GENETIC VARIABILITY FOR YIELD, YIELD COMPONENTS AND FATTY ACID TRAITS IN OIL PALM (*Elaeis guineensis* Jacq.) GERMPLASM USING MULTIVARIATE TOOLS

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ABSTRACT

Knowledge of genetic variability and relations among germplasm materials is crucial for selection of promising breeding materials and also to ease their utilization by plant breeders. Hence, this study was undertaken to explore the pattern of variation and identify the characters which delineate the MPOB-Nigerian oil palm germplasm materials. The data on the oil palm materials obtained from Malaysian Palm Oil Board (MPOB) were subjected to principal component analysis (PCA) and Ward's clustering method after standardization. The first six principal components (PCs) with eigenvalue >1 accounted for 85.52 % of the total variability with yield and yield component characters accounting for the most variation. Distribution pattern of the oil palm germplasm materials into six distinct clusters indicate the presence of wide variations among the germplasm materials for the twenty-traits evaluated. Selections for the characters which had large positive significance on the extracted PCs could possible enhance oil palm improvement and hybridization between accessions of different clusters with high cluster means for desired traits could be achieved.

Key words: Oil palm, Germplasm, Genetic Variability, Principal Components Analysis, Clusters Analysis.

Introduction

Oil palm is a tropical crop grown mainly for its industrial production of vegetable oil. According to the World Bank report (2010), oil palm provides one of the leading vegetable oils produced globally and it accounts for one quarter of global consumption and 60% of international trade in vegetable oils. The oil extracted from the oil palm is of two types; the palm oil and palm kernel oil, 90% of which is used mainly for food purposes and the other 10% for non-food purposes (industrial) (Jalani, 2012). The modern oil palm industry of the world was sown from only four oil palm trees that were introduced from Amsterdam botanical garden and Bogor. These four palms were planted 1848 in java as ornamental plants (Jalani, 2012). This shows that the oil palm planting materials have a very narrow genetic base and a lot of concern was generated amongst researchers in Malaysia

and thus, provided the initial impulsion for the collection of oil palm genetic materials from its area of endemism (centre of origin such as the *Elaeis guineensis* from West Africa and *E. oleifera* from South America), as genetic diversity is a crucial factor of any agricultural production (Rajanaidu, 1994; Rajanaidu & Jalani, 1994). Some of these prospected materials have been introgressed into existing breeding programmes.

Collection, conservation and evaluation of germplasm materials provide opportunity for exploring advantages of natural diversity for improvement (Sarkar et al., 2012) and these have been accelerated in the past decades to prevent the extinction of landraces and wild relatives (Sapey et al., 2012). The concept of germplasm conservation therefore, requires that collection methods initially seize maximum variation and to this essence, plant genetic resources conservation entails collecting, conservation and management, identification of potentially valuable material by characterization and evaluation for subsequent utilization (Rao, 2004). Adequate characterization for agronomic and morphological traits is necessary to ease utilization of germplasm materials by breeders (Upadhyaya et al., 2008). The utilization of grounded multivariate statistical algorithms have become significant in classifying germplasm, ordering variability for large number of accessions and studying genetic relationships in any breeding materials (Mohammadi & Prassana, 2003).

Multivariate analysis consists of a collection of methods than can be utilized when several measurements are made on each individual or objects in one or more samples (Rencher, 2002), and of all multivariate tools, principal components analysis and clustering have been extensively used to classify germplasm materials. Principal component analysis (PCA) generates the general relationship between variables while clustering is an exploratory data analysis tool for grouping accessions (Richard & Wichern, 2007). Principal component analysis (PCA) and cluster analysis (CA) have been successfully used in germplasm evaluation of crops for years as they reveal the relationship and correlation among variables studied (Zafar et al., 2008; Maji & Shaibu, 2012; Odewale et al., 2012; Ahmad et al., 2014; Hamza et al., 2014). However, as at the time this research was undertaken, the use of principal component analysis and clustering in characterizing oil palm germplasm is limited. Thus, this study explored the pattern of variability in the MPOB-Nigerian oil palm germplasm using PCA and classified the materials based on similarity using cluster analysis, so that those possessing desired agronomic characters could be selected for further improvement and development of oil palm breeding materials. The methodologies employed, research findings and justifications of the study are further explained in the other sections of this paper.

