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# GENETIC VARIABILITY OF MPOB-CAMEROON OIL PALM GERMPLASM BASED ON MORPHOLOGICAL TRAITS USING MULTIVARIATE ANALYSIS

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## ABSTRACT

*Understanding genetic variability and its distribution among breeding materials is a prerequisite to improve conservation programmes and design breeding strategies. In this study, 31 populations of* dura *palms from MPOB-Cameroon oil palm germplasm were evaluated for 21 quantitative traits. Data retrieved from the MPOB Breeding Information System (MPOB-BIS™) was investigated for genetic variability using principal component analysis (PCA) and cluster analysis (CA). The first six principal components (PC1-PC6) with eigenvalue >1.0, accounted for 91.89% of the total variability. The first principal component, PC1 which accounted for 38.35% of the total variation was the largest, contributed by oil yield and total economic product. Whilst PC2 with 16.86% total variation was positively associated with bunch index, bunch number and kernel yield. Population CMR 03 is considered extremely distinct and most positive along PC1 as it performed well in most of bunch quality traits. Population CMR 13 is most positive towards PC2 and among the most negative towards PC1 due to good performance in some vegetative traits studied. CA revealed greater variation among the materials evaluated. Complementing this study with molecular analysis provides the impetus for leveraging new genetic resources in future oil palm improvements and more tractable conservation of oil palm germplasm.*

**Keywords**: cluster analysis, core collection, genetic resources, morphological characteristics, principal component analysis.

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## INTRODUCTION

Oil palm has been recognised as the highest oil-producing tropical perennial crop. It is one of the key sources of vegetable oils in the world. Malaysia and Indonesia contribute more than one-third of the global vegetable oil production (OECD/FAO, 2019). Palm oil offers great potential in food and non-food applications such as cooking, production of shortening, soap, surfactant, *etc*. Global population growth, with rapidly improving living standards and dietary customs, has led to a gradual increase in market demand for palm oil consumption (Verheye, 2010). This is also reflected in Malaysia's oil palm plantation areas, which have grown exponentially from 54 700 ha in 1960 to 5.90 million hectares in 2019 (MPOB, 2020).

Oil palm (*Elaeis guineensis* Jacq.) is native to West Africa where the oil palm belt runs through Sierra Leone, Liberia, Ivory Coast, Ghana, Cameroon, Nigeria and the Democratic of Congo (formerly known as Zaire) (Hartley, 1988). The highest allelic diversity was identified among the Nigerian oil palm populations, suggesting the possible centre of oil palm origin (Bakoumé *et al*., 2015; Zeven,

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1964). In Southeast Asia, the African oil palm was initially introduced with four seedlings planted in Bogor Botanical Gardens, Indonesia in 1848, giving rise to the Deli *dura* populations. It was brought into Malaysia in 1878 and has become the backbone of oil palm planting materials in the country (Rajanaidu *et al*., 2013). Due to the extremely narrow genetic base of oil palm caused by the restriction in a number of ancestral progenitors, researchers from the Malaysian Palm Oil Board (MPOB) have mounted a series of prospection exercises throughout the oil palm belt in Africa and America to explore new genetic resources for future breeding programmes (Corley and Tinker, 2016; Rajanaidu, 1994).

Oil palm germplasm was collected from 11 African countries including Nigeria, Cameroon, Zaire, Angola, Ghana, Guinea, Gambia, Madagascar, Sierra Leone, Senegal and Tanzania to form the largest *ex-situ* conservation programme (Rajanaidu *et al*., 2013). This is imperative to broaden the genetic base of current oil palm materials to improve yield potential, enhance nutritional qualities and tackle future challenges in the oil palm industry. In 1984, through scientific collaboration efforts between MPOB and Pamol, Unilever successfully amassed oil palm materials from the Western and Eastern parts of Cameroon of West Africa (Rajanaidu, 1986). One to 15 open-pollinated palms were collected from 32 different sites in Cameroon, to cover the entire country as much as possible within the available time frame. A total of 58 *dura* bunches were sampled during the prospection and the data was recorded *in situ*. Bunch weight, stalk weight, fruit diameter, nut diameter and mean fruit weight showed a significant difference between the sites. In terms of material quality, the Cameroon *duras* had a mean bunch weight of 16.83 kg, a mean fruit weight of 10.33 g and a mesocarp to the fruit of 39.69% (Rajanaidu, 1986).

Currently, oil palm genetic resources in MPOB are maintained in the form of field genebank to safeguard the long term interest of the Malaysian oil palm industry. Despite being readily available for use, conservation in the form of field genebank necessitates large space and high maintenance costs. Aside from that, it is also a labour and time-intensive effort. Understanding and assessing the genetic diversity of oil palm germplasm is a key pillar for establishing a core collection and crop improvement. According to Frankel *et al*. (1984), a core collection is a small number of accessions that represent the genetic diversity of a crop species and wild relatives with the least amount of repetition. Morphological (Sapey *et al*., 2017), biochemical (Hayati *et al*., 2004), cytological (Castilho *et al*., 2000) and molecular techniques (Zulkifli *et al*., 2012) were employed to gauge germplasm diversity, with morphological traits being commonly evaluated as they are direct, rapid and inexpensive (Suzana *et al*., 2020).

Plant breeders frequently measure a large number of variables, some of which may lack sufficient discriminatory power for germplasm evaluation, characterisation and evaluation (Das *et al*., 2017). In this case, multivariate analysis enables discrimination by eliminating variables that are difficult to measure and contribute little to explaining variation (Arandas *et al*., 2017). Over the years, the use of multivariate analysis in evaluating the genetic diversity of various crops such as tomato (Evgenidis *et al*., 2011), rice (Sohrabi *et al*., 2012), wheat (Ahmad *et al*., 2014), groundnut (Jonah *et al*., 2014), cauliflower (Aleem *et al*., 2021), bean (Girgel, 2021) has increased as they help to explain variations among the genotypes. Among the multivariate tools, principal component analysis (PCA) and cluster analysis (CA) are widely utilised to assess genetic divergence and classify germplasm materials (Li-Hammed *et al*., 2016). PCA is a data reduction technique by transforming the multi-correlated variables into another set of uncorrelated variables for further study, whilst CA is an exploratory data analysis method for grouping accessions based on phenotypic performance and depicts the pattern of relatedness between genotypes (Bhandari *et al*., 2017). In this study, these techniques are adopted to assess the genetic variability in the MPOB-Cameroon oil palm germplasm. Various researches have been conducted on MPOB oil palm germplasm, however, these studies have yet to cover the entire population of MPOB-Cameroon germplasm. The findings from this study may provide important information for oil palm conservation and breeding strategies.

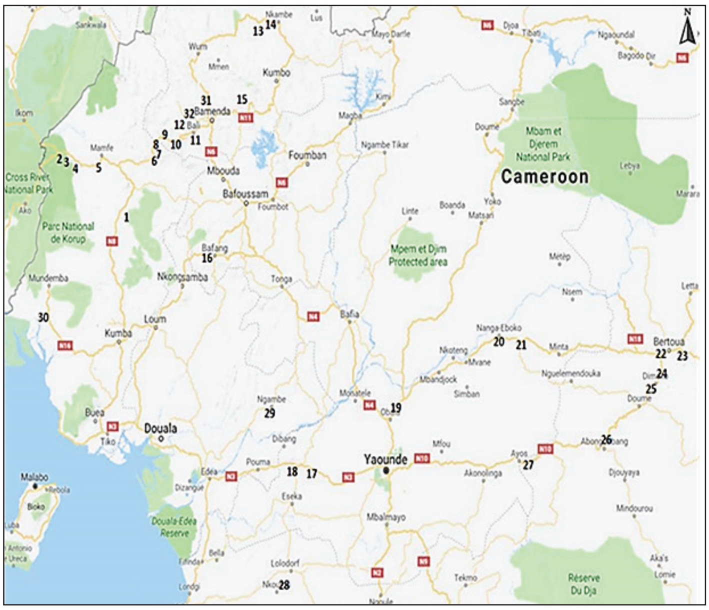
## MATERIALS AND METHODS

### Planting Materials

A total of 3590 open-pollinated palms collected from 32 sites throughout Cameroon (*Figure 1*) were planted in MPOB Kluang Research Station Johor, Malaysia in 1986. A total of 1800 palms were laid down in two replicates using the Randomised Complete Block Design (RCBD) and named Trial 0.218 while another 1790 palms were grown using Complete Randomised Design (CRD) with two replications planted in Trial 0.219. All populations were planted at both trials. The palms at each site represent populations labelled as CMR (Cameroon) 01-32, hence a total of 32 populations were made. Population CMR 06, however no longer exists in both trials.

