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Full Length Research Paper

Genotype by trait relations of yield and other physiological traits of coconut (*Cocos nucifera L.)* hybrids based on GT biplot

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Abstract

Adequate knowledge of the interrelationships among physiological traits is essential in planning and evaluating breeding programmes for coconut improvement. The Genotype by Trait (GT) biplot can be used to compare cultivars on the basis of multiple traits and to identify cultivars that are particularly good in certain traits and therefore can be candidates for parents in plant breeding program. The objective of this study was to evaluate the coconut hybrids based on Genotype by Traits (GT) biplot to examine its usefulness in visualizing coconut trait relationship and its application in hybrids comparison. The GT biplot analysis revealed close associations among the physiological traits. Correlation coefficient between the studied traits showed that there is a strong positive relationship between number of fruit and number of bunches. These two traits were however negatively correlated with other traits except number of fronds. Based on the *Auto Find QTL function* of GGE biplot, bunch yield and width of leaflets were identified as traits suitable for indirect selection for nut yield improvement. H4 was identified as an ideal cultivar as it combines several good traits in its genetic composition and thus could serve as a good genetic raw material from which better cultivars, synthetic varieties and pure lines can be developed. H1 was the best in terms of nut and bunch yield, indicating that it can be used as parents in the development of variety hybrids and populations that are outstanding in these traits.

Keywords: *Coconut*, genotype by trait biplot, ideal cultivar and correlation coefficient.

INTRODUCTION

In many crops including the coconut palm (*Cocos nucifera L.*), selection for yield is a major objective for improvement. One of the main objectives in coconut breeding is to increase nut yield which is a complex character dependent on interaction of number of component characters. For achieving a reasonable improvement in yield, an understanding of correlation between characters would be very useful. Earlier, Patel (1937), Satyabalan and Mathew (1984) and Ganesamurthy *et* al. (2002) had worked out correlation between nut characters. Nut yield is very important in coconut cultivation, hence breeding programs aimed at improving the crop is mainly directed towards increased nut yield. Yield is the major breeding objective of any crop improvement programme. It represents the final product from physiological and developmental processes which occur from time of sowing to plant maturity (Obisesan, 2004). From the crop production view point, yield is the sum total of all production efforts on the farm. It is always measured in terms of the quantity of desired crop part per unit area of land and it can be partitioned into several components that constitute physiological determinants of yield. Although yield is the universal breeding objective, cultivars gain acceptability as a package of various multiple traits. This is because a cultivar is more or less a complex biological system rather than simple collection of independent traits, and an effective breeding programme requires a proper understanding of the essential components of the system and the interrelationship among them (Yan and Kang, 2003). Yield in crop plants is governed by yield components. According to Obisesan (1986), yield can be analysed using two different approaches: the yield system analysis (YSA) and the systematic modelling approach. One of the main objectives in coconut breeding is to increase nut yield which is a complex character dependent on interaction of number of component characters. Selection of characters could be done only if there is genetic variation. To obtain maximum benefits from selection procedure, plant breeders must be able to identify and manipulate a combination of morphological and phenological traits that positively enhance nut yield increase in coconut palm. Several studies on the interrelationship among agronomic traits of crops have been reported. Ogunbodede, 1989; Musvosvi, 2009, used correlation and regression analysis in cowpea. C. Natarajan *et al*., 2010 also studied genetic variability analysis of morphological growth characters, nut yield and nut characters in coconut and concluded that Nut yield exhibits positive correlation with number of functional leaves, length of leaves and petiole genotypes. Recently, the GGE biplot methodology was developed originally for analysing multi-environment trial data (Yan and Kang 2003). However, it can also be equally used for all types of 2-way data that assume an entry × tester structure (Yan 2001). The genotypes can be generalized as entries, and the multiple traits as testers (Rubio et al. 2004). Yan and Rajcan (2002) used a GT biplot, which is an application of the GGE biplot technique to study the GT data. A GT biplot is an effective tool for exploring multi-trait data. It graphically displays the genotype by trait table, and allows the visualization of the associations among traits across the genotypes and of the trait profile of the genotypes (Yan and Kang 2003).The genotype-by-trait (GT) biplot analysis, proposed by Yan and Kang (2003) is another powerful statistical tool for studying relationships among traits, evaluating cultivars based on multiple traits and for identifying those that are superior in certain traits. These could be candidates for use as parents in a breeding programme or directly released for commercial production. The genotype by trait biplot (Yan and Rajcan, 2002; Okoye et al., 2007) facilitates identification of traits that can be used in indirect selection for a target trait and those that may be redundantly measured. It also helps to visualize the trait profiles (strength and weakness) of genotypes, which is important for parent as well as variety selection (Yan and Kang 2003). A GT biplot can also be used to visualize the merits and shortcomings of individual genotypes which are important for both cultivar evaluation and parent selection (Okoye et al., 2007). The GT analysis allows visual display of the genetic correlation among traits (Yan and Rajcan, 2002; Lee*et al*., 2003). It also provides information on the usefulness of cultivars for production as well as information that help to detect less important (redundant) traits, and identify those that are appropriate for indirect selection for a target trait. Research data is expensive and precious, yet it is seldom fully utilized due to our ability of comprehension. Graphical display is desirable, if not absolutely necessary, for fully understanding large data sets with complex interconnectedness and interactions. The newly developed GGE biplot methodology is a superior approach to the graphical analysis of research data and may revolutionize the way researchers analyse data. The objective of this study was to use the genotype by trait (GT) biplot, which is an application of the GGE biplot technique to study the genotype by trait data and its effectiveness in visualization of the associations among coconut yield traits across the genotypes and of the trait profile of the genotypes.

