Malaysian Applied Biology (2024) 53(2): 125-133
https://doi.org/10.55230/mabjournal.v53i2.2975

Research

Genetic Variability of Oil Palm (*Elaeis guineensis* Jacq.) Deli *Dura* Inter-Crosses Population in The MPOB Research Station Hulu Paka, Terengganu, Malaysia

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ABSTRACT

The oil palm Deli *dura* breeding population is the most widely used *dura* for breeding and seed production. Due to its narrow genetic base, with current material originating from the four initial *dura* palms of Bogor, the Deli *dura* is presumed to have low genetic diversity. A total of 35 MPOB Deli *dura* inter-crosses from eight paternal parents were characterized based on 22 different traits including bunch yields, bunch quality components, as well as other vegetative and physiological traits. Based on the principal component analysis of the collected data, the first five components (PC1-PC5) possessing eigenvalues surpassing 1, contributed to 97.83% of the overall variance. PC1, with the highest variation (30.88%), was characterized mainly by vegetative and physiological traits, while PC2, with about 26.02% variation, was primarily associated with bunch quality components. The principal component score plot suggests that populations of the Johor Labis paternal parents 0.278/318 and 0.278/295 are unique populations and can be used in further breeding programmes. Besides, the populations from Ulu Remis (0.280/68) and Ulu Remis × Elmina (0.281/44) paternal parents were positively associated with PC2, suggesting strong performance in bunch quality components. Cluster analysis indicated that all populations were clustered into three main groups comprised of several sub-clusters, with populations of paternal parents 0.279/48 (Banting) and 0.281/74 (Banting) were outliers in the second and third clusters, respectively. In overall, the study revealed the presence of variation among the Deli *dura* inter-crosses based on the traits evaluated. These results will be useful for the selection of specific populations for genetic improvements of bunch yield, bunch quality, as well as vegetative and physiological characteristics.

Key words: Cluster analysis, Deli *dura*, genetic variability, principal component analysis

Article History
Accepted: 11 May 2024
First version online: 30 June 2024

Cite This Article:
Fadila, A.M., Marhalil, M., Zulkifli, Y., Shamsudin, N.A.A. & Oyebamiji, Y.O. 2024. Genetic variability of oil palm (*Elaeis guineensis* Jacq.) Deli *Dura* inter-crosses population in the MPOB Research Station Hulu Paka, Terengganu, Malaysia. Malaysian Applied Biology, 53(2): 125-133. https://doi.org/10.55230/mabjournal.v53i2.2975

INTRODUCTION

Oil palm (*Elaeis guineensis* Jacq.) has been the main contributor to Gross Domestic Product (GDP) in Malaysia at 35.2%, followed by other agriculture (29.3%), livestock (16.7%), fisheries (11.3%), forestry and logging (5.2%), as well as rubber (2.5%) in 2021 (DOSM, 2022). The remarkable growth of the oil palm industry in Malaysia started with the plantation of a significant 54,000 hectares in 1960 and reached an astonishing increase of more than 5 million hectares in the past year. In 2023, the Malaysian oil palm industry produced crude palm oil (CPO) of 18.6 million tonnes, an average fresh fruit bunch (FFB) yield of 15.8 tonnes ha^{-1}, and an average oil extraction rate (OER) of 19.9% (MPOB, 2024). Due to its high productivity per hectare, which accounts for about 40% of globally traded vegetable oil, oil palm is well known as the most important oil crop in the world (Murphy *et al*., 2021).

