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GENETIC VARIABILITY OF CAMEROON AND ANGOLA OIL PALM GERMPLASM FOR TROPICAL BREEDING PROGRAMME

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ABSTRACT

Breeding populations of restricted origin (BPRO), such as Deli dura*, have been widely utilised in oil palm (*Elaeis guineensis*) breeding programmes and seed production since the early 20th century. However, there is growing interest in leveraging genetic diversity from introduced germplasm to develop new varieties. Indonesia introduced 230 oil palm accessions from Cameroon (CMR) and Angola (AGO) in 2008 and 2010, respectively. These accessions, collected from diverse ecological zones, were planted in multiple locations in Indonesia. This study aimed to evaluate the phenotypic diversity of this germplasm, focusing on bunch components, oil quality and vegetative morphology. Results revealed moderate to high levels of diversity in both germplasm sets. The CMR exhibited shorter palms and rachises, as well as a higher shell to fruit and fruit to bunch ratio. In contrast, the AGO showed a higher oleic acid and lower palmitic acid, indicating favourable oil quality traits. Additionally, the AGO exhibited the most favourable values for oil yield, mesocarp to fruit and fruit weight. Both sets of germplasm showed high levels of carotene and unsaturated fatty acids. These findings highlight the potential of germplasm for enriching genetic diversity in the oil palm breeding programmes.*

Keywords: bunch components, correlation, diversity, oil quality, vegetative.

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INTRODUCTION

Natural oil palm (*Elaeis guineensis*) groves are scattered across West to Central Africa. As the centre of oil palm genetic diversity, this region has been the focus of extensive exploration efforts to conserve and broaden the genetic base of oil palm germplasm (Purba et al., 2017; Rajanaidu, 1994; Rajanaidu et al., 2013). The African oil palm was introduced to Indonesia in 1848 and first planted at the Bogor Botanical Garden (Ariati et al., 2019). The progeny derived from these early introductions, known as Deli *dura*, became the foundation of modern oil palm breeding programmes (Corley & Tinker, 2016; Lubis, 2008), thriving under Indonesia's high and stable annual rainfall (Corley & Tinker, 2016).

The phenotypic diversity of African-derived germplasm has been widely evaluated, particularly for yield potential, bunch components and vegetative traits. Studies such as Nor Azwani et al. (2020) and Norziha et al. (2020, 2024) assessed the performance and selection criteria of MPOB germplasm originating from Cameroon, Nigeria, Zaire, Angola and other sources. Similarly, Wan Nor Salmiah et al. (2023) evaluated morphological variability within the MPOB-Cameroon germplasm.

In 2008 and 2010, Indonesia introduced 230 oil palm accessions from Cameroon (CMR) and Angola (AGO), respectively. These collections covered a wide geographical range from Northwestern to the Eastern regions bordering the Democratic Republic of Congo and spanned an altitudinal gradient of 9

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to 1,326 m. Substantial variation in bunch weight was observed (4.2–50.0 kg; mean 20.9 kg), and the collected seeds were established in North Sumatra, Riau, Central Kalimantan, and Bengkulu. The early field performance of the CMR germplasm under Indonesian conditions was later reported (Purba et al., 2017). In addition, several studies have examined the genetic diversity of these germplasm populations, particularly focusing on their response to *Ganoderma boninense* (Nugroho et al., 2019; Nur et al., 2024).

Breeding to enhance oil palm productivity remains essential to meet the rising global demand amid limited land expansion. Climate change, ecological shifts and evolving market preferences necessitate the redefinition of ideotypes for future cultivars (Soh et al., 2017). Desirable cultivars should combine high yield, disease resistance, compact growth, long bunch stalks, virescens fruit colour, improved oil quality and broad adaptability (Norziha et al., 2020; Rajanaidu et al., 1989; Rao & Chang, 2021; Yue et al., 2021). These traits require access to well-characterised and genetically diverse germplasm (Gan et al., 2021; John Martin et al., 2022). Therefore, this study evaluated the phenotypic diversity of bunch components, oil quality and vegetative morphology in oil palm accessions from the CMR and AGO germplasm, and applied the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) (Olivoto & Nardino, 2020) to identify high-performing accessions that integrate favourable traits for ideotype-based breeding.

MATERIALS AND METHODS

Planting Material

The collected oil palm germplasm originated from open pollination, leading to unique genetic backgrounds for each palm. This study evaluated 224 *dura* types from 62 accessions of CMR (*Figure 1*) and 135 *dura* types from 33 accessions of AGO (*Figure 2*). In 2010 and 2012, the Indonesian Oil Palm Research Institute (IOPRI) planted the CMR and AGO oil palm accessions in the Simalungun and Serdang Bedagai regencies, North Sumatra, Indonesia.

Bunch components assessment. Bunch component analysis was conducted between 2014 and 2024, with at least three bunches per palm evaluated for all accessions. Mature *dura*-type fruit bunches, identified by either a minimum of 10 detached fruits or a maximum moisture content of 35%, were selected for analysis. Bunch components were analysed according to the IOPRI standard adopted from Corley & Tinker (2016). Sixteen bunch component traits were observed, including bunch weight (BW), stalk weight (StW), spikelet weight (SpW), stalk to bunch (St/B), spikelet to bunch (Sp/B), fruit to bunch (F/B), fruit weight (FW), mesocarp weight (MW), mesocarp to fruit (M/F), kernel to fruit (K/F), oil to dry mesocarp (O/DM), oil to wet mesocarp (O/WM), oil to bunch (O/B), kernel to bunch (K/B), shell to fruit (S/F) and industrial extraction ratio (IER).