Materials and Methods

Plant Breeding Materials

The Malaysian Agricultural Research and Development (MARDI) and the Nigerian Institute for Oil Palm Research (NIFOR) in 1973 jointly made collections of oil palm genetic materials in Nigeria to broaden the genetic base of the oil palm. The oil palm germplasm materials were collected at 45 sites. The palms from each site represents a population designated NGA (Nigeria) thus, 45 populations were made. The prospected oil palm breeding materials were planted using eight cubic lattice design on September, 1975 and identified as Trial 0.149 at the Malaysian Palm Oil Board Station, Kluang, Malaysia.

Data Collection

Data on yield and yield components were evaluated from 1982 – 1986. Harvesting of oil palm usually begins at 36 months after field planting with subsequent operations carried out at regular intervals of seven to ten days, i.e. three rounds in a month. The bunch yield components were fresh fruit bunch (FFB), bunch number (BNO), and average bunch weight (ABW) and other derivatives used in this study. The fatty acid compositions on the other hand were evaluated from 1981 until 1997. The fatty acid composition was evaluated using the method proposed by Timms (1978) for routine analysis using Gas chromatography.

Statistical Analysis

Prior to performing PCA and clustering on the dataset, data for traits were standardized to a mean of zero and a standard deviation of one to annihilate the biasness due to dissimilar magnitude of the units of measurement (Jolliffe, 2002). The average of the quantitative was standardized using the formula (Microsoft Office Excel, 2010);

$$z = \frac{x - \mu}{\sigma} \qquad (1)$$

Where;

x = value to standardize

μ = arithmetic mean

σ = standard deviation of the distribution

PCA was performed with the aid of "THE UNSCRAMBLER®X" software (CAMO software version 10.1). PCA has been described as a powerful technique for pattern recognition that attempts to explain the variance of a large set of inter-correlated variables and transforming into a smaller set of independent (uncorrelated) variables (principal components) (Svetlana et al.,

2012). PCA analyzes a data table representing observations described by several dependent variables which are, in general, inter-correlated. PCA also represents the pattern of similarity of the observations and the variables by displaying them as points in maps (Abdi & Williams, 2010).

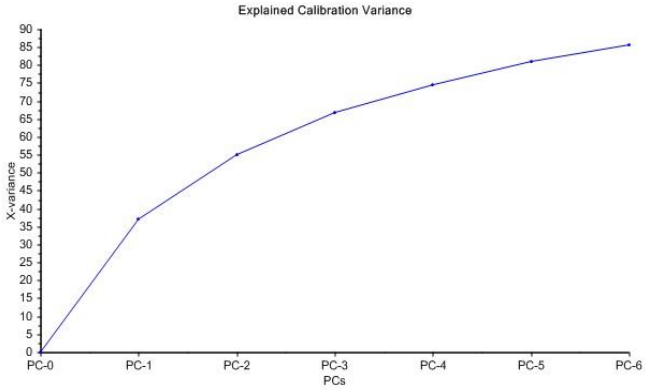
Cluster analysis on the other hand was carried out using minimum variance method of WARD (1963) also with the aid of "THE UNSCRAMBLER®X" software (CAMO software version 10.1). The theory behind clustering is an expected positive relationship between the variables Euclidean distance and the similarity of the observations. As a result, cluster analysis is driven between minimizing the Euclidean distance of observations within a cluster, and maximizing the Euclidean distance between clusters (Vural & Karasu, 2007).

Results and Discussion

Principal Component Analysis

As stated by Abdi (2003), the goal of PCA is to decompose a data table with correlated measurements into a new set of uncorrelated (i.e. orthogonal variables). Thus, to have an insight about the independent impact of the variables studied, principal component analysis was undertaken. The result of PCA studied indicated six components with eigenvalues >1 contributing 85.52% of the total variability underlying the characters of the MPOB-Nigerian oil palm germplasm (Figure 1). The eigenvalue can be used as a criterion to determine how many PCs should be retained (Iezonni & Pritts, 1991) while the explained variance graph measures the proportion in the data accounted for by the individual principal component (PC) (Ahmadizadeh & Felenji 2011). PC 1 with eigenvalue of 9.28 accounted for 37.13% of the total variability, while PC 2 with eigenvalue 4.49 accounted for 17.97 of the total variation observed among the 44 MPOB-Nigerian oil palm germplasm. PC 3 had eigenvalue of 2.95 with total variability of 11.82%. PC 4, PC 5 and PC 6 on the other hand had eigenvalues of 1.88, 1.67 and 1.11 respectively and accounted for 7.50%, 6.66% and 4.44% of the total variability. PC 1 is generally better correlated with the variables than PC 2; this is expected as PCs are extracted successively, each one accounting for as much of the remaining variance as possible (Beebe et al., 1998).