The Malaysian oil palm (*Elaeis guineensis* Jacq.) sector originated from the planting of four *dura* palms at the Bogor Botanical Gardens, Indonesia, in 1848. A pair of these palms hailed from the Amsterdam Botanic Gardens, their origins undisclosed, while the remaining duo originated from either

Mauritius or Reunion Island (Hartley, 1988). The current Deli *dura* breeding population is formed from the offspring of these original four Bogor palms and has since spread worldwide (Rajanaidu & Jalani, 1999). In the 1920s, the establishment of Malaysia's oil palm breeding initiative was led by the Department of Agriculture (DOA) using materials planted in Serdang and Elmina Estates (Kushairi & Rajanaidu, 2000). Another pair of enterprises, namely the Oil Palm of Malaya (OPM) under Kumpulan Guthrie Berhad in Ulu Remis and Elaeis Estates, as well as *Societe Financiere de Caoutchouces* (Socfin) in Johore Labis Estate, started their breeding programs in 1933. Four sub-populations of the Deli *dura* were formed through their programs, with each considered to be independent breeding populations of restricted origin (BPRO): Johore Labis (Socfin), Elmina (DOA), Serdang Avenue (DOA) and Ulu Remis (Guthrie) (Rosenquist, 1985). The development of these BPROs was thoroughly recorded by Hardon and Thomas in 1968. The Malaysian Agricultural Research and Development Institute (MARDI) subsequently took over the administration of DOA's oil palm breeding materials. The management was later shifted to the establishment formed in 1979, initially named the Palm Oil Research Institute of Malaysia (PORIM), and currently recognized as the Malaysian Palm Oil Board (MPOB).

As the Deli *dura* populations descended from a limited number of palms, the Deli *dura* populations in Malaysia were extremely narrow (Fadila *et al*., 2019). Jin *et al*. (2016) found over 18 million single nucleotide polymorphisms (SNPs) and discovered a low genetic diversity among *dura* palms in Southeast Asia by sequencing 18 palms from Southeast Asia, Africa, and Central America. Meanwhile, MPOB initiated introgressed crosses of Nigerian *dura* x Deli *dura* to broaden the genetic base of the *dura* population in Malaysia (Noh *et al*., 2014). There was a significant level of genetic variability in the introgressed crosses for bunch yield and its components, bunch quality components, and vegetative characters that would assist in further selection programs for the improvement of these traits. Marhalil *et al*. (2016) reported that an FFB yield improvement of 12%-16% was observed in the Banting and Elmina progenies from the fifth generation compared to the previous generation. This outcome aligns with the assessment made by Hardon *et al*. (1987) regarding selection progress of 10-15% per generation in the second and succeeding generations.

Meanwhile, a multivariate statistical technique known as the principal component analysis (PCA) can be deployed to analyze various inter-correlated quantitative dependent variables. It has been widely used to classify germplasm materials, including germplasm collections of MPOB such as MPOB-Nigeria by Li-Hammed *et al*. (2016), MPOB-Sierra Leone by Suzana *et al*. (2016), MPOB-Guinea by Norziha *et al*. (2019), and MPOB-Cameroon by Tun Mohd Salim *et al*. (2023). It also generates a pattern of similarity between variables and explains the variation among genotypes, which is very helpful in selecting desired traits for breeding programs. On the other hand, cluster analysis (CA) is used to complement PCA in representing genetic differences. It is an exploratory data analysis tool to gather accessions (Richard & Wichern, 2007). Hence, this study is conducted to select superior Deli *dura* inter-crosses for future breeding and commercial seed production.

MATERIALS AND METHODS

Materials

A total of 35 MPOB Deli *dura* inter-crosses were planted in Trial 0.493 at the MPOB Research Station Hulu Paka, Terengganu, in 2007 (Table 1). This trial followed a randomized complete block design (RCBD) with three replications, each consisting of 16 palms per cross. The Deli *dura* inter-crosses were derived from crosses between Ulu Remis Chemara *duras* as maternal parents and eight paternal parents from Johor Labis, Banting, Ulu Remis, and Ulu Remis × Elmina.

