

Principal Component and Cluster Analysis of Agromorphological Traits in *Momordica cochinchinensis* Accessions from Peninsular Malaysia

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ABSTRACT

Momordica cochinchinensis (Lour.) Spreng ($2n = 28$), a medicinal and nutraceutical cucurbit, remains poorly characterised in Peninsular Malaysia, constraining effective germplasm conservation and breeding. This study assessed the agromorphological diversity of 21 *M. cochinchinensis* accessions utilising 27 agromorphological traits. Principal Component Analysis (PCA) revealed that the first two components (PC1 = 29.50%, PC2 = 19.84%) explained 49.34% of the variation, with fruit biomass traits dominating PC1, while yield-associated and phenological traits defined PC2. In total, eight PCs explained 88.85% of the variance. Hierarchical clustering using UPGMA based on Gower dissimilarity distance showed strong fidelity (cophenetic $r = 0.831$) and clustered the accessions into five clusters at a cut height of 0.293. Bootstrap resampling (1000 replicates) confirmed high stability for Cluster II (0.951), Cluster III (0.859), and Cluster I (0.819), moderate support for Cluster IV (0.771), and weaker support for Cluster V (0.608). PCA and UPGMA analyses were largely congruent, revealing consistent clustering patterns among the accessions. Compact, small-fruited types, including BMA, BMB, and BMC (Bukit Mertajam, Penang), and ME (Merlimau, Malacca), formed a tight cluster, while late-harvesting, agromorphologically distinct accessions such as KK (Kubang Kerian, Kelantan) and BPC (Batu Pahat, Johor) grouped separately. In contrast, large-fruited elite types, including PS (Pokok Sena, Kedah) and KL (Kuala Lipis, Pahang), were clearly distinguished, highlighting their potential as promising accessions for yield-oriented improvement. The PP (Pasir Puteh, Kelantan) held an intermediate yet strategically important position, bridging elite and generalist types. Meanwhile, a broad assemblage of accessions from diverse regions displayed intermediate fruit size and heterogeneous morphological characteristics, reflecting generalist profiles. The Mantel test revealed no significant association between agromorphology and geography, consistent with farmer-mediated exchange of planting material across regions. These findings demonstrate substantial agromorphological variation within Malaysian *M. cochinchinensis*, with fruit biomass and reproductive traits emerging as the principal axes of diversity, providing a foundation for targeted breeding, germplasm conservation, and domestication strategies.

Keywords: Agromorphological diversity, dendrogram, germplasm, *Momordica cochinchinensis*, principal component analysis

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INTRODUCTION

Momordica cochinchinensis, known as Gac, is a perennial melon found throughout Southeast Asia, Southwestern China, and Northeastern Australia (Mai & Debaste, 2019). Traditionally cultivated in home gardens, *M. cochinchinensis* has long been valued for its culinary and medicinal uses. Its bright red aril is exceptionally rich in bioactive compounds such as β -carotene,

lycopene, fatty acids, and phenolics, which underpin its growing nutraceutical appeal (Anunthawan *et al.*, 2022; Erşan & Müller-Maatsch, 2022). Despite these attributes, domestication and systematic improvement remain limited, and currently available varieties often underperform in terms of fruit yield and nutrient consistency.

In Malaysia, the potential of *M. cochinchinensis* remains underexploited due to a lack of comprehensive agromorphological evaluation of local germplasm. Prior studies conducted by Othman *et al.* (2020) and Mohd Khairi and Othman (2023) have either provided only preliminary descriptions or been limited by small sample sizes and limited trait coverage. As a result, the extent of agromorphological diversity within Peninsular Malaysian accessions remains poorly understood, hindering conservation, breeding, and commercialisation efforts. Addressing this gap is crucial because agromorphological characterisation provides the baseline needed to identify promising genotypes, evaluate adaptability, and guide improvement and conservation programs (Itoh & Sato, 2023).

The present study, therefore, undertakes the first systematic evaluation of 21 *M. cochinchinensis* accessions collected from various regions across Peninsular Malaysia. These accessions represent a broad geographic range, encompassing northern, southern, eastern, and western states, thereby ensuring coverage of diverse agroecological zones. All plant material was cultivated under a single experimental regime at the Bukit Kor experimental plot of Universiti Malaysia Terengganu. The site was chosen for its uniform topsoil, tropical humid climate, and low spatial heterogeneity, while consistent management practices such as organic fertilisation, daily irrigation, and controlled hand-pollination minimised environmental variation. This design ensured that observed trait differences largely reflected genetic and agromorphological variation rather than ecological noise.

