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Genotype by Trait Relations between Yield and some Morphological Traits of Coconut (*Cocos nucifera* L.*)* Hybrid Varieties Based on GT Biplot

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Authors' contributions

All the authors were involved in all aspects of this study.

Original Research Article

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ABSTRACT

The objective of this study was to evaluate the coconut hybrid varieties based on Genotype by Traits (GT) biplot to examine its usefulness in visualizing coconut trait relationship and its application in genotypes comparison. The experimental design was a randomized complete block design 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. This experiment was conducted at the Main Research Station of the Nigerian Institute for Oil Palm Research (NIFOR), Benin City, Edo State, Nigeria. The materials for the present study consisted of 5 hybrid varieties of Coconut palm. Data on individual palms were recorded on seven quantitative traits: thickness of petiole (TP), number of fronds (NFD), number of leaflets (NL), number of fruits per palm (NF), number of bunches per palm (NB), width of leaflet (WL) and circumference of the stem 20 cm from the soil level (CF).The GT biplot analysis revealed close associations among the studied traits. The two

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axes explained 90.4% of the total variation among the cultivars due to the various traits measured thus reflecting the accuracy of inter-relationships among the measured characters. 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 genotype 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 yields, indicating that it can be used as parents in the development of hybrid varieties and populations that are outstanding in these traits.

Keywords: Coconut; Genotype by Trait biplot; ideal cultivar; correlation coefficient.

1. 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 polygenic character which is directly or indirectly dependent on a number of traits known as yield components [1,2]. For achieving a reasonable improvement in yield, an understanding of correlation between characters would be very useful. Earlier, [3-5] 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. It represents the final product from physiological and developmental processes which occur from time of sowing to plant maturity [6]. 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 [7].

Yield in crop plants is governed by yield components. According to [8], yield can be analysed using two different approaches: the yield system analysis 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 [9] and Musvosvi [10] used correlation and regression analysis in cowpea. Natarajan et al. [11] also studied genetic variability analysis of morphological 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.

Recently, the GGE biplot was developed originally for analysing multi-environment trial data [7]. However; it can also be equally used for all types of 2-way data that assume an entry × tester structure [12]. The genotypes can be generalized as entries and the multiple traits as testers [13]. Yan and Rajcan [14] 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 [7]. The genotype-by-trait (GT) biplot analysis, proposed by [7] 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. The genotype by trait biplot [14,15] 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 [7]. 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 [15]. The GT biplot analysis allows visual display of the genetic correlation among traits [14,16]. 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.

2. MATERIALS AND METHODS

The materials for the present study consisted of 5 hybrid varieties of Coconut palm. They were crossing between the following coconut cultivars: Malayan Yellow Dwarf (MYD), Vanuatu tall (VTT), Malayan Green Dwarf (MGD), Sri-Lanka 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 hybrid varieties used in the present study.

Table 1. Codes and origin of 5 coconut hybrids

S.no	Hybrids code	Status	Introduced from	Year
1	H1	Germplasm	Ghana	2003
2	H2	Germplasm	Ghana	2003
3	H3	Germplasm	Ghana	2003
4	H4	Germplasm	Nigeria	-
5	H5	Germplasm	Nigeria	-

This experiment was conducted at the Main Research Station of the Nigerian Institute for Oil Palm Research (NIFOR), Benin City, Edo State, Nigeria. About 137 coconut palms consisting of the five hybrids varieties were planted in 2003. The experimental design was a randomized complete block design 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 (TP), number of fronds (NFD), number of leaflets (NL), number of fruits per palm (NF), number of bunches per palm (NB), width of leaflet (WL) and circumference of the stem 20 cm from the soil level (CF). All palms were planted at 7.5m triangular spacing at a density of 204 palms ha^{-1}.The genotypes used in this work were labelled H1 to H5 (Table 1). Genotype by Trait analysis using GGE biplot analysis [17,7] 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 standardized 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 standardized (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 visualizing the relationships among traits and genotypes. The GGE biplot model equation for genotype by trait interaction biplot analysis is presented as follows:

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

Where:

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

μ is the mean of all combinations involving trait j;

Bj is the main effect of trait j;

λ_1 and λ_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*;
dj is the phenotypic standard deviation; and ∑ij is the residual of the model associated with the combination of genotype i and trait j [18]. All analyses reported in this study were conducted by using the GGE biplot software [17,7] (www.ggebiplot.com).

