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Assessment of fruit component characters among coconut genotypes using multivariate analysis for breeding optimisation

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Abstract

Coconut (*Cocos nucifera* L.) is a vital economic crop supplying food, oil, and raw materials. Breeding programmes require superior varieties with improved fruit composition, which depend on understanding trait variation among genotypes. This study evaluated 30 coconut genotypes at MARDI Bagan Datuk, Perak, using multivariate techniques principal component analysis (PCA), cluster analysis, and biplot analysis to assess variation in fruit components. The analysis showed significant differences in fruit weight (483.0 – 1765.0 g) and nut weight (208.2 – 1248.3 g). Kernel and copra weights were highest in RIL (518.6 g) and TAGT (274.7 g), respectively. Oil content averaged 62.8%, peaking at 66.2% in LAGT. PCA identified three principal components that explain 98.39% of the variation, with split nut weight, kernel weight and fruit weight being the major contributors. Biplot analysis revealed strong positive correlations among fruit weight, nut weight and kernel weight, supporting trait-based selection. Cluster analysis grouped genotypes into three main clusters reflecting trait similarities rather than geographic origin. These results highlight the importance of multivariate analysis for identifying key traits for coconut improvement. The findings provide valuable insights for selecting promising genotypes. Integrating molecular tools into future research could further enhance the precision of selection and breeding efficiency.

Keywords: *biplot, coconut germplasm, fruit component analysis, multivariate analysis, PCA*

Introduction

Coconut (*Cocos nucifera* L.) is indeed a vital economic crop for millions globally, providing essential products such as food, oil and construction materials. The significance of coconut breeding programmes lies in their aim to develop improved varieties that exhibit enhanced yield, disease resistance and desirable fruit composition. Characterising the variation in fruit component traits among coconut genotypes is crucial for achieving these breeding objectives, as it informs selection strategies and enhances genetic diversity within breeding programmes.

Traditionally, univariate analysis methods have been applied to assess individual fruit component traits, including nut weight, husk percentage, copra weight, kernel weight and water content (Geethanjali et al. 2018). However, these methods are limited as they do not adequately capture the complex interrelationships among these traits. Multivariate analysis techniques, in contrast, offer a more comprehensive understanding of the variation in fruit components among coconut genotypes. Studies have demonstrated that employing multivariate approaches can elucidate the intricate relationships between traits, which is essential for effective breeding strategies (Sivakumar et al. 2021).

Principal component analysis (PCA) is a foundational technique in multivariate analysis that transforms correlated variables into a set of uncorrelated principal components, thereby maximising the variance explained in the data (Jerard et al. 2017). Research has successfully employed PCA to identify key traits influencing coconut fruit characteristics and to discern primary sources of variation in genotypes. For instance, Maizura et al. (2024) utilised PCA to analyse morphological traits and genetic inheritance among dwarf coconut varieties, Shunmugiah Veluchamy et al. (2023) utilised multivariate analysis to reveal the genetic variations in the nutritionally important biochemical components

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among various coconut genotypes, and Yao et al. (2019) utilised multivariate analysis to revealed the genetic relationships among regenerated tall coconut accessions of morphological descriptors. Moreover, this method enables the visualisation of patterns among genotypes, which is essential for identifying potential groupings based on fruit composition (Gunn et al. 2011).

Cluster analysis complements PCA by grouping genotypes with similar fruit component profiles. Researchers have effectively utilised hierarchical clustering and K-means clustering to classify coconut genotypes based on trait similarities. For example, the application of these techniques has facilitated the classification of coconut groups that may exhibit desirable agronomic traits, such as larger nut sizes and higher copra yields (Faramitha et al. 2024). This highlights the importance of accurately assessing fruit characteristics for effective breeding strategies and genetic improvement in coconut.

Biplot analysis further visualises trait-genotype relationships, offering insights into genotype performance across multiple traits. This technique is crucial for identifying relationships among various fruit characteristics and can aid in selecting coconut genotypes with desirable fruit components. The application of biplots to coconut fruit analysis has been supported by studies that investigated the relationships between fruit morphology and chemical composition, confirming its relevance in breeding programmes aimed at enhancing quality traits (Shunmugiah Veluchamy et al. 2023).