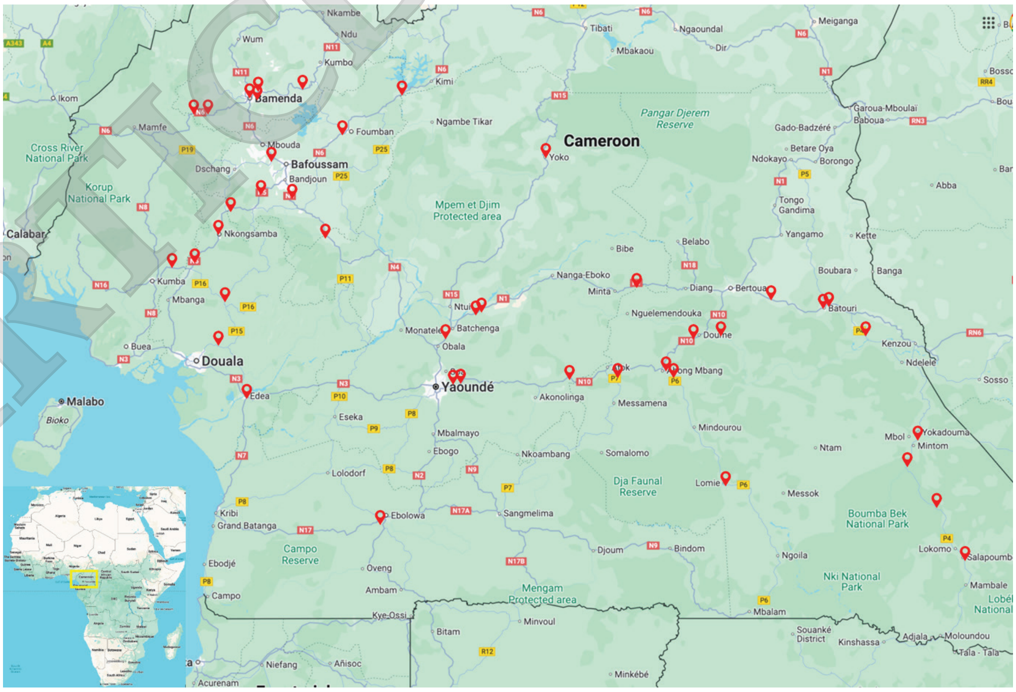

Figure 1. Distribution of 62 red-marked points indicating collection sites in Cameroon (CMR). Some points are not individually distinguishable due to the overlapping caused by the proximity of collection locations.

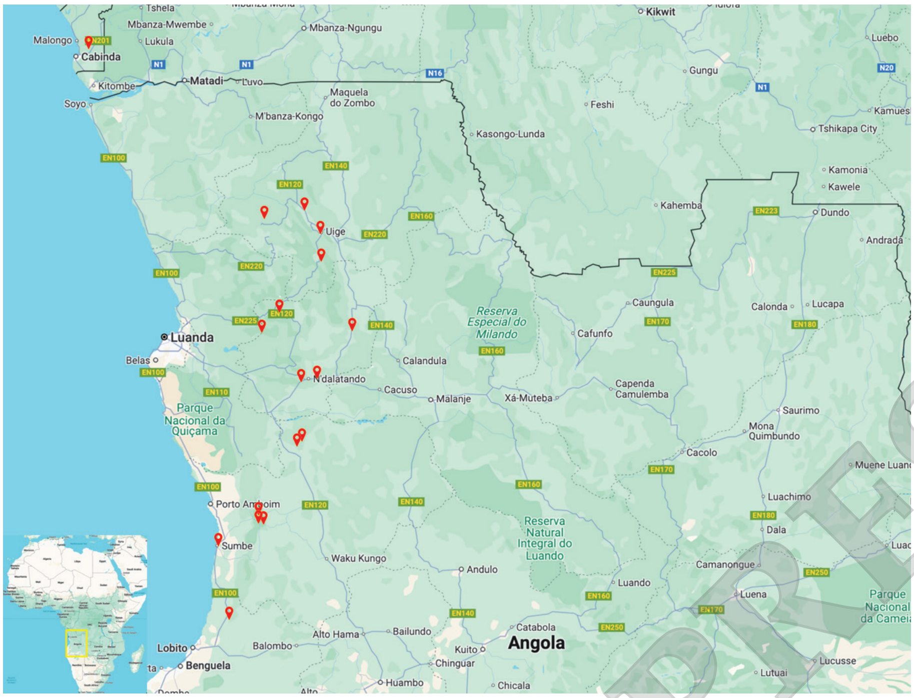

Figure 2. Distribution of 33 red-marked points indicating collection sites in Angola (AGO). Some points are not individually distinguishable due to the overlapping caused by the close proximity of collection locations.

Oil quality assessment. Oil quality analysis followed the same harvest maturity criteria used for bunch component sampling. Eleven variables were assessed: myristic (C14:0), palmitoleic (C16:1), arachidic (C20:0), linolenic (C18:3), stearic (C18:0), oleic (C18:1), palmitic (C16:0), linoleic (C18:2), unsaturated fatty acids (USFA), saturated fatty acids (SFA) and carotene (CAR). The fatty acid composition was measured using the MPOB Test Method p3.5 (Malaysian Palm Oil Board [MPOB], 2004a) with a 9C-2010 plus gas chromatograph (Shimadzu Corporation, Japan). Carotene content was simultaneously quantified using MPOB Test Method P.2.6 Part 2 (MPOB, 2004b), PORIM Test Method (Siew et al., 1995) and the standard curve method, utilising a UV-visible spectrophotometer.

Vegetative traits assessment. The vegetative traits were assessed approximately seven years after planting. Vegetative trait measurements adhered to the IOPRI standards based on Corley & Tinker (2016). Seven phenotypic traits were evaluated: palm height (PH), rachis length (RL), petiole width (PW), petiole thickness (PT), leaflet count (LC), leaflet length (LL) and leaflet width (LW).

Data analysis. Bunch component analysis for the CMR and AGO involved 941 and 405 bunch samples, respectively. Oil quality analysis was performed on 234 mesocarp oil samples from CMR and 150 samples from AGO. Vegetative morphological traits were measured from 147 CMR and 72 AGO palms. All quantitative data were analysed and visualised using Microsoft Excel, Python (Pandas, Matplotlib, and Seaborn), ACE tools, and R (adegenet, ggplot2, circlize and qgraph packages).

RESULTS AND DISCUSSION

Bunch Components

Diverse germplasm serves as a fundamental resource for breeders in developing superior varieties (Kenworthy, 2019). Genetic diversity is a critical factor in breeding programmes, as it enables the identification and incorporation of desirable traits (Govindaraj et al., 2015). The coefficient of variation (CV) measures trait variability, with values below 10% indicating low variability and above 20% suggesting substantial diversity (Bertolino et al., 2024; Kozak et al., 2013).

The AGO and CMR germplasm displayed broadly similar CV distribution patterns for bunch component traits, except for St/B and FW (*Table 1*). Traits such as F/B, M/K, O/DM, O/WM, and S/F exhibited low variability, while St/B (AGO), FW (CMR), K/F, O/B, K/B and IER showed moderate variability (10% ≤ CV ≤ 20%). High variability was observed for BW, StW, SpW, St/B (CMR), Sp/B, FW (AGO) and MW.

The variability of common traits such as F/B, M/F, K/F, S/F, O/DM, O/WM, O/B and K/B was lower in this study, ranging from –14% to –69% compared with Zambia and Cameroon germplasm (Pedapati et al., 2021), and –16% to –31% lower relative to the Nigerian germplasm (Abimbola et al., 2014). For instance, wider mean-range intervals were observed for key traits such as S/F (7.50%–40.00%), M/F (31.40%–67.20%), and O/B (7.26%–24.53%) in the Zambia-Cameroon germplasm and S/F (22.13%–57.43%), M/F (26.33%–64.00%) and O/B (6.73%–25.81%) in the Nigerian germplasm. The Zambian germplasm exhibited extensive variability in S/F, which may explain the broader overall variation observed when the Zambia and CMR accessions were analysed together. The AGO-CMR in the present study exhibited more stable variability for these traits, which may reflect both their genetic background and environmental adaptation under tropical plantation conditions.