MATERIALS AND METHODS

The materials for the present study consisted of 5 genotypes of Coconut palm .They were hybrids between the following varieties: NIFOR MYD, Vanuatu tall (VTT), Malayan Green Dwarf (MGD), Srinlanka Green Dwarf (SGD), and West Africa Tall (WAT) with Vanuatu and West Africa Tall as the pollen parents. Table 1 reveals detailed information about the 5 genotypes used in the present study. This experiment was conducted at the Main Research Station of the Nigerian Institute for Oil Palm Research (NIFOR), Benin City, Edo State, Nigeria. NIFOR is located within latitude 6°33'N and longitude 5°37'E and lies 156m above sea level. About 137 palms consisting of the five hybrids of coconut were planted in 2003.The experimental design was a randomized complete block design (RCBD) with two replications; each block consisted of 5 plots with a total of eight palms per plot while the remaining palms were used as guard rows. Data on individual palms were recorded on seven quantitative traits: thickness of petiole, number of fronds, number of leaflets, number of fruits, number of bunches width of leaflet, and circumference of the trunk 20cm from

Table 1. Codes and origin of 5 coconut hybrids

S.no	Hybrids code	Status	Introduced from
1	H1	Germplasm	Ghana
2	H2	Germplasm	Ghana
3	H3	Germplasm	Ghana
4	H4	Germplasm	Nigeria
5	H5	Germplasm	Nigeria

the base. The genotypes used in this work were labelled H1 to H5 as in Table 1.Genotype by trait analysis using GGE biplot analysis (Yan, 2001; Yan and Kang, 2003) was used to determine which variety was best and for what trait. This would aid selection of genotypes for the agro-ecological zone. The biplots were generated using the standardised values of the traits means. The biplot analyses were based on Model 2 (i.e., dataset was not transformed (Transform=0) within-trait standard deviation standardised (Scale=1), and trait-centred (Centering=2). The polygon views were based on genotype-focused singular value partitioning (SVP=2), while the vector views were based on the trait-focused singular value partitioning and is, therefore, appropriate for visualising the relationships among traits and genotypes. The GGE biplot model equation for genotype by trait interaction biplot analysis is presented as follows:

$$(Y_{ij} - \mu - \beta_j)/d_j = \lambda_1 g_{i1} e_{1j} + \lambda_2 g_{i2} e_{2j} + \Sigma_{ij}$$

Where:

Yij is the genetic value of the combination between genotype i and trait j;

μ is the mean of all combinations involving traitj;

β_j is the main effect of trait j;

λ_1 and $\lambda_2$are the singular values for principal component (PC)1 and PC2;

g_{i1} and g_{i2} are the PC1 and PC2 eigenvectors, respectively, for genotype*I*;

e_{1j} and $e_{2j}$are the PC1 and PC2 eigenvectors, respectively, for trait *j*;

djis the phenotypic standard deviation; and □ij is the residual of the model associated with the combination of genotype i and trait j. All analyses reported in this study were conducted by using the GGE biplot software (Yan, 2001; Yan and Kang, 2003) (www.ggebiplot.com).

