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Genetic Diversity and Interrelationship among Some *Dura* × *Tenera* Oil Palm (*Elaeis guineensis* Jacq.) Genotypes in Cameroon

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Abstract: In this study, the multivariate tools, namely principal component analysis (PCA) and cluster analysis, were used to classify and measure the pattern of genetic diversity and evaluate the correlation of nine oil palm traits in 25 progenies. Fresh fruit bunch weight (FFB), kernel to fruit (K/F) and kernel to bunch (K/B) ratios showed significant variance, while bunch number (BN), kernel yield (KY) and oil yield (OY) showed little variance. Positive significant correlation between these traits and yield was appreciated through PCA, where 90.55% of the variation was explained by the first three principal components. Progeny grouping was performed and revealed three clusters of oil palm progenies. Cluster I contained progenies with high production of FFB, BN, OY and KY, while low height increment (HI) of palm trees was found in cluster II. However, most of progenies with high mean values of bunch spikelet weight (SpW), average fruit weight (AFW), K/F and K/B were grouped in cluster III. This grouping could help oil palm breeders to identify progenies with the traits of interest for breeding and commercial seed production.

Key words: Oil palm, *Elaeis guineensis* Jacq., cluster analysis, correlation, genetic diversity, principal component analysis.

1. Introduction

Oil palm (*Elaeis guineensis* Jacq.) is a major crop that ranks first in the world market as a product of vegetable fats and oils. An estimated 74% of global palm oil usage is for food products and 24% is for industrial purposes [1]. A mastery of the genetic diversity and structure of oil palm is particularly important for the conservation of genetic resources, identification of oil palm populations, exploration of plant genetic resources and development of future breeding programs. Significant progress in crop improvement could be achieved by exploitation of relationships between characters in a genetically diverse population [2]. In the oil palm, analysis of yield components and their relative contributions towards yield will give a better chance of selecting high yielding progeny [3, 4]. Several works have previously estimated the genetic variation of the different oil yield components of oil palm [5-7]. There is a high genetic variability among the oil palm progenies, indicating ample scope for further breeding and selection [8].

Principal component analysis (PCA) used in this study is a descriptive procedure for analyzing relationships that may exist in a set of quantitative variables. Genetic diversity could be estimated with such quantitative traits using multivariate analysis tools, like PCA and a tree diagram hierarchical clustering technology analysis [9]. These taxonomic relationships analysis tools were chosen as efficient approaches to perform genetic diversity of quantitative agronomical characters of the new oil palm progenies test population. The objective of this study was to

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evaluate the magnitude of genetic diversity within the introgressed *Dura* × *Tenera* (D × T) oil palm progenies of the third selection cycle of the Specialized Centre for Oil Palm Research (CEREPAH) of Cameroon, using multivariate and clustering tools and to determine correlation among the studied important agronomic traits under Cameroonian climatic conditions.

2. Materials and Methods

In this study, 25 *Dura* × *Tenera* progenies (Table 1) of the third selection cycle of oil palm breeding program were evaluated in the experimental field of CEREPAH, Cameroon (3°46′-4°01′ N latitude and 9°44′-10°04′ E longitude) from 2004 to 2014. A total of 2,730.49 mm of annual mean rainfall and 27.36 °C of annual mean temperature were recorded during this study. The progeny test experiment was conducted in a randomized complete block design with three replications. The palms were laid down in a triangular planting system at 9 m apart with 12 palm plants per progeny. The oil palm field agronomic protocol steps were applied to achieve healthy plants. The collection of data was focused on nine oil palm agronomical traits, namely, fresh fruit bunch weight (FFB), bunch number (BN), spikelet weight (SpW), average fruit weight (AFW), kernel to fruit ratio (K/F), kernel to bunch ratio (K/B), oil yield (OY) and kernel yield (KY), following the method implemented by Mandal and Kochu [10]; while the vegetative trait, namely, palm height increment (HI) of trees, was determined in cm per year [11], following Eq. (1):

Table 1 *Dura* × *Tenera* oil palm progenies from CEREPAH, Cameroon (2004-2014) used in this study.