The CMR demonstrated greater variability in bunch components than the AGO (*Table 1*). This finding aligns with Abu-Bakar et al. (2021), who reported high variability in several bunch component traits within the TxT CMR. Conversely, the AGO germplasm has exhibited relatively low variability for bunch index traits (Fadila et al., 2016), yet remains distinct from the Deli population (Nur et al., 2024). A comparable observation was made by Wan Nor Salmiah et al. (2023), who examined 31 accessions of the MPOB-Cameroon; compared with that study, our CMR showed higher means and greater variability for BW, F/B, K/F and K/B, but lower values for MW, M/F and IER.

Mean comparisons between the CMR and AGO were not conducted due to age differences between the populations. Nevertheless, the variability among accessions revealed distinct trends (*Table 1*). The AGO exhibited significant variability FW, MW, M/F, K/F, O/B, K/B, S/F and IER. In contrast, the CMR showed significant variability across all traits except spikelet weight and spikelet to bunch. Despite being approximately two years younger, the AGO demonstrated superior performance in several traits related to crude palm oil (CPO) yield-namely BW, FW, MW, O/WM, O/DM, O/WM, O/B and IER. Conversely, the CMR showed higher means for traits associated with palm kernel oil (PKO) yield and shell biomass, such as F/B, K/F, K/B and S/F.

TABLE 1. STATISTICAL SUMMARY OF BUNCH COMPONENTS IN THE ANGOLA AND CAMEROON OIL PALM GERMPLASM

Bunch components	135 *Dura* palms of Angola (AGO)						224 *Dura* palms of Cameroon (CMR)					
	Mean	Min	Max	*p*-value		CV	Mean	Min	Max	*p*-value		CV
BW (kg)	13.63	7.13	32.25	0.99	ns	44.20	12.07	5.63	27.05	0.00	***	54.41
StW (kg)	1.74	0.85	3.55	0.99	ns	46.61	1.35	0.47	4.25	0.00	***	62.47
SpW (kg)	2.36	1.47	5.20	0.93	ns	35.13	2.06	1.18	3.25	0.06	ns	38.52
St/B (%)	12.98	8.71	20.19	0.07	ns	18.04	10.98	6.60	17.33	0.00	***	21.64
Sp/B (%)	19.22	10.51	29.60	0.60	ns	33.93	19.83	9.41	32.06	0.08	ns	31.29
F/B (%)	63.95	52.37	71.13	0.88	ns	7.79	66.23	50.59	71.81	0.00	***	6.26
FW (g)	11.61	7.66	19.70	0.00	***	21.49	8.59	5.62	13.87	0.00	***	19.99
MW (g)	5.80	3.16	10.29	0.00	***	23.27	3.43	1.98	6.60	0.00	***	20.75
M/F (%)	49.78	36.20	64.77	0.00	***	8.35	40.08	28.03	61.81	0.00	***	9.76
K/F (%)	11.49	6.35	16.98	0.00	***	15.51	13.42	7.55	23.12	0.00	***	16.21
O/DM (%)	78.08	69.96	83.53	0.25	ns	4.33	74.95	68.39	81.19	0.00	***	3.58
O/WM (%)	56.88	46.95	62.82	1.00	ns	9.69	53.69	46.06	62.20	0.00	***	7.13
O/B (%)	18.08	12.41	25.84	0.01	**	14.67	14.30	8.77	22.64	0.00	***	14.90
K/B (%)	7.34	4.11	10.97	0.00	***	16.65	8.87	4.84	15.09	0.00	***	17.26
S/F (%)	38.74	28.64	46.96	0.00	***	9.85	46.51	24.16	58.57	0.00	***	8.59
IER (%)	15.46	10.61	22.10	0.01	**	14.67	12.22	7.50	19.36	0.00	***	14.90

Note: ns - not significant ($p > 0.05$); * - significant at $p \leq 0.05$; ** - $p \leq 0.01$; *** - $p \leq 0.001$; BW - bunch weight; StW - stalk weight; SpW - spikelet weight; St/B - stalk to bunch; Sp/B - spikelet to bunch; F/B - fruit to bunch; FW - fruit weight; MW - mesocarp weight; M/F - mesocarp to fruit; K/F - kernel to fruit; O/DM - oil to dry mesocarp; O/WM - oil to wet mesocarp; O/B - oil to bunch; K/B - kernel to bunch; S/F - shell to fruit; IER - industrial extraction ratio; CV - coefficient of variation.

Oil Quality Traits

The variability patterns of oil quality traits were generally consistent between the AGO and CMR, except for C16:1 and C18:3 (*Table 2*). Approximately half of the oil quality traits, including C16:0, C18:1, C18:2, SFA and USFA, showed low to moderate variability, whereas traits such as C18:3, C14:0, C16:1, C18:0, C20:0 and carotene exhibited high variability. The CMR displayed a broader range of variability in six fatty acids (C14:0, C18:0, C18:1, C18:2, C18:3 and USFA) compared with the AGO. Similar levels of variability were reported in the Nigerian germplasm, particularly for C14:0, C16:0, C18:0, C18:1 and C18:2 (Abimbola et al., 2014).

Significant and highly significant differences were observed for all oil quality traits among the evaluated germplasm. The AGO population exhibited higher levels of USFA, with mean and maximum values 3.97% and 1.42% higher than those of the CMR. Conversely, the CMR showed higher SFA levels, with mean and maximum values 4.94% and 6.68% higher than those of AGO. Carotene content was also markedly higher in the CMR, with a 16.54% higher mean and 32.82% higher maximum than the AGO. The mean C18:1 for both AGO and CMR was higher than that reported for the *Elaeis oleifera* Taisha and some of its hybrids and backcrosses (Mendoza et al., 2023), but lower than that observed in other *E. oleifera* hybrids (Mozzon et al., 2015; Valentim et al., 2019). The carotene ranges in both AGO and CMR were comparable to those reported for *E. oleifera* by Valentim et al. (2019).

Vegetative Traits

The AGO and CMR germplasm exhibited low to moderate levels of vegetative diversity, with CV ranging from 4.10% to 17.52% (*Table 2*). Overall, the vegetative diversity of AGO and CMR was substantially lower than that of their bunch components (CV range: 3.58%–62.47%) (*Table 1*) and lower than Nigerian germplasm (CV: 8.71%–30.42%) (Abimbola et al., 2014). Despite these low to moderate levels of variation, the observed diversity remains adequate for genetic association studies (Ong et al., 2018).

The AGO demonstrated significantly higher means for vegetative traits than the CMR across all traits (*Table 2*). Means of RL for AGO and CMR were 496.17 and 483.51 cm, respectively, with a minimum of 342.00 and 348.00 cm. In contrast, the CMR exhibited the lowest mean for PH (358.68 cm, minimum 215.00 cm). Both RL and PH are key traits in oil palm breeding, influencing harvest efficiency, planting density and overall productivity (Corley & Tinker, 2016; John Martin et al., 2022; Nor Azwani et al., 2020; Norziha et al., 2020). Consistent with previous findings, Wan Nor Salmiah et al. (2023) reported RL variability ranging from 4.08 to 5.17 m, with an annual vertical growth rate of ≈ 24.42 cm in the MPOB-Cameroon germplasm. Similarly, the Madagascar germplasm is noted for its exceptionally short RL of 3.22 m at eight years of age (Norziha et al., 2020). In the present study, both RL and PH exhibited moderate variability (*Table 2*), aligning with results from other germplasm collections (Norziha et al., 2020; Ong et al., 2018; Pasaribu et al., 2022).