RESULTS AND DISCUSSION

The GT biplot of mean performance of coconut genotypes explained 90.4%of the total variation of the standardized data (Figure 1). This relatively high percentage variation reflects the accuracy of inter-relationships among the measured characters/traits. According to Kroonenberg (1995) the fundamental patterns among the traits should be captured by the biplots. In the GT biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships between and among the traits. The vector length of the trait measures the magnitude of its effects (positive or negative) on nut yield (Yan and Tinker, 2005). Provided that the biplot explained a sufficient amount of the total variation, the correlation coefficient between any 2 traits is approximated by the cosine of the angle between their vectors (Yan and Rajcan 2002).On this premise, two traits are positively correlated if the angle between their vectors is an acute angle (< 90°) while they are negatively correlated if their vectors is an obtuse angle (> 90°) (Yan and Kang,2003).Across the 5 tested genotypes, nut yield and bunch yield were positively associated (an acute angle) as shown in figure 1. These two traits were negatively correlated with other traits (obtuse angles), and they were independent of the number of fronds (near right angles).These relationships suggest that it is possible to combine higher nut yield, higher bunch yield, lower number of fronds, lower number of leaflets, lower circumference of the trunk, smaller thickness of petiole, and smaller width of leaflets in a single genotype. The negative association between yields and number of leaflets could be due to the fact that more of the photosynthate is diverted towards the production of more fruits and bunches at the expense of the production of leaflets. This also applies to the circumference of the trunk, thickness of petiole and width of leaflets. Figures 2 is biplots showing the polygon view of the genotype x traits analysis on the morphological traits based on Principal Component axes (PC) 1and PC2. The traits were considered as the tester and the cultivars as entries. The two axes explained 90.4% of the total variation among the cultivars due to morphological traits measured. Figure 2 shows which cultivar(s) were best at what trait. The cultivar(s) at each vertex (vertex cultivar) of the polygon in the biplot were the best in terms of the trait(s) found within the sector demarcated by any two lines that meet at the origin of the polygon. From Figure 2, H1was the best in terms of nut and bunch yield, indicating that it can be used as parents in the development of variety hybrids and populations that are outstanding in these traits. H4was the best cultivars for circumference of the trunk, thickness of petiole, width of leaflets, number of leaflets, and number of fronds .Even though H4was identified for good performance in these traits, it was not the best for nut and bunch yield,