### Data Collection

A total of 21 quantitative traits were recorded for all accessions and their replications. Yield data collection of individual palms was conducted from



| Site No. | Area |
|---|---|
| 1 | 30 km from Nguti |
| 2 | 11 km from Eyumojok |
| 3 | Near to Site 2 |
| 4 | 16 km from Eyumojok |
| 5 | 6 km South of Mamfe |
| 6 | Kendem - 43 km from Mamfe |
| 7 | Mbeme - 50 km from Mamfe |
| 8 | Numba - 64 km from Mamfe |
| 9 | Widikum |
| 10 | Batibo |
| 11 | 8 km from Bali |
| 12 | Teze-Andek |
| 13 | Kikangko - 20 km from Miseje |
| 14 | Kamine - 16 km from Nkambe |
| 15 | Babessie - 40 km North of Ndop |
| 16 | 12 km from Bafang |
| 17 | 12 km from Yaounde-Douala Road |
| 18 | 15 km from Yaounde-Douala Road |
| 19 | 6 km from Obala-Bertoua Road |
| 20 | Nanga Eboko |
| 21 | At the junction of Betoua |
| 22 | 20 km from Bertoua |
| 23 | 14 km from Bertoua |
| 24 | 39 km from Betoua |
| 25 | Obila |
| 26 | 13 km from Abang Mbang |
| 27 | 7 km from Ayos |
| 28 | 101 km from Ebolowa |
| 29 | Ngambe |
| 30 | Ndian |
| 31 | Bafut - 18 km from Bamenda |
| 32 | Mbengwi |

*Figure 1. Collection sites in Cameroon.*

1990 until 1995 (Rajanaidu *et al*., 2017). The traits related to yield were fresh fruit bunch (FFB), bunch number (BNO) and average bunch weight (ABWT). Bunch quality components were evaluated from 1991-1993 by using the bunch analysis method developed by Blaak *et al.* (1963). Twelve bunch traits parameters were measured such as mean fruit weight (MFW), mean nut weight (MNW), mesocarp to fruit (MTF), kernel to fruit (KTF), shell to fruit (STF), oil to dry mesocarp (OTDM), fruit to bunch (FTB), oil to bunch (OTB), kernel to bunch (KTB), oil yield (OY), kernel yield (KY) and total economic product (TEP). Vegetative measurement was carried out in 1995 using a protocol developed by Corley and Breure (1981). Six parameters measured for vegetative traits were frond production (FP), petiole cross-section (PCS), rachis length (RL), height increment (HI), leaf area index (LAI) and bunch index (BI).

### Statistical Analysis

A dataset of 31 populations consisting of 2633 *dura* palms was systematically extracted from MPOB Breeding Information System (MPOB-BIS™) (Mohd Din *et al*., 2012) and the population means were calculated using Microsoft Excel version 14.0. The mean data were converted into a new dataset with a mean of zero and a standard deviation of one to remove all biases due to the different scales of variables (Bhandari *et al*., 2017). Correlation, coefficient of variation (CV) and multivariate analyses of PCA and CA were conducted using SAS version 9.4 (SAS Inc). In SAS software, the PRINCOMP procedure was used to execute a PCA, while the PRINQUAL method was applied to perform a multidimensional preference analysis. Average linkage cluster analysis known as the Unweighted Pair-Group Method with Arithmetic average (UPGMA) was employed to construct phylogenetic relationships among the populations from a distance matrix (Sokal and Michener, 1958).

## RESULTS AND DISCUSSION

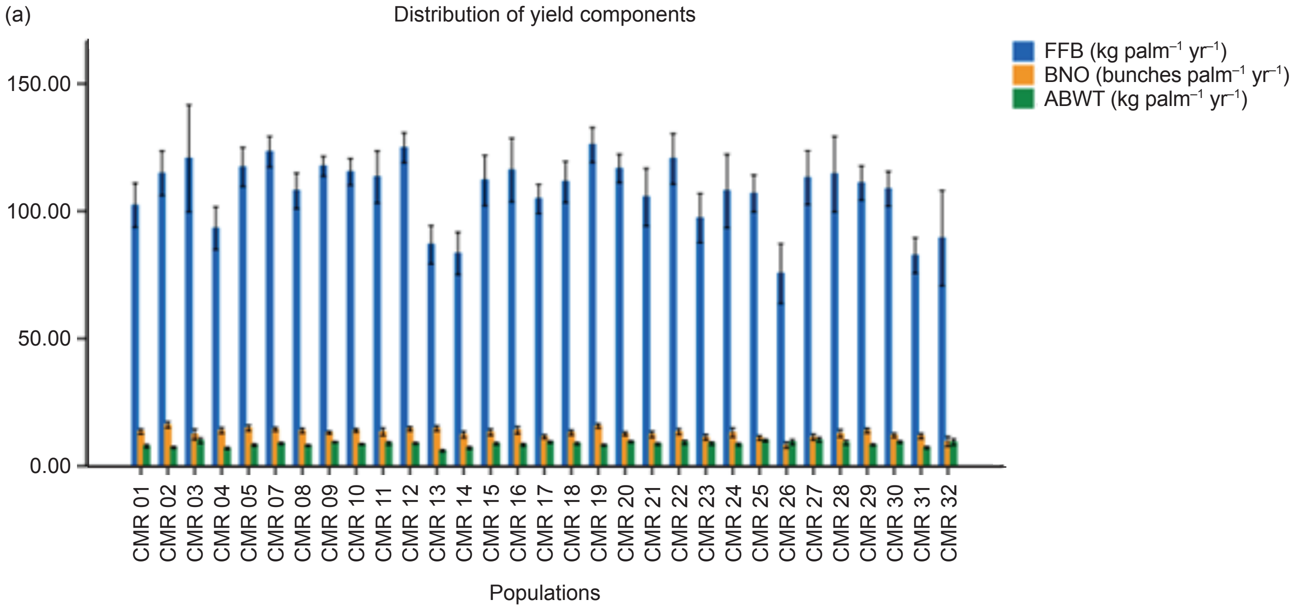
### Performance of Yield, Bunch Quality Components and Vegetative Traits

Among the 31 *dura* populations, CMR 19 produced the highest FFB yield (125.99 kg palm$^{-1}$ yr$^{-1}$) with a CV of 31%, attributed to the high BNO (15.69 bunches palm$^{-1}$ yr$^{-1}$) and moderate ABWT (8.22 kg palm$^{-1}$ yr$^{-1}$) (*Figure 2a*). In contrast, CMR 26 produced the lowest FFB yield (75.51 kg palm$^{-1}$ yr$^{-1}$) due to low BNO (8.22 bunches palm$^{-1}$ yr$^{-1}$) despite its high ABWT (9.37 kg palm$^{-1}$ yr$^{-1}$).

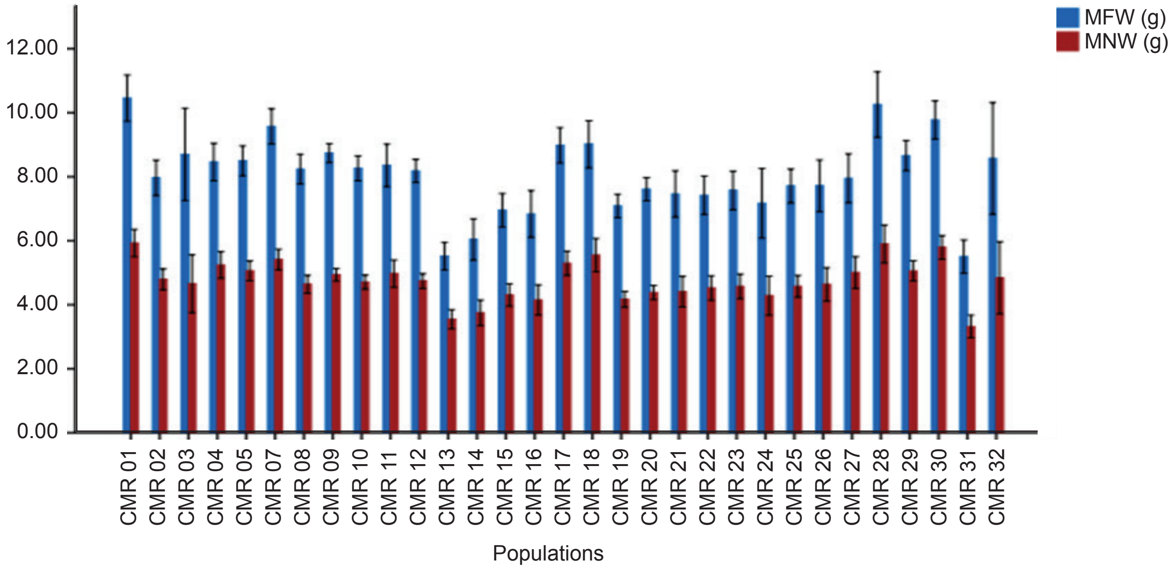
On the other hand, even with the highest BNO (16.19 bunches palm$^{-1}$ yr$^{-1}$), CMR 02 was not among the top FFB yielders due to its low ABWT (7.26 kg palm$^{-1}$ yr$^{-1}$), which is below the grand mean (8.61 kg palm$^{-1}$ yr$^{-1}$). These results suggest that high BNO together with moderate ABWT may contribute to high FFB yields as observed by Noh *et al.* (2012). As the selection of high-yielding palms is important for breeding purposes, the selection of CMR palms can be based on high BNO and moderate ABWT as these two traits are associated with high FFB yields. Therefore, CMR 19, CMR 12 and CMR 07 performed the best in terms of FFB, BNO and ABWT with CV values between 21%-35%. A CV of 20%-30% is tolerable for bunch yield traits of perennial crops, such as the oil palm (Hartley, 1988).