This study evaluated 27 qualitative and quantitative agromorphological traits spanning vegetative and reproductive traits. Multivariate approaches, including Principal Component Analysis (PCA) and hierarchical clustering (UPGMA) using Gower distance, were applied to assess patterns of variation and identify distinct accession groups. This study hypothesised that fruit size and biomass traits would explain the largest share of variance, and agromorphological clusters would show only weak associations with geographic origin, reflecting farmer-mediated exchange of planting material. By integrating rigorous sampling, uniform cultivation, and multivariate statistics, this study provides the first statistically validated

baseline of agromorphological diversity in Malaysian *M. cochinchinensis*. The findings not only establish a foundation for germplasm grouping and conservation but also highlight promising accessions for future breeding and domestication strategies.

MATERIALS AND METHODS

Accessions Collection

A total of 21 accessions of *M. cochinchinensis* were collected between 2021 and 2022 from four major regions of Peninsular Malaysia (Northern, Southern, Eastern, and Western states) to ensure broad geographic representation (Table 1). Propagation was performed using semi-hardwood cuttings, selected for their high survival rates (Tran *et al.*, 2020) and suitability for this dioecious species. Cuttings were prepared at 25–30 cm length, containing at least three nodes and a basal diameter of 3–6 mm, with a single halved leaf retained (Hamidon *et al.*, 2020). To enhance rooting, cuttings were treated with 1000 ppm indole-3-butyric acid (IBA) (Hamidon *et al.*, 2020). Topsoil was used as the propagation medium, and rooted cuttings were maintained under shaded nursery conditions with daily irrigation for four weeks before field transplantation.

Experimental Site and Design

Transplanted plants were established at the Bukit Kor experimental plot, Universiti Malaysia Terengganu, Marang, covering 0.15 ha. The site is located at 5°21'N and 103°2'E, at an altitude of ~32 m above sea level, within a humid tropical climate (mean annual rainfall ≈2552.5 mm; mean temperature 26–28 °C). The soil was classified as topsoil (pH 6.1), well-drained, and relatively homogeneous in texture and fertility, making it suitable for common plot experiments. The field experiment followed a Completely Randomised Design (CRD), selected based on the relatively uniform environmental conditions across the site, which exhibited minimal spatial heterogeneity (Mudi & Usman, 2012). Each accession was represented by three replicates, with one plant per replicate. Plants were established in rows with 3 m inter-row and 2 m intra-row spacing. To reduce pseudo-replication, replicates were positioned across different rows. For agromorphological trait evaluation, three leaves, three flowers, and three fruits were

sampled per plant, yielding a total of nine leaves, nine flowers, and nine fruits per accession for each trait measurement. For fruit traits, only mature fruits were selected to ensure consistency.

A coding system was employed to trace the origin of each accession (Table 1). For single-word locations, the first two letters were used (e.g., Baling → BA), while for two-word locations, the first letter of each word was combined (e.g., Bukit Kor → BK). Multiple accessions from the same region were distinguished with alphabetical suffixes (e.g., Bukit Mertajam → BMA, BMB, BMC). Routine management practices included daily irrigation

and fertilisation with organic chicken manure. Fungicide and pesticide applications were conducted periodically to suppress disease and pest pressure, ensuring that observed variation reflected genetic and agromorphological differences rather than uncontrolled biotic stress. Controlled hand-pollination was performed across all accessions using a single male plant as the pollen donor. This standardised approach ensured uniform pollination but is acknowledged as a limitation, as paternal effects may have influenced seed and fruit traits. Pollinated flowers were tagged for tracking, and fruits were harvested upon reaching maturity, identified by peel colour change to orange-red.