Methods

The bunch yield recording was initiated in 2010 and carried out at two monthly rounds with intervals of 15 days. Its components consist of FFB (sum of BWT), bunch number (BNO), and average bunch weight (ABW) (quotient between FFB and BNO). The summarised bunch yields of four consecutive years, from 2014 to 2017, were used for data analysis. Meanwhile, bunch analysis was carried out from 2012 to 2017 based on methods devised by Blaak *et al*. (1963) and adjusted by Rao *et al*. (1983). As proposed by Corley and Breure (1981), a single instance of the non-destructive vegetative measurements (VM) approach was conducted in 2015, eight years after field planting. A single year of vegetative measurements and four consecutive years of bunch yield data were used to estimate physiological parameters. Based on the eight paternal parents, some 22 traits were used for analysis, where population means were standardized to eliminate bias due to the different magnitudes of the measurement units. Ward's minimum variance technique (Ward, 1963) was used to cluster the eight paternal parents. Statistical Analysis Software (SAS) version 9.4 was utilized to conduct both PCA and CA.

Table 1. Details of MPOB Deli *dura* inter-crosses in Trial 0.493, MPOB Research Station Hulu Paka, Terengganu

No.	Progeny	Female Parent	Male Parent	Cross Type
1	ECP HP 469	0.338/110	0.278/295 (Johor Labis)	D × D
2	ECP HP 470	0.338/373		
3	ECP HP 471	0.338/264		
4	ECP HP 472	0.338/300		
5	ECP HP 480	0.338/420		
6	ECP HP 578	0.338/63	0.278/318 (Johor Labis)	D × D
7	ECP HP 592	0.338/422		
8	ECP HP 595	0.338/339		
9	ECP HP 597	0.338/406		
10	ECP HP 498	0.338/420	0.279/48 (Banting)	D × D
11	ECP HP 511	0.338/420		
12	ECP HP 512	0.338/423		
13	ECP HP 433	0.338/127	0.280/64 (Ulu Remis)	D × D
14	ECP HP 434	0.338/209		
15	ECP HP 507	0.338/299		
16	ECP HP 508	0.338/304		
17	ECP HP 534	0.338/436		
18	ECP HP 624	0.338/384		
19	ECP HP 629	0.338/422		
20	ECP HP 451	0.338/302	0.280/68 (Ulu Remis)	D × D
21	ECP HP 453	0.338/148		
22	ECP HP 454	0.338/420		
23	ECP HP 489	0.338/148	0.281/44 (Ulu Remis x Elmina)	D × D
24	ECP HP 491	0.338/420		
25	ECP HP 493	0.338/302		
26	ECP HP 551	0.338/332		
27	ECP HP 552	0.338/262		
28	ECP HP 588	0.338/84		
29	ECP HP 589	0.338/89		
30	ECP HP 590	0.338/373		
31	ECP HP 605	0.338/127	0.281/57 (Johor Labis)	D × D
32	ECP HP 607	0.338/63		
33	ECP HP 615	0.338/357	0.281/74 (Banting)	D × D
34	ECP HP 625	0.338/331		
35	ECP HP 632	0.338/389		

RESULTS AND DISCUSSION

Principal component analysis

Principal component analysis (PCA) offers an advantage in pinpointing the primary contributor to overall variation on each axis of differentiation. The eigenvalues dictate the number of relevant principal components to preserve, typically equating to the total number of variables when summed. Among the MPOB Deli *dura* inter-crosses, PCA indicates that the first five components (PC1-PC5) with eigenvalues greater than 1.0 accounted for 97.83% of the total variation observed (Table 2). PC1, which had the largest eigenvalue of 6.79, accounted for 30.88% of the total variability. PC2, with an eigenvalue of 5.73, accounts for an additional 26.02% of the variation. PC3, PC4, and PC5 had eigenvalues of 4.91, 3.04, and 1.05, respectively, and accounted for 22.33% (PC3), 13.81% (PC4), and 4.78% (PC5) of the total variation observed among the MPOB Deli *dura* inter-crosses. Suzana *et al*. (2016) also reported five principal components with eigenvalues greater than 1.0 among the 14 populations of MPOB-Sierra Leone germplasm, with a total variation of 95.72%.