Figure 1: Explained variance curve



On each principal axis, a number of characters contributed to the total variation (Table 1). The first PC accounting for the highest variation was characterized mostly by the yield and yield components. The traits that contributed highly to this PC include fresh fruit bunch (FFB), average bunch weight (ABW), mean fruit weight (MFW), mean nut weight (MNW), kernel to fruit ratio (K/F), shell to fruit ratio (S/F), oil to dry mass (ODM), oil to bunch proportion (O/B), kernel to bunch ratio (K/B), oil yield (OY) and total economic product (TEP). PC 2 was characterized by the fatty acid traits only and the traits which contributed highly to this PC include iodine value (IV), lauric acid (C12:0), myristic acid (C14:0), palmitic acid (C16:0), stearic acid (C18:0) and oleic acid (C18:1). PC 3 was related to parthenocarpic fruit to bunch ratio (PB) and palmitoleic acid (C16:1). PC 4, PC 5 and PC 6 were related to kernel yield (KY), lauric acid (C12:0) and linoleic acid (C18:2) respectively. Variables that have significant positive as well as negative impact on the PCs can be said to contribute mostly to the diversity, especially those on PC1 are likely to be the source of variation and can be said to be the characters which differentiate the accessions in the oil palm germplasm (Denton & Nwangburuka; 2011; Iannucci et al., 2011; Ahmad et al., 2014; Hamza et al., 2014). Therefore, these traits can be used in the selection of diverse genotypes (Ashfaq et al., 2012).

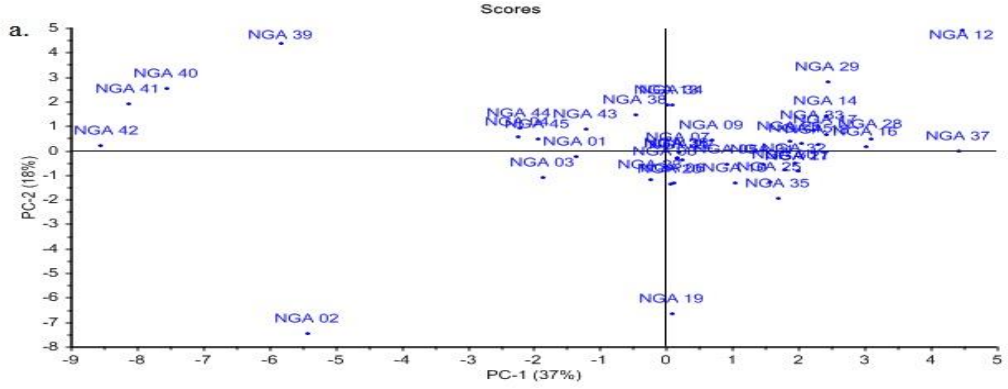
Table 1: Variables correlation loading matrix, eigenvalues, total variation and cumulative variance for different principal components in MPOB-Nigerian oil palm germplasm