3. RESULTS AND DISCUSSION

The biplot in Fig. 1 presents data of 5 coconut hybrid varieties determined for seven traits in the coconut performance trials: thickness of petiole (TP), number of fronds (NFD), number of leaflets (NL), number of fruits per palm (NF), number of bunches per palm (NB), width of leaflet (WL) and circumference of the stem 20 cm from the soil level (CF). It is trait-metric preserving (SVP = 2) and is, therefore, appropriate for visualizing the relationships among the traits. H1 and H2 both had the highest bunch and nut yields, intermediate for number of fronds and were below average for the other traits. H1 and H2 were similar in their performance as revealed in their trait profile and therefore crosses between these hybrids should not be encouraged.H4 was intermediate for both nut and bunch yields and were higher than H1 and H2 for the other traits. If it is desirable to further improve the nut and bunch yield of H4, crosses of H1 - H4 or H2 - H4 may be useful. The GT biplot of mean performance of coconut genotypes explained 90.4% of the total variation of the standardized data (Fig. 1).

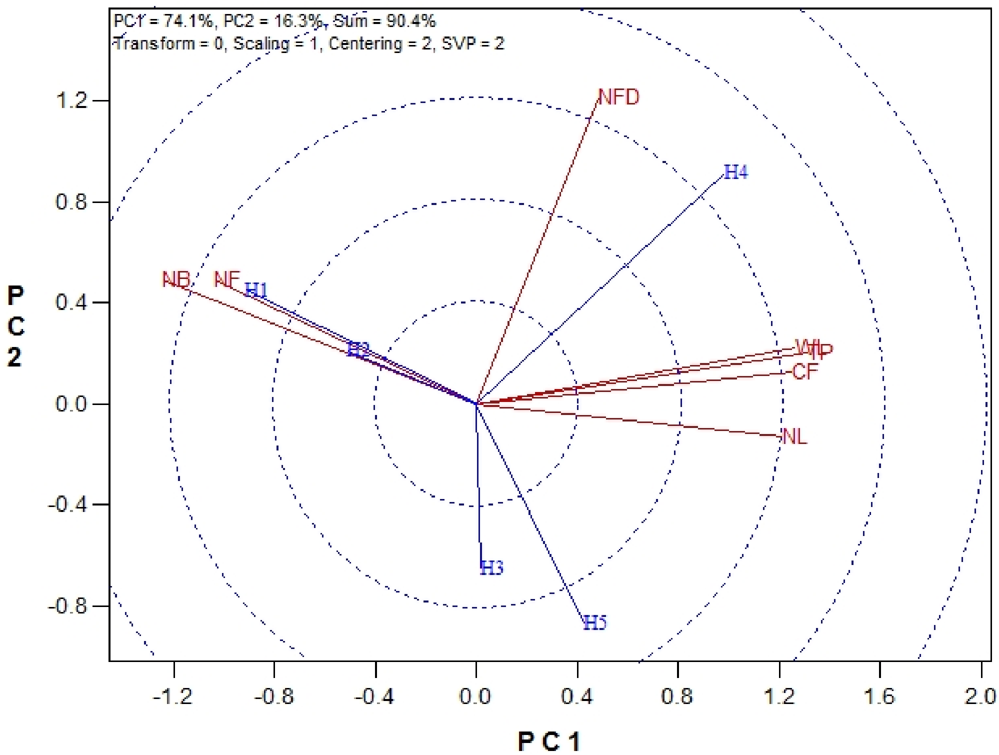

Figure 1.The polygon view of the hybrid by traits fron 5 coconut genotypes evaluated at NIFOR in Nigeria. See Table 1 for codes of hybrids.