The integration of these multivariate analysis techniques provides a robust framework for characterising fruit component variation in coconut genotypes. All data from the fruit component analysis among the coconut genotypes planted in MARDI Bagan Datuk, Sungai Sumun, Perak were explained using multivariate analysis to gain a deeper understanding of the complex interactions between various fruit component traits. The insights derived from these analyses are invaluable for enhancing coconut breeding programmes, ultimately leading to the development of superior varieties with improved fruit composition and economic value.

Materials and method

Experimental site

The experiment was conducted at the Malaysian Agricultural Research and Development Institute (MARDI), situated in MARDI Bagan Datuk, Sungai Sumun, Perak, at a latitude of 3°54’ 03.7” N and a longitude of 100° 51’ 45.4” E at an altitude of 4 m above mean sea level. The trial was conducted under rain-fed conditions, with an annual rainfall of more than 1900 mm, an annual temperature of 24 – 36°C, and relative humidity of 79 – 83%. The soil type in MARDI Bagan Datuk was generally classified as riverine, with medium pH and low availability of Nitrogen (N) and Potassium (K).

Planting materials and experimental design

The experimental material consisted of 30 coconut genotypes, including dwarf and tall germplasms and hybrid crosses, planted in MARDI Bagan Datuk, Sungai Sumun, Perak. The germplasm collections were planted in blocks and evaluated since 2008 for fruit component analysis. Dwarf varieties were planted at distances 7 m x 7 m triangle planting, Dwarf x Tall hybrid crosses at 8.2 m x 8.2 m triangle planting, Dwarf x Dwarf hybrid crosses at 7 m x 7 m triangle planting and tall varieties at 9 m x 9 m triangle planting system. Hybrid seed nuts were produced through controlled pollination using emasculation and pollination methods, and have been planted in replicated field trials for evaluation since 2005. The fruit component analysis data were obtained from the average value of data collected from the genotypes twice a year for at least one year to a maximum of 10 years, at ages ranging from six to 20 years. Fruit component analysis data in terms of fruit and nut weight, kernel and copra weight, and oil content were recorded from two mature fruits per palm, consisting of 30 palms per variety, as recommended in the coconut descriptor (Santos et al. 1996). The oil content was calculated as a percentage after Soxhlet extraction using a method described by AOAC (2002). The details of the varieties involved in the study are given in *Table 1*.

Data analysis

The mean values were subjected to statistical analysis from data of at least one year to a maximum of ten years (*Table 2*). A biplot analysis was conducted to visualise the association between traits and genotypes. The data matrix with columns representing traits, and rows representing the genotypes, was first standardised and then subjected to principal component analysis (PCA) to obtain the information on the traits most effective in discriminating genotypes on the first three principal components (PC) using the R package through General R-shiny based Analysis Platform Empowered by Statistics in Agriculture part-1 (grapesAgri1) (Gopinath et al. 2020). The cluster tree was constructed using semi-partial R^2 following Ward’s method by SAS package software (SAS Institute Inc. 2023).

Results and discussion

Mean performance of fruit component analysis among coconut genotypes

The study aimed to assess the genetic diversity and phenotypic variation of fruit components among 30 coconut genotypes evaluated at MARDI Bagan Datuk, utilising multivariate analysis as a tool to enhance breeding programmes. The findings reveal significant variability in fruit and nut weights, ranging from 483.0 g (JANTONG) to 1765.0 g (MT. BCHK) for fruit weight, and from 208.2 g (JANTONG) to 1248.3 g (MT. BCHK) for nut weight. The mean fruit and nut weights were 1166.5 g and 796.3 g, respectively, underscoring the wide range of performances among these genotypes. The highest recorded kernel and copra weights were 518.6 g (RIL) and 274.7 g (TAGT), respectively. The average oil percentage across the 30 genotypes was 62.8%, varying from 59.5% (RIL) to 66.2% (LAGT).