For bunch quality traits, population CMR 01 in Western Cameroon had the highest MFW (10.45 g) and MNW (5.93 g) (*Figure 2b*). Similarly, CMR 28 sourced from the South Province of Cameroon showed the same trend, with MFW and MNW values that were not significantly different from CMR 01. KTF varied from 10.93% to 15.47% with a trial mean of 12.55%, meanwhile, KTB ranged from 6.73% to 9.31% with a trial mean of 7.83%. The highest KTF and KTB were observed in CMR 13, with 15.47% and 9.31% respectively (*Figure 2d*). The highest FTB value was also recorded in CMR 01 (70.49%) and the lowest was found in CMR 14 (61.01%) (*Figure 2e*). As an indicator of pollination efficiency, high FTB is necessary to produce high OTB (Myint *et al.*, 2019; Noh *et al.*, 2010). It is interesting to note that the average FTB for MPOB-Cameroon germplasm (65.55%) is comparable with other MPOB-*dura* germplasm collections from Nigeria, Zaire and Angola with the range of 65.39% to 67.85% (Rajanaidu *et al.*, 2017). OY was highest in CMR 03 (*Figure 2f*) due to its high OTB (15.69%) (*Figure 2e*) and MTF (46.80%) (*Figure 2c*), which also contributed to the highest TEP (24.96 kg palm$^{-1}$ yr$^{-1}$) (*Figure 2f*) observed in this MPOB-Cameroon germplasm.

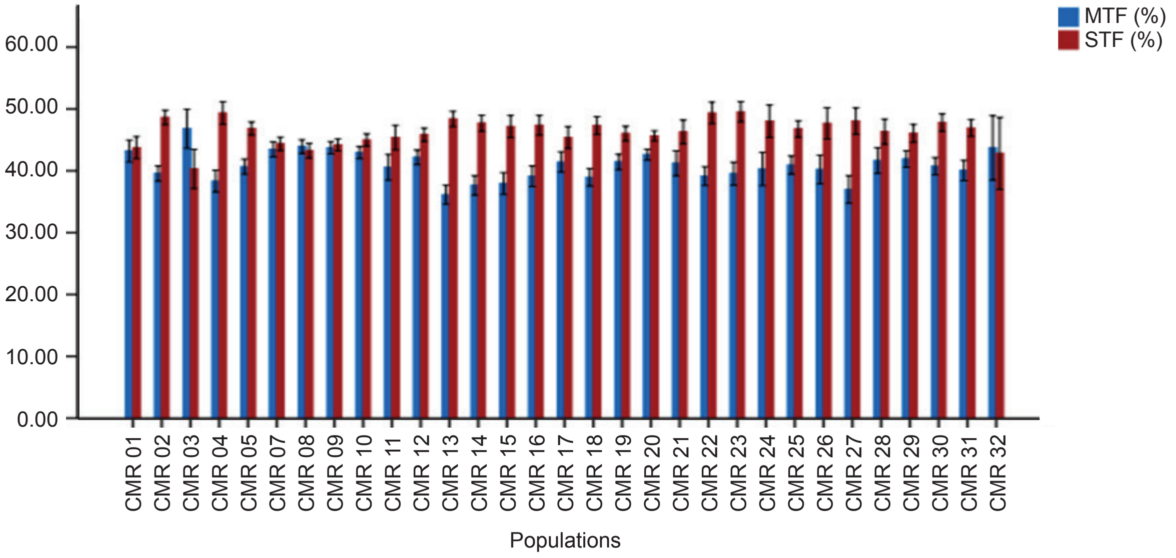
Vegetative traits can be an important character for the improvement of oil palm. Among the populations, CMR 18 and CMR 14 exhibited the highest FP of 30.49 and 30.41 fronds palm$^{-1}$ yr$^{-1}$ respectively, which have the potential to produce high yields (*Figure 2g*). Besides FP, smaller PCS and shorter RL are favoured characters to increase yield per unit area as they can be planted at higher density (Noh *et al.*, 2010). In this study, the PCS ranged from 12.67 cm$^2$ to 23.89 cm$^2$ whereas the RL varied from 4.08 m to 5.17 m. The smallest PCS and shortest RL were observed in populations CMR 13 and CMR 14, respectively (*Figures 2g, 2h*). The mean values of PCS (19.66 cm$^2$) and RL (4.75 m) of Cameroon *dura* materials were 49.32% and 16.67% respectively, lower than the DxP standard cross. The mean value for HI of this germplasm (24.42 cm yr$^{-1}$) is comparable to the DxP standard cross (24.46 cm yr$^{-1}$). With the lowest HI (20.43 cm yr$^{-1}$) and highest BI (0.46) (*Figures 2g, 2h*), CMR 02 is the best population for future breeding programmes not only for better yields but also in reducing harvesting costs. Among the MPOB germplasm collections, the *dura*s from Cameroon showed a high BI (trial mean of 0.42) in addition to Nigeria, Tanzania and Angola with a value ranging from 0.48 to 0.55 (Rajanaidu *et al.*, 2017). This was corroborated by Fadila *et al.* (2016) with regard to *dura*s from Cameroon.



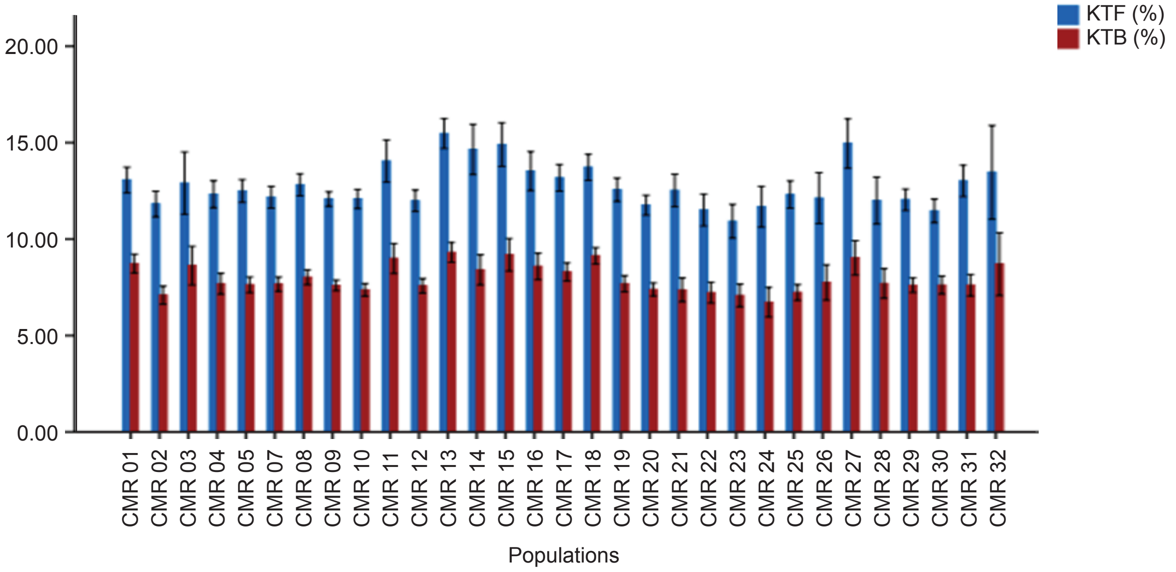
(b) Distribution of bunch quality traits (I)