NFD: number of fronds; NF: number of fruits per palm; NB: number of bunches per palm; NL: number of leaflets; CF: circumference of the stem 20_cm from soil level; WL: width of leaflet; TP: thickness of petiole

This relatively high percentage variation reflects the accuracy of inter-relationships among the measured traits. According to [18] 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 [20]. 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 [14]. 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 are an obtuse angle (> 90°) [7]. Across the 5 tested genotypes, nut yield and bunch yield were positively associated (an acute angle) as shown in Fig. 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 bulb, 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 bulb, thickness of petiole and width of leaflets. Fig. 2 is biplots showing the polygon view of the genotype x traits analysis on the morphological traits based on Principal Component axes (PC1 and PC2).

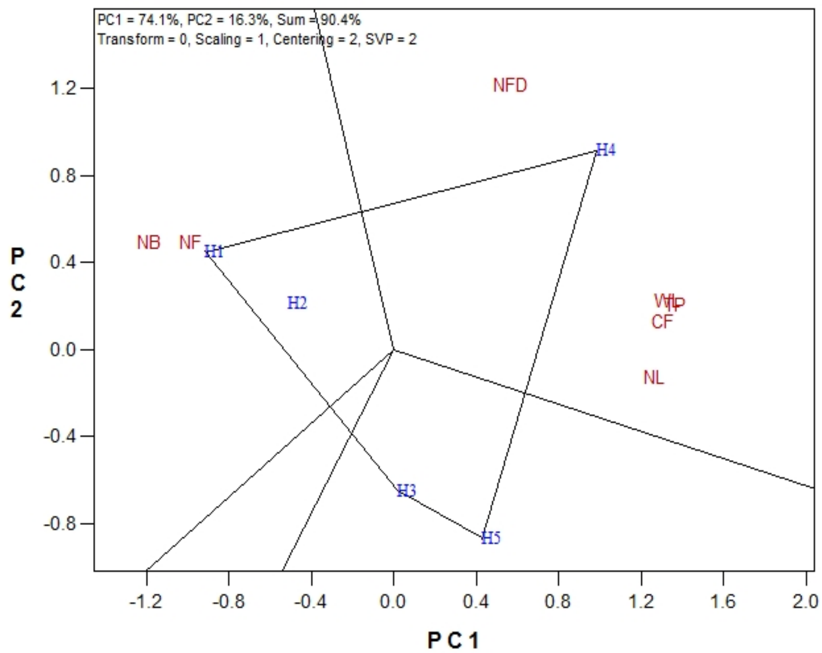

Figure 2. A "Which is best for what" genotype x traits biplot of morphogical traits of 5 coconuts genotypes evaluated at NIFOR in Nigeria. PC1 and PC2 explained 90.4% of the variation among genotypes. See Table 1 for codes of the genotypes.

NFD: number of fronds; NF: number of fruits per palm; NB: number of bunches per palm; NL: number of leaflets; CF: circumference of the stem 20 cm from soil level; WL: width of leaflet; TP: thickness of petiole

The traits were considered as the tester and the cultivars as entries [17] .The two axes explained 90.4% of the total variation among the cultivars due to morphological traits measured. Fig. 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 Fig. 2, H1 was the best in terms of nut and bunch yield, indicating that it can be used as parents in the development of varieties, hybrids and populations that are outstanding in these traits [17]. H4 was the best cultivars for circumference of the bulb, thickness of petiole, width of leaflets, number of leaflets, and number of fronds. Even though H4 was identified for good performance in these traits, it was not the best for nut and bunch yield, indicating that circumference of the bulb, thickness of petiole, width of leaflets, number of leaflets, and number of fronds might not be a good trait-indicator 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*. [18], working on cowpea cultivars also recorded some cultivars with no trait in their respective sector. The biplot in Fig. 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 Fig. 2.