Trait correlations and yield-contributing characteristics

Correlation studies elucidated the relationships between different fruit component traits (*Table 3*, *Figure 1*), showing significant positive correlations between fruit weight and husked weight (r = 0.813), nut weight (r = 0.965), split nut weight (r = 0.961), shell weight (r = 0.927), kernel weight (r = 0.961) and copra weight (r = 0.937) at $p < 0.05$. In a correlation study conducted by Suchithra & Paramaguru (2019), shell weight is considered one of the major yield-contributing traits. Positive correlations between traits, such as mature fruit weight and nut weight, indicate that selection for one trait may indirectly improve the other. These findings corroborate those of Sivakumar et al. (2021) who identified positive associations among several fruit component traits in coconut hybrids, supporting the notion that selecting for one trait may enhance others.

Table 1. List of 30 genotypes evaluated for fruit component analysis evaluated in MARDI Bagan Datuk

Genotypes	Identification code	Population structure
Malayan red dwarf	MRD	Dwarf
Malayan yellow dwarf	MYD	Dwarf
Malayan green dwarf	MGD	Dwarf
Malayan brown dwarf	MBD	Dwarf
Nias green dwarf	NGD	Dwarf
Catigan green dwarf	CATD	Dwarf
Cameroon red dwarf	CRD	Dwarf
Aromatic green dwarf	AROD	Dwarf
Malayan dwarf v. ribu	RIBU	Dwarf
Malayan dwarf v. pink husk	PINKHUSK	Dwarf
Malayan dwarf v. jantong	JANTONG	Dwarf
Niu leka dwarf	NLAD	Dwarf
Rennel island tall	RIT	Tall
Tagnanan tall	TAGT	Tall
Malayan tall v. Bachok	MT.BCHK	Tall
Malayan tall v. Kota Bharu	MT.KTBR	Tall
Malayan tall v. Blenheim Estate	MT.BLES	Tall
Malayan tall v. Pasir Putih	MT.PSPT	Tall
Malayan tall v. Pinggan-Pinggan	MT.PPT	Tall
Niu damu tall	NDMT	Tall
Fiji tall	FIT	Tall
Laguna tall	LAGT	Tall
MRDxNLAD	MARLECA	Hybrid
MRDxLAGT	MARENA	Hybrid
MYDxNLAD	MYLECA	Hybrid
MYDxLAGT	MYLAG	Hybrid
CRDxNGD	CARENI	Hybrid
CRDxCATD	CARECA	Hybrid
CRDxAROD	CAMEARO	Hybrid
CRDxMGD	CAMEREEN	Hybrid

Table 2. The average performance of fruit component traits among the genotypes evaluated in MARDI Bagan Datuk

Variety	FW (g)	HW (g)	NW (g)	SNW (g)	SW (g)	KW (g)	CW (g)	OC (%)
JANTONG	483.0	281.8	208.2	180.4	63.1	117.3	54.4	65.9
CRD	615.6	207.7	407.9	307.1	121.5	185.6	97.7	60.0
MGD	947.3	272.9	674.4	446.2	139.7	306.5	151.5	64.5
MBD	950.5	310.2	640.3	419.9	139.6	280.3	158.4	64.1
MRD	1134.0	427.2	706.8	465.5	156.6	309.4	156.7	62.7
MYD	802.7	251.9	550.8	368.5	118.8	249.7	125.6	59.8
NGD	827.1	227.3	599.8	445.0	164.8	280.2	132.3	62.9
CATD	1467.1	664.8	802.3	541.4	176.8	364.5	194.9	61.2
PINKHUSK	852.0	192.2	659.8	473.5	172.3	301.2	152.4	65.4
MYLAG	1179.0	349.1	832.8	574.3	199.1	375.4	184.6	63.3
MYLECA	1217.1	366.1	850.7	606.1	211.2	394.9	182.4	63.3
MARLECA	1293.2	401.8	892.1	617.7	218.3	399.4	189.6	63.2
MARENA	1286.1	374.4	913.9	621.0	216.1	405.0	210.1	63.3
MATAG	1328.2	386.1	946.2	645.1	220.6	427.0	213.8	62.6
CARENI	866.1	233.3	633.0	472.8	187.7	298.7	148.6	63.0
CARECA	1012.8	284.7	717.4	500.8	182.0	318.6	154.1	61.4
CAMEARO	1035.1	279.3	759.3	524.5	186.4	337.6	173.7	60.6
CAMEREEN	886.4	246.3	641.0	452.7	166.1	286.7	144.8	60.5
NLAD	1102.1	461.5	640.7	499.1	206.2	292.9	136.8	62.8
NDMT	1190.5	473.7	716.8	527.2	202.1	325.1	167.2	63.5
LAGT	1200.6	374.8	826.3	594.8	216.7	378.1	174.5	66.2
AROD	882.7	318.3	564.4	402.7	128.0	274.7	143.4	65.6
MT.KTBR	1729.0	506.8	1223.7	795.2	295.3	499.9	240.4	62.7
MT.BCHK	1765.0	517.6	1248.3	801.5	288.5	503.2	233.5	63.5
MT.PSPT	1643.9	514.0	1140.7	745.7	268.9	476.8	234.7	62.2
MT.BLES	1586.1	500.2	1095.5	722.0	273.8	446.7	203.9	62.4
RIL	1664.5	450.2	1224.6	784.5	265.5	518.6	268.5	59.5
TAGT	1634.4	407.1	1233.9	803.9	292.8	511.9	274.7	60.3
MT.PPT	1363.9	463.1	904.6	631.4	236.1	399.0	189.7	62.4
FIT	1048.4	415.9	632.4	498.9	184.8	314.1	144.2	64.6
Average	1166.5	372.0	796.3	549.0	196.6	352.6	174.6	62.8
Min	483.0	192.2	208.2	180.4	63.1	117.3	54.4	59.5
Max	1765.0	664.8	1248.3	803.9	295.3	518.6	274.7	66.2