indicating that circumference of the trunk, thickness of

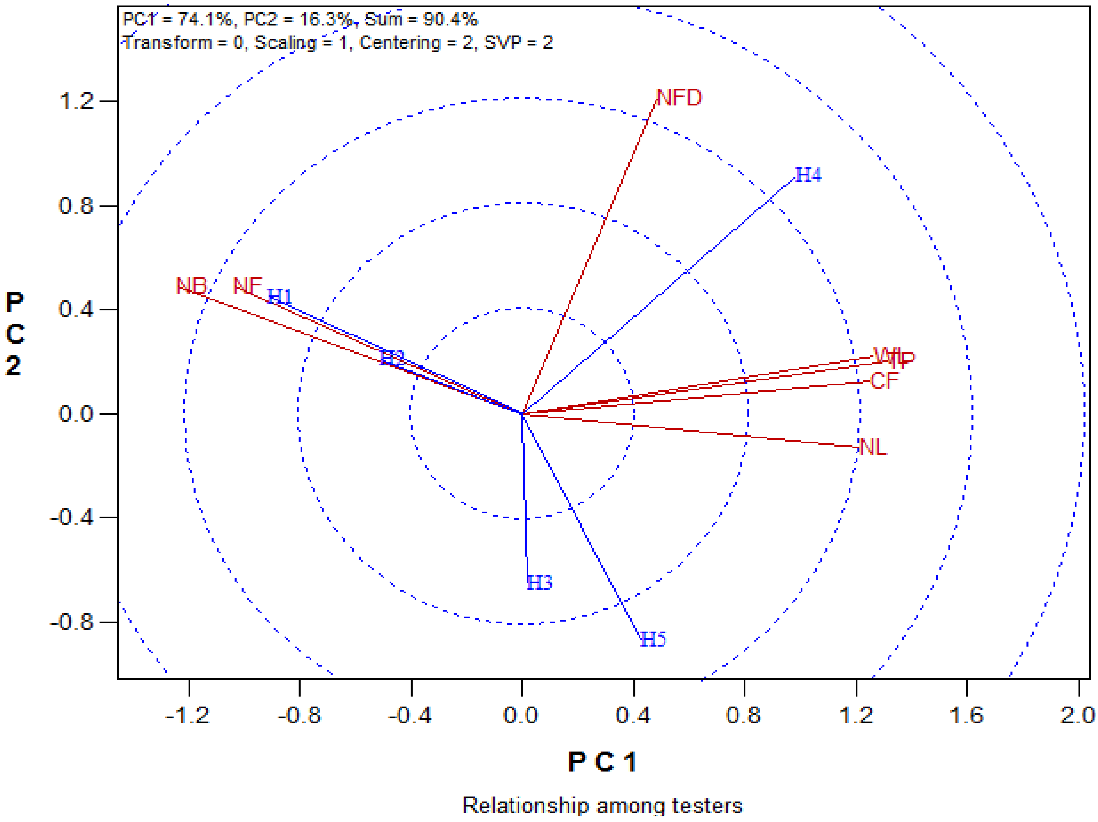

Figure 1. Vector view of the genotype-by-trait biplot on physiological traits of 5 coconuts genotypes showing the interrelationships among all traits of 5 coconut genotypes evaluated at NIFOR in Nigeria.

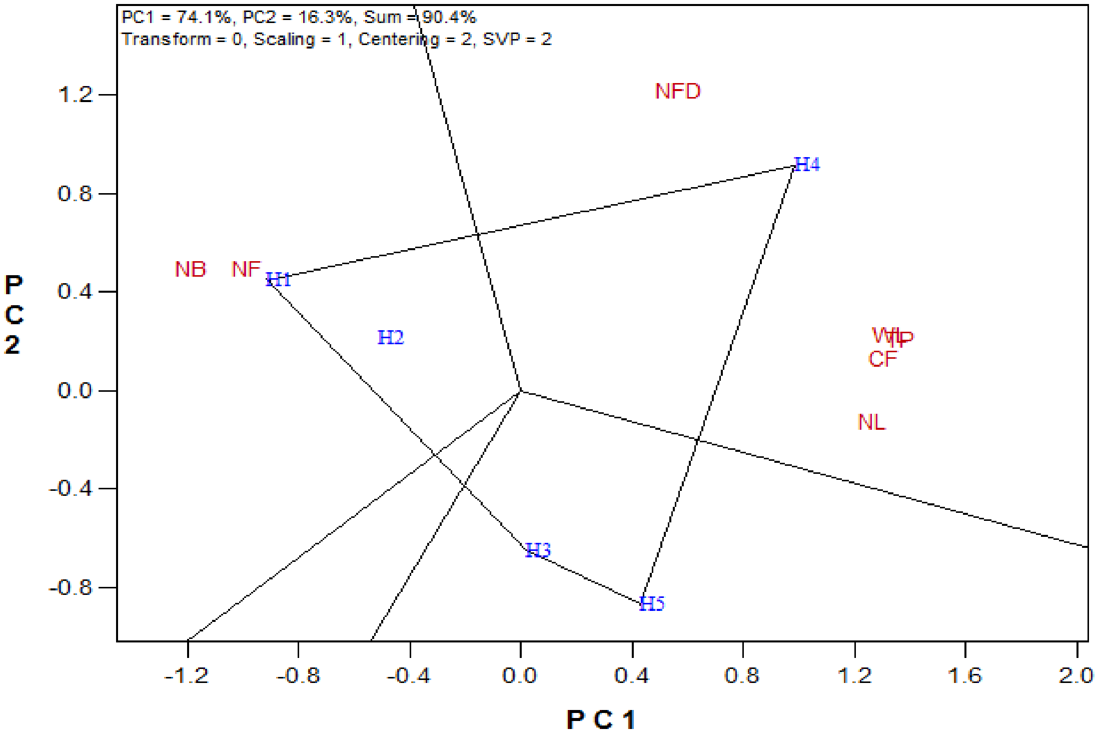

Figure 2. A ''Which is best for what'' genotype x traits biplot of morphogical traits of 5 coconuts genotypes evaluated at NIFOR in Nigeria. PC1 and PC2 explained 90.4% of the variation among genotypes. See Table 1 for codes of the genotypes