Cluster Analysis

Cluster analysis of bunch components, oil quality and vegetative traits was performed using the Bayesian Information Criterion (BIC), which identifies the optimal number of clusters by balancing model fit and complexity. The BIC analysis identified two main clusters for each phenotypic group, reflecting two dominant groupings (*Figure 3*).

In the circular heatmap of the bunch component (*Figure 3a*), accessions were separated into three sub-clusters, primarily driven by variation in M/F, S/F, O/B and IER. These traits effectively differentiate populations due to their high correlations, heritability and phenotypic diversity across germplasm, making them essential indicators for distinguishing population structure (Constantin et al., 2017; Nor Azwani et al., 2020; Nouy et al., 2006; Putri et al., 2009). For instance, these four traits distinctly separated the reference population DxP PPKS 540 from the AGO and CMR, as shown by distinct colour gradations. The largest sub-cluster was dominated by CMR accessions, exhibiting relatively lower M/F, O/B, and IER, but higher S/F. The smaller sub-cluster was mainly composed of AGO accessions, which displayed the opposite pattern: higher M/F, O/B, and IER, but lower S/F. On the other hand, DxP PPKS 540 accessions formed a distinct cluster characterised by more uniform and optimised values across these key traits, reflecting their genetic improvement for yield stability.

The heatmap of vegetative traits (*Figure 3b*) revealed a clear clustering pattern, primarily driven by PH, which showed the greatest variability among vegetative traits. The contrasting colour gradients at cluster boundaries reflected substantial phenotypic diversity in PH. Previous studies reported moderate to high heritability for PH, indicating strong genetic control (Constantin et al., 2017; Ting et al., 2023). The primary cluster, composed of accessions from both germplasms, represented taller palms distributed across several

TABLE 2. STATISTICAL ANALYSIS OF OIL QUALITY AND VEGETATIVE TRAITS IN THE ANGOLA AND CAMEROON GERMPLASM

Traits	Angola				Cameroon				Significance
	Mean	Min	Max	CV	Mean	Min	Max	CV	
C14:0 (%)	0.65	0.20	1.40	36.05	0.73	0.00	1.90	41.10	***
C16:0 (%)	40.77	32.20	50.90	9.80	42.56	30.90	52.30	9.48	***
C16:1 (%)	0.10	0.00	0.80	78.65	0.12	0.00	0.60	50.76	*
C18:0 (%)	3.97	1.90	7.00	23.84	4.25	1.70	10.00	27.48	***
C18:1 (%)	44.80	34.30	56.00	9.26	42.97	29.50	55.50	10.78	***
C18:2 (%)	9.24	5.00	15.30	15.63	8.89	4.50	18.70	19.08	***
C18:3 (%)	0.13	0.10	0.30	36.54	0.12	0.00	0.30	57.86	*
C20:0 (%)	0.16	0.00	0.30	48.20	0.19	0.10	0.50	44.16	*
CAR (ppm)	656.03	43.21	2028.83	56.31	764.54	21.95	2694.64	53.11	**
SFA (%)	45.59	35.60	55.40	8.69	47.84	36.70	59.10	8.49	***
USFA (%)	54.25	44.50	64.30	7.43	52.18	40.90	63.40	7.89	***
PH (cm)	413.25	301.00	520.00	12.32	358.68	215.00	535.00	17.52	***
RL (cm)	496.17	342.00	596.00	10.75	483.51	348.00	618.00	10.67	ns
PW (mm)	69.28	55.00	98.00	13.51	63.56	44.00	85.00	13.10	***
PT (mm)	39.39	31.00	77.00	17.03	32.86	21.00	49.00	15.02	***
LC (leaves)	162.79	144.00	178.00	4.10	151.67	127.00	182.00	6.06	***
LL (cm)	87.42	46.84	122.00	14.94	85.60	58.33	106.83	12.30	***
LW (cm)	5.08	3.37	6.60	12.76	4.54	2.95	6.50	16.01	***

Note: ns - not significant ($p > 0.05$); * - significant at $p \leq 0.05$; ** - $p \leq 0.01$; *** - $p \leq 0.001$; PH - palm height; RL - rachis length; PW - petiole width; PT - petiole thickness; LC - leaf count; LL - leaflet length; LW - leaflet width; CAR - carotene; SFA - saturated fatty acids; USFA - unsaturated fatty acids; C18:1 - oleic acid; C16:0 - palmitic acid; C18:0 - stearic acid; C18:2 - linoleic acid; C18:3 - linolenic acid; C16:1 - palmitoleic acid; C14:0 - myristic acid; C20:0 - arachidic acid; CV - coefficient of variation.

sub-clusters. In contrast, the secondary cluster, dominated by CMR accessions, consisted of palms with lower palm. This pattern suggests that CMR exhibits broader variability in PH, spanning both extremes of the height spectrum, whereas AGO showed a more moderate range. Overall, the results suggest that PH is a key discriminating trait among the vegetative variables and may serve as an essential criterion in selection programme targeting plant architecture and harvest efficiency.

The circular heatmap of oil quality (*Figure 3c*) revealed two main clusters, primarily shaped by variation in C16:0 and C18:1, whose strong correlation (Lamaisri et al., 2015) underscores their combined influence on population differentiation. Accessions from both AGO and CMR, along with the reference DxP PPKS 540 variety, were evenly distributed across these clusters. A similar two-cluster pattern was observed for carotene (*Figure 3d*), reflecting the substantial phenotypic range in total carotene content among accessions. Together, these results indicate that variation in oil quality and carotene traits is not associated with geographical origin but rather with phenotypic differences among individual accessions.

Overall, the clustering of bunch components and vegetative traits largely followed the geographical origins of the AGO and CMR germplasm, except for oil quality and carotene traits. This finding indicates that phenotypic variation occurs not only between germplasm populations but also among individual accessions within each population. Similar clustering patterns have been reported in germplasm from Zaire, Cameroon, and Nigeria (Nasir et al., 2024; Wan Nor Salmiah et al., 2023). Such clustering patterns are likely influenced by high levels of genetic exchange facilitated by seed dispersal (Arias et al., 2013). These results highlight the importance of phenotypic diversity in identifying superior palms and selecting elite genotypes for future breeding programmes.