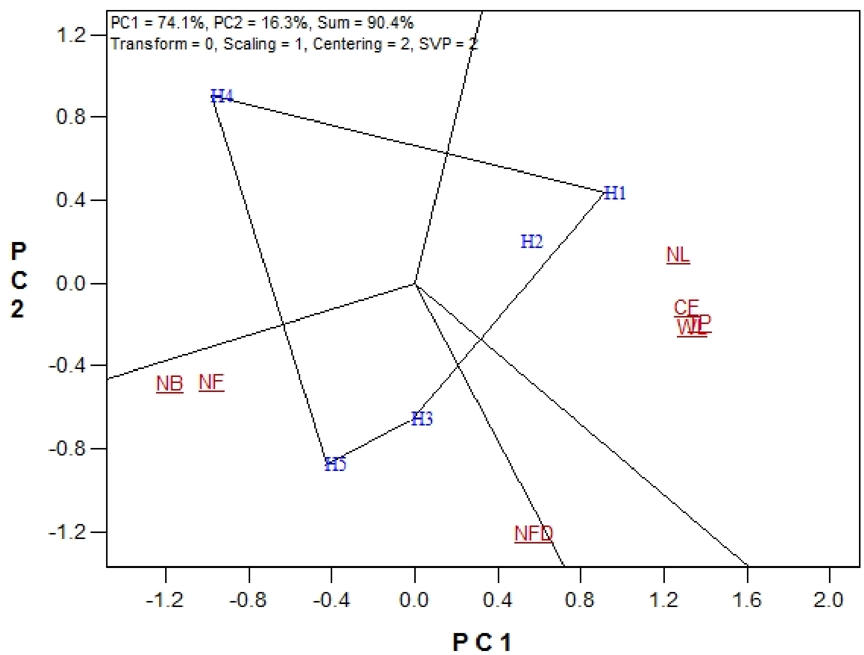

Figure 3. A "Which is worst for what" genotype x traits biplot of morphogical traits of 5 coconuts genotypes evaluated at NIFOR in Nigeria. PC1 and PC2 explained 90.4% of the variation among genotypes. See Table 1 for codes of the hybrids.

NFD: number of fronds; NF: number of fruits per palm; NB: number of bunches per palm; NL: number of leaflets; CF: circumference of the stem 20 cm from soil level; WL: width of leaflet; TP: thickness of petiole.

Based on this biplot, H3 and H5 were the poorest in terms of nut yield, bunch yield and number of fronds while H1 and 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 [21]. An ideal cultivar should possess the highest mean performance across traits (i.e., longest projection onto the average tester axis or 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 [7]. 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 Fig. 4, the single-arrow line that passes through the biplot origin is referred to as ATC and on this line is ranked the cultivars in terms of their morphological performance.

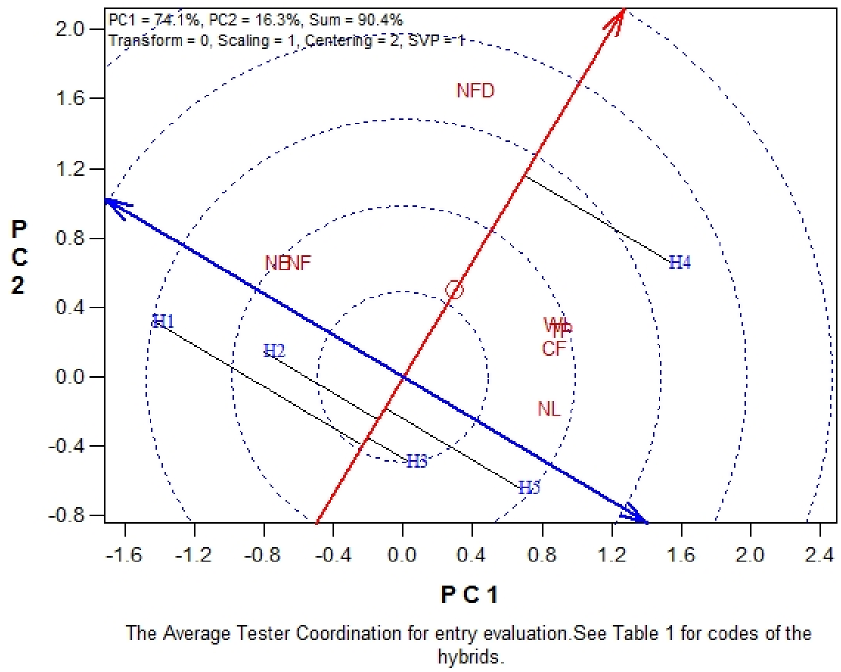

Fig. 4. An entry/tester genotype x trait biplot of morphological traits from 5 coconut genotypes evaluated at NIFOR, Nigeria. See Table 1 for codes of the hybrids

NFD: number of fronds; NF: number of fruits per palm; NB: number of bunches per palm; NL: number of leaflets; CF: circumference of the stem 20 cm from soil level; WL: width of leaflet; TP: thickness of petiole.