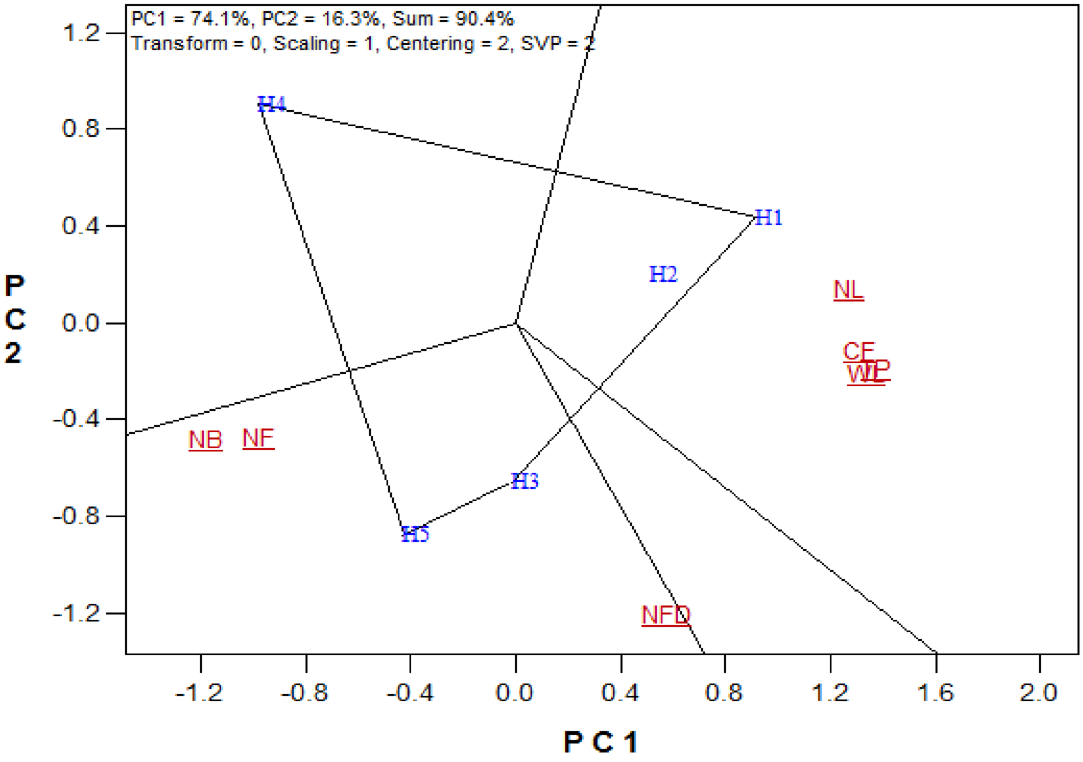

Figure 3. A ''Which is worst for what'' genotype x traits biplot of morphogical traits of 5 coconuts genotypes evaluated at NIFOR in Nigeria. PC1 and PC2 explained 90.4% of the variation among genotypes. See Table 1 for codes of the hybrids