Phenotypic Correlation

Pearson correlation analysis revealed broadly similar correlation patterns and trends in both germplasm (*Figure 4*). However, the number of variables meeting the significance threshold ($|r| > 0.7$ and p-value < 0.01) differed between the two populations: 22 significant correlations in CMR and 15 in AGO. Notably, carotene did not

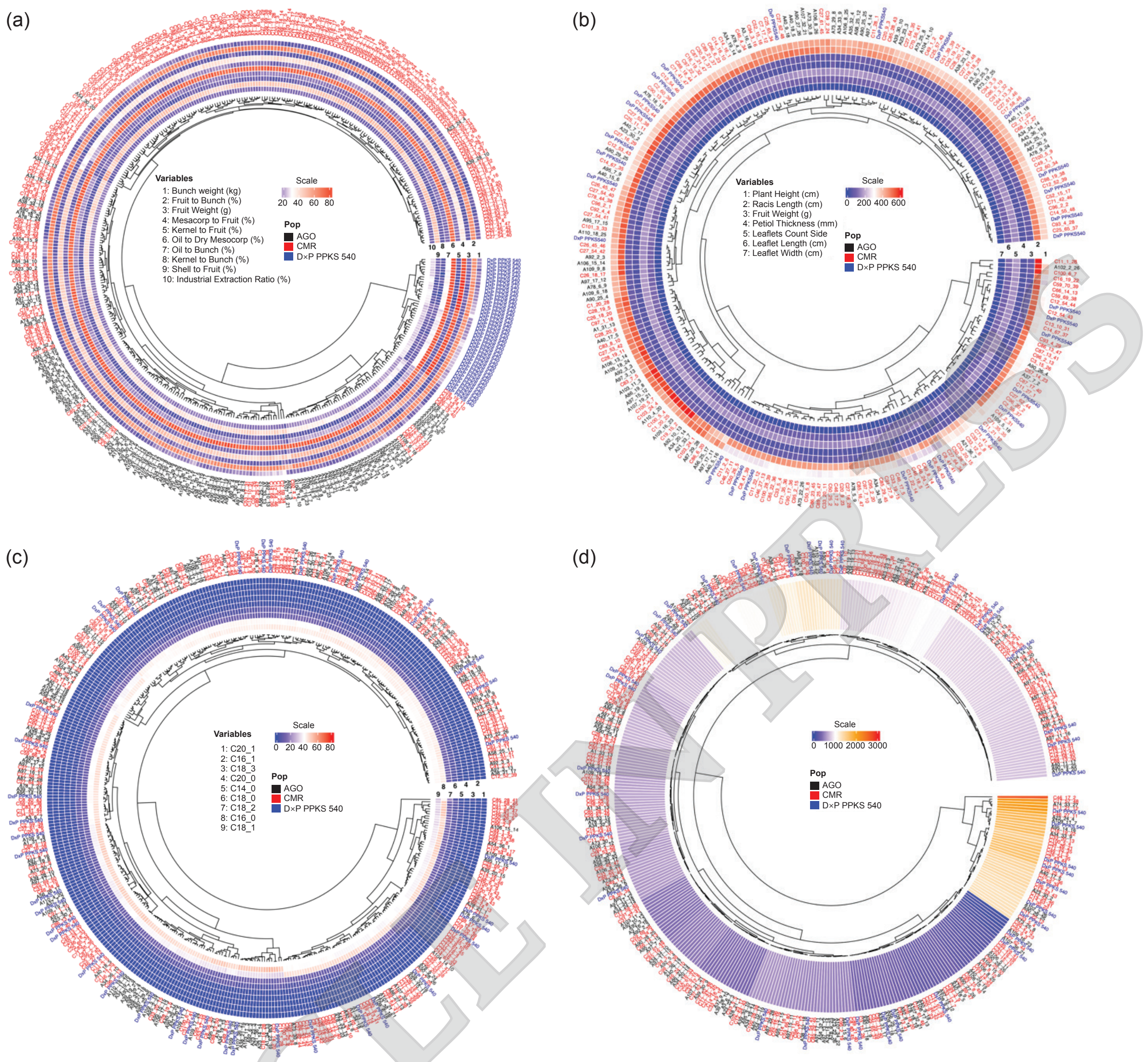

Figure 3. Circular heatmaps of the Angola and Cameroon germplasm based on phenotypic variability across four trait groups: (a) bunch components, (b) vegetative traits, (c) oil quality and (d) carotene content.

meet this threshold, showing weak correlations with all traits. Furthermore, no strong correlations were observed among the traits related to bunch components, vegetative morphology and oil quality in either germplasm. These results align with previous studies that also reported limited or non-significant interactions among these major trait groups (Abimbola et al., 2014; de Almeida Rios et al., 2018; Norziha et al., 2020).

Overall, the correlation patterns observed in this study align closely with those in earlier studies (Abimbola et al., 2014; De Almeida Rios et al., 2018), suggesting that strong correlations among variables may be universal across different germplasms and primarily influenced by underlying genetic factors. Among the bunch component traits, IER consistently showed positive correlations with M/F and O/B, but negative correlations with S/F, reinforcing the importance of M/F and S/F as major selection traits for achieving high yield, as previously reported by Kushairi et al. (1999). The high heritability estimates of M/F and S/F further confirm their breeding relevance (Hardon et al., 1985; Norziha et al., 2020).

On the other hand, traits such as oil O/DM, MW and K/F did not show strong correlations with any other traits, except with O/WM, FW and K/B, respectively. The BW exhibited positive correlations with StW and SpW, but negative correlations with Sp/B ratio. For oil quality traits, C18:1 showed positive correlations with USFA percentage but negative correlations with C16:0 and SFA percentage. Regarding vegetative traits, RL and PH were positively correlated with LC and PT, respectively, within the CMR.