FW= fruit weight, HW= husk weight, NW= nut weight, SNW= split nut weight, KW= kernel weight, CW= copra weight, and OC= oil content percentage.

Table 3. The Pearson correlation coefficients and their corresponding significant levels among the fruit component traits, evaluated at p <0.05, at MARDI Bagan Datuk, Perak

	FW	HW	NW	SNW	SW	KW	CW
HW	0.813**						
NW	0.965**	0.632**					
SNW	0.961**	0.642**	0.990**				
SW	0.927**	0.623**	0.953**	0.979**			
KW	0.961**	0.636**	0.992**	0.993**	0.951**		
CW	0.937**	0.609**	0.973**	0.961**	0.903**	0.979**	
OC	-0.235	-0.086	-0.275	-0.237	-0.231	-0.238	-0.307

FW= Fruit weight, NW= nut weight, SNW= split nut weight, SW= shell weight, KW= kernel weight, CW= copra weight, OC= oil content percentage.

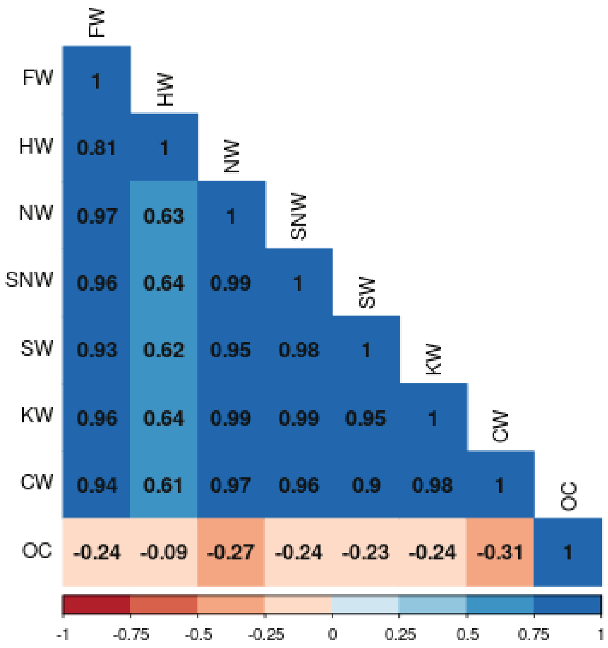

Figure 1. Correlogram of Pearson coefficients among the fruit component traits in 30 coconut genotypes evaluated at MARDI Bagan Datuk, Perak
FW= fruit weight, HW= husk weight, NW= nut weight, SNW= split nut weight, KW= kernel weight, CW= copra weight, and OC= oil content percentage