Progenies	Parents	Origin of *Tenera*/*Pisifera*	Origin of *Dura*	Origin of grandparent *Tenera*/*Pisifera*	Origin of grandparent *Dura*
LM21661	LM2T × DA115D	BRT10	Dabou		
LM22478	LM5100D × LM11096T	DA2356	LM9838	DA115D × LM269D	LM2T × WI10T
LM21761	LM11087T × LM2749D	LM9175	DA787	LM5T × WI15T	DA10D × DA 3D
LM22099	LM11087T × LM7409D	LM9175	LM7899	LM5T × WI15T	LM3257D AF
LM22001	LM11088T × LM2531D	LM9175	DA507	LM5T × WI15T	DA115D AF
LM22527	LM11088T × LM2781D	LM9175	DA787	LM5T × WI15T	DA10D × DA3D
LM22534	LM11088T × LM7811D	LM9175	LM7899	LM5T × WI15T	LM3257D AF
LM21884	LM11089T × LM2749D	LM9175	DA787	LM5T × WI15T	DA10D × DA3D
LM21864	LM12963T × LM5100D	LM9175	DA2356	LM5T × WI15T	DA115 D × LM269D
LM22130	LM11091T × LM2749D	LM9287	DA787	LM5T × WI1T	DA10D × DA3D
LM21709	LM11091T × LM5100D	LM9287	DA2356	LM5T × WI1T	DA115 D × LM269D
LM21706	LM11097T × LM2531D	LM9927	DA507	LM5T × WI10T	DA115D AF
LM21787	LM11097T × LM5100D	LM9927	DA2356	LM5T × WI10T	DA115 D × LM269D
LM21839	LM11097T × LM7422D	LM9927	LM7899	LM5T × WI10T	LM3257D AF
LM21925	LM7422D × LM11091T	LM7899	LM9287	LM3257D × LM3257D	LM5T × WI1T
LM21728	LM12960T × LM5100D	LM9287	DA2356	LM5T × WI1T	DA115D × LM269D
LM21790	LM12960T × LM7409D	LM9287	LM7899	LM5T × WI1T	LM3257D AF
LM21881	LM12961T × LM2509D	LM9287	DA507	LM5T × WI1T	DA115D AF
LM22575	LM12961T × LM2749D	LM9287	DA787	LM5T × WI1T	DA10D × DA3D
LM21852	LM12961T × LM5155D	LM9287	LM2911	LM5T × WI1T	LM269D × DA115D
LM21886	LM12965T × LM2509D	LM9927	DA507	LM5T × WI10T	DA115D AF
LM21867	LM12965T × LM2749D	LM9927	DA787	LM5T × WI10T	DA10D × DA3D
LM21874	LM12967T × LM2781D	LM9927	DA787	LM5T × WI10T	DA10D × DA3D
LM21836	LM12967T × LM2509D	LM9927	DA507	LM5T × WI10T	DA115D AF

$$\text{HI (cm/year)} = \frac{\text{height at year } t}{t - 2} \quad (1)$$

where, t is the age of the palm.

The recorded data for statistical analysis of all parameters were mean values. Determination of the level of interrelationship between traits was done with Pearson's correlation coefficients [12]. Cluster analysis was performed to determine genetic distance between progenies and cluster diagram was constructed following grower's method to study the dissimilarities among progenies with the help of R program statistic tool version 3.0.3. Scatter plots were visualized based on the principal components (PCs) to illustrate the variability patterns in the studied oil palm progeny test population.

3. Results and Discussion

An important prerequisite for breeding programs in crop improvement is the estimation of genetic variability. The co-association of economical traits can be evaluated on the basis of the presence of genetic variability among the traits. By this approach, very high variability was observed among the studied traits in the present study. The described basic features of statistical analysis showed a wide diversity of the nine studied traits in the 25 oil palm progenies of the test population. Traits, such as FFB (kg), K/F (%) and K/B (%) showed wide range of high variance values. On the other hand, OY (tons), AFW (g), BN, SpW (kg) and KY (tons) showed little variant values (Table 2).