Table 1. List of the collected *M. cochinchinensis* accessions

No	Region	State	District	Code	Longitude	Latitude
1	North Region	Perlis	Beseri	BE	100.174491	6.519567
2	North Region	Perlis	Chuping	CHA	100.302217	6.610053
3	North Region	Perlis	Chuping	CHB	100.291639	6.541444
4	North Region	Kedah	Pokok Sena	PS	100.652622	6.195422
5	North Region	Kedah	Baling	BA	100.621631	5.507086
6	North Region	Penang	Bukit Mertajam	BMA	100.472276	5.378969
7	North Region	Penang	Bukit Mertajam	BMB	100.472276	5.378969
8	North Region	Penang	Bukit Mertajam	BMC	100.472276	5.378969
9	West Region	Selangor	Jenjarom	JE	101.513079	2.883574
10	West Region	Selangor	Sungai Buloh	SB	101.5225	3.194833
11	South Region	Johor	Batu Pahat	BPA	102.945498	1.87119
12	South Region	Johor	Batu Pahat	BPB	102.923497	1.827411
13	South Region	Johor	Batu Pahat	BPC	102.928179	1.827365
14	South Region	Johor	Batu Pahat	BPD	102.928179	1.827365
15	South Region	Malacca	Merlimau	ME	102.361546	2.176589
16	South Region	Malacca	Alor Gajah	AG	102.192521	2.342708
17	East Region	Kelantan	Pasir Puteh	PP	102.466343	5.777787
18	East Region	Kelantan	Kubang Kerian	KK	102.290874	6.090133
19	East Region	Pahang	Kuala Lipis	KL	101.43457	4.408947
20	East Region	Terengganu	Kuala Berang	KB	102.957954	4.967162
21	East Region	Terengganu	Bukit Kor	BK	103.165883	5.210298

Agromorphological Assessment of *M. cochinchinensis*

Twenty-seven traits were assessed (10 qualitative, 17 quantitative), as summarised in Table 2. Qualitative traits were encoded into categorical scores (e.g., leaf margin: entire = 0, dentate = 1; fruit shape: round = 0, oblong = 1, ellipsoid = 2). Qualitative and quantitative traits

were measured utilising standard botanical guides and calibrated instruments. Traits were selected from a larger pool of descriptors but were limited to those consistently scorable across all accessions and sufficiently variable to distinguish between genotypes. Traits prone to high subjectivity or low repeatability were excluded.

Table 2. Morphological and agronomic characters of *M. cochinchinensis* with methodology, instruments, and units

Character Type	Trait	Methodology / Instrument	Unit / Category
Qualitative	Fruit shape, sepal shape	Categorised by comparison with standard shapes using botanical guides.	Categories
	Leaf apex	Categorised by observation using a botanical guide.	Categories
	Leaf margin	Categorised by observation using a botanical guide.	Categories
	Leaf lobes number	Counted manually.	Number
	Degree of leaf dissection	Categorised by comparison with the botanical guide.	Categories
	Leaf colour, petal colour, skin colour, seed colour	Scored using ECPGR (2008) standard descriptors and colour categories.	Descriptor terms
	Spike density	Categorised as sparse, medium, dense, based on the distance between spikes (mm).	Categories
Quantitative	Days to female flower bud appearance	Days from transplanting until the first female bud is observed.	Days
	Number of female flowers per season	Counted regularly; flowers tagged to prevent duplication.	Number
	Number of fruits per season	Counted regularly; fruits were tagged to prevent duplication.	Number
	Days to fruit harvest	Days from pollination until fruit maturity/harvest.	Days
	Fruit length, width, diameter	Measured with a ruler (cm).	cm
	Ovary length	Measured with ruler (cm).	cm
	Spike diameter	Measured with ruler (mm).	mm
	Pulp thickness	Measured with a ruler (cm).	cm
	Fresh fruit weight, pulp weight, peel weight, aril weight	Measured with digital weighing balance (HR-250AZ, Japan).	gram
	Seed weight (10 seeds)	Measured with digital weighing balance (HR-250AZ, Japan).	gram
	Seed number	Counted manually per fruit.	Number

Qualitative characters = categorical; Quantitative characters = numerical. Standard descriptors adapted from Simpson (2019), ECPGR (2008), John & Antony (2011), Bootprom *et al.* (2015), Wimalasiri *et al.* (2016), Toan *et al.* (2018) and Mohd Khairi & Othman (2023)

Data Collection

Agromorphological assessments were performed on living plants under tropical field conditions. Only characteristics that effectively distinguished among the accessions were considered for the current analysis. Measurements were taken from three healthy plants per accession, and the resulting data were averaged for subsequent analysis. Data collection was conducted directly in the field during the study period.