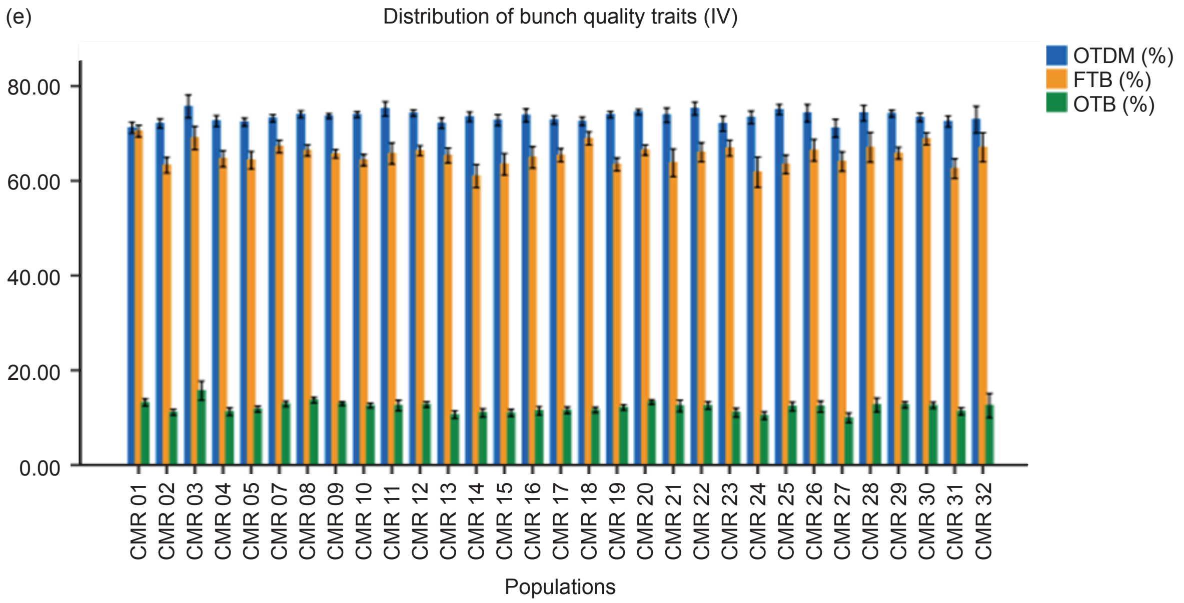


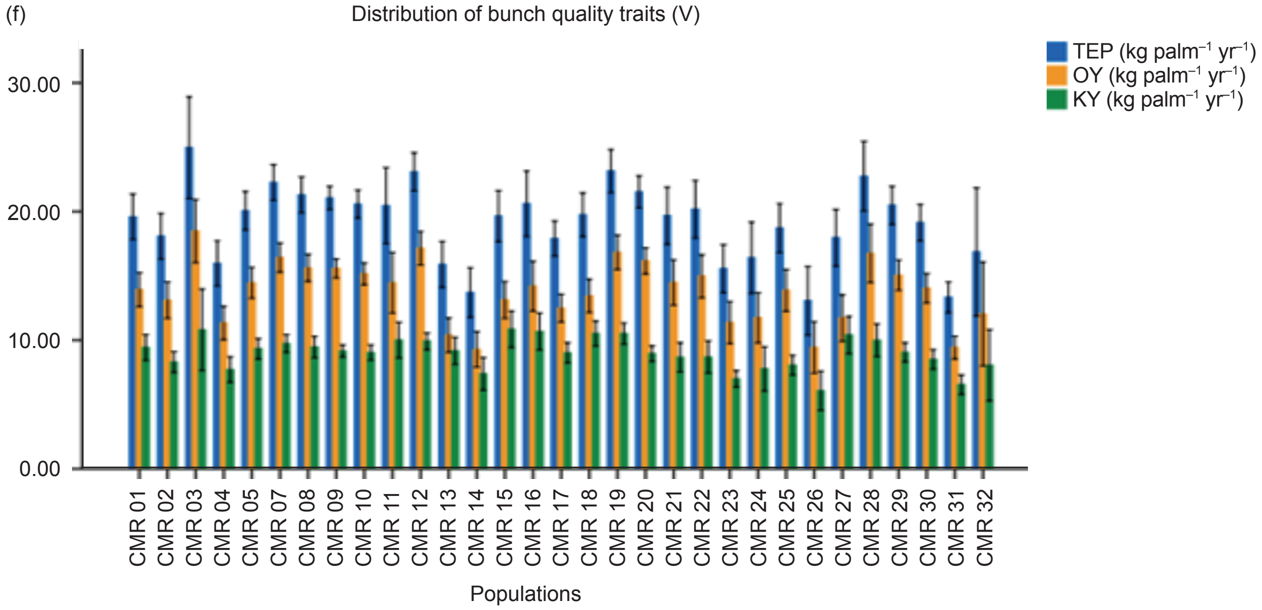
(c) Distribution of bunch quality traits (II)

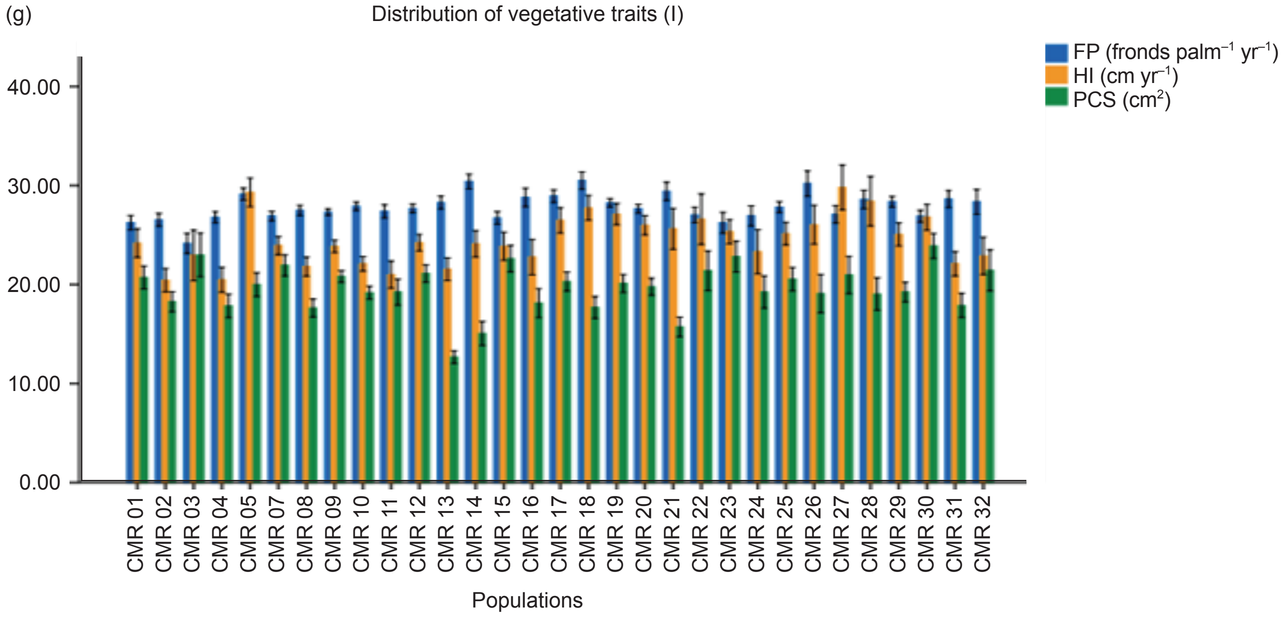


(d) Distribution of bunch quality traits (III)




(e) Distribution of bunch quality traits (IV)


(f) Distribution of bunch quality traits (V)


(g) Distribution of vegetative traits (I)

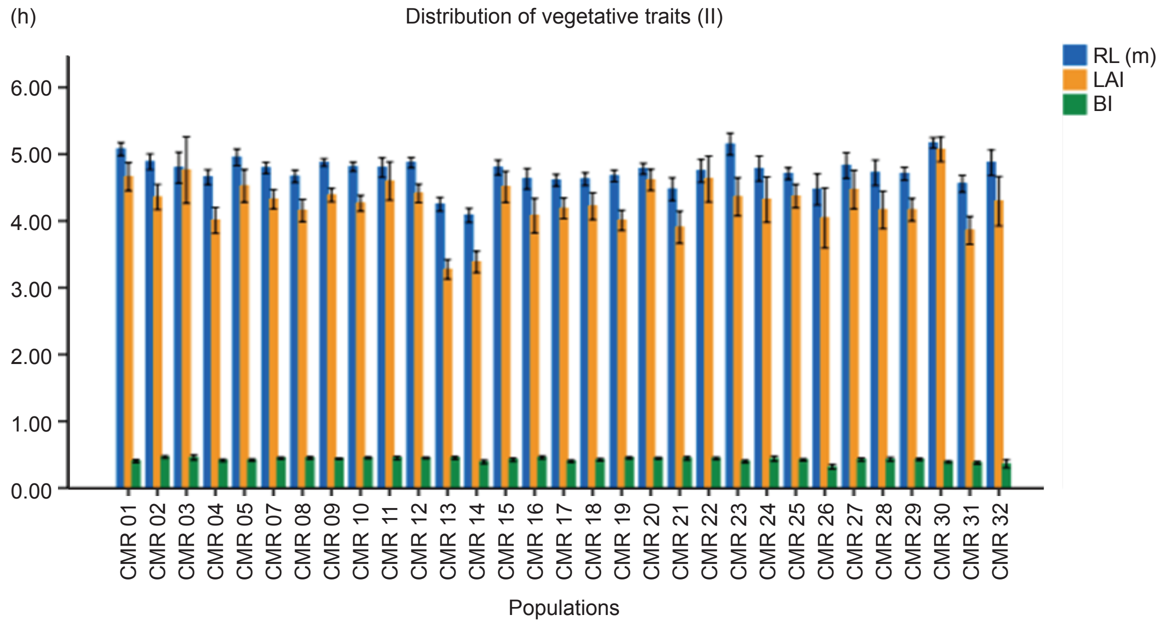


*Figure 2. Performance of MPOB-Cameroon* duras *germplasm. (a) Population mean of yield and its component, (b-f) population mean of bunch quality traits and (g-h) population mean of vegetative traits.*

## Correlation between Morphological Traits

Correlation analysis was computed to study the relationships between 21 traits among the 31 populations of Cameroon oil palm germplasm (*Table 1*). The correlations between yield-related traits were weak to moderate. FFB was positively correlated to both BNO ($r$=0.58, $p$≤0.01) and ABWT ($r$=0.41, $p$≤0.05). As expected, BNO was negatively correlated to ABWT ($r$=-0.50, $p$≤0.01). This result is in agreement with Suzana *et al*. (2020) who reported a negative correlation between BNO and ABWT as well for MPOB-Tanzania oil palm germplasm ($r$=-0.42). Okwuagwu *et al*. (2008) showed moderate ($r$=0.67) to strong ($r$=0.86) correlation between FFB-BNO while low ($r$=0.20) correlation between FFB-ABWT in their populations studied. These results indicated that an increase in BNO and ABWT likely corresponds to higher FFB yields. In contrast, BNO and ABWT seemed to be negatively correlated, usually considered antagonistic, as reported in several studies (Corley and Tinker, 2016; Marhalil *et al*., 2013). Henson and Mohd Tayeb (2003) reported that the mean ABWT increased with palm age while reducing the BNO.