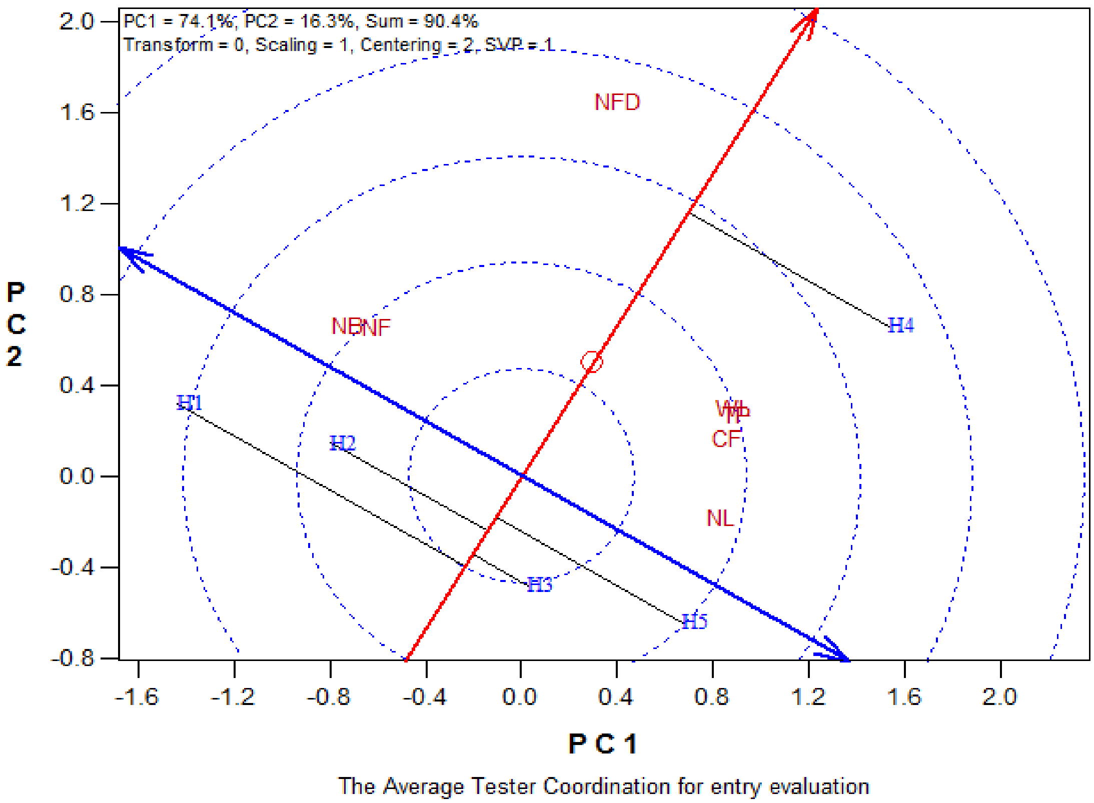

Figure 4. An entry/tester genotype x trait biplot of morphological traits of 5 coconut genotypes evaluated at NIFOR, Nigeria. See Table 1 for codes of the hybrids.