Principal component analysis of fruit component traits

The patterns observed in the fruit component analysis were further examined using principal component analysis (PCA) (*Figure 2*). Three major eigenvectors with values greater than one accounted for 98.39% of the total variability among the 30 coconut genotypes. The first principal component explained 79.66% of the total variation (*Table 4*), with notable contributions from split nut weight (0.39), kernel weight (0.39), nut weight (0.39), and fruit weight (0.39). The second principal component accounted for 12.00% of the variability, with significant negative contributions from oil content percentage (-0.96) and husked weight (-0.26). The third principal component explained 6.73% of the total variation, with contributions from husked weight (0.87) and a negative contribution from oil content percentage (-0.25). This demonstrates that a limited number of key traits largely explain the observed phenotypic differences among genotypes, aligning with the findings of Odufale et al. (2021), who reported substantial morphological variability among coconut accessions. Key traits such as nut weight, nut circumference, split nut weight and fresh meat weight had high eigenvalues, emphasising their importance in distinguishing accessions. These findings reinforce the effectiveness of PCA in identifying critical traits for selection, demonstrating its potential to enhance coconut breeding programmes through targeted trait improvement and hybrid development.

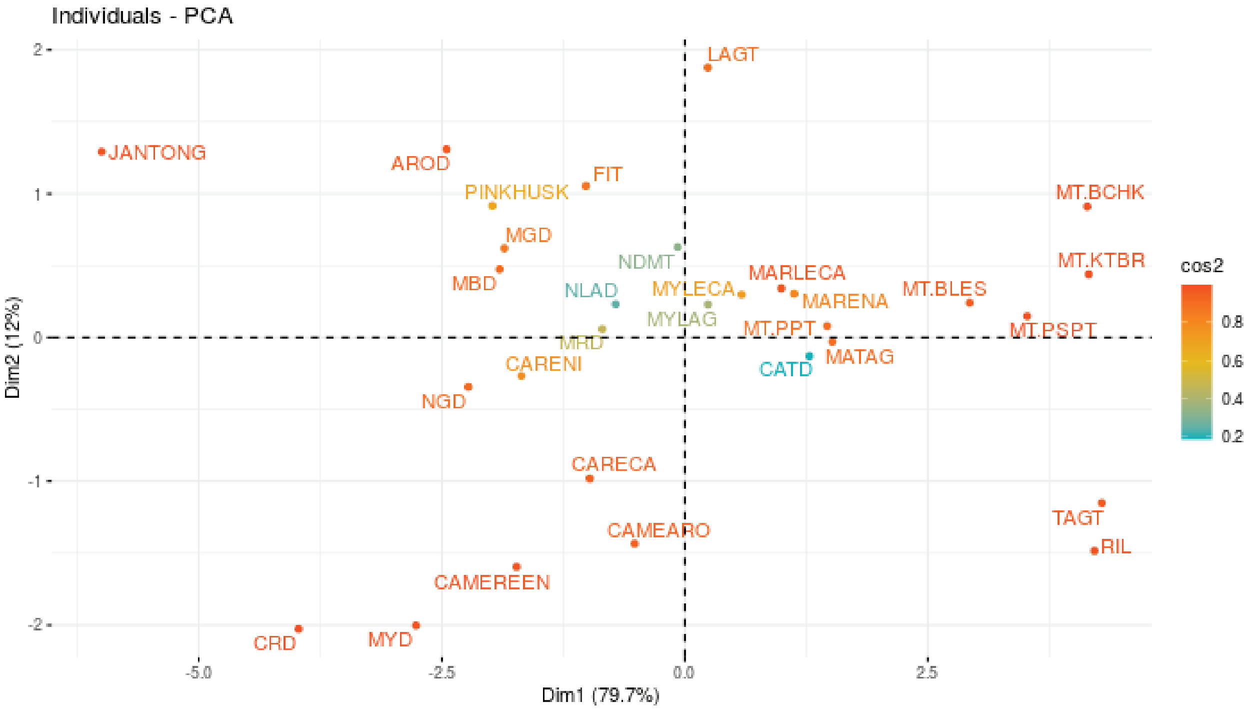

Figure 2. Principal component analysis (PCA) of fruit component traits among the 30 coconut genotypes evaluated at MARDI Bagan Datuk, Perak