The quality of bunches is also important to breeders as this characteristic is highly associated with the quality of palm oil. Strong positive correlations were observed between OY-TEP ($r$=0.98, $p$≤0.01) and MFW-MNW ($r$=0.97, $p$≤0.01). It is interesting to note that STF is negatively correlated with all bunch analysis traits and the highest correlation was observed between STF and MTF ($r$=-0.88, $p$≤0.01). Shi *et al*. (2019) reported that STF was negatively correlated to MTF ($r$=-0.96) and KTF ($r$=-0.50). This strong negative relationship between STF and MTF suggests that an increase in shell thickness would associate with a reduced mesocarp content and *vice versa*. While for vegetative traits, the LAI was positively and highly correlated to RL ($r$=0.86, $p$≤0.01) and PCS ($r$=0.85, $p$≤0.01), whereby both traits are important for palm compactness. A positive significant correlation between PCS-RL ($r$=0.39) and PCS-LAI ($r$=0.65) was also observed by Marhalil *et al.* (2013) in the evaluation of elite germplasm of MPOB-Nigerian *dura* × AVROS *pisifera* progenies. The MPOB-Cameroon germplasm thus, showed stronger relationships between LAI and RL, as well as with PCS. An increase in LAI promotes better photosynthetic capability in the crop, thus, enhancing yield production (Noor and Harun, 2004). In addition, FP was negatively correlated with all other vegetative traits except HI ($r$=0.31, $p$>0.05). Correlation between traits is indispensable for breeders to select vital characters from the studied traits (Sohrabi *et al*., 2012).

## PCA Indicating CMR 03 and CMR 13 Potential for Breeding Programme

PCA is a powerful tool for data compression and is capable of providing an overview of complex multivariate data (Bro and Smilde, 2014). PCA's task is to reduce the dimension of the data while retaining most of its original information. The PCA indicated that about 91.89% of the total variation of all studied traits is accounted for from the first six principal components (PCs) with eigenvalues of >1.0 (*Table 2*). As highlighted by Kaiser (1960), PCs with eigenvalues of >1.0 should be retained as it is

**TABLE 1. THE CORRELATION COEFFICIENT ANALYSIS OF MPOB-CAMEROON OIL PALM GERMPLASM BETWEEN 21 TRAITS**

| | Bunch yield | | | Bunch quality | | | | | | | | | | | | Vegetative measurement | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **FFB** | **BNO** | **ABWT** | **MFW** | **MNW** | **MTF** | **KTF** | **STF** | **OTDM** | **FTB** | **OTB** | **KTB** | **OY** | **KY** | **TEP** | **FP** | **PCS** | **RL** | **HI** | **LAI** | **BI** |
| FFB | 1.00 | | | | | | | | | | | | | | | | | | | | |
| BNO | 0.58$^{**}$ | 1.00 | | | | | | | | | | | | | | | | | | | |
| ABWT | 0.41$^{*}$ | -0.50$^{**}$ | 1.00 | | | | | | | | | | | | | | | | | | |
| MFW | 0.38$^{*}$ | -0.01$^{ns}$ | 0.44$^{**}$ | 1.00 | | | | | | | | | | | | | | | | | |
| MNW | 0.33$^{ns}$ | -0.01$^{ns}$ | 0.39$^{*}$ | 0.97$^{**}$ | 1.00 | | | | | | | | | | | | | | | | |
| MTF | 0.36$^{*}$ | -0.04$^{ns}$ | 0.44$^{*}$ | 0.54$^{**}$ | 0.32$^{ns}$ | 1.00 | | | | | | | | | | | | | | | |
| KTF | -0.27$^{ns}$ | -0.02$^{ns}$ | -0.26$^{ns}$ | -0.36$^{*}$ | -0.29$^{ns}$ | -0.44$^{**}$ | 1.00 | | | | | | | | | | | | | | |
| STF | -0.26$^{ns}$ | 0.06$^{ns}$ | -0.31$^{ns}$ | -0.41$^{*}$ | -0.20$^{ns}$ | -0.88$^{**}$ | -0.05$^{ns}$ | 1.00 | | | | | | | | | | | | | |
| OTDM | 0.31$^{ns}$ | -0.07$^{ns}$ | 0.38$^{*}$ | 0.00$^{ns}$ | -0.11$^{ns}$ | 0.43$^{*}$ | -0.30$^{ns}$ | -0.31$^{ns}$ | 1.00 | | | | | | | | | | | | |
| FTB | 0.17$^{ns}$ | -0.14$^{ns}$ | 0.33$^{ns}$ | 0.71$^{**}$ | 0.66$^{**}$ | 0.48$^{**}$ | -0.19$^{ns}$ | -0.43$^{*}$ | 0.04$^{ns}$ | 1.00 | | | | | | | | | | | |
| OTB | 0.35$^{*}$ | -0.01$^{ns}$ | 0.38$^{*}$ | 0.49$^{**}$ | 0.30$^{ns}$ | 0.88$^{**}$ | -0.35$^{ns}$ | -0.79$^{**}$ | 0.62$^{**}$ | 0.60$^{**}$ | 1.00 | | | | | | | | | | |
| KTB | -0.15$^{ns}$ | -0.08$^{ns}$ | -0.08$^{ns}$ | -0.02$^{ns}$ | 0.03$^{ns}$ | -0.22$^{ns}$ | 0.89$^{**}$ | -0.24$^{ns}$ | -0.25$^{ns}$ | 0.26$^{ns}$ | -0.07$^{ns}$ | 1.00 | | | | | | | | | |
| OY | 0.87$^{**}$ | 0.44$^{**}$ | 0.41$^{*}$ | 0.50$^{**}$ | 0.37$^{*}$ | 0.68$^{**}$ | -0.35$^{*}$ | -0.56$^{**}$ | 0.53$^{**}$ | 0.40$^{*}$ | 0.73$^{**}$ | -0.15$^{ns}$ | 1.00 | | | | | | | | |
| KY | 0.75$^{**}$ | 0.49$^{**}$ | 0.23$^{ns}$ | 0.30$^{ns}$ | 0.28$^{ns}$ | 0.18$^{ns}$ | 0.35$^{*}$ | -0.38$^{*}$ | 0.11$^{ns}$ | 0.28$^{ns}$ | 0.25$^{ns}$ | 0.50$^{**}$ | 0.68$^{**}$ | 1.00 | | | | | | | |
| TEP | 0.89$^{**}$ | 0.48$^{**}$ | 0.39$^{*}$ | 0.48$^{**}$ | 0.37$^{*}$ | 0.60$^{**}$ | -0.19$^{ns}$ | -0.55$^{**}$ | 0.45$^{**}$ | 0.40$^{*}$ | 0.65$^{**}$ | 0.01$^{ns}$ | 0.98$^{**}$ | 0.80$^{**}$ | 1.00 | | | | | | |
| FP | -0.38$^{*}$ | -0.21$^{ns}$ | -0.18$^{ns}$ | -0.25$^{ns}$ | -0.17$^{ns}$ | -0.34$^{ns}$ | 0.23$^{ns}$ | 0.25$^{ns}$ | -0.03$^{ns}$ | -0.28$^{ns}$ | -0.32$^{ns}$ | 0.09$^{ns}$ | -0.37$^{*}$ | -0.22$^{ns}$ | -0.36$^{*}$ | 1.00 | | | | | |
| PCS | 0.44$^{**}$ | -0.21$^{ns}$ | 0.71$^{**}$ | 0.50$^{**}$ | 0.45$^{**}$ | 0.43$^{*}$ | -0.41$^{*}$ | -0.26$^{ns}$ | 0.11$^{ns}$ | 0.41* | 0.34$^{ns}$ | -0.15$^{ns}$ | 0.40$^{*}$ | 0.18$^{ns}$ | 0.37$^{*}$ | -0.57$^{**}$ | 1.00 | | | | |
| RL | 0.46$^{**}$ | 0.07$^{ns}$ | 0.44$^{**}$ | 0.59$^{**}$ | 0.57$^{**}$ | 0.38$^{*}$ | -0.50$^{**}$ | -0.15$^{ns}$ | -0.16$^{ns}$ | 0.47$^{**}$ | 0.24$^{ns}$ | -0.24$^{ns}$ | 0.39$^{*}$ | 0.17$^{ns}$ | 0.36$^{*}$ | -0.62$^{**}$ | 0.80$^{**}$ | 1.00 | | | |
| HI | 0.24$^{ns}$ | -0.24$^{ns}$ | 0.53$^{**}$ | 0.27$^{ns}$ | 0.34$^{ns}$ | -0.10$^{ns}$ | -0.10$^{ns}$ | 0.16$^{ns}$ | -0.07$^{ns}$ | 0.15$^{ns}$ | -0.07$^{ns}$ | -0.04$^{ns}$ | 0.14$^{ns}$ | 0.18$^{ns}$ | 0.16$^{ns}$ | 0.31$^{ns}$ | 0.29$^{ns}$ | 0.15$^{ns}$ | 1.00 | | |
| LAI | 0.56$^{**}$ | -0.04$^{ns}$ | 0.67$^{**}$ | 0.60$^{**}$ | 0.57$^{**}$ | 0.43$^{*}$ | -0.41$^{*}$ | -0.25$^{ns}$ | 0.16$^{ns}$ | 0.50$^{**}$ | 0.43$^{*}$ | -0.14$^{ns}$ | 0.50$^{**}$ | 0.28$^{ns}$ | 0.48$^{**}$ | -0.59$^{**}$ | 0.85$^{**}$ | 0.86$^{**}$ | 0.24$^{ns}$ | 1.00 | |
| BI | 0.77$^{**}$ | 0.77$^{**}$ | -0.06$^{ns}$ | -0.02$^{ns}$ | -0.07$^{ns}$ | 0.14$^{ns}$ | -0.01$^{ns}$ | -0.15$^{ns}$ | 0.25$^{ns}$ | -0.08$^{ns}$ | 0.18$^{ns}$ | -0.06$^{ns}$ | 0.66$^{**}$ | 0.66$^{**}$ | 0.70$^{**}$ | -0.38$^{*}$ | -0.09$^{ns}$ | 0.08$^{ns}$ | -0.19$^{ns}$ | 0.11$^{ns}$ | 1.00 |