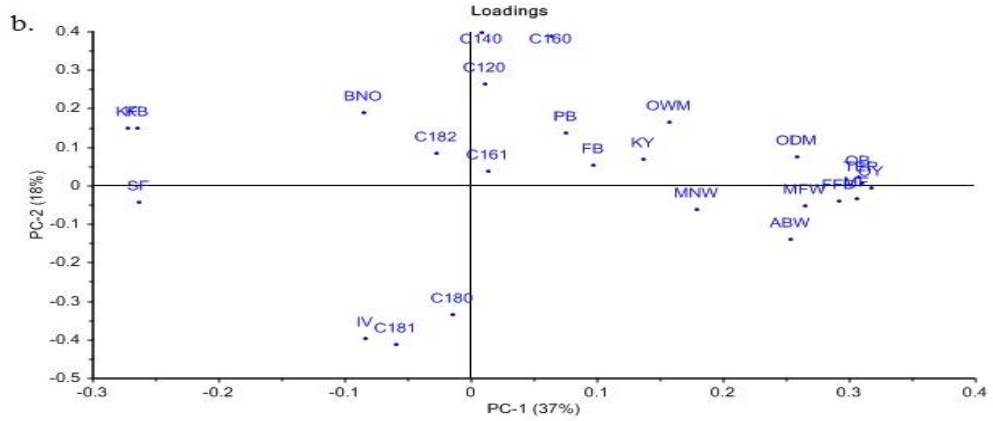
Variables	Component					
	PC1	PC2	PC3	PC4	PC5	PC6
FFB (fresh fruit bunch)	0.891	-0.084	-0.023	0.371	-0.15	-0.016
BNO (bunch number)	-0.259	0.403	-0.477	0.13	-0.497	-0.153
ABW (average bunch weight)	0.774	-0.297	0.311	0.156	0.24	0.076

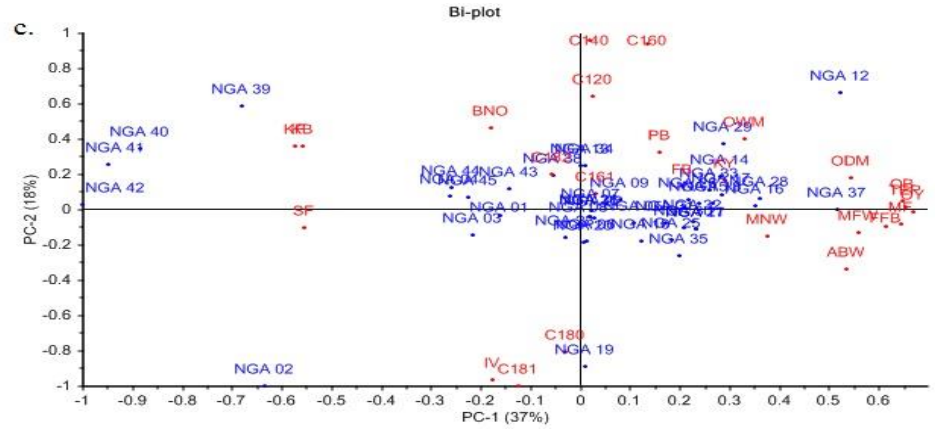
MFW (mean fruit weight)	0.81	-0.113	0.461	-0.109	-0.036	-0.035
MNW (mean nut weight)	0.546	-0.134	0.702	-0.088	-0.087	-0.025
PB (Parthenocarpic fruit/bunch)	0.23	0.287	-0.798	0.09	0.046	-0.067
MF (mesocarp/fruit)	0.934	-0.075	-0.264	-0.026	0.097	-0.004
KF (kernel/fruit)	-0.827	0.317	-0.078	0.297	0.218	-0.002
SF (shell/fruit)	-0.802	-0.09	0.419	-0.147	-0.27	0.007
ODM (oil/dry mass)	0.789	0.16	-0.071	-0.451	-0.073	0.104
OWM (oil/wet mass)	0.479	0.351	-0.315	-0.477	-0.168	0.142
FB (fruit/bunch)	0.298	0.113	0.489	-0.039	0.427	-0.148
OB (oil/bunch)	0.936	0.044	-0.215	-0.155	0.112	0.004
KB (kernel/bunch)	-0.806	0.314	0.06	0.295	0.273	-0.014
OY (oil yield)	0.968	-0.014	-0.139	0.166	-0.049	-0.015
KY (kernel yield)	0.419	0.147	0.115	0.846	0.093	-0.005
TEP (total economic product)	0.945	0.01	-0.108	0.285	-0.029	-0.015
IV (iodine value)	-0.254	-0.846	-0.02	-0.119	0.025	0.242
C120 (lauric acid)	0.035	0.56	0.059	-0.166	0.636	-0.003
C140 (myristic acid)	0.027	0.841	0.222	-0.171	0.276	0.084
C160 (palmitic acid)	0.194	0.822	0.19	0.086	-0.39	-0.078
C161 (palmitoleic acid)	0.044	0.079	0.595	0.228	-0.458	0.148
C180 (stearic acid)	-0.044	-0.71	-0.394	0.205	0.195	0.174
C181 (oleic acid)	-0.179	-0.877	-0.027	-0.083	0.006	-0.233
C182 (linoleic acid)	-0.081	0.174	-0.024	0.11	-0.022	0.918
Eigenvalue	9.283	4.492	2.954	1.875	1.665	1.11
% variance	37.131	17.967	11.818	7.502	6.662	4.438
Cumulative variance	37.131	55.098	66.916	74.417	81.079	85.518