PC1, which had the highest variation, was characterized mostly by vegetative and physiological traits. It exhibits the largest positive associations with rachis length (0.372), vegetative dry matter (0.329), and petiole cross-section (0.326). Conversely, it demonstrates a negative relationship with frond production (-0.335) and bunch index (-0.303). In the oil palm germplasm, the majority of the diversity can be attributed to variables that significantly affect the principal component in both positive and negative ways, particularly variables associated with PC1. These variables tend to be the source of variation that distinguishes the different accessions (Denton & Nwangburuka, 2011; Iannucci *et al*., 2011; Ahmad *et al*., 2014; Hamza *et al*., 2014). Thus, these vegetative and physiological traits can be used to differentiate Deli *dura* populations in MPOB. As for PC2, it has the largest association with bunch quality components such as oil to dry mesocarp (0.393), oil yield (0.378), oil to bunch (0.365), shell to fruit (-0.356), and total economic product (0.355). PC3 is related to the high total dry matter (0.373), FFB yield (0.356), bunch dry matter (0.356), and mean fruit weight (-0.315). PC4 has large negative associations with fruit to bunch (-0.453), kernel to bunch (-0.436), and kernel to fruit (-0.364). PC5 has positive relations with palm height (0.556), trunk diameter (0.353), and fruit to bunch (0.346), but a negative association with mean fruit weight (-0.454). In general, PCA scores are centered at zero, where zero denotes an observation with an average PCA score. Lower than-average component scores are indicated by negative values. Negative loadings and negative correlations between the variables do not highlight specific issues in PCA. A negative loading in PCA simply indicates that a specific trait is lacking from a latent variable linked to the designated principal component (Burstyn, 2004). For example, in PC1, frond production with negative loading is associated with vegetative dry matter, a derived trait that also requires petiole cross-section, trunk diameter, and palm eight in its estimation. In addition, vegetative dry matter is one of the components of the bunch index, along with bunch dry matter. However, a detailed analysis may reveal associations between traits with positive and negative loadings in the same principal components.

Table 2. Variables correlation loading matrix, eigenvalues, variance, and cumulative variance for five principal components in MPOB Deli *dura* inter-crosses

	Eigenvectors				
Traits	PC1	PC2	PC3	PC4	PC5
FFB	-0.085	0.053	0.356	0.315	0.104
BNO	-0.273	0.276	0.080	0.066	-0.080
ABW	0.248	-0.261	0.147	0.145	0.125
MFW	0.122	0.047	-0.315	0.172	-0.454
M/F	0.119	0.299	-0.234	0.140	0.205
K/F	-0.206	-0.071	0.230	-0.364	-0.071
S/F	-0.049	-0.356	0.194	0.005	-0.235
O/DM	0.081	0.393	-0.050	-0.104	-0.157
F/B	0.137	0.111	0.040	-0.453	0.346
O/B	0.142	0.365	-0.023	-0.175	0.047
K/B	-0.168	-0.069	0.193	-0.436	0.056
OY	0.001	0.378	0.180	0.044	0.042
TEP	-0.036	0.355	0.226	0.000	0.053
FP	-0.335	-0.119	-0.096	-0.089	0.161
PCS	0.326	0.012	0.227	-0.063	-0.097
RL	0.372	-0.064	0.057	0.056	-0.029
HT	-0.207	-0.123	-0.187	0.152	0.556
DIA	0.262	-0.041	-0.247	0.109	0.353
VDM	0.329	-0.063	0.204	-0.077	0.078
BDM	-0.084	0.0542	0.356	0.315	0.106
TDM	0.180	-0.005	0.373	0.150	0.127
BI	-0.303	0.117	0.081	0.278	-0.033
Eigenvalue	6.79	5.73	4.91	3.04	1.05
Variance (%)	30.88	26.02	22.33	13.81	4.78
Cumulative variance (%)	30.88	56.91	79.24	93.05	97.83