Exploitation of variability for selection of these traits in the studied population could yield good response. Other studies found significant variability and diversity among *Dura* × *Pisifera* progeny populations [7, 8, 13]. Okwuagwu et al. [3] also reported significant variability and diversity in *Dura* × *Tenera* oil palm population for FFB trait. It has also been reported by Talebi et al. [14] that in quantitative study, agronomic features with high variance and significant variability can be used in breeding programs for genetic improvement of varieties. OY, AFW, BN, SpW and KY showed little variance in the present study. Little variance values were also reported by Malik et al. [15] in their genetic diversity analysis of morpho-genetic traits in Desi chickpea (*Cicer arietinum*).

In this study, the correlation coefficients between the nine studied traits of 25 oil palm progenies (Table 3) were estimated. OY showed positive and high significant association with FFB ($P < 0.001$; $r = 0.97$), BN ($P < 0.001$; $r = 0.85$) and KY ($P < 0.001$; $r = 0.55$). The result showed that OY trait is thus an expression of multi-association trait components resulting from action of various other oil palm traits. There was also high strong positive association between KY and FFB ($P < 0.001$; $r = 0.66$), BN ($P < 0.001$; $r = 0.71$), KF ($P < 0.001$; $r = 0.88$) and KB ($P < 0.001$; $r = 0.91$). KY was also significantly correlated with AFW ($P < 0.05$; $r = 0.49$). Moreover,

Table 2 Descriptive statistics for the nine studied quantitative traits in 25 oil palm progenies from CEREPAH, Cameroon.

Traits	Range	Mean ± SE	σ^2	σ
Height increment (cm)	21.4-35.8	25.6 ± 0.4	14.1	3.8
Fresh weight of fruit bunch (kg)	90.3-140.3	112.4 ± 1.2	134.3	11.6
Total bunches number	8.1-14.6	11.6 ± 0.2	2.7	1.6
Spikelet weight (kg)	7.5-12.4	9.8 ± 0.1	1.3	1.1
Average fruit weight (g)	6.8-9.4	8.1 ± 0.1	0.6	0.8
Kernel to fruit ratio (%)	43.5-85.5	61.4 ± 1.2	145.6	12.1
Kernel to bunch ratio (%)	27.6-56.1	40.3 ± 0.8	70.7	8.4
Kernel yield (tons)	4.99-9.7	6.5 ± 0.2	3.0	1.7
Oil yield (tons)	4.04-7.4	5.7 ± 0.1	0.4	0.6

σ^2 = variance; σ = standard deviation; SE = standard error.

Table 3 Correlation coefficients among nine quantitative traits of 25 oil palm progenies.

Variables	FFB	BN	SpW	AFW	KF	KB	KY	OY
HI	0.26	0.17	0.11	0.24	0.22	0.22	0.28	0.18
FFB		0.91^a	-0.35	-0.16	0.24	0.30	0.66^a	0.97^a
BN			-0.65^a	-0.05	0.37	0.41^b	0.71^a	0.85^a
SpW				-0.10	-0.31	-0.29	-0.37	-0.31
AFW					0.76^a	0.71^a	0.49^b	-0.29
KF						0.99^a	0.88^a	0.11
KB							0.91^a	0.19
KY								0.55^a

HI: height increment; FFB: fresh fruit bunch weight; BN: bunch number; SpW: spikelet weight; AFW: average fruit weight; KF: kernel to fruit ratio; KB: kernel to bunch ratio; KY: kernel yield; OY: oil palm yield.

^{a} Significant at $P < 0.001$; ^{b} significant at $P < 0.05$.

Table 4 Eigenvalue, proportion of variability and quantitative traits that contributed to the three principal components (PCs) in 25 oil palm progenies of Cameroon.

Traits	PC1	PC2	PC3
Height increment (cm)	0.292	0.122	0.850
Fresh fruit bunch (kg)	0.771	-0.583	0.177
Total bunches number	0.807	-0.546	-0.098
Spikelet weight (kg)	-0.532	0.348	0.567
Average fruit weight (g)	0.339	0.847	-0.046
Kernel to fruit (%)	0.721	0.673	-0.097
Kernel to bunch (%)	0.752	0.624	-0.067
Kernel yield (tons)	0.946	0.266	0.020
Oil yield (tons)	0.679	-0.667	0.166
Eigenvalue	4.169	2.851	1.130
Cumulative eigenvalue	4.169	7.020	8.150
Variance (%)	46.321	31.676	12.554
Cumulative of variance (%)	46.321	77.997	90.551

KB showed strong positive association ($P < 0.001$) with AFW, KF and positive significant correlation ($P < 0.05$) with BN. KF and BN also showed positive significant association with AFW and FFB, respectively. These results could be exploited to improve yields by indirect selection for these traits. The characters that showed positive significant correlation can be exploited to achieve high yield *Tenera* hybrid of oil palm elites for seed production in Cameroon.