The configurations of the forty-four oil palm populations (scores), twenty-five characters (loadings) and the bi-plot for scores and loadings along the first two principal component axes, are shown in Figure 2. The ordination of the oil palm germplasm materials (Fig. 2a) revealed that accessions NGA 02, NGA 19, NGA 12, NGA 37, NGA 39, NGA 40, NGA 41 and NGA 42 were distinct for the characters studied. The ordination of the characters (Fig. 2b) on PC 1 and PC 2 showed that some of the variables were highly inter-correlated as seen in the overlapping pattern of the variables. Also, the variables accounting for most of the variation can be seen on the right and left hand quadrant of the plot. Variables that are on the same PC and are very close to each other signify that there are positive correlations between them, and the increase in one will lead to the increase in the other, while variables at opposite end to each other are anti-correlated and the increase in one will bring about decrease in the other and vice versa. Jonah et al. (2014) reported similar result in groundnut. The bi-plot (Fig. 2c) indicates the oil palm populations and the characters that best portrait them closely. According Firincioglu et al. (2009) biplot diagrams can be used to select genotypes that might have favourable combinations of traits for use in a breeding project.

Figure 2: Principal component analysis plots: (a) scores plot of the MPOB-Nigerian oil palm populations; (b) loadings plot of variables on PC1 and PC2; (c) bi-plot of 44 MPOB-Nigerian oil palm populations and 25 variables.







Ward's Cluster Analysis

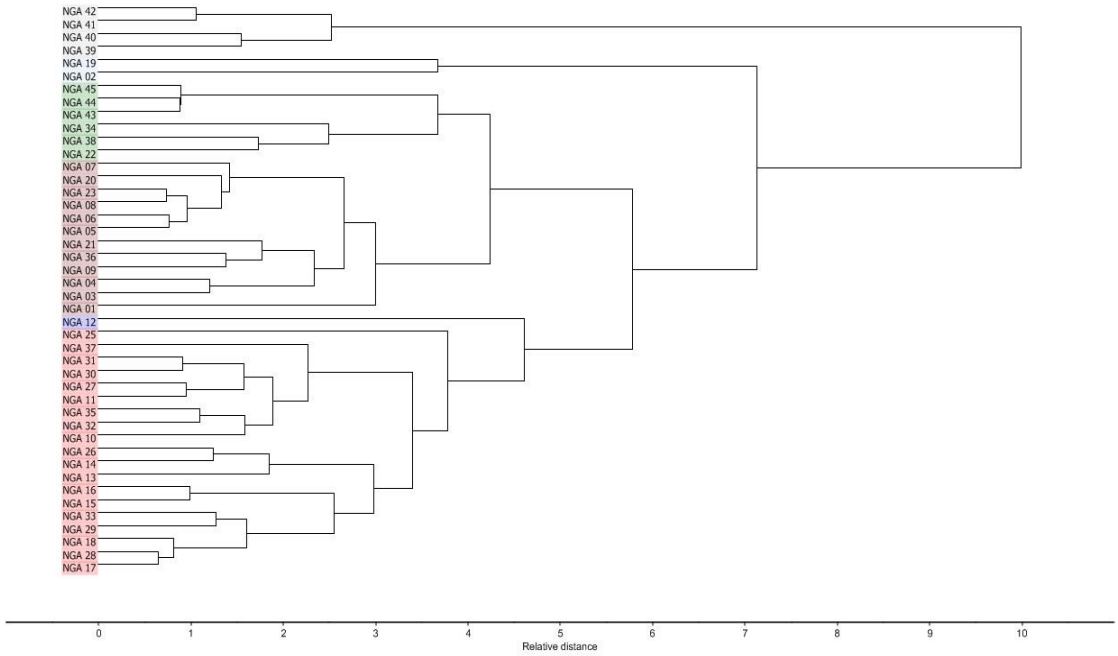
Ward's method was used because it has generally been considered to be very efficient and the most common approach to doing hierarchical clustering analysis (Siracli et al., 2013). According to Hossain et al. (2011), samples will be grouped in terms of their nearness or similarity. Ward's hierarchical cluster analysis based on the principal component extracted resulted in six clusters (Figure 3). The first cluster (2.27%) was a singleton comprising of only NGA 12. The second cluster (43.18%) had the highest number of members and comprised of nineteen populations (NGA 10, NGA 11, NGA 13, NGA 14, NGA 15, NGA 16, NGA 17, NGA 18, NGA 25, NGA 26, NGA 27, NGA 28, NGA 29, NGA 30, NGA 31, NGA 32, NGA 33, NGA 35 and NGA 37). The third cluster (13.64%) comprised six populations which include NGA 22, NGA 34, NGA 38, NGA 43, NGA 44 and NGA 45. Cluster 4 (4.55%) had only two populations which include NGA 2 and NGA 19. Cluster 5 (27.27%) only the other hand comprised of twelve populations which include NGA 01, NGA 03, NGA 04, NGA 05, NGA 06, NGA 07, NGA 08, NGA 09, NGA 20, NGA 21, NGA 23 and NGA 36 while the sixth cluster (9.09%) comprised of four populations which include NGA 39, NGA 40, NGA 41 and NGA 42.

