

CHAPTER V

DISCUSSION

A clear relationship between agronomic traits as stated by Deyong (2011) will not only address the fundamental principle of plant breeding but will also facilitate the plant breeding practice. Most of the characters such as the agronomic traits investigated in the current study contribute to crop yield. The high variability unveiled in some of the yield, morpho-physiological and fatty acid traits are essential and important for efficient selection of elite oil palm accessions with high yield and yield component characters. This finding supports the result reported by Li-Hammed et al. (2014) in variation and correlation studies of MPOB-Nigerian oil palm germplasm. The existence of variation is nonetheless vital for diversity and adaptability in breeding population (Marhalil et al., 2013).

5.1 Principal Component Analysis (PCA)

Deyong (2011) stated that when agronomic character contributed mostly to yield, it complicates the designing of an ideal crop architecture and that finding out several typical agronomic traits of a crop is of assistance in architecture designing and / or in designing high crop yield. This conception according to Deyong (2011) could be materialized through multivariate statistical analysis. PCA through its dimension reduction method is of immense help in knowing the traits contributing most to variation. In present study, nine PCs with Eigen values greater than one and total cumulative variance of 88% were extracted from the numerous variables through PCA with ABW and BWT, PCS, BNO, C16:0, carotene, MNW, HT, IV and K/B

contributing mostly to PC1, PC 2, PC 3, PC 4, PC 5, PC 6, PC 7, PC 8 and PC 9 respectively. This translates that oil palm accession with higher scores for these traits seems probably will attain high yield more easily and as a result, these traits should be given utmost importance in breeding program of oil palm germplasm under study. This result follows similar trends to that of Deyong (2011) in analysis among main agronomic traits of spring wheat. Furthermore, it can also be observed from the PCA results that most of the yield contributing traits was poor on other PCs except on PC 1. From the findings of this study, it is obvious that a good hybridization breeding program can be initiated by the selection of genotypes from PC 1 and PC 2. This result also agrees with the findings of Maqbool et al. (2010) on morphological diversity and traits association in bread wheat.

5.1.1 Score Plot

The score plot is a visual aid for determining an appropriate number of PCs. It shows the eigenvalue against the component number. The eigenvalues measure the amount of variation explained by each PC and will be largest for the first PC and smaller for the subsequent PCs. An eigenvalue of greater than one indicates PCs accounted for more variance than accounted by one of the original variables in standardized data and it is commonly used as a benchmark for which PCs are retained (Fernandez, 2002). The score plot in this study showed that maximum variation was present in the first PC and according to Maqbool et al. (2010), selection of genotypes from PC 1 will be useful.

5.1.2 Loadings

PC loadings are correlation coefficients between the PC scores and the original variables. PC loadings measure the importance of each variable in accounting for the

variability in the PC (Fernandez, 2010). In this study, variables on the left quadrant with high loadings on PC 1 include TDM, P/B, MFW, ABW, BWT, OY, M/F, OY, TEP, FFB, BDM, O/B and e while those on the right quadrant with high loadings include S/F, K/F and K/B; these set of variables can be said to be anti-correlated. That is to say, those on the left quadrant are traits conferring high yield to palms while those on the right quadrant are not yield contributing traits and oil palm with high percentage of S/F, K/F and K/B will be low in yield. This is evident from the strong negative correlation that was unveiled between variables and FFB and other yield traits in the research carried out by Li-Hammed et al. (2014) on association between oil palm traits.

Variables with high contribution to PC 2 include BNO, PCS, RL, FP, DIAM and BI. Also from the loadings plot, variables that lie close together along the same PC can be said to be highly correlated (CAMO, 2014). As stated by Fernandez (2010), high correlation between PC 1 and a variable indicates that the variable is associated with the direction of the maximum amount of variation in the dataset al. so, more than one variable might have a high correlation between with PC 1. A strong correlation between a variable and PC 2 indicates that the variable is responsible for the next largest variation in the data perpendicular to PC 1 and so on.

Furthermore on the PC, some variables particularly amongst the fatty acid traits had no significant loadings on any of the extracted PCs. This suggests that the variables have little or no contribution to the variation in the Senegal and Gambia oil palm germplasm. Therefore, PCA may often indicate which variables in a dataset are important and which ones maybe of little importance (Fernandez, 2010).

5.1.3 Scores

PC scores are the derived composite scores computed for each observation based on the eigenvectors for each PC (Fernandez, 2010). From the scores of the oil palm germplasm summarized in Table 3, oil palm genotypes with high scores on PC 1 can be said to be the most diverse. Those with high negative scores, i.e., SSC 3, SEN 09.04 and SEN 01.02 can be said to compliment variables with high negative loadings on PC 1 while those with high positive scores, i.e., SEN 13.07 and SEN 02.08 are complementary to variables with high positive loadings on PC 1 (CAMO, 2014). The oil palm genotypes with high negative scores are of the high yield type as yield traits as observed from the loading plots were loaded negatively on PC 1 (38 traits) while the non-yield traits were also positively loaded on PC 1 (for 11 traits) and genotypes with high positive scores can be said to be non-yield type. Therefore, from the scores given to the Senegal and Gambia oil palm germplasm, breeders can select genotypes with highest score having desirable characters for further breeding programs.