PCA is a multivariate tool analysis, which helps to obtain at the same time component groups with more important traits. This approach was widely implemented by several other plant scientists for specific breeding [16-20]. In this study, PCA revealed that the first three principal components (PC) with eigenvalue greater than 1, accounted for 90.55% variation within the 25 progenies (Table 4). The first principal component (PC1) related to the following progenies: LM21674, LM22130, LM21709, LM21925, LM21728, LM21790, LM21661, as determined with 46.32% of variation, while eight characters gave positive values apart from SpW, which produced negative value. KY, BN, FFB, KB, KF and OY per progeny were the main traits that respectively contributed more to the variation among the studied oil palm progenies. PC2 explained 31.68% of all the accumulated variation, in which AFW, KF and KB were the main contributing traits in this component.

HI and SpW were the major traits in PC3.

Based on the first two principal components of the biplot graph, the studied individual genetic differences were observed between *Dura* × *Tenera* progenies and can be visualized on the scatter plot (Fig. 1). An important genetic diversity was revealed by the high

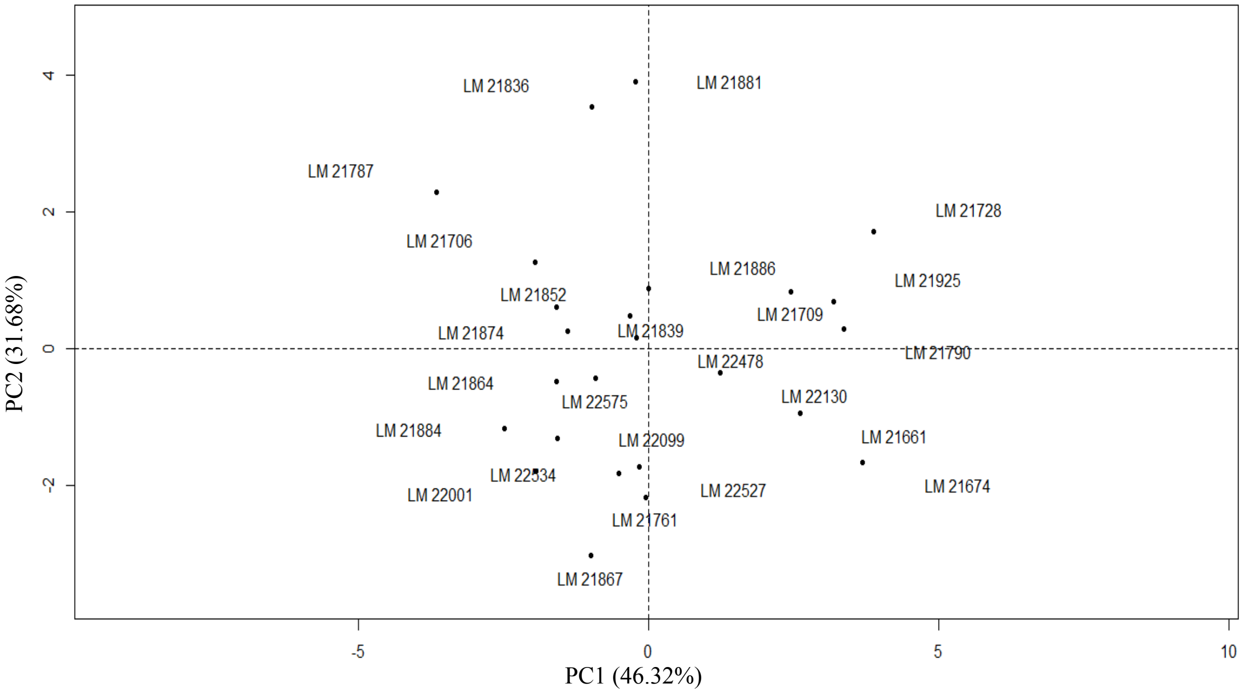

Fig. 1 Scatter plot of first two principal components contributing 78% of the total variation for nine quantitative traits in 25 oil palm progenies of Cameroon.