In order to envision the pattern of clustering of the oil palm germplasm materials, the mean performance of the clusters was computed and is presented in Table 2. Germplasm material NGA 12 alone formed cluster 1, mainly attributing to its maximum fresh fruit bunch weight, bunch number, parthenocarpic to bunch ratio, mesocarp to fruit ratio, oil to dry mass, oil to wet mass, oil to bunch proportion, oil yield, kernel yield, total economic product and palmitic content. Rajanaidu and Rao (1987) also found NGA 12 to have the highest fresh fruit bunch yield. Cluster 2 shows second highest value of fresh fruit bunch weight, mesocarp to fruit, oil to dry mesocarp, oil to weight mesocarp, oil to bunch, oil yield and total economic product. This cluster is also attributed by maximum mean fruit weight and fruit to bunch ratio. Cluster 3, cluster 4 and cluster 5 showed average mean values for all the yield associated traits. In addition, cluster 3 and cluster 4 showed maximum mean values for the fatty acid traits. Cluster 3 shows maximum values for lauric acid, myristic acid and linoleic acid while cluster 4 shows maximum values for iodine value, stearic acid and oleic acid.

Cluster 6 was quite distinct and well separated from the other oil palm populations as it shows the minimum mean values for yield associated traits as well as fatty acid traits. Rajanaidu and Rao (1987) reported populations that make up this cluster to be of low yield because they were collected from dry areas (Northern Nigeria). However, this cluster also had maximum mean values for shell to fruit proportion, kernel to fruit ratio as well as kernel to bunch. These traits that are characteristics of this cluster were also found to contribute highly to PC 1 and they are anti-correlated with yield associated traits. Thus, hybridization

between populations of different clusters with high cluster mean will result into palms which will perform better than their parents (Kumar & Singh, 2006).

Figure 3: Dendrogram showing the 44 MPOB-Nigerian oil palm germplasm derived from Ward's cluster



According to Mohammadi and Prasanna (2003), analysis of genetic relations in crop species is a significant component of crop species as it provides information about genetic diversity. Among the oil palm germplasm materials, the least genetic distance was between NGA 17 and NGA 28 (2.441) as indicated by the proximity matrix of squared Euclidean distance while the highest genetic distance was between NGA 02 and NGA 12 (275.621), followed by NGA 12 and NGA 42 (218.540). Also, inter cluster distance was maximum between cluster 1 and cluster 6 and minimum between cluster 3 and cluster 5 (Table 3). Crossing between morphologically distant populations will result in maximum degree of heterosis (Mohammadi & Prassana, 2003; Singh et al., 2008; Odewale et al., 2012). Hence, the use of populations with high genetic distant between them for breeding programs should be given utmost importance while those with the least genetic distance should be avoided (Odewale et al., 2012). The high level of genetic variability encountered in this oil palm germplasm was also recorded by Zulkifli et al. (2012). Furthermore, in this study, there was random pattern distribution of the populations from different geographic locations into various clusters. Hence, there was no association of genetic diversity with geographic distribution (Kumar & Singh, 2006; Khan et al., 2009; Makinde & Ariyo, 2010; Odewale et al., 2012).