Table 4. Percentage of variance of the three main principal components and loading of each variable of the fruit component traits among the 30 coconut genotypes

Principal components	PC1	PC2	PC3
Eigenvalue	6.37	0.96	0.54
Percentage of variance	79.66	12.00	6.73
Cumulative percentage	79.66	91.66	98.39
FW	0.39	-0.08	0.17
HW	0.29	-0.26	0.87
NW	0.39	0.01	-0.17
SNW	0.39	0.03	-0.18
SW	0.38	-0.03	-0.18
KW	0.39	-0.02	-0.19
CW	0.38	0.06	-0.17
OC	-0.12	-0.96	-0.25

FW= Fruit weight, NW= nut weight, SNW= split nut weight, SW= shell weight, KW= kernel weight, CW= copra weight, OC= oil content percentage

Genotype-trait relationships from biplot analysis

The principal component analysis (PCA) biplot (*Figure 3*) revealed two distinct groups of traits contributing to variability among coconut genotypes. The first group comprised fruit component traits, including fruit weight (FW), nut weight (NW), husk weight (HW), shell weight (SW), kernel weight (KW), and copra weight (CW), all of which were positively correlated and oriented in the same direction, indicating their joint contribution to fruit size and yield potential. In contrast, oil content (OC) was positioned in an opposing direction, suggesting an antagonistic relationship with the fruit size traits and signifying its role as a quality-related parameter independent of yield components. These findings highlight the importance of utilising multivariate techniques to uncover relationships among traits that can inform coconut breeding strategies and cultivar improvement.

Classification of genotypes through cluster analysis

Cluster analysis using Ward's method grouped the 30 coconut genotypes into three clusters (*Figure 4*). Group 1 included improved hybrids and high-yielding selections such as MATAG, MARLECA, MYLECA, MYLAG, MARENA, and other Tall varieties and Malayan Tall accessions, which were closely associated with larger fruit and nut components, with an average of 1291.9 g fruit weight (*Table 5*), 871.1 g nut weight, 392.9 g kernel weight, and an average oil content of 63.2%. The largest cluster, Group 2, mainly comprised traditional and dwarf varieties, including JANTONG, CRD, MGD, NGD, MBD and PINKHUSK, characterised by smaller fruit components but relatively higher oil content, as well as improved Dwarf x Dwarf hybrids such as CARECA, CARENI, CAMEREEN, and CAMEARO, Malayan Dwarf (MYD and MRD), and three Fijian