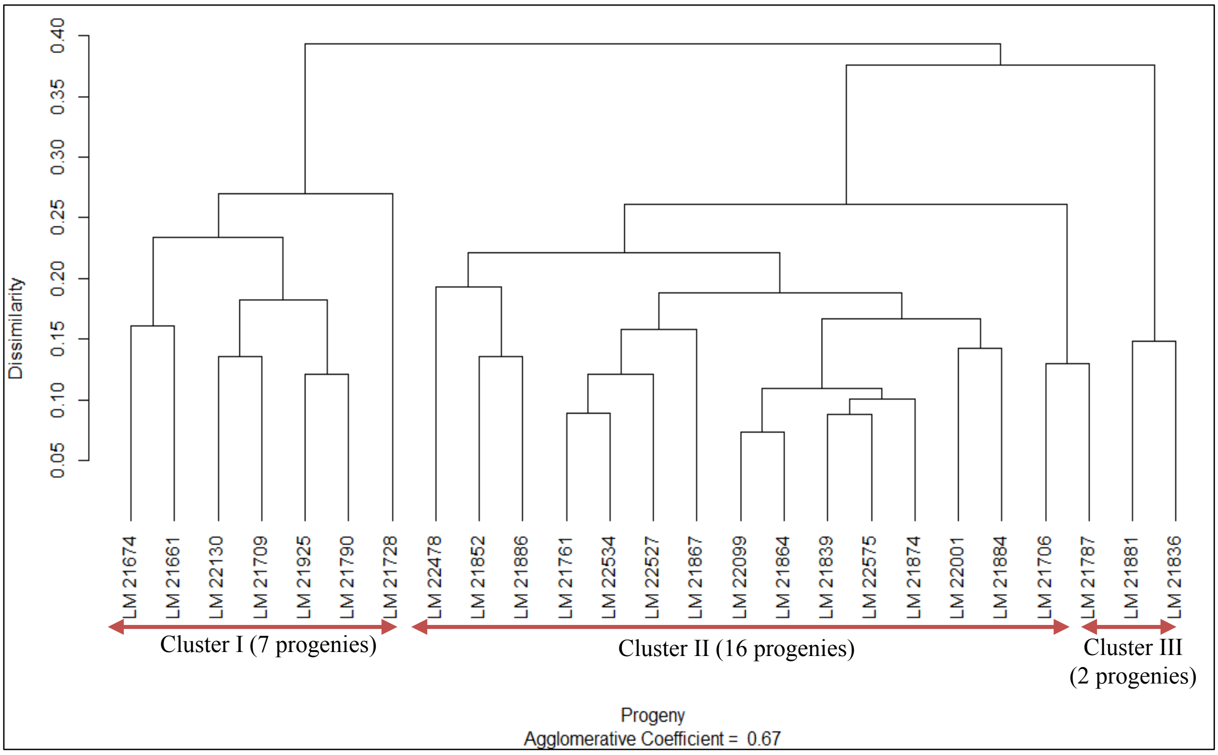

Fig. 2 Dendrogram depicting genetic relationships of 25 oil palm progenies based on nine studied characters.

Table 5 Means and standard errors of the nine studied oil palm variables in the three clusters with the related number of progenies.