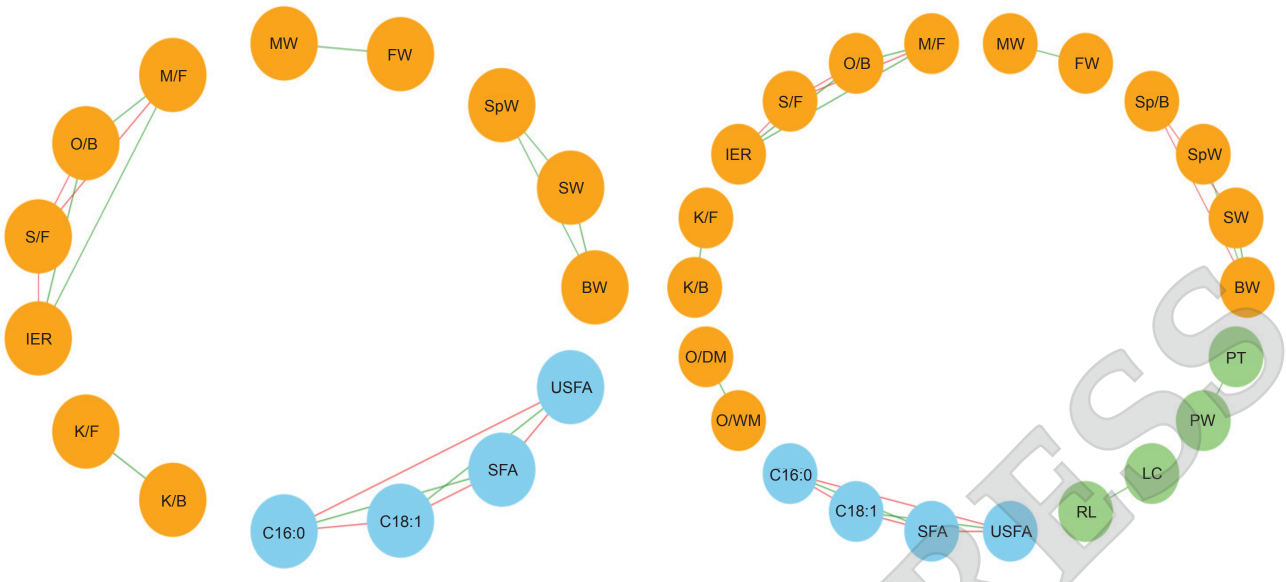

Figure 4. Circular correlation network among variables of bunch components, vegetative morphology, and oil quality. The threshold was set at $|r| > 0.7$ *and* p-*value* < 0.01. *The thickness of the lines represents the strength of the correlations, with green lines indicating positive correlations and red lines indicating negative correlations.*

MGIDI Selection Analysis

The MGIDI was employed to identify superior palms based on bunch components, oil quality and vegetative traits across both germplasms (Olivoto & Nardino, 2020). Traits such as M/F, O/DM, S/F, IER, PH, RL, C18:1, USFA, carotene and F/B were used as selection criteria due to their strong association with oil productivity, compact palm architecture, and superior oil quality.

The MGIDI classified the traits into four groups derived from factor analysis (FA), based on their correlations and interrelationships. The first FA group encompassed bunch component (M/F, O/DM, S/F and IER). The second and third groups represented vegetative traits (PH and RL) and oil quality (C18:1 and carotene), respectively. The fourth FA group was associated with the bunch component trait F/B. Theoretical selection gains (SGPerc) predicted by MGIDI-based selection ranged from –15.10% to 47.10% (*Table 3*).

The MGIDI-based selection analysis using nine traits successfully identified 18 top-performing accessions (*Figure 5*), comprising seven from the AGO and 11 from the CMR. The strengths and weaknesses of each accession are illustrated in the MGIDI factor index (*Figure 5b*). Among these, accession BC71_41_4 exhibited one of the shortest distances from the ideotype, reflecting a balanced and desirable combination of traits. It displayed favourable values for multiple parameters, including M/F (40.99%), O/DM (73.60%), IER (12.68%), C18:1 (44.3%), F/B (68.89%) and carotene (886.39 ppm), together with desirable S/F (41.15%), RL (533 cm) and PH (315 cm). This comprehensive profile suggests that BC71_41_4 is a strong multi-trait ideotype candidate for the *dura* parental line in future oil palm breeding.

CONCLUSION

This study revealed distinct variability patterns between the AGO and CMR germplasms, with bunch components exhibiting greater diversity than vegetative traits and oil quality traits. The CMR consistently displayed higher variability across most traits. The AGO performed better for traits linked to CPO yield, while CMR accessions excelled in kernel oil yield and carotene. Cluster analysis generally grouped accessions by geographic origin based on bunch traits and vegetative traits, whereas oil quality showed a more admixed clustering pattern. Pearson correlation analysis revealed no strong associations among bunch components, vegetative, and oil quality traits. However, critical yield-related traits, such as M/F ratio and IER, exhibited meaningful correlations. The MGIDI analysis identified 18 superior accessions, with BC71_41_4 showing one of the shortest ideotype distances, underscoring the value of MGIDI for multi-trait selection in oil palm breeding.

TABLE 3. MGIDI SELECTION DIFFERENTIAL

Variables	Factor	Xo	Xs	SD	SDPerc	h^{2*}	SG	SGPerc	Goal
M/F	FA1	43.10	43.40	0.33	0.77	0.691	0.228	0.532	Ö
O/DM	FA1	75.90	75.90	0.02	0.02	0.312	0.006	0.006	Ö
S/F	FA1	44.10	43.20	-0.93	-2.12	0.625	-0.581	-1.325	Ö
IER	FA1	13.20	13.50	0.30	2.30	0.514	0.154	1.184	Ö
PH	FA2	378	321	-57.20	-15.10	1	-57.2	-15.1	Ö
RL	FA2	489	443	-45.70	-9.35	1	-45.7	-9.35	Ö
C18:1	FA3	43.60	48.29	4.55	10.40	1	4.55	10.4	Ö
Car	FA3	612	900	288	47.10	1	288	47.1	Ö
F/B	FA4	65.60	66	0.37	0.56	0.096	0.0355	0.054	Ö

Note: M/F - mesocarp to fruit; O/DM - oil content in dry mesocarp; S/F - shell to fruit; IER - industrial extraction ratio; PH - palm height; RL - rachis length; C18:1 - oleic acid; CAR - carotene content; F/B - fruit to bunch; Xo - original population mean; Xs - selected mean; SD - selection differential (Xs – Xo); SDPerc - selection differential expressed as a percentage; h^2 - narrow-sense heritability; SG - selection gain (SD × h^2); SGPerc - selection gain expressed as a percentage; * - heritability values were computed from a single-environment mixed model; therefore, traits with very low residual variance resulted in heritability values approaching 1.

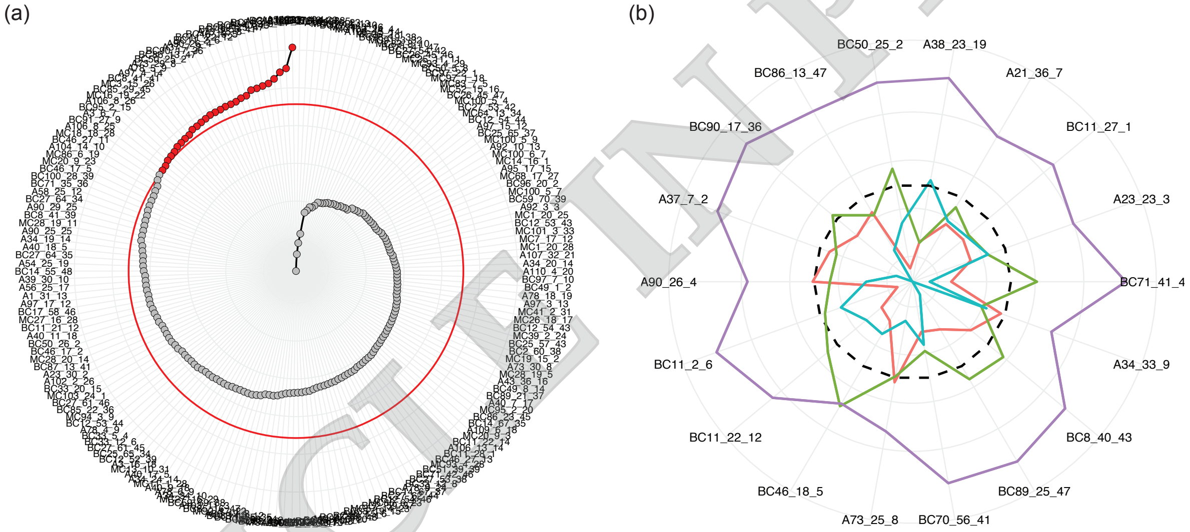

Figure 5. (a) Accession ranking based on the MGIDI index and (b) the strengths or weaknesses of selected accessions represented as the proportion of each factor in the MGIDI index. A smaller proportion explained by a factor indicates that the traits within that factor are closer to the ideotype (further toward the external edge). The dashed line represents the theoretical value if all factors contributed equally. FA1: M/F, O/DM, S/F, IER; FA2: PH, RL; FA3: C18:1, CAR; FA4: F/B.