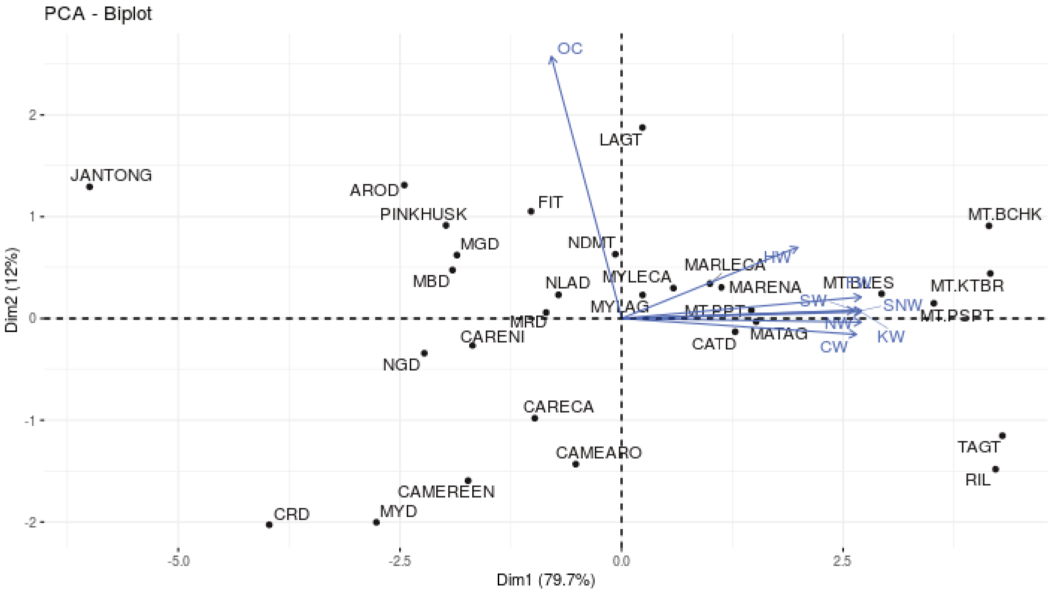

Figure 3. Biplot analysis for 30 coconut genotypes and the fruit component traits evaluated at MARDI Bagan Datuk.
FW= fruit weight, HW= husk weight, NW= nut weight, SNW= split nut weight, KW= kernel weight, CW= copra weight, and OC= oil content percentage

coconut varieties. These showed greater variability with intermediate performance, possibly balancing yield and oil content. Group 3 consisted primarily of tall varieties like RIL, TAGT, and four from the Malayan Tall group (MT. BLES, MT.PSPT, MT.KTBR, and MT BCHK), which achieved the highest fruit weight traits, with an average of 1670.5 g for fruit weight, 1194.5 g for nut weight, 482.7 g for husk weight, 492.9 g for kernel weight, and 242.6 g for copra weight, but exhibited the lowest average oil content at 61.8%. The overall clustering pattern did not reflect the geographical diversity, supporting conclusions by Perera et al. (2016) and Subramanian et al. (2019). This suggests that certain morphological traits may be more indicative of a variety's functionality, such as nut production, than their origin. Collectively, these results reveal a clear divergence between yield-oriented and oil-oriented traits, indicating that improved hybrids and advanced materials are more suitable for breeding programmes targeting copra and kernel yield, whereas dwarf and local varieties may serve as valuable genetic resources for enhancing oil quality.

The potential of using multivariate analysis for identifying superior coconut genotypes with desirable traits is evident in this study. While the genetic relationships between different genotypes and the underlying architecture of fruit component characters were examined, certain limitations must be acknowledged. The assessment of the 30 genotypes was based on the average value that predominantly represents open-pollinated populations, which may encompass the full genetic diversity of coconut. Furthermore, the current study concentrated solely on fruit component traits; therefore, future studies should explore additional essential traits, including yield, disease resistance and adaptability to diverse environmental conditions. In future research, advanced molecular techniques such as genomic selection and marker-assisted selection could be explored to accelerate the breeding process and enhance the accuracy of selection. By addressing the identified limitations and pursuing the recommended future research directions, coconut breeding programmes can be further optimised, leading to the development of superior cultivars that meet the needs of both farmers and consumers.

