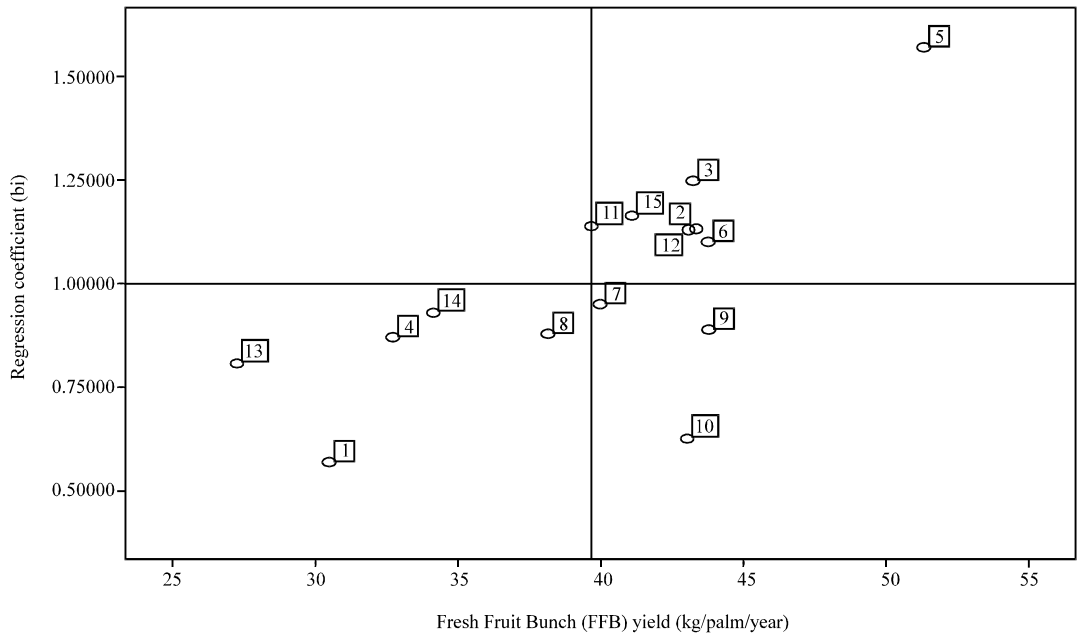

Fig. 1: Regression coefficient plotted against mean fresh fruit bunch yield (kg/palm/year)

The most stable genotype as indicated by SH method were DT 7, DT 9, DT 11 and DT 15 (Table 2). The genotypes with poor stability according to this parameter were DT 5, DT 10, DT 12, DT 3 and DT 1.

Following the genotype grouping technique, five genotypes using the FK method were considered to be highly stable (Fig. 2, Table 2) because of the high mean bunch yield and low CV. The group II genotypes produced bunch yield above the grand mean but had high CV which made them unreliable. Yield consistency is more important than absolute yield to subsistence farmers who need to be assured of harvest from season to season or year to year (Evans, 1993; Hassanpanah, 2010). The genotypes in group III had low CV but produced below grand mean bunch yield. They are therefore, considered stable and could be selected for further improvement by increasing their yield potential. FK method will be amenable to use especially in screening a large number of genotypes for yield stability. This conforms to Ataga (2010) report in the yield stability study of oil palm using descriptive method of grouping genotypes.

Using the cultivar performance measure (LB method), the genotypes with the lowest p_i values (DT 7, DT 11, DT 15, DT 9 and DT 8) were judged most stable (Table 2).

The most unstable genotypes according to this analysis were DT 5, DT 13, DT 1, DT 4 and DT 10. The genotypes DT 6, DT 2 and DT 3 which respectively ranked 3rd to 5th for mean FFB yield, showed intermediate stability and ranked 6th to 8th for LB.

The visual display of the average yield and stability of genotypes from the GGE biplot method classified DT 15, DT 9, DT 13, DT 7 and DT 11 as the most stable genotypes for FFB yield due to the lesser absolute values (Fig. 3, Table 2). It is however worthy to note that genotype DT 13 has the lowest bunch yield performance. This model selected DT 12, DT 3, DT 2, DT 5 and DT 14 as the least stable genotypes because of the greater absolute values.

The Spearman's rank correlation among environments and stability indices of the five methods based on ranking of FFB yield of 15 oil palm genotypes was generally weak (Table 3).