Note: FFB = fresh fruit bunch, BNO = bunch number, ABW = average bunch weight, MFW = mean fruit weight, M/F = mesocarp to fruit, K/F = kernel to fruit, S/F = shell to fruit, O/DM = oil to dry mesocarp, F/B = fruit to bunch, O/B = oil to bunch, K/B = kernel to bunch, OY = oil yield, TEP = total economic product, FP = frond production, PCS = petiole cross-section, RL = rachis length, HT = palm height, DIA = trunk diameter, VDM = vegetative dry matter, BDM = bunch dry matter, TDM = total dry matter, BI = bunch index

Based on the score plot, PC1 loadings for populations of the Johor Labis paternal parents, 0.278/318 and 0.278/295, were the most positive and negative, respectively (Figure 1). This indicates that they are unique among the other populations. Population 0.278/318, with the most positive loading on PC1, recorded the highest fruit to bunch (69.58%), rachis length (5.45 m), and vegetative dry matter (15.06 t ha^{-1} yr^{-1}) (Table 3). It also had the lowest FFB yield (173.98 kg palm^{-1} yr^{-1}), BNO (10.39 bunches palm^{-1} yr^{-1}), palm height (1.87 m), bunch dry matter (13.65 t ha^{-1} yr^{-1}) and bunch index (0.47). On the other hand, population 0.278/295 with the most negative loading on PC1, was associated with the lowest mesocarp to fruit (61.69%), petiole cross-section (24.60 cm^2), rachis length (4.91 m), trunk diameter (0.58 m), and vegetative dry matter (12.63 t ha^{-1} yr^{-1}). Besides kernel to fruit (7.33%) and kernel to bunch (4.4%), it also had the highest frond production (26.76 frond palm^{-1} yr^{-1}) and bunch index (0.54). Norziha *et al*. (2020) reported that palms with short rachis lengths (less than 5 m) are desirable for high-density planting, which can increase the yield per unit land area. In addition, palms with narrow petiole cross-sections allow ease of harvesting. Besides, increasing the bunch index is an alternative way to increase oil production since the bunch index has been reported to be highly correlated to FFB yield and oil yield production (Junaidah *et al*., 2004; Fadila *et al*., 2016). Therefore, population 0.278/295 can be considered in the parental selection to breed high-density planting materials with a high bunch index.

Populations from both Ulu Remis (0.280/68) and Ulu Remis × Elmina (0.281/44) paternal parents had high positive loadings for PC2, which were associated with good performance in bunch quality components such as mesocarp to fruit (65.46% & 66.13%), oil to dry mesocarp (79.71% & 79.86%), oil to bunch (23.04% & 22.53%), and oil yield (44.76 kg palm^{-1} yr^{-1} & 43.77 kg palm^{-1} yr^{-1}) (Table 3). The findings align with the assertion of Saleh *et al*. (2018) that closer populations tend to share similar values for specific variables, while those more distant show significantly different values. Conversely, the population of Ulu Remis paternal parent (0.280/64) had the highest negative loading for PC2, which was linked to its lowest means of oil to dry mesocarp (77.57%), oil to bunch (19.79%), oil yield (35.78 kg palm^{-1} yr^{-1}), total economic product (40.17 kg palm^{-1} yr^{-1}), and total dry matter (27.42 t ha^{-1} yr^{-1}).