Table 2: Mean values of yield, yield components and fatty acid traits of oil palm gerrmplasm under different clusters

Traits	cluster 1	cluster 2	cluster 3	cluster 4	cluster 5	cluster 6
FFB	190.29	160.21	150.46	144.85	150.33	102.07
BNO	17.23	13.53	12.56	13.18	12.84	15.33
ABW	11.22	12.36	12.68	11.39	12.30	7.02
MFW	9.69	9.91	9.00	8.19	9.51	6.68
MNW	4.96	5.23	5.03	4.54	5.32	4.08
PB	5.08	2.45	2.38	2.71	2.07	2.58
MF	48.55	47.22	44.11	45.02	44.10	38.86
KF	12.24	11.81	13.72	12.24	12.40	15.58
SF	39.22	40.97	42.17	42.74	43.50	45.56
ODM	75.07	75.06	73.71	73.08	74.40	73.26
OWM	50.57	49.10	47.65	46.86	48.71	48.56
FB	65.44	67.13	66.88	65.69	66.61	66.42
OB	16.13	15.58	14.08	13.94	14.31	12.53
KB	7.41	7.64	8.84	7.69	8.00	9.93
OY	30.21	25.07	21.33	20.15	21.50	12.89
KY	13.86	12.27	13.35	10.96	12.01	10.22
TEP	38.52	32.44	29.34	26.73	28.71	19.03
IV	50.82	54.23	53.92	57.32	54.53	54.14

C12:0	1.00	0.78	1.33	0.00	0.48	0.99
C14:0	1.35	1.21	1.43	0.40	1.11	1.39
C16:0	42.35	38.68	38.14	32.95	38.95	38.79
C16:1	0.00	0.06	0.04	0.00	0.09	0.03
C18:0	5.75	6.28	6.35	9.10	6.21	5.94
C18:1	38.55	41.31	40.76	46.10	41.51	41.09
C18:2	10.20	10.05	10.74	10.20	10.61	10.69

Table 3: Inter cluster proximity matrix of squared Euclidean distance

Proximity Matrix						
	Squared Euclidean Distance					
Case	1:cluster 1	2:cluster 2	3:cluster 3	4:cluster 4	5:cluster 5	6:cluster 6
1:cluster 1	0.000	32.746	52.220	92.717	52.711	109.520
2:cluster 2	32.746	0.000	19.638	48.039	10.850	75.896
3:cluster 3	52.220	19.638	0.000	47.222	11.626	41.471
4:cluster 4	92.717	48.039	47.222	0.000	39.542	65.417
5:cluster 5	52.711	10.850	11.626	39.542	0.000	50.383
6:cluster 6	109.520	75.896	41.471	65.417	50.383	0.000

Conclusion

The wealth of any germplasm collection is quantified in terms of the extent of genetic variability of the accessions it contains. It can be concluded from this study that there is wide variability for yield, agronomic and oil quality traits in the MPOB-Nigerian oil palm germplasm especially for fresh fruit bunch and its related components, kernel/bunch, oil yield, total economic product, bunch dry mass, myristic acid and stearic acid. Also, populations that are genetically distant from each other have been identified and these can be used for selection of oil palms with hybrid vigor. Populations with good amount of genetic divergent (NGA 12 and NGA 41; NGA 12 and NGA 02; NGA 12 and NGA 19) and superior agronomic characters (NGA 12, NGA 14, NGA 15, NGA 16, NGA 19 and NGA 34) will be of practical use and can be used to derive superior offspring .The variation in this oil palm material may be only a portion of the variability in oil palm worldwide, and subsequent evaluation may be needed to conserve these valuable genetic materials. Subsequent breeding programmes need to further exploit the existing oil palm germplasm variation to broaden the oil palm narrow genetic base, as excessive use of a limited number of germplasm lines for reselection and hybridization will result in a decline of genetic diversity. The use of multivariate tools will help to explore the unutilized genetic diversity for future generation.

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