According to Huhn (1996), this is an indication of cross order pattern due to strong g×e interaction. Consequently, the order of ranking of genotypes in an environment would not predict

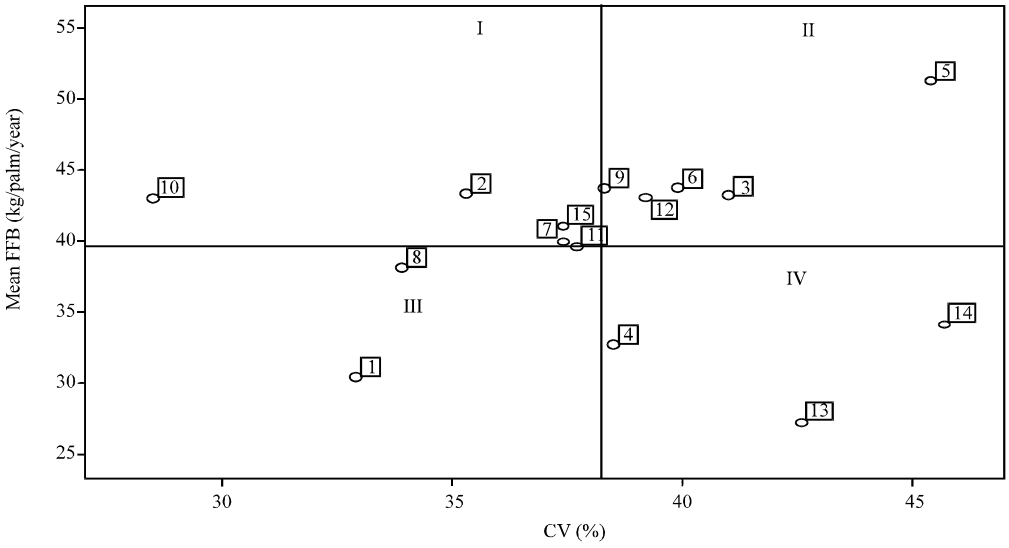

Fig. 2: Mean FFB yield (kg/palm/year) plotted against CV (%)

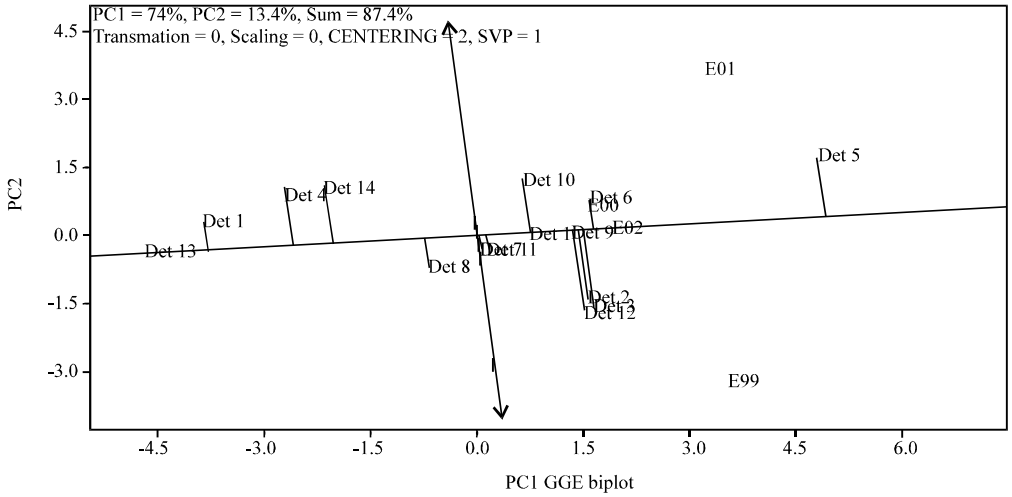

Fig. 3: Average tester coordinate (ATC) view of FFB yield for 15 oil palm genotypes

Table 3: Rank correlations among environments and stability parameters of five stability methods for 15 oil palm genotypes

	E99	E00	E01	E02	FFB	ER	FK	SH	LB	GGE
E99	1.000	0.682**	0.732**	0.525*	0.854**	0.193	-0.104	0.232	-0.018	-0.007
E00		1.000	0.654**	0.418	0.832**	0.400	0.222	0.209	-0.229	0.446
E01			1.000	0.479	0.829**	0.125	0.091	0.009	-0.229	-0.179
E02				1.000	0.646**	0.161	-0.336	0.177	-0.296	0.189
FFB					1.000	0.193	0.134	0.113	-0.179	0.114
ER						1.000	0.266	0.795**	0.475	0.011
FK							1.000	-0.011	0.304	-0.232
SH								1.000	0.720**	-0.050
LB									1.000	-0.482
GGE										1.000