Note: FFB - fresh fruit bunch; BNO - bunch number; ABWT - average bunch weight; MFW - mean fruit weight; MNW - mean nut weight; MTF - mesocarp to fruit ratio; KTF - kernel to fruit; STF - shell to fruit ratio; OTDM - oil to dry mesocarp ratio; FTB - fruit to bunch ratio; OTB - oil to bunch ratio; KTB - kernel to bunch ratio; OY - oil yield; KY - kernel yield; TEP - total economic product; FP - frond production; PCS - petiole cross section; RL - rachis length; HI - height increment; LAI - leaf area index; BI - bunch index.

*, **, and ns indicate significant at $p \leq 0.05$, $p \leq 0.01$ and not significant, respectively.

one of the criteria for principal component selection, also known as Kaiser's criterion or eigenvalue-one criterion. Sujadi *et al*. (2019) also reported six PCs with eigenvalues >1.0, which however only explained a total variation of 73.81% among the 47 accessions of oil palm germplasm introduced from Cameroon that were planted in Indonesia. The greatest eigenvalue (8.05) accounted for 38.35% of the total variation contributed by PC1 followed by PC2 (3.54) with 16.86% of the total variation. PC3 with an eigenvalue of 2.41 accounted for 11.47% of the total variation while the eigenvalue of PC4 is 2.30 with 10.96% of the total variation. The subsequent decreasing eigenvalue of PC5 (1.67) and PC6 (1.32) represent 7.97% and 6.29% of total variation among the 31 populations tested, respectively.

The highest variance (PC1) was largely associated with bunch traits including OY (0.313) and TEP (0.303). This PC showed positive effect for all variables studied except for STF (-0.210), FP (-0.190), KTF (-0.155) and KTB (-0.044). PC2 had large positive associations with BI (0.436), BNO (0.412) and KY (0.319) but displayed negative associations with PCS (-0.246), ABWT (-0.225), MNW (-0.199) and RL (-0.199). PC3 is related to the high KTB (0.588) and KTF (0.480). As for PC4, it is characterised by high STF (0.423) with low OTB (-0.398), OTDM (-0.354) and MTF (-0.349). The traits that contribute greatly to PC5 were HI (0.570) and FP (0.434). PC6 has large positive associations with MNW (0.404), FP (0.383) and MFW (0.379) but negative associations with PCS (-0.350) and ABWT (-0.314).

From the score plot between PC1 and PC2, four groups were obtained based on the morphological data of MPOB-Cameroon germplasm (*Figure 3*). Group 1 is the largest group comprising 26 populations positioned at the centre of the plane in the plot, suggesting that they represent the average performance of the variables studied. Populations that are closer to each other have similar values for the respective variables, whereas those far from one another have quite different values (Saleh *et al*., 2018). Group 2, represented by population CMR 03, is distinct and most positive towards PC1 since

TABLE 2. CONTRIBUTIONS OF 21 VARIABLES TO PC1-PC6 IN MPOB-CAMEROON OIL PALM GERMPLASM

| Field evaluation | Trait | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 |
|---|---|---|---|---|---|---|---|
| Bunch yield | FFB | 0.272 | 0.236 | -0.060 | 0.226 | 0.187 | -0.039 |
| | BNO | 0.064 | 0.412 | -0.100 | 0.273 | -0.164 | 0.244 |
| | ABWT | 0.218 | -0.225 | 0.055 | -0.042 | 0.375 | -0.314 |
| Bunch quality | MFW | 0.260 | -0.180 | 0.172 | 0.047 | -0.085 | 0.379 |
| | MNW | 0.217 | -0.199 | 0.218 | 0.156 | -0.045 | 0.404 |
| | MTF | 0.264 | -0.034 | -0.107 | -0.349 | -0.128 | 0.075 |
| | KTF | -0.155 | 0.197 | 0.480 | -0.064 | -0.016 | -0.249 |
| | STF | -0.210 | -0.068 | -0.140 | 0.423 | 0.151 | 0.051 |
| | OTDM | 0.134 | 0.101 | -0.256 | -0.354 | 0.300 | -0.128 |
| | FTB | 0.219 | -0.157 | 0.256 | -0.100 | -0.182 | 0.206 |
| | OTB | 0.262 | 0.015 | -0.055 | -0.398 | -0.062 | 0.069 |
| | KTB | -0.044 | 0.118 | 0.588 | -0.094 | -0.090 | -0.183 |
| | OY | 0.313 | 0.205 | -0.066 | -0.047 | 0.121 | 0.081 |
| | KY | 0.195 | 0.319 | 0.326 | 0.113 | 0.120 | -0.078 |
| | TEP | 0.303 | 0.247 | 0.029 | -0.009 | 0.129 | 0.045 |
| Vegetative measurement | FP | -0.190 | -0.020 | 0.107 | -0.141 | 0.434 | 0.383 |
| | PCS | 0.246 | -0.246 | -0.017 | 0.144 | -0.016 | -0.350 |
| | RL | 0.241 | -0.199 | -0.047 | 0.301 | -0.228 | -0.106 |
| | HI | 0.069 | -0.175 | 0.165 | 0.192 | 0.570 | 0.111 |
| | LAI | 0.279 | -0.179 | -0.005 | 0.184 | -0.050 | -0.237 |
| | BI | 0.141 | 0.436 | -0.111 | 0.151 | 0.002 | -0.039 |
| Eigenvalue | | 8.05 | 3.54 | 2.41 | 2.30 | 1.67 | 1.32 |
| Variance (%) | | 38.35 | 16.86 | 11.47 | 10.96 | 7.97 | 6.29 |
| Cumulative variance (%) | | 38.35 | 55.20 | 66.67 | 77.63 | 85.60 | 91.89 |

Note: FFB - fresh fruit bunch; BNO - bunch number; ABWT - average bunch weight; MFW - mean fruit weight; MNW - mean nut weight; MTF - mesocarp to fruit ratio; KTF - kernel to fruit; STF - shell to fruit ratio; OTDM - oil to dry mesocarp ratio; FTB - fruit to bunch ratio; OTB - oil to bunch ratio; KTB - kernel to bunch ratio; OY - oil yield; KY - kernel yield; TEP - total economic product; FP - frond production; PCS - petiole cross section; RL - rachis length; HI - height increment; LAI - leaf area index; BI - bunch index.

they performed well in variables which exhibited the highest positive loading in PC1 such as OY (18.48 kg palm$^{-1}$ yr$^{-1}$), TEP (24.96 kg palm$^{-1}$ yr$^{-1}$) and FFB (120.71 kg palm$^{-1}$ yr$^{-1}$). Other traits such as MTF (46.80%), OTDM (75.68%), OTB (15.69%) and KY (10.80 kg palm$^{-1}$ yr$^{-1}$) were also promising in population CMR 03.

Population CMR 13 in Group 3 showed the most positive along PC2 and the most negative toward PC1. This might be due to the good performance in PCS (12.67 cm$^2$), RL (4.25 m) and BI (0.45). While having the best performance in some vegetative traits, CMR 13 had the highest KTB (9.31%) and KTF (15.47%), with the lowest LAI (3.27), MTF (36.14%) and ABWT (5.96 kg palm$^{-1}$ yr$^{-1}$), as well as low FFB (86.83 kg palm$^{-1}$ yr$^{-1}$) caused CMR 13 to be distinctly placed from other populations. The poor performance of some variables related to PC1 has caused CMR 14 and CMR 31 grouped in Group 4. Both populations have the lowest OY (9.27 kg palm$^{-1}$ yr$^{-1}$ and 9.43 kg palm$^{-1}$ yr$^{-1}$), TEP (13.71 kg palm$^{-1}$ yr$^{-1}$ and 13.34 kg palm$^{-1}$ yr$^{-1}$), and among the lowest LAI (3.39 and 3.86) and FFB (83.40 kg palm$^{-1}$ yr$^{-1}$ and 82.60 kg palm$^{-1}$ yr$^{-1}$). Population CMR 14 was slightly positive towards PC2 because the RL was shorter (4.08 m) than the rest, while the CMR 31 was slightly negative towards PC2 due to the lowest MNW (3.32 g) and MFW (5.50 g).