Statistical Analysis

Quantitative traits were standardised to z-scores (mean = 0, SD = 1) before analysis to minimise scale effects. Principal Component Analysis (PCA) was conducted on 27 agromorphological characteristics to reduce dimensionality and identify patterns of trait variation among accessions. These characteristics were selected based on Plant Systematics by Simpson (2019), standard cucurbit descriptor lists (ECPGR, 2008), previous studies (John & Antony, 2011; Bootprom *et al.*, 2015; Wimalasiri *et al.*, 2016; Toan *et al.*, 2018; Mohd Khairi & Othman,

2023), and preliminary screening. Dataset suitability for PCA was verified utilising the Kaiser–Meyer–Olkin (KMO) measure of sampling adequacy and Bartlett’s test of sphericity. Principal components (PCs) with eigenvalues greater than 1.0 were retained, and traits with loading coefficients ≥ 0.40 were considered biologically meaningful contributors to each component (Paredes-Espinosa *et al.*, 2023).

Hierarchical clustering was carried out utilising the unweighted pair-group method with arithmetic mean (UPGMA) based on Gower distance, which accommodates both quantitative and qualitative traits (Pavoine *et al.*, 2009). The robustness of the dendrogram was assessed utilising the cophenetic correlation coefficient (r), which measures the concordance between the original distance matrix and the dendrogram structure. To assess the relationship between agromorphological and geographic variation, a Mantel test was performed with 999 permutations, comparing Euclidean

agromorphological distance matrices with great-circle geographic distances derived from collection coordinates. The test statistic (Mantel r) and associated p-value were utilised to evaluate the degree of correlation between agromorphology and geography. All analyses were performed using R (v4.5.1), SPSS (v26) and Past (v4.17).

RESULTS AND DISCUSSION

Principal Component Analysis (PCA)

The Kaiser–Meyer–Olkin statistic was 0.548, indicating mediocre but acceptable sampling adequacy, and Bartlett’s test was highly significant ($\chi^2 = 2564.12$, $df = 351$, $p < 0.001$) (Table 3), confirming the dataset was suitable for multivariate analysis (Kaiser, 1974; Mason *et al.*, 2003). All 27 agromorphological traits were z-standardised before analysis. Traits with loading ≥ 0.70 were considered salient contributors, while those with loading 0.40 – 0.69 were treated as moderate (Hair *et al.*, 2013).

Table 3. Kaiser–Meyer–Olkin (KMO) and Bartlett’s test of sphericity for PCA suitability

Kaiser-Meyer-Olkin Measure of Sampling Adequacy.		0.548
Bartlett's Test of Sphericity	Approx. Chi-Square	2564.123
	Df	351
	Sig.	0.001

Principal Component Analysis (PCA) confirmed substantial agromorphological variation among *M. cochinchinensis* accessions. Eight principal components with eigenvalues greater than one explained 88.85% of the total variance, indicating that the observed differences were structured rather than random (Paredes-Espinosa *et al.*, 2023). Table 4

summarises the contribution of the principal components, including eigenvalues, Percentage of variance, and Percentage of cumulative variance. These eight components adequately capture the overall variations within the germplasm, indicating meaningful variability among the collected *M. cochinchinensis* accessions.

Table 4. Principal component analysis of agromorphological traits of *M. cochinchinensis* for the first eight components

Principal component	Eigenvalue	Variance (%)	Cumulative (%)
PC1	8.36	29.50	29.50
PC2	5.62	19.84	49.34
PC3	2.87	10.14	59.48
PC4	2.35	8.31	67.79
PC5	2.10	7.42	75.21
PC6	1.66	5.86	81.07
PC7	1.15	4.06	85.13
PC8	1.05	3.72	88.85

The first principal component (PC1, 29.50%) was dominated by fruit biomass characteristics, including fruit weight, size, pulp weight, peel weight, and pulp thickness (all loadings ≥ 0.70), confirming fruit weight and size as the major axis of phenotypic variation among *M. cochinchinensis* accessions. Moderate contributions were observed for aril weight (0.592), seed colour (0.516), and seed number (0.681), suggesting that aril quality and seed traits were partially correlated with fruit biomass. This indicates that selection for larger fruits may impact aril yield and seed characteristics, which are crucial for both nutritional value and propagation (Parks *et al.*, 2013). These findings were consistent with Abdul Rahman *et al.* (2024), who identified fruit biomass as a primary determinant of both diversity and consumer acceptance in *M. cochinchinensis*. Similar patterns have been documented in related *Momordica* species, with Yadagiri (2017) reporting that fruit biomass serves as the dominant driver of morphological variation in *Momordica charantia*.