** Correlation is significant @ 0.01 level, * Correlation is significant @ 0.05 level

the pattern in other environments. The bunch yield at E99 had the highest correlation ($r = 0.854$, $p<0.01$) with the mean FFB yield over all the environments. It could be inferred that the mean performance at E99 may be representative of the performance at the other three environments. Shukla's stability index procedure (SH) was highly significantly correlated with ER deviation parameter and LB cultivar performance value. Martin (2004) reported highly significant correspondence between SH and ER procedures in his comparative studies of statistical methods to describe g×e interactions and yield stability in multi-location maize trials. This may suggest similarity to the procedures of ER and LB. GGE biplot method showed the greatest deviation from all other procedures, having negative rank correlation coefficients compared to the other procedures (Table 3). The weak correlation among the stability procedures may be due to genotypes sensitivity to different procedures as a result of the principles underlying the choice of stable genotypes.

There was a high concordance among the stability models (Table 4). The level of convergence between any two of the stability models ranged between 25 and 67%. The highest agreement (66.7%) on stable genotypes was between ER and SH, SH and LB, SH and GGE and LB and GGE. These were followed by ER and LB, ER and GGE, FK and SH, FK and LB and FK and GGE

Table 4: Concordance analysis for number of genotypes jointly selected by two or more analytical methods

Methods[a]	Method 1	Method 2	Method 3	Method 4	Method 5	No. of common selections	CC[b] (%)
1.2	3	3	-	-	-	2	25.0
1.3	1	-	1	-	-	4	66.7
1.4	2	-	-	2	-	3	42.9
1.5	2	-	-	-	2	3	42.9
2.3	-	2	2	-	-	3	42.9
2.4	-	2	-	2	-	3	42.9
2.5	-	2	-	-	2	3	42.9
3.4	-	-	1	1	-	4	66.7
3.5	-	-	1	-	1	4	66.7
4.5	-	-	-	1	1	4	66.7
1.2.3	1	1	-	-	-	2	50.0
1.2.4	2	2	-	1	-	2	28.6
1.2.5	2	2	-	-	1	2	28.6
2.3.4	-	2	1	1	-	2	33.3
2.3.5	-	2	1	-	1	3	42.9
3.4.5	-	-	1	1	1	4	57.1
1.2.3.4	1	2	-	1	-	2	33.3
1.2.3.5	1	2	-	-	1	2	33.3
1.2.3.4.5	1	2	-	1	1	2	28.6

[a]Method 1 = ER, Method 2 = FK, Method 3 = SH, Method 4 = LB, Method 5 = GGE, [b]CC = Concordance

(42.9%). However, the concordance between any of the three or five methods was between 28.6 and 57.1%. The high percent divergence in the choice of stable genotypes as seen in this study is similar to earlier reports of Lin *et al.* (1986), Becker and Leon (1988) and Baiyeri *et al.* (1999). It is interesting to note that there were genotypes selected as stable by the five methods based on a 28.6% concordance (Table 4). These genotypes are superior and therefore more reliable for future breeding programmes (Papadopoulos *et al.*, 2007).

Although, there may be some differences in the identification and selection of stable genotypes using different stability procedures, stability models with the same concordance percentage is an indication of similarity in selection efficiency of stable genotypes. This suggests availability of close substitutes or alternative procedures. For instance, the high level of concordance between methods 1.5, 2.5, 3.5 and 4.5 shows that each of the methods could be used in lieu of method 5 (GGE) whilst achieving the same results. This is especially when the model is very complex, rare or expensive for the scientist or researcher.

CONCLUSION

Fresh fruit bunch yield showed significant differences for the genotype, environment and g×e interaction terms. The marked influence of environment on the magnitude of genetic variance suggests the responsiveness of FFB yield to environmental conditions or fluctuations. The combined use of the five stability procedures implicated genotypes DT 7 and DT 11 to be highly stable for FFB yield. These genotypes will be very reliable for future breeding programmes to develop high yielding planting materials with stable performance. Notably however, DT 5 which produced high FFB yield was rated as unstable by all the stability methods. Hence, this study shows that high yielding genotypes may not necessarily be highly stable over environments. The high percent divergence in the number of genotypes identified as stable is due to the inherent variation

associated with the respective procedures for identification of stable genotypes. It has been concluded that the simultaneous use of different statistics would protect the breeders from grievous errors of selecting a wrong genotype especially when testing new varieties. In addition, the high concordance observed in some of the methods suggests availability of alternative procedures. It is therefore recommended that ER, FK, SH and LB methods could be used in lieu of the GGE biplot method particularly where the software is not available.

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