A PCA biplot was constructed from multidimensional preference analysis to study the inter-relationship between the populations and variables, and to identify the best variables contributing to the population. The variables on the right quadrant such as TEP, OY, LAI, FFB, OTB and MTF were correlated to PC1, however, variables in the left quadrant, *i.e.*, KTB, KTF, FP and STF, were anti-correlated to PC1 (*Figure 4*). Among others, the most important variables that contributed positively to PC2 were BNO, BI, and KY, while PCS, ABWT, MNW and RL negatively contributed to PC2. *Figure 4* clearly shows that PC1 is negatively influenced by KTB, KTF, FP and STF; however, there was a low correlation between KTF and KTB with FP and STF. Variables that are closer to one another indicate positive associations between them. Thus, the increased value of OY is important to entail a high TEP value. CMR 03 and CMR 13 are distinctly located in quadrants 1 and 2 of the plot, respectively, suggesting that CMR 03 could be selected as a potential population for breeding programmes as it has good characters in bunch quality components and vegetative measurements such as OTDM, OTB, OY, TEP, FTB, KY and BI. Population CMR 13 could be further exploited for breeding for non-edible purposes due to the best characteristics in KTB and KTF, which suggests potential for increasing the yield of palm kernel oil.

## Highly Diverse Populations Should be Prioritised in Conservation Programme

The average linkage cluster analysis classified the materials depending on the environment or correlation of the individuals as suggested by Granato *et al.* (2018). The result from CA is slightly

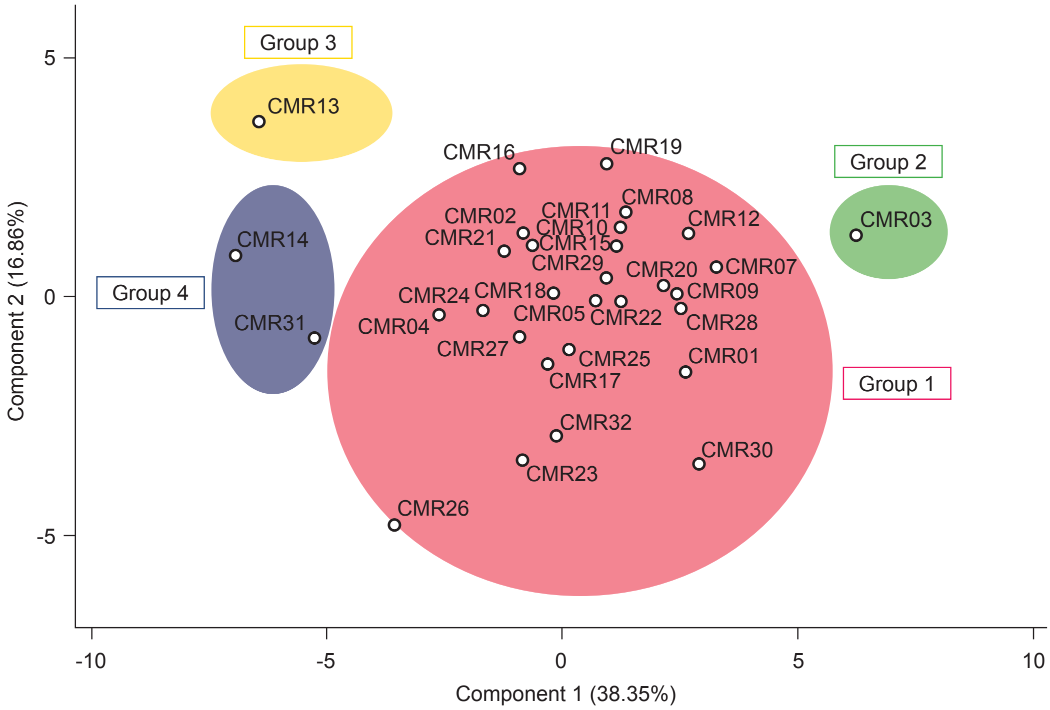


*Figure 3. Scores plot of MPOB-Cameroon oil palm germplasm.*

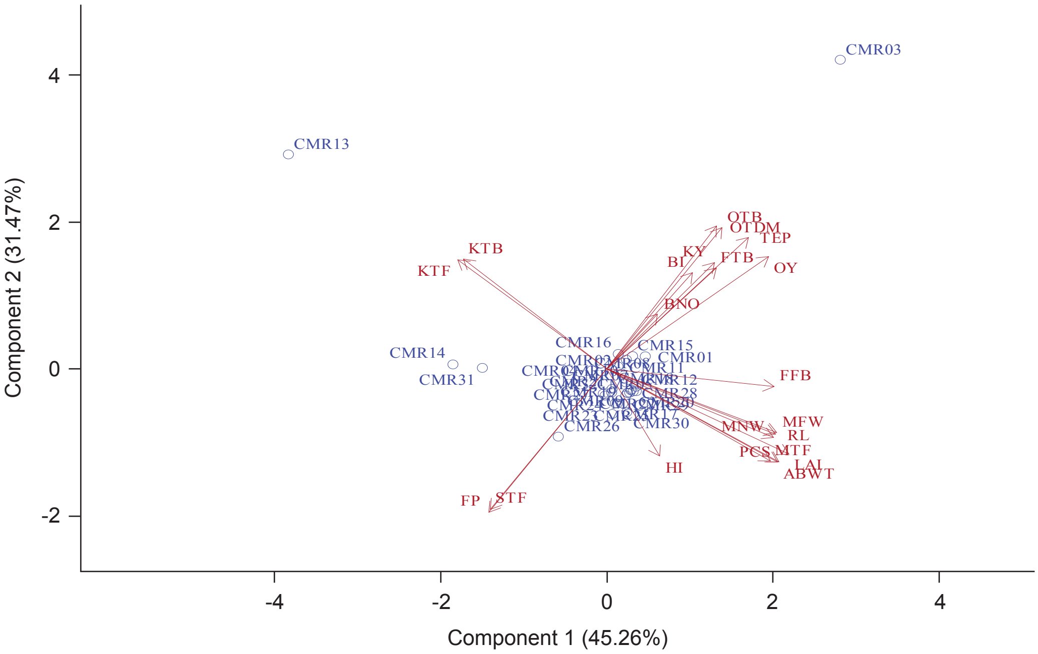


*Figure 4. PCA biplot of 21 morphological traits and 31 populations of MPOB-Cameroon oil palm germplasm.*

different from PCA as CA groups observations while PCA groups variables rather than observations. Based on the result, it showed that 31 populations of MPOB-Cameroon oil palm germplasm can be grouped into three major clusters with the highest Pseudo F-value of 6.3 (*Figure 5*). All three clusters have two sub-clusters each. Cluster I consist of seven populations with the first sub-cluster containing CMR 30, CMR 23 and CMR 01 joined together with the second sub-cluster which has four populations namely, CMR 18, CMR 26, CMR 32 and CMR 17. Cluster II consists of 11 populations which are CMR 03, CMR 08, CMR 07, CMR 09, CMR 10, CMR 12, CMR 28 and CMR 29 grouped in the first sub-cluster at the distance of 0.81 while CMR 20, CMR 22 and CMR 25 were grouped in second sub-cluster at the distance of 0.65. Cluster III had the largest group, consisting of 13 populations (41.9% of the entire germplasm populations studied). Four populations were grouped in the first sub-cluster at the distance of 0.88 which are CMR 02, CMR 04, CMR 24 and CMR 05, while the remaining populations were clustered together in the second sub-cluster at the distance of 0.96.

Based on *Figure 5*, among the MPOB-Cameroon oil palm germplasm materials, paired populations of CMR 16 and CMR 30 were found extremely diverse, while paired populations of CMR 07 and CMR 09 exhibited the closest relationship. According to Odewale *et al.* (2012), priority should be given to the use of populations with a high genetic distance between them, whilst avoiding those with less genetic distance. This study suggested that the clustering pattern of the MPOB-Cameroon populations did not depend on their geographical locations, as the populations from different locations were randomly distributed into various clusters. This might be due to the high rate of genetic exchange through seed dispersal (Arias *et al*., 2013). This finding conforms with the results from other studies on the genetic variability of Nigeria and Sierra Leone oil palm germplasm (Li-Hammed *et al*., 2016; Suzana *et al*., 2016). On the other hand, a strong relationship between genetic distance and geographical location has been reported during the evaluation of MPOB-oil palm germplasm (Hayati *et al*., 2004; Zulkifli *et al*., 2012).

Based on trait-specific clustering (*Table 3*), Cluster II showed the best performance in yield related traits with the highest mean of FFB and ABWT supplemented with high BNO. On the contrary, Cluster I had the lowest FFB contributed by the low BNO, despite their moderate ABWT which placed most of the populations in quadrant 3 and 4 of the score plot (*Figure 3*). The highest BNO of Cluster III would not result in the highest FFB due to the lowest ABWT. In terms of bunch traits, Cluster II was found to have the highest cluster mean of OY owing to its highest MTF, OTDM and OTB, in addition to the lowest STF. On a similar note, Cluster II was also highest in KY and TEP while the lowest cluster mean was found in Cluster 1. For vegetative traits, Cluster I had the highest mean cluster for all vegetative characters except BI. In conjunction with high FP and BI, Cluster III showed better performance with minimum mean clusters for PCS, RL and HI. Meanwhile, Cluster II showed a moderate mean of all vegetative traits except for the highest BI and lowest FP.