Characters	Cluster I (7 progenies)	Cluster II (16 progenies)	Cluster III (2 progenies)
Height increment (cm)	26.43 ± 1.36	25.41 ± 2.40	25.59 ± 2.37
Fresh weight of fruit bunch (kg)	123.70 ± 4.05	108.31 ± 5.23	94.45 ± 5.24
Total bunches number	13.37 ± 0.46	10.79 ± 0.48	8.94 ± 0.14
Spikelet weight (kg)	8.81 ± 0.48	10.24 ± 0.67	11.18 ± 0.74
Average fruit weight (g)	8.56 ± 0.31	7.75 ± 0.25	9.23 ± 0.25
Kernel to fruit (%)	74.35 ± 4.54	54.08 ± 3.75	78.66 ± 4.88
Kernel to bunch (%)	49.44 ± 4.03	35.26 ± 2.52	51.59 ± 3.98
Kernel yield (tons)	8.74 ± 0.79	5.45 ± 0.44	6.90 ± 0.41
Oil yield (tons)	6.20 ± 0.36	5.50 ± 0.32	4.64 ± 0.19

progeny dissemination in all the four compartments of the biplot graphic display. The progenies closest to each other in this biplot graph presented less or no differences in the expression of the phenotypic specific studied traits (Fig. 1). However, progenies occurring far from the origin illustrated more variability in the expression of traits. Thus, the parent crosses of these progenies can be effectively used for the hybrid breeding program, with the evidence to also improve the oil palm germplasm genetic potential.

Cluster analysis used in this study further helped to group or show dissimilarity relationships among progenies depending on morpho-genetic traits. Cluster diagram based on Euclidean dissimilarity constructed by gower's method, grouped the 25 oil palm progenies into three clusters at 0.35 dissimilarity value level (Fig. 2).

Table 5 shows the range, means and standard errors of the nine studied oil palm variables in the three clusters of the 25 oil palm progenies. The similarity matrix is presented in Table 6. Cluster I contained seven progenies, which were characterized by high production of FFB and BN per progeny, OY and KY per hectare. Cluster II comprised of 16 progenies, classified by low HI per year, moderate production of FFB and BN, progeny with moderate SpW, AFW, KF and KB, medium OY and KY per hectare. Cluster III contained two progenies, which were characterized by moderate HI and KY, low OY, FFB and BN, high mean values for SpW, AFW, KF and KB. Such hierarchical grouping of individuals is useful to oil palm breeders for the selection of progenies with traits of interest needed in the production of superior hybrid commercial varieties. Oil palm crosses can be selected from the displayed clusters.

Cluster analysis, which supported the results of correlation analysis, both indicated that OY per hectare, FFB, BN, KY, KF and KB may be improved simultaneously and put together in a single progeny for yield improvement. This was obvious from the fact that these components are positively associated with yield and with themselves. Furthermore, progenies with high mean values for these characters and those with high OY and KY were grouped in same cluster. Camillo et al. [21] reported evidence of correlation between oil palm seed trait components in their oil palm clustering study of Brazilian germplasm bank.

4. Conclusions

Through the characterization of the oil palm population of introgressed progenies in this study, some interesting crosses with specific traits were identified. The studied oil palm population was found to exhibit wide genetic diversity for most of the expressed oil palm characters. To improve overall yield, the following traits must be considered: FFB, BN, KF, KB and KY. There was a positive significant correlation between these traits and yield as confirmed

Table 6 Similarity matrix of oil palm progenies studied.