The second principal component (PC2, 19.84%) reflected yield-associated and phenological traits, with salient contributions from seed weight (0.962) and time to fruit harvesting (0.906). Moderate loadings were observed for skin colour (0.616) and leaf lobe number (0.635), indicating that variation in maturity and seed vigour is associated with visible vegetative and fruit characteristics that may be useful for field-level identification. Divergent accessions such as KK (Kubang Kerian, Kelantan) and BPC (Batu Pahat, Johor) were displaced along this axis, highlighting their unique reproductive allocation strategies. These findings align with Wimalasiri *et al.* (2016), who identified seed weight and leaf lobe number as key traits differentiating *M. cochinchinensis* accessions, and with Sundaram *et al.* (2019), who similarly highlighted fruit harvest timing as a discriminating trait in *Kabuli chickpea*.

PC3 (10.14%) was primarily defined by leaf margin (0.849), with moderate contributions from fruit shape (0.484) and time of flowering (0.472). This axis reflects vegetative and reproductive variation, traits that may aid in taxonomic discrimination or adaptation to local environments. Mohd Khairi and Othman (2023) demonstrated that leaf margins contribute substantially to variation in *M. cochinchinensis*, while Yan *et al.* (2021) highlighted flowering time as a key driver of adaptive differentiation across diverse environments. PC4 (8.31%) reflected reproductive output, defined primarily by the number of fruits (0.708) and flowers per accession (0.708), thereby capturing variation in overall productivity. Similar emphasis on reproductive traits has been reported in cucurbit studies, where fruit and flower count strongly influence yield-based grouping and serve as key indicators of accession performance (Vásquez Gamboa *et al.*, 2017).

PC5 (7.42%) was defined primarily by seed colour (−0.718), with moderate contributions from aril weight (0.494) and petal colour (0.464), suggesting trade-offs between seed traits, pigmentation, and aril quality. These traits are key to market preference, since seed pigmentation and aril yield determine nutritional and economic value (Wimalasiri *et al.*, 2016; Yadav, 2022). Previous studies have similarly emphasised the importance of the aril in *M. cochinchinensis*, indicating that the concentration of carotenoids, often reflected in aril colour, is one of the key factors determining fruit quality (Abdul Rahman *et al.*, 2024). PC6–PC8 each accounted for less than 6% of the variance, primarily reflecting minor contributions from traits such as leaf colour, sepal shape and length of ovary. The loading coefficients of all 27 agromorphological traits across the first eight components were presented in Table 5, and Table 6 provides a summary of the variance explained, salient and moderate loadings, and their biological interpretation.

Table 5. Principal Component Analysis (PCA) loadings of 27 agromorphological traits of *M. cochinchinensis* across the first eight components

Trait	PC1 (29.50%)	PC2 (19.84%)	PC3 (10.14%)	PC4 (8.31%)	PC5 (7.42%)	PC6 (5.86%)	PC7 (4.06%)	PC8 (3.72%)
FRWT (Fruit weight) (g)	0.989	0.137	−0.172	−0.114	0.006	0.031	0.057	−0.001
FRL (Fruit length) (cm)	0.861	−0.154	−0.398	−0.064	0.014	−0.026	0.072	−0.078
FRW (Fruit width) (cm)	0.902	0.375	0.048	−0.076	0.172	0.003	0.01	0.047
FRD (Fruit diameter) (cm)	0.972	−0.264	−0.057	0.012	0.067	0.005	0.008	0.117

Table 5. (continued)