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REFERENCES

Abimbola, L. H. M., Din, A. K., Rajanaidu, N., Hassan, M. S., Ngah, C., & Sukaimi, J. (2014). Variation and correlation studies in the MPOB-Nigerian oil palm (*Elaeis guineensis* Jacq.) germplasm. *Proceedings of the 13th Symposium of the Malaysian Society of Applied Biology*, Cherating, Pahang, Malaysia, Article ID 2014014.

Abu-Bakar, N. A., Amiruddin, M. D. & Nookiah, R. (2021). Preliminary evaluation of intra-crosses MPOB-Cameroon and their inter-crosses with MPOB-Zaire breeding population (*Elaeis guineensis* Jacq.). *IOP Conference Series: Earth and Environmental Science*, 736(1), Article 012002. https://doi.org/10.1088/1755-1315/736/1/012002

Arias, D., Montoya, C., & Romero, H. (2013). Molecular characterisation of oil palm *Elaeis guineensis* Jacq. materials from Cameroon. *Plant Genetic Resources*, *11*(2), 140–148. https://doi.org/10.1017/S1479262112000482

Ariati, S. R., Astuti, R. S., Supriyatna, I., Yuswandi, A. Y., Setiawan, A., Saftaningsih, D., & Pribadi, D. O. (2019). *An alphabetical list of plant species cultivated in the Bogor Botanic Gardens.* Center for Plant Conservation, Indonesian Institute of Sciences.

Bertolino, F., Columbu, S., Manca, M., & Musio, M. (2024). Comparison of two coefficients of variation: A new Bayesian approach. *Communications in Statistics: Simulation and Computation*, *53*(12), 6260–6273. https://doi.org/10.1080/ 10.1080/03610918.2023.2231179

Constantin, M., Ridwani, S., Syukur, M., & Suwarno, W. B. (2017). Performance, heritability and genetic advance for oil yield and some economical characters in oil palm (*Elaeis guineensis* Jacq.) of Cameroon. *Jurnal Agronomi Indonesia (Indonesian Journal of Agronomy)*, *45*(2), 212–219.

Corley, R. H. V., & Tinker, P. B. (2016). *The oil palm* (5th ed.). Wiley-Blackwell.

De Almeida Rios, S., da Cunha, R. N. V., Lopes, R., Barcelos, E., da Rocha, R. N. C., & de Lima, W. A. A. (2018). Correlation and path analysis for yield components in *Dura* oil palm germplasm. *Industrial Crops and Products*, 112, 724–733. https://doi.org/10.1016/j.indcrop.2017.12.054

Fadila, A. M., Norziha, A., Mohd Din, A., Rajanaidu, N., & Kushairi, A. (2016). Evaluation of bunch index in MPOB oil palm (*Elaeis guineensis* Jacq.) germplasm collection. *Journal of Oil Palm Research*, *28*(4), 442–451.

Gan, S. T., Teo, C. J., Manirasa, S., Wong, W. C., & Wong, C. K. (2021). Assessment of genetic diversity and population structure of oil palm (*Elaeis guineensis* Jacq.) field genebank: A step towards molecular-assisted germplasm conservation. *PLOS ONE*, *16*(7), Article e0255418.

Govindaraj, M., Vetriventhan, M., & Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Genetics Research International*, 2015, Article 431487. https://doi.org/10.1155/2015/431487

Hardon, J. J., Rao, V., & Rajanaidu, N. (1985). A review of oil palm breeding. In G. E. Russell (Ed.), *Progress in plant breeding* (pp. 139–163). Butterworths.

John Martin, J. J., Yarra, R., Wei, L., & Cao, H. (2022). Oil palm breeding in the modern era: Challenges and opportunities. *Plants*, *11*(11), Article 1395. https://doi.org/10.3390/plants11111395

Kenworthy, W. J. (2019). Strategies for introgressing exotic germplasm in breeding programs. In *World soybean research conference II* (pp. 217–223). CRC Press.

Kozak, M., Bocianowski, J., & Rybinski, W. (2013). Note on the use of coefficient of variation for data from agricultural factorial experiments. *Bulgarian Journal of Agricultural Science*, *19*(4), 644–646.

Kushairi, A., Rajanaidu, N., Jalani, B. S., & Zakri, A. H. (1999). Agronomic performance and genetic variability of *dura* × *pisifera* progenies. *Journal of Oil Palm Research*, *11*(2), 1–24.

Lamaisri, C., Punsuvon, V., Chanprame, S., Arunyanark, A., Srinives, P. & Liangsakul, P. (2015). Relationship between fatty acid composition and biodiesel quality for nine commercial palm oils. *Songklanakarin Journal of Science & Technology*, *37*(4), 389–395.

Lubis, A. U. (2008). *Kelapa sawit (Elaeis guineensis Jacq.) di Indonesia* (2nd ed.). Pusat Penelitian Kelapa Sawit.

Malaysian Palm Oil Board. (2004a). *MPOB Test method p3.5: Determination of fatty acid composition (FAC) as their methyl esters by capillary column gas chromatography.*

Malaysian Palm Oil Board. (2004b). *Test method: A compendium of tests on palm oil products, palm kernel products, fatty acids, food related products and others.*

Mendoza, L., Barba, J., & Ligarreto, G. (2023). Bunch oil and fatty acid profile in *Elaeis oleifera* Taisha-Ecuador, *E. guineensis* Jacq., interspecific hybrids and backcrosses. *Journal of Oil Palm Research*, *35*(3), 504–516. https://doi.org/10.21894/jopr.2022.0057

Mozzon, M., Pacetti, D., Frega, N. G., & Lucci, P. (2015). Crude palm oil from interspecific hybrid *Elaeis oleifera* × *E. guineensis*: Alcoholic constituents of unsaponifiable matter. *Journal of the American Oil Chemists' Society*, *92*(5), 717–724. https://doi.org/10.1007/s11746-015-2628-1

Nasir, F. M., Mustaffa, S., Marjuni, M., Mohd Salim, W. N. S. T., & Yaakub, Z. (2024). Genetic diversity of MPOB-Zaire oil palm (*Elaeis guineensis* Jacq.) germplasm population by multivariate analysis. *Journal of Oil Palm Research.* https://doi.org/10.21894/jopr.2024.0050

Nor Azwani, A. B., Fadila, A. M., Mohd Din, A., Rajanaidu N., Norziha, A., Suzana, M., Marhalil, M., Zulkifli, Y., & Kushairi, A. (2020). Potential oil palm genetic materials derived from the introgression of germplasm (MPOB-Nigeria, MPOB-Zaire, and MPOB-Cameroon accessions) to advanced (AVROS) breeding populations. *Journal of Oil Palm Research*, *32*(4), 569–581.