Furthermore, score plot which is a dimensional scatter plot signifies how well the data is distributed and gives information about the samples. In the scores plot of the present study, oil palm genotypes that are closer to one another have close values for the corresponding variables while those that are far away from one another are quite different in values for corresponding variables (CAMO, 2014). The scores plot of the Senegal and Gambia materials portrayed that genotypes that are close together are sensed as being similar when rated on all the variables studied while genotypes which are further apart are more diverse from other accessions (Smiullah, 2013).

In the present study, SSC 3 was the most distant oil palm genotype from other oil palm accessions. The reason for this is glaring distance as SSC 3 is a standard cross;

i.e. hybrid between a *dura* and a *pisifera* and standard crops also known as *tenera* are known to be of high commercial value as they are high yielding genotypes as compared to their *dura* counterparts (*pisifera* is normally trail) used in this study (Teoh, 2002; Corley & Tinker, 2003). Besides from SSC 3, genotypes which are also diverse as can be seen from the scores plot include SEN 01.02, SEN 09.04 and GAM 05.08. The Gambia material GAM 05.08 was expected to be different because it is not of the same origin with the “SEN” genotypes.

5.1.4 Bi-Plot

Bi-plot display is a visualization technique for investigating the inter-relationships between the observations and variables in multivariate data (Fernandez, 2010). From the bi-plot (Figure 5), genotypes SSC 3, SEN 09.04 and SEN 01.02 will be good choice for genetic improvement. GAM 05.08 will be the best choice for high carotene palm. The result of this is in conformity with that of Doumbia et al. (2013) who used the bi-plot graph to suggest good candidates of cowpea accessions to be used in genetic improvement of the crop.

5.2 Cluster Analysis

Estimating genetic diversity and determining the relationships between collections are very useful for ensuring efficient germplasm collections and different markers are available for studying variability among accessions (Rabbani et al., 1998). Several techniques have also been used to classify and measure the patterns of phenotypic diversity in the relationships of species and germplasm collections for a variety of crops. However, morphological characterization constitutes the first step in the description and classification of germplasm (Mostafa & Hamed, 2011).

Doumbia et al. (2013) stated that PCA alone may not give a clear character representation in terms of their contribution to genetic diversity and hence, the need for PCA to be complemented with other techniques such as cluster analysis which provides more information about the relative positions of the accessions. Cluster analysis of the germplasm resources is helpful for parental selection in the plant breeding program (Deyong, 2011). In this study, all the Senegal and Gambia oil palm germplasm were clustered into six types with each group having its own peculiar characters. Such information would be effective in selecting parental materials to breed new expected oil palm varieties. The MPOB-Nigerian oil palm germplasm also grouped into eight types by cluster analysis (Li-Hammed et al. 2014).

Though cluster analysis was able to group accessions with greater morphological similarity together, the grouping did not necessarily group accessions from the same origin together. This can be observed in the grouping of Gambia materials which were not in the same cluster group but were found grouped together with some of the Senegal materials. This shows that there is no consistency between geographical origin and genetic distance. Seymus and Brulent (2010), Lacis et al. (2010), Talebi and Rockzadi (2013) and Ajmal et al. (2013) also reported lack of relationship between geographical origin and distance. Sonnante and Pignone (2007) were of the opinion that the association between genetic similarity and geographic distance among genotypes is not always clear. This may be due to migration of the oil palm materials from one region to another in collection site.

Based on the means value for each cluster, cluster-I, cluster-II and cluster-III contained genotypes with high yield characters and as stated by Ajmal et al. (2013), increased yield potential is a stated goal for plant breeders. Hence, these genotypes

could be exploited for their release as high yielding accessions after testing them on a wide range of environments. Furthermore, these genotypes can also be utilized as parents in hybridization programs to develop high yielding oil palm varieties. This finding is in conformity with research of Ajmal et al. (2013). Also cluster-II had the lowest height and hence, the genotype in this group could be used for breeding of short palms as it is a preferred trait in oil palm breeding for easy harvesting of fresh fruit bunch (Sapey et al., 2012). Groups with desired traits can also be exploited directly for such traits.

5.2.1 Genetic Distance

According to squared Euclidean distances (D^2) among genotypes, the largest genetic distance was between SEN 13.07 and SSC 3; this was followed by SEN 02.08 and SSC 3. Hence, crosses between morphologically distant genotypes will result in maximum heterosis. The importance of genetic diversity to maximum heterosis has been reported by many researchers. WeldeMicheal et al. (2013) reported maximum heterosis in some germplasm accessions of some Ethiopian specialty coffee based on morphological traits.

Genotypes with the largest genetic distance between them can be hybridized as hybrids of maximum distance result in high yield. On the other hand, the least genetic distance was recorded in SEN 02.06 and SEN 07.08. Therefore, crosses between genotypes of close proximity should be avoided. However, Rahim et al. (2010) suggested that crosses between close genotypes could be useful for backcross breeding programs. Similar to the findings of Khodadadi et al. (2010), who reported that cluster analysis can be used for finding high yielding genotypes in wheat.