The double-arrow line (ATC ordinate) divides the ATC abscissa into two at the middle [22]. 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 [18]. Fig. 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 [22]. 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 180°(directly opposite) are negatively correlated [22]. From Fig. 5, 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 any one 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. 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 [23] working on cowpea cultivars. The biplot in Fig. 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.

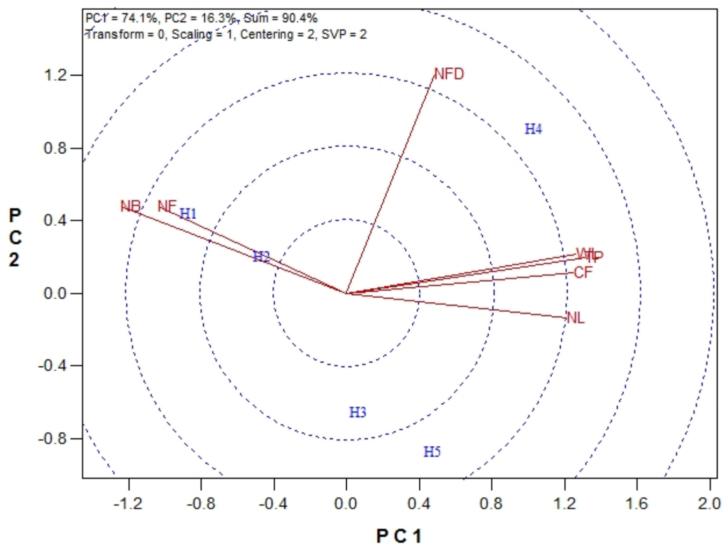

Figure 5: Relationships among morphological traits assessed in 5 coconut hybrids. See Table 1 for codes of the hybrids.

NFD: number of fronds; NF: number of fruits per palm; NB: number of bunches per palm; NL: number of leaflets; CF: circumference of the stem 20 cm from soil level; WL: width of leaflet; TP: thickness of petiole.

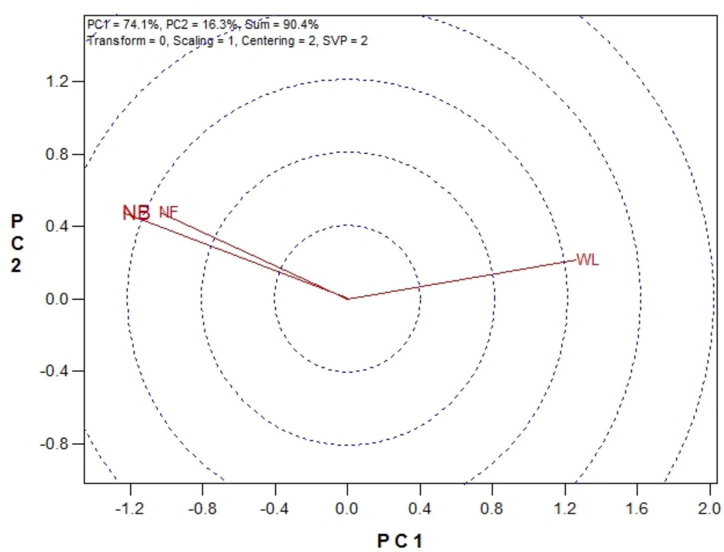

Figure 6. Vector view showing traits that are most suitable for indirect selection for nut yield at R-square value e"100% and P<0.01. See Table 1 for codes of the hybrids

NF: number of fruits per palm; NB: number of bunches per palm; WL: width of leaflet.

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. Results indicate that the GT biplot explained high proportion of the total variation of the data .Therefore, the GT biplot describes the interrelationships among traits and it was used to identify ideal genotype and hybrids that are good for some particular traits [24].

4. CONCLUSION

The relatively high percentage variation explained by the GT biplot reflects the accuracy of inter-relationships among the measured traits. H4 was identified as the closest to the position of an ideal cultivar and therefore most desirable 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. If it is desirable to further improve the nut and bunch yield of H4, crosses of H1 - H4 or H2 - H4 may be useful.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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