Table 3. Means of 11 traits based on eight paternal parents

Dura male	FFB	BNO	ABW	MFW	M/F	K/F	S/F	O/DM	F/B	O/B	K/B
0.278/295 (Johor Labis)	195.04	13.26	14.84	15.81	**61.69**	**7.33**	30.98	77.92	67.01	19.85	**4.40**
0.278/318 (Johor Labis)	**173.98**	**10.39**	16.93	17.14	64.36	6.13	29.51	79.20	**69.58**	22.53	3.85
0.279/48 (Banting)	190.66	11.11	17.33	16.97	65.35	**5.10**	29.55	77.82	66.34	20.03	**3.11**
0.280/64 (Ulu Remis)	176.98	11.03	16.25	16.36	62.17	6.55	31.28	**77.57**	68.67	**19.79**	4.05
0.280/68 (Ulu Remis)	191.85	13.33	14.45	**15.40**	65.46	6.56	**27.98**	79.71	69.54	**23.04**	4.10
0.281/44 (Ulu Remis × Elmina)	186.14	**13.50**	**13.92**	**18.03**	**66.13**	5.52	28.35	**79.86**	67.15	22.53	3.25
0.281/57 (Johor Labis)	**210.24**	11.96	**17.93**	15.88	62.25	6.34	**31.41**	78.27	67.37	20.73	3.74
0.281/74 (Banting)	186.29	12.01	15.84	16.97	63.20	6.29	30.52	78.43	**65.81**	20.10	3.74
Dura male	OY	TEP	FP	PCS	RL	HT	DIA	VDM	BDM	TDM	BI
0.278/295 (Johor Labis)	40.28	45.55	**26.76**	**24.60**	**4.91**	2.19	**0.58**	**12.63**	15.30	27.91	**0.54**
0.278/318 (Johor Labis)	40.13	44.20	24.43	33.87	**5.45**	**1.87**	0.63	**15.06**	**13.65**	28.77	**0.47**
0.279/48 (Banting)	38.30	41.90	25.17	27.48	5.29	**2.24**	**0.64**	13.54	14.96	28.50	0.52
0.280/64 (Ulu Remis)	**35.78**	**40.17**	25.75	27.74	5.22	2.11	0.60	13.53	13.88	**27.42**	0.50
0.280/68 (Ulu Remis)	**44.76**	**49.48**	24.99	28.80	5.11	1.98	0.60	13.37	15.05	28.41	0.53
0.281/44 (Ulu Remis × Elmina)	43.77	47.54	25.17	26.95	5.15	2.03	0.60	12.79	14.60	27.44	0.53
0.281/57 (Johor Labis)	42.84	47.56	**24.31**	**34.54**	5.41	1.87	0.59	15.01	**16.49**	**31.51**	0.52
0.281/74 (Banting)	38.42	42.64	25.04	27.94	5.16	1.90	0.60	12.99	14.61	27.54	0.53

Note: Figures in bold within each column are the minimum and maximum values. FFB = fresh fruit bunch (kg palm^{-1} yr^{-1}), BNO = bunch number (no. palm^{-1} yr^{-1}), ABW = average bunch weight (kg), MFW = mean fruit weight (g), M/F = mesocarp to fruit (%), K/F = kernel to fruit (%), S/F = shell to fruit (%), O/DM = oil to dry mesocarp (%), F/B = fruit to bunch (%), O/B = oil to bunch (%), K/B = kernel to bunch (%), OY = oil yield (kg palm^{-1} yr^{-1}), TEP = total economic product (kg palm^{-1} yr^{-1}), FP = frond production (no. palm^{-1} yr^{-1}), PCS = petiole cross-section (cm^2), RL = rachis length (m), HT = palm height (m), DIA = trunk diameter (m), VDM = vegetative dry matter (t ha^{-1} yr^{-1}), BDM = bunch dry matter (t ha^{-1} yr^{-1}), TDM = total dry matter (t ha^{-1} yr^{-1}), BI = bunch index