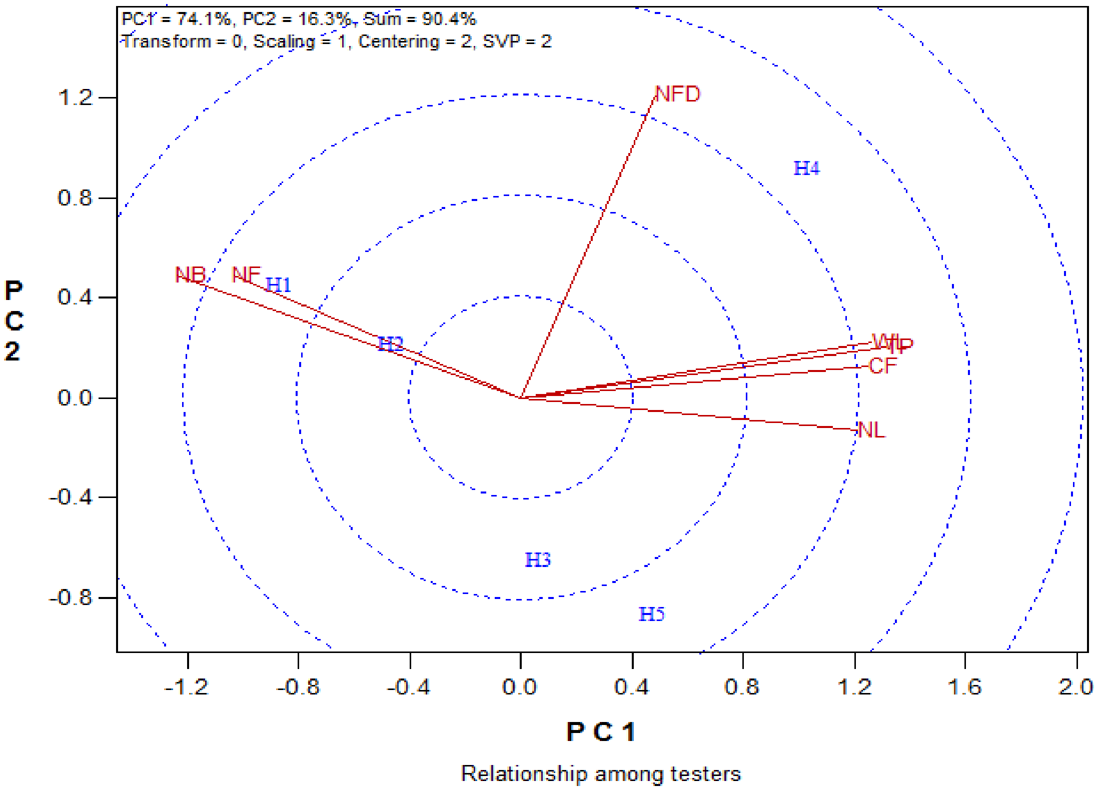

Figure 5. Relationships among traits

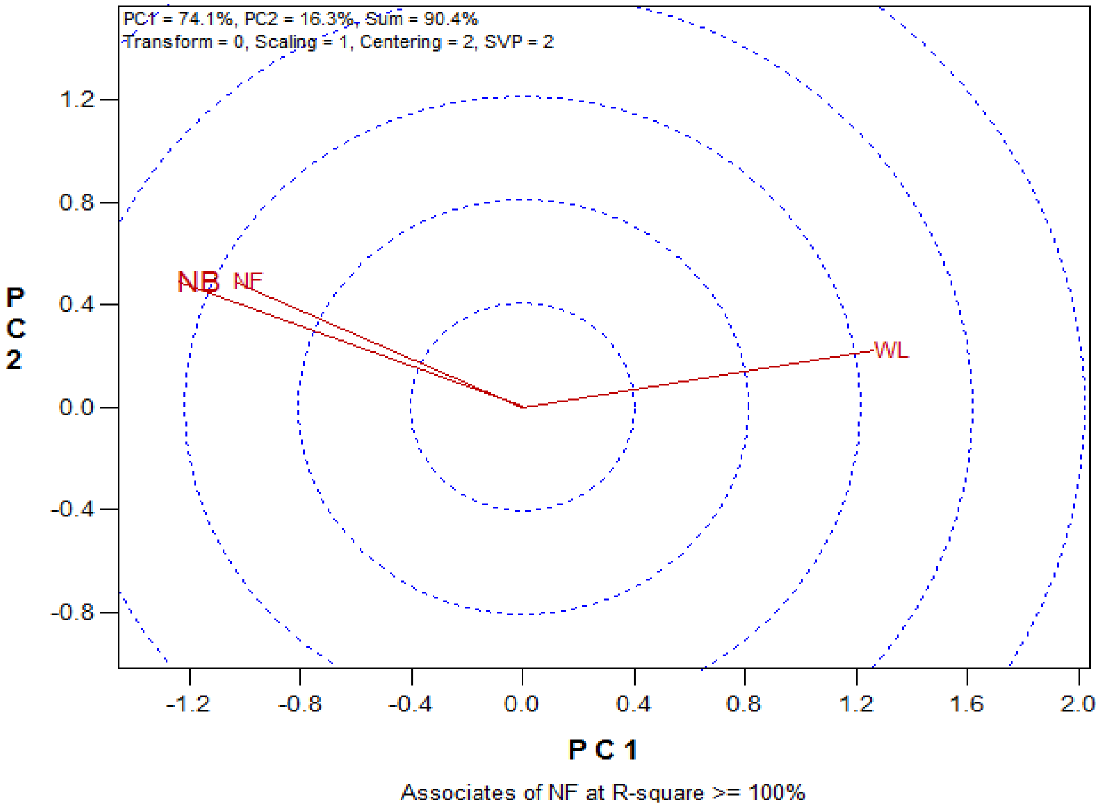

Figure 6. Vector view of the genotype-by-trait biplot on physiological traits of 5 genotypes of coconut showing traits that are most suitable for indirect selection for grain yield at R-square value e”100% and P<0.01. PC 1 and PC 2 explained 90.4% of the total variation.