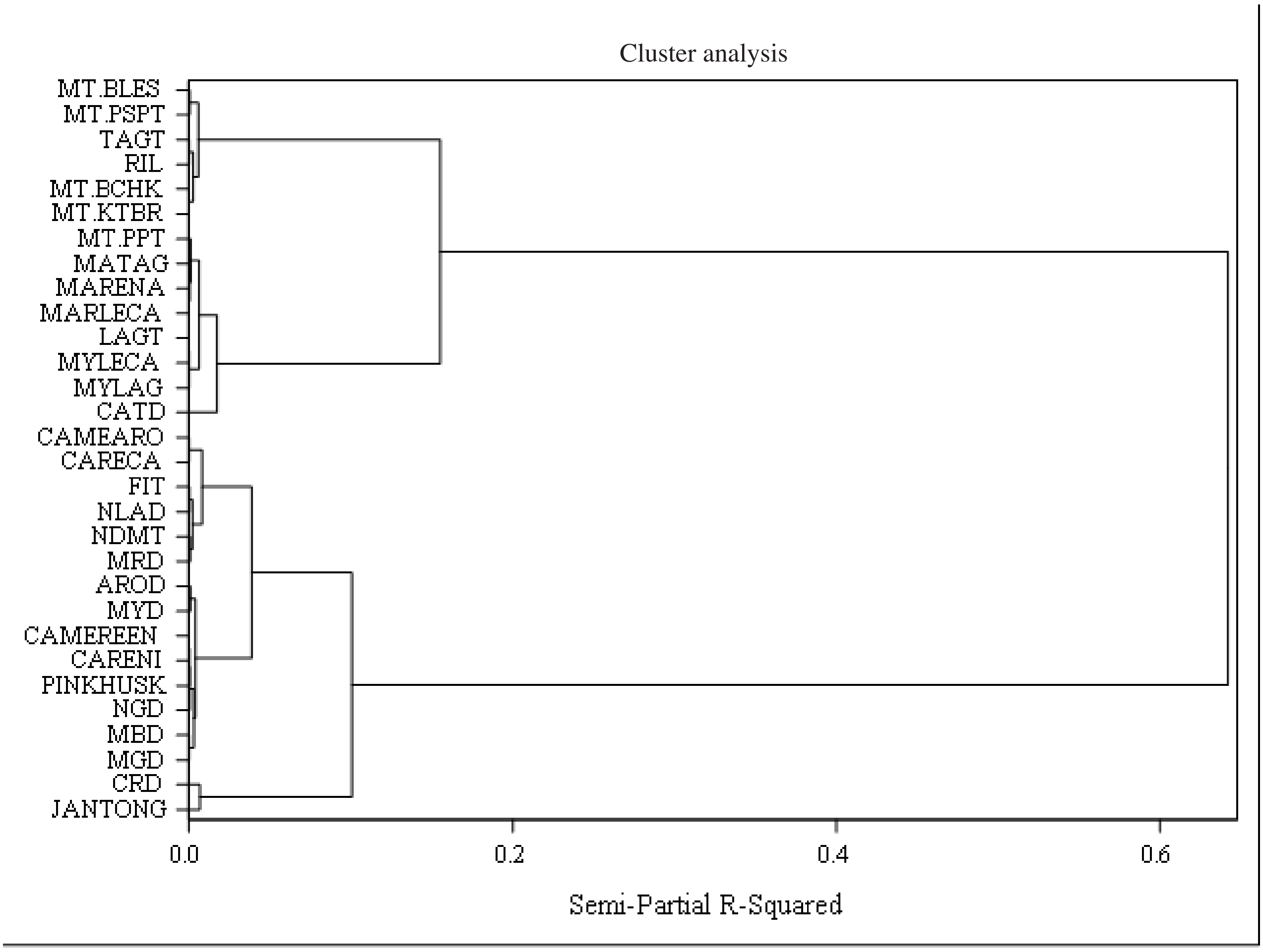

Figure 4. Cluster analysis of fruit component traits among 30 coconut genotypes using semi-partial R-squared by Ward's method.

Table 5. The average performance on fruit component traits of 30 coconut genotypes is separated from the dendrogram tree

Traits	Group 1	Group 2	Group 3
FW	1291.9	914.8	1670.5
HW	422.5	305.3	482.7
NW	871.1	609.6	1194.5
SNW	604.0	436.6	775.5
SW	211.9	157.5	280.8
KW	392.9	279.9	492.9
CW	192.5	140.1	242.6
OC	63.2	63.0	61.8

FW= Fruit weight, NW= nut weight, SNW= split nut weight, SW= shell weight, KW= kernel weight, CW= copra weight, OC= oil content percentage.

Conclusion

The genetic diversity and phenotypic variation observed among the 30 coconut genotypes offer essential insights for targeted breeding and selection efforts. Strong positive correlations among fruit component traits, such as fruit weight, nut weight, and kernel weight, suggest that selecting for one trait may improve others, thereby increasing overall fruit yield. Conversely, the negative correlation between oil content and fruit weight highlights a potential trade-off that breeders need to consider. The PCA and cluster analyses clearly divided fruit component traits into two primary groups: yield-related (FW, NW, HW, SNW, SW, KW, and CW) and quality-related (OC). Improved hybrids and advanced selections clustered with yield traits, while dwarfs and traditional types grouped with oil content, emphasising their complementary value in breeding programmes aimed at either boosting productivity or enhancing quality. These findings collectively provide a robust foundation for optimising breeding strategies to develop high-yielding and superior-quality coconut cultivars.

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