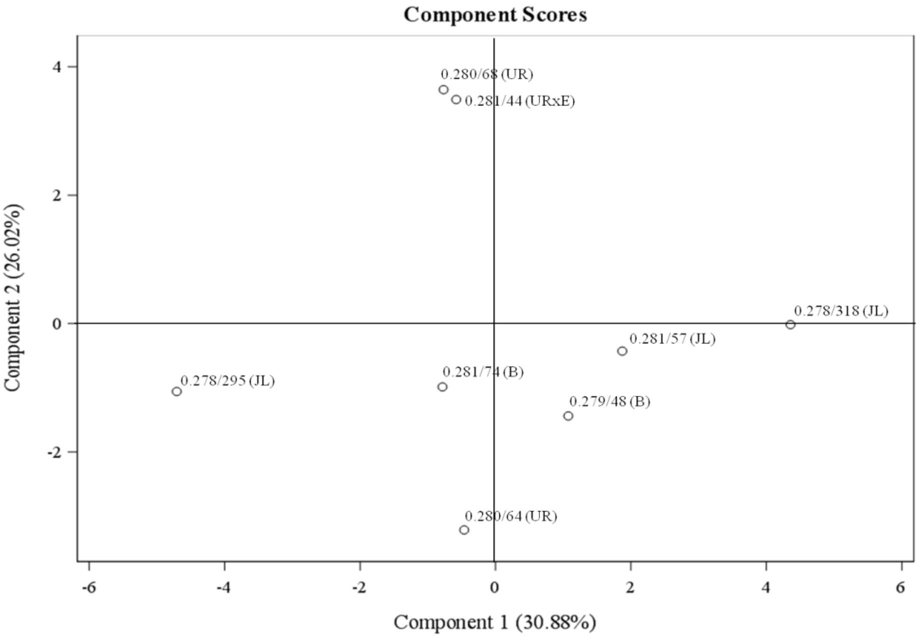

Fig. 1. Score plot of the eight paternal parents of MPOB Deli *dura* inter-crosses on the first two principal components. Note: JL = Johor Labis, B = Banting, UR = Ulu Remis, UR×E = Ulu Remis × Elmina

Cluster analysis

Cluster analysis is used to complement the principal components analysis in representing genetic divergence. It illustrates how various genotypes can be distinguished and organized into groups. All eight populations of paternal parents clustered into three main groups (clusters), with several sub-clusters (Figure 2). Overall, populations were not clustered according to their backgrounds, resulting in populations from different Deli origins being grouped within the same cluster. Arolu *et al*. (2017) reported that 34 Deli *dura* × Nigeria *pisifera* progenies were clustered based on their performance of certain characteristics. In this study, cluster I comprised two sub-clusters, formed by populations 0.281/44 (Ulu Remis × Elmina) and 0.280/68 (Ulu Remis). Clusters II and III each contained two sub-clusters. One sub-cluster comprised singleton Banting paternal parents: 0.279/48 in Cluster II and 0.281/74 in Cluster III. The other sub-cluster in Cluster II included populations 0.281/57 (Johor Labis) and 0.278/318 (Johor Labis), while in Cluster III, it consisted of populations 0.280/64 (Ulu Remis) and 0.278/295 (Johor Labis).

The cluster analysis also showed that population 0.281/44 (Ulu Remis × Elmina) had the most genetic distance to population 0.278/295 (Johor Labis) than the rest. A high degree of heterosis can be achieved by crossing morphologically distant populations (Mohammadi & Prassana, 2003). Thus, inter-crosses between these two Deli populations may be advantageous not only to achieve the maximum expression of heterosis, as both populations were superior in different groups of traits (bunch quality components for 0.281/44 as well as vegetative and physiological traits for 0.278/295) but also to gain the most genetic divergence among these Deli *duras* for further breeding programs.