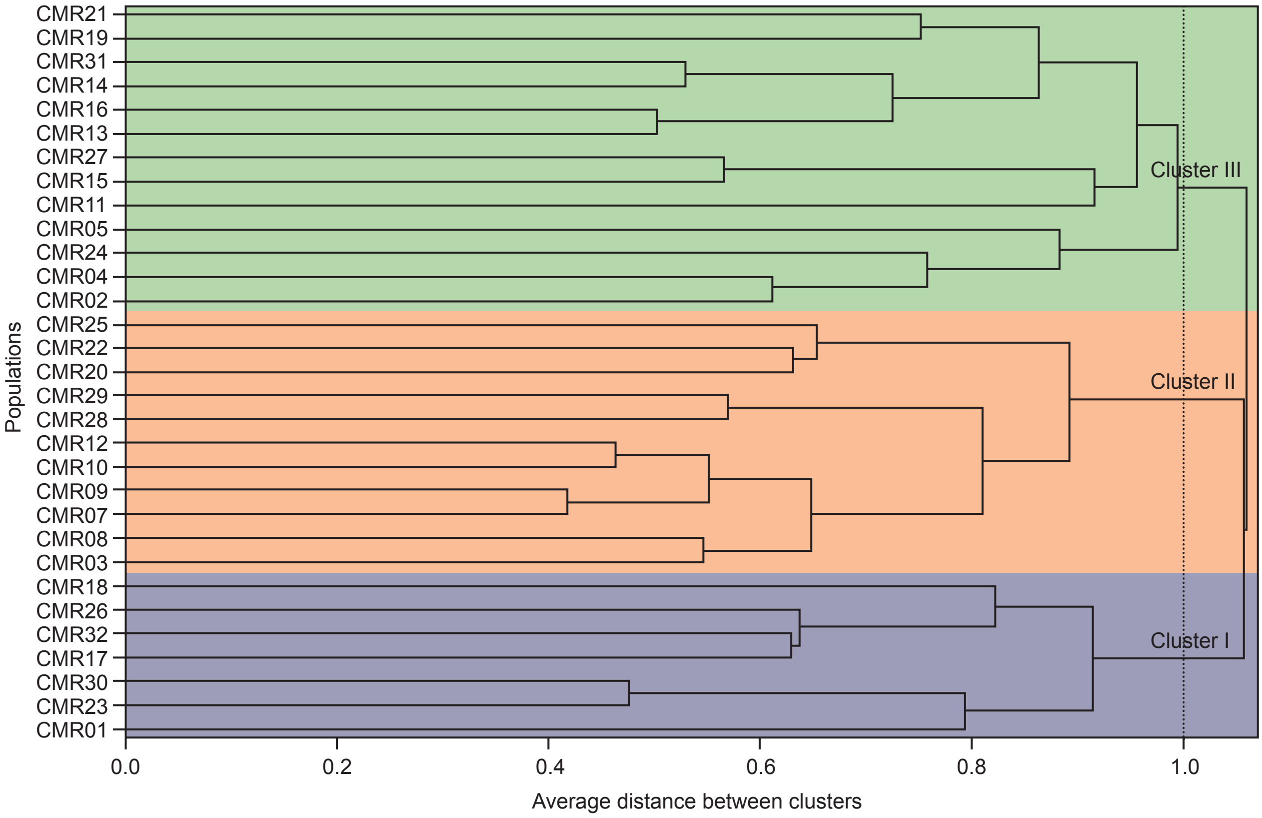


*Figure 5. Dendrogram of 31 MPOB-Cameroon germplasm populations based on 21 morphological traits.*

High genetic variability was identified in MPOB-Cameroon oil palm germplasm, which was corroborated by Zulkifli *et al*. (2012), who revealed a high level of polymorphism (100%) in the Cameroon germplasm material through molecular markers (EST-SSRs) which could be exploited for oil palm improvement programmes. The germplasm from Cameroon also had the highest heterozygosity, implying that these materials represent a rich source of genes and may possess unique genes associated with traits which may not be found in the current oil palm planting materials. Morphological data in conjunction with molecular data could be very useful for the effective characterisation and utilisation of MPOB-Cameroon oil palm germplasm. Apart from the exploitation for the improvement of planting materials, stratification using multivariate analysis is one of the approaches that can be used to establish a good core collection (van Hintum *et al*., 2000). Creating a core collection is a cost-effective way to improve the conservation strategy, characterisation and utilisation of genetic resources. A core collection can reflect the entire genetic diversity of a large collection with a limited number of accessions as suggested by Brown (1995).

From cluster analysis, the number of palms or families or populations in the same cluster could be reduced as they possess genetic similarities for future regeneration and conservation purposes. Selection and conservation should be taken into account for those traits that contribute to a higher variation in the MPOB-Cameroon oil palm germplasm. Based on this study, the most distant populations, namely CMR 16 and CMR 30 from different clusters are having a higher genetic difference, and populations with unique characteristics, *i.e*., CMR 03 and CMR 13, are recommended for inclusion in the conservation programme for future breeding utilisation.

## CONCLUSION

This study compared 21 parameters of yield, bunch quality components and vegetative measurement, and identified high genetic variability in Cameroon oil palm germplasm. It can be concluded from this study that multivariate analysis successfully characterised the MPOB-Cameroon oil palm germplasm populations based on the phenotypic characters. Principal component analysis was able to identify some traits that play an important role in classifying the variation in this germplasm that can be used for oil palm improvement and conservation. The results of the principal component analysis are not in agreement with cluster analysis. Cluster analysis successfully grouped the populations into three major clusters and revealed that there was no relationship between the geographical origin of the

TABLE 3. CLUSTER GROUPS AND QUANTITATIVE TRAITS MEANS

| Field evaluation | Trait | Unit | Cluster | | |
|---|---|---|---|---|---|
| | | | I | II | III |
| Bunch yield | FFB | kg palm$^{-1}$ yr$^{-1}$ | 98.5 | 116.32 | 105.56 |
| | BNO | bunches palm$^{-1}$ yr$^{-1}$ | 11.31 | 13.29 | 13.63 |
| | ABWT | kg palm$^{-1}$ yr$^{-1}$ | 8.99 | 9.08 | 8.01 |
| Bunch quality | MFW | g | 8.87 | 8.49 | 7.22 |
| | MNW | g | 5.23 | 4.87 | 4.38 |
| | MTF | % | 41.11 | 42.66 | 39.23 |
| | KTF | % | 12.56 | 12.15 | 13.38 |
| | STF | % | 46.33 | 45.19 | 47.39 |
| | OTDM | % | 72.74 | 74.37 | 73.03 |
| | FTB | % | 67.73 | 66.18 | 63.73 |
| | OTB | % | 12.13 | 13.1 | 11.32 |
| | KTB | % | 8.19 | 7.64 | 8.1 |
| | OY | kg palm$^{-1}$ yr$^{-1}$ | 12.39 | 15.92 | 12.66 |
| | KY | kg palm$^{-1}$ yr$^{-1}$ | 8.37 | 9.35 | 9.02 |
| | TEP | kg palm$^{-1}$ yr$^{-1}$ | 17.41 | 21.53 | 18.07 |
| Vegetative measurement | FP | fronds palm$^{-1}$ yr$^{-1}$ | 28.19 | 27.35 | 28.03 |
| | PCS | cm$^2$ | 20.85 | 20.33 | 18.28 |
| | RL | m | 4.85 | 4.77 | 4.64 |
| | HI | cm yr$^{-1}$ | 25.64 | 24.55 | 23.96 |
| | LAI | - | 4.41 | 4.39 | 4.1 |
| | BI | - | 0.38 | 0.44 | 0.43 |

Note: FFB - fresh fruit bunch (kg palm$^{-1}$ yr$^{-1}$); BNO - bunch number (bunches palm$^{-1}$ yr$^{-1}$); ABWT - average bunch weight (kg palm$^{-1}$ yr$^{-1}$); MFW - mean fruit weight (g); MNW - mean nut weight (g); MTF - mesocarp to fruit ratio (%); KTF - kernel to fruit (%); STF - shell to fruit ratio (%); OTDM - oil to dry mesocarp ratio (%); FTB - fruit to bunch ratio (%); OTB - oil to bunch ratio (%); KTB - kernel to bunch ratio (%); OY - oil yield (kg palm$^{-1}$ yr$^{-1}$); KY - kernel yield (kg palm$^{-1}$ yr$^{-1}$); TEP - total economic product (kg palm$^{-1}$ yr$^{-1}$); FP - frond production (fronds palm$^{-1}$ yr$^{-1}$); PCS - petiole cross section (cm$^2$); RL - rachis length (m); HI - height increment (cm yr$^{-1}$); LAI - leaf area index; BI - bunch index.

31 populations and their clustering patterns. This finding should be further verified with a molecular-based diversity study to efficiently exploit the collected germplasm materials and improve the conservation strategies to a manageable level towards a sustainable future for the oil palm sector.

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