Norziha, A., Fadila, A. M., Marhalil, M., Zulkifli, Y., Mohd Din, A., Rajanaidu, N., Ong-Abdullah, M., & Kushairi, A. (2020). MPOB oil palm (*Elaeis guineensis* Jacq.) germplasms linked to compact trait for high-density planting. *Journal of Oil Palm Research*, *32*(3), 394–405.

Norziha, A., Zamri, Z., Zulkifli, Y., Fadila, A. M., & Marhalil, M. (2024). Selection criteria of MPOB-Angola germplasm collection for yield improvement of the oil palm. *Oil Crop Science*, *9*(1), 20–28. https://doi.org/10.1016/j.ocsci.2023.12.003

Nouy, B., Jacquemard, J. C., Suryana, E., Potier, F., Konan, K. E., & Durand-Gasselin, T. (2006). The expected and observed characteristics of several oil palm (*Elaeis guineensis* Jacq.) clones. In *Proceedings of the International Oil Palm Conference (IOPC).* Indonesian Oil Palm Research Institute.

Nugroho, Y. A., Tanjung, Z. A., Yono, D., Mulyana, A. S., Simbolon, H. M., Ardi, A. S., Yong, Y. Y., Utomo, C., & Liwang, T. (2019). Genome-wide SNP discovery and analysis of genetic diversity in oil palm using double digest restriction site-associated DNA sequencing. *IOP Conference Series: Earth and Environmental Science*, *293*(1), Article 012041. https://doi.org/10.1088/1755-1315/293/1/012041

Nur, F., Forster, B. P., & Caligari, P. D. (2024). Breeding using parents of restricted origins. *IOP Conference Series: Earth and Environmental Science*, *1308*(1), Article 012021. https://doi.org/10.1088/1755-1315/1308/1/012021

Olivoto, T., & Nardino, M. (2020). MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics*, *37*(10), 1383–1389. https://doi.org/10.1093/bioinformatics/btaa981

Ong, P. W., Maizura, I., Marhalil, M., Rajanaidu, N., Abdullah, N. A. P., Rafii, M. Y., & Singh, R. (2018). Association of SNP markers with height increment in MPOB-Angolan natural oil palm populations. *Journal of Oil Palm Research*, *30*(1), 61–70.

Pasaribu, A., Yulismawati, S. B., & Fathoni, A. (2022). Pemilihan karakter seleksi pada kelapa sawit berdasarkan koefisien keragaman fenotipik dan principal component analysis (PCoA) [Identification of selection parameter on oil palm based on phenotypic coefficient of variance and principal component analysis]. *In Prosiding Seminar Nasional Peripi*, 249–255.

Pedapati, A., Mathur, R. K., Ravichandran, G., Babu, B. K., & Bhagya, H. P. (2021). Evaluation of bunch quality components in *Dura* × *Dura* progenies of Zambia and Cameroon sources of oil palm germplasm. *Journal of Environmental Biology*, *42*(6), 1567–1577.

Purba, A. R., Nookiah, R., Boon, A. B., Kohar, M., Syahputra, I., & Siregar, H. A. (2017). Ekspedisi kelapa sawit (*Elaeis guineensis* Jacq.) Kamerun dan keragaan di lapangan [Cameroon oil palm (*Elaeis guineensis* Jacq.) expedition and field performance]. *Warta PPKS*, *22*(2), 66–75.

Putri, L. A. P., Aswidinnoor, H., & Asmono, D. (2009). Genetic performance and heritability estimations on yield component and β-carotene content of oil palm progenies. *Jurnal Agronomi Indonesia (Indonesian Journal of Agronomy)*, *37*(2), 102–107.

Rajanaidu, N. (1994). *MPOB oil palm genebank: Collection, evaluation, utilisation and conservation of oil palm genetic resources.* Malaysian Palm Oil Board.

Rajanaidu, N., Ainul, M. M., Kushairi, A., & Mohd Din, A. (2013). Historical review of oil palm breeding for the past 50 years: Malaysian journey. In *Proceedings of the International Seminar on Oil Palm Breeding: Yesterday, Today and Tomorrow*, (pp. 11–28). Malaysian Palm Oil Board.

Rajanaidu, N., Rao, V., Hassan, A. H., & Ong, A. S. H. (1989). *Genetic resources: New developments in oil palm breeding*. Malaysian Palm Oil Board (MPOB).

Rao, V., & Chang, K. C. (2021). Breeding virescens oil palm. *Journal of Oil Palm Research*, *33*(4), 565–576.

Siew, W. L., Tang, T. S., & Tan, Y. A. (1995). *PORIM test methods – Methods of test for oil and palm* *oil products.* Palm Oil Research Institute of Malaysia.

Soh, A. C., Mayes, S., & Roberts, J. A. (Eds.). (2017). *Oil palm breeding: Genetics and genomics.* CRC Press.

Ting, N. C., Chan, P. L., Buntjer, J., Ordway, J. M., Wischmeyer, C., Ooi, L. C. L., Low, E. T. L., Marjuni, M., Sambanthamurthi, R., & Singh, R. (2023). High-resolution genetic linkage map and height-related QTLs in an oil palm (*Elaeis guineensis*) family planted across multiple sites. *Physiology and Molecular Biology of Plants*, *29*(9), 1301–1318.

Valentim, J., Silva, M. S., Ferreira, A. M., & Souza, A. G. (2019). Fatty acids composition and carotenoids in *caiaué* (*Elaeis oleifera*) genotypes. *Anais do 13º Simpósio Latino Americano de Ciência de Alimentos*, [In *Proceeding of the 13th Latin American Symposium on Food Science*]. Galoá.

Wan Nor Salmiah, T.M.S., Zulkifli, Y., Suzana, M., Nor Azwani, A.B., Fatin, M.N., Marhalil, M, & Ong-Abdullah, M. (2023). Genetic variability of MPOB-Cameroon oil palm germplasm based on morphological traits using multivariate analysis. *Journal of Oil Palm Research, 35*(3), 476–490. https://doi.org/10.21894/jopr.2022.0038

Yue, G. H., Ye, B. Q., & Lee, M. (2021). Molecular approaches for improving oil palm for oil. *Molecular Breeding*, *41*, 1–17.