CONCLUSION

This study revealed the variation among the Deli *dura* inter-crosses, especially in the vegetative and physiological traits such as rachis length, vegetative dry matter, and petiole cross-section. The unique population from Johor Labis (0.278/295) with desired traits of short rachis length and narrow petiole cross-section, as well as the Ulu Remis × Elmina (0.281/44) and Ulu Remis (0.280/68) populations with superior bunch quality traits, could be suggested to be used in the genetic improvements of the current Deli *dura* parent through introgression among these populations. These populations can also be used to derive superior *dura* × *pisifera* (D×P) offspring. In addition, further evaluation of the MPOB Deli *dura* inter-crosses from each population may be needed to identify valuable genetic materials for conservation and utilization for future use in breeding programs.

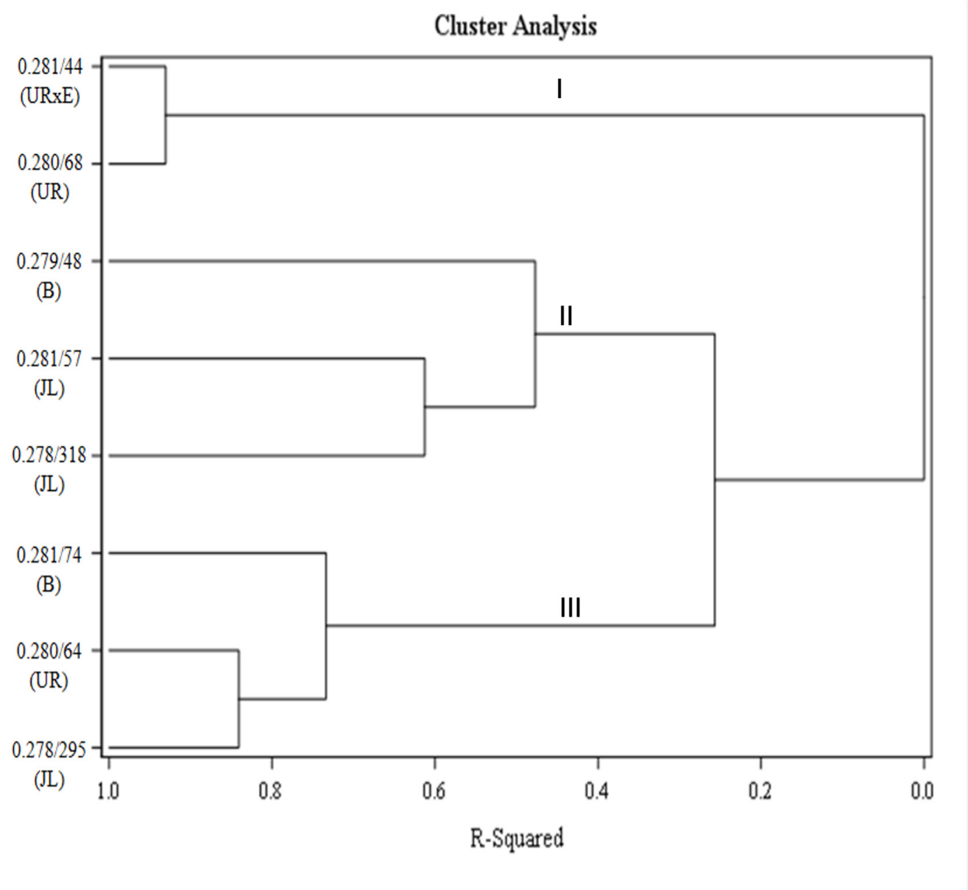

Fig. 2. Dendogram of the eight paternal parents of MPOB Deli *dura* inter-crosses based on 22 traits evaluated with root mean square distance between observations (R2) = 1.066318. Note: JL = Johor Labis, B = Banting, UR = Ulu Remis, UR×E = Ulu Remis × Elmina

ACKNOWLEDGEMENTS

The authors thank the Malaysian Palm Oil Board (MPOB) for providing research materials, facilities, and financial support to carry out this study. We also acknowledge Universiti Kebangsaan Malaysia (UKM) for the research and learning experience.

ETHICAL STATEMENT

Not applicable.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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