Progeny	LM21674	LM21661	LM22478	LM21761	LM22099	LM22001	LM22527	LM22534	LM21884	LM21864	LM22130	LM21709	LM21706	LM21787	LM21839	LM21925	LM21728	LM21790	LM21881	LM22575	LM21852	LM21886	LM21867	LM21874	LM21836
LM21674	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21661	0.838775	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22478	0.533177	0.625707	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21761	0.671326	0.759727	0.755680	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22099	0.541579	0.632801	0.784315	0.855119	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22001	0.470729	0.614730	0.680459	0.797789	0.877728	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22527	0.609025	0.746494	0.788746	0.870539	0.868255	0.849662	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22534	0.618060	0.720045	0.800463	0.910667	0.856215	0.830130	0.888057	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21884	0.492078	0.576768	0.765647	0.788004	0.844636	0.857618	0.794461	0.856723	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21864	0.565524	0.656746	0.816022	0.856205	0.926145	0.849763	0.845702	0.861292	0.878901	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM22130	0.674791	0.826631	0.756582	0.801267	0.733263	0.727060	0.827606	0.768661	0.652908	0.755769	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21709	0.699884	0.838315	0.640815	0.671791	0.605583	0.599380	0.709543	0.648802	0.534845	0.629528	0.864562	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21706	0.467559	0.587758	0.747353	0.709998	0.792098	0.779164	0.731913	0.730708	0.756919	0.826826	0.742956	0.653326	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21787	0.382279	0.481340	0.706685	0.644242	0.726601	0.693837	0.635881	0.646043	0.720312	0.784751	0.636538	0.535105	0.870121	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21839	0.541052	0.640114	0.798823	0.767089	0.860060	0.803306	0.767143	0.765341	0.795403	0.894717	0.760245	0.632565	0.868302	0.809353	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21925	0.769707	0.844611	0.613760	0.649476	0.543020	0.513048	0.657892	0.638415	0.503259	0.567145	0.779684	0.873488	0.577800	0.471381	0.570182	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21728	0.623660	0.700744	0.607319	0.493672	0.4110029	0.395507	0.540351	0.504151	0.399359	0.434975	0.656214	0.788978	0.458772	0.340551	0.438011	0.835806	NA	NA	NA	NA	NA	NA	NA	NA	NA
LM21790	0.685386	0.787391	0.533577	0.607144	0.5260757	0.536710	0.597773	0.566352	0.423075	0.525937	0.770167	0.847252	0.552235	0.434159	0.572779	0.878973	0.775675	NA	NA	NA	NA	NA	NA	NA	NA

(Table 6 continued)

Progeny	LM21674	LM21661	LM22478	LM21761	LM22099	LM22001	LM22527	LM22534	LM21884	LM21864	LM22130	LM21709	LM21706	LM21787	LM21839	LM21925	LM21728	LM21790	LM21881	LM22575	LM21852	LM21886	LM21867	LM21874	LM21836
LM 21881	0.502859	0.592096	0.587421	0.532551	0.5770359	0.525950	0.551022	0.541147	0.557089	0.629403	0.658511	0.730702	0.746786	0.702238	0.680962	0.686478	0.638313	0.643984	NA	NA	NA	NA	NA	NA	NA
LM 22575	0.592027	0.691089	0.813080	0.849582	0.897046	0.849301	0.848678	0.839077	0.803673	0.906534	0.812035	0.684354	0.845366	0.760496	0.912171	0.621972	0.489801	0.619402	0.633249	NA	NA	NA	NA	NA	NA
LM 21852	0.630575	0.723105	0.817589	0.757161	0.780418	0.676563	0.785126	0.780925	0.732519	0.821011	0.820416	0.701145	0.728961	0.702878	0.836164	0.664400	0.532229	0.590584	0.651808	0.810560	NA	NA	NA	NA	NA
LM 21886	0.664278	0.756809	0.795974	0.747188	0.785118	0.715595	0.784182	0.784989	0.788982	0.829718	0.820715	0.730193	0.754028	0.689567	0.848340	0.698607	0.585310	0.618423	0.720551	0.842174	0.864222	NA	NA	NA	NA
LM 21867	0.557185	0.701186	0.670506	0.843052	0.770531	0.846204	0.838667	0.844881	0.807844	0.786827	0.782207	0.672007	0.674733	0.601028	0.681545	0.599504	0.478986	0.584943	0.450903	0.768558	0.670315	0.660341	NA	NA	NA
LM 21874	0.566718	0.659248	0.859622	0.788549	0.865185	0.781597	0.827852	0.837177	0.848727	0.918520	0.747570	0.629507	0.829497	0.797416	0.905279	0.597921	0.470316	0.517737	0.656517	0.893805	0.865136	0.866791	0.716689	NA	NA
LM 21836	0.509751	0.590484	0.640736	0.537693	0.599342	0.525893	0.566527	0.556652	0.586714	0.658225	0.658454	0.711687	0.746729	0.751335	0.719702	0.649845	0.543946	0.572888	0.851667	0.637855	0.775364	0.760459	0.450846	0.718419	NA

NA: non available.

by the used PCA multivariate analysis tool. Obtained clusters of studied progenies could be exploited by oil palm breeders for identification and selection of interesting progeny crosses needed to boost and improve the oil palm breeding program and genetic resource materials, in terms to develop superior hybrid *Tenera* varieties with the introgessed traits of interest that will be distributed to oil palm farmers.

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