petiole, width of leaflets, number of leaflets, and number of fronds might not be a good trait-indicators for nut yield. H3 and H5 were also vertex cultivars but no trait was found in their respective sector, an indication that they are not outstanding for any of the morphological traits. Oladejo *et al*., 2011, working on cowpea cultivars also recorded some cultivars with no trait in their respective sector. The biplot in Figure 3 was generated by choosing ‘Reverse Sign of All Traits’ function of the GGE biplot software to show the exact opposite of the biplot in Figure 2. Based on this biplot, H3 and H5 were the poorest in terms of nut yield, bunch yield and number of fronds while H1and H2 were the worst in terms of circumference of the trunk, thickness of petiole, width of leaflets and number of leaflet. In the context of genotype-by-trait analysis, an ideal cultivar has been defined as the cultivar that combines several good traits in its genetic composition (Badu-Apraku and Akinwale, 2011) cited in Oladejo et al., 2011. An ideal cultivar should possess the highest mean performance across traits (i.e., longest projection onto the average tester axis (ATC abscissa) and shortest entry-vector, thus, it should be close to the ideal genotype represented by the innermost concentric circle with an arrow pointing to it (Yan and Kang, 2003). Such ideal cultivar can, therefore, be used as a reference check in subsequent trials where the set of morphological traits will be measured. In the biplot displayed in Figure 4, the single-arrow line that passes through the biplot origin is referred to as the average-tester axis (ATC) abscissa, and on this line is ranked the cultivars in terms of their morphological performance. The double-arrow line (ATC ordinate) divides the ATC abscissa into two at the middle (Yan *et al*., 2007). The portion of the ATC towards the right displays the above average cultivars and towards the left shows those cultivars below average. Based on this biplot, the genotypes that performed above average was H4; while H1, H2, H3, and H5 performed below average in terms of morphological parameters.H4 is closest to the position of an ideal cultivar. It is ranked the highest in term of morphological performance because it is desirable in terms of most of the morphological traits. This cultivar could serve as a good genetic raw material from which better cultivars, synthetic varieties and pure lines can be developed. A vector is drawn from the biplot origin to each marker of the trait to enhance visualization of the relationships between and among the traits (figure 1). The vector length of a trait measures its effect (positive or negative) on yield (Yan and Tinker, 2005). Though this is not possible to observe visually in most cases, the GGE BIPLOT tester stratification was used to separate the traits with long vectors from those with short vectors. The number of bunches, thickness of petiole, width of leaflets and number of fronds were selected as long vector traits, suggesting that they had relatively large effects on nut yield while the circumference of the trunk and number of leaflets selected as short vector traits had little association with nut yield due to their relatively short vectors. Figure 5 is a vector view of GGE biplot showing the interrelationship among all the traits measured. Principal components (PC1 and PC2) explained 90.4% of the total variation observed among the cultivars based on all the traits. The lines connecting each trait marker to the origin of the biplot are called the trait vectors and the length of each trait vector approximates the standard deviation of each trait (Yan *et al*., 2007). The cosine of the angle between the vectors of any two traits approximates the correlation coefficient (degree of association) between the traits. Trait vectors that are approximately at right angle are not closely related and traits that are at angle 180º (directly opposite) are negatively correlated (Yan *et al*., 2007). From Figure 1, circumference of the trunk, thickness of petiole, width of leaflets and number of leaflets were highly positively correlated and it shows they all gave similar information about variability among the genotypes. Considerable efforts, time and funds can be saved without sacrificing useful information if one or two traits are taking instead of all. Nut and bunch yield are closely correlated and taking anyone of the two will give the same information with less effort. Nut and bunch yield was negatively correlated with all the morphological traits, except number of fronds, which had approximately right angled (very weak) correlation with it. This means that the lower the values of these morphological traits, the more the nut and bunch yield. The morphological traits were not redundant. They were mutually exclusive and each supplies useful and unique information about the genotypes. This was indicated by various angle sizes and vector lengths displayed in the biplot. Similar results were obtained by Imran *et al*. (2010) working on cowpea cultivars. The biplot in Figure 6 is a vector view of the *Auto Find QTL function* of GGE biplot that selects and displays traits that have close association with a target trait among other traits. Based on the biplot, bunch yield and width of leaflets were identified as traits suitable for indirect selection for nut yield improvement. Thus, selecting for these traits is expected to lead to improved nut yield under optimal growing conditions. This suggests that selection index that incorporates these traits will not only result in the development of high yielding genotypes but with other desirable agronomic traits that enhance wide acceptability of such genotypes.

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