Trait	PC1 (29.50%)	PC2 (19.84%)	PC3 (10.14%)	PC4 (8.31%)	PC5 (7.42%)	PC6 (5.86%)	PC7 (4.06%)	PC8 (3.72%)
FRS (Fruit shape)	-0.314	-0.085	0.484	-0.062	-0.073	-0.035	0.007	-0.057
SKC (Skin colour)	-0.267	0.616	0.423	-0.307	0.184	-0.237	0.202	0.103
SPD (Spike density) (mm)	-0.378	-0.389	-0.119	-0.005	-0.094	-0.264	-0.035	-0.375
SPDI (Spike diameter) (mm)	0.141	-0.672	-0.227	-0.032	-0.077	-0.540	-0.282	-0.041
PUT (Pulp thickness) (cm)	0.835	-0.018	0.146	-0.092	0.367	0.001	0.327	-0.062
PUW (Pulp weight) (g)	0.964	0.01	0.146	-0.163	0.126	0.012	-0.003	-0.003
ARW (Aril weight) (g)	0.592	-0.005	-0.552	0.086	0.494	-0.289	-0.069	0.069
PEW (Peel weight) (g)	0.92	0.273	0.051	-0.097	0.076	0.042	-0.096	0.083
SEN (Seed number) (count)	0.681	-0.107	-0.106	-0.035	-0.169	-0.127	0.024	-0.049
SEW (10-seed weight) (g)	0.121	0.962	0.003	0.141	0.003	0.122	-0.006	0.145
SEC (Seed colour)	0.516	0.054	0.258	-0.031	-0.718	-0.278	-0.055	0.173
LO (length of Ovary) (cm)	-0.211	-0.254	-0.262	-0.345	-0.305	-0.405	-0.043	-0.328
SP (Sepal shape)	-0.193	-0.625	-0.162	-0.007	0.032	-0.549	0.154	0.243
PC (Petal colour)	0.15	0.567	-0.016	-0.404	0.464	-0.046	-0.446	0.053
LD (Leaf division)	0.184	0.263	-0.284	0.072	-0.034	0.033	0.319	-0.163
NOL (number of leaf lobes) (count)	-0.219	0.635	-0.191	0.51	-0.238	0.097	0.026	0.077
LA (Leaf apex)	-0.449	-0.003	-0.091	-0.471	0.171	-0.365	-0.127	0.127
LC (Leaf colour)	-0.025	-0.137	-0.056	0.124	0.112	-0.687	-0.052	0.552
LM (Leaf margin)	0.132	0.051	0.849	0.028	-0.414	-0.234	-0.202	0.099
NOR (Number of flowers) (count)	0.195	0.093	-0.471	0.557	0.357	0.074	-0.010	0.025
NOF (Number of fruits) (count)	0.309	0.126	0.427	0.708	0.229	-0.006	-0.186	-0.091
TOR (Time of flowering) (days)	0.404	0.289	0.472	-0.186	-0.128	0.212	-0.527	-0.284
TOF (Time of fruit harvesting) (days)	-0.340	0.906	-0.105	0.108	-0.100	-0.052	-0.216	0.044

Table 6. Summary of PCA components with variance explained, salient/moderate loadings, and biological interpretation

Principal Component	% Variance	Salient Traits (≥ 0.70)	Moderate Traits (0.40–0.69)	Biological Interpretation
PC1	29.50%	fruit weight (g), fruit size (cm), pulp thickness (cm), pulp weight (g), peel weight (g) (≥ 0.70)	Aril weight (g) (0.592), seed colour (0.516), seed number (count) (0.681)	Fruit biomass axis: strong yield traits with linked aril and seed attributes
PC2	19.84%	Seed weight (g) (0.962), time of fruit harvesting (days) (0.906)	Skin colour (0.616), number of leaf lobes (count) (0.635)	Reproductive timing & seed vigour; associated with visible vegetative/fruit markers
PC3	10.14%	Leaf margin (0.849)	Fruit shape (0.484), time of flowering (days) (0.472)	Vegetative & phenological differentiation
PC4	8.31%	Number of fruits per accession (count) (0.708)	Number of flowers per accession (count) (0.557),	Reproductive output axis (flowers and fruits)
PC5	7.42%	Seed colour (-0.718)	Aril weight (g) (0.494), petal colour (0.464)	Seed–fruit trade-offs; pigmentation and aril quality variation
PC6–PC8	<6% each	None	Leaf colour (0.552, PC8) Length of ovary (cm) (-0.405, PC6), and sepal shape (-0.549, PC6)	Minor axes; isolated vegetative or pigmentation signals and floral variation

The PCA scatter plots separated the accessions into three broad groups. Large-fruited types, including PS (Pokok Sena, Kedah) and KL (Kuala Lipis, Pahang), were positioned at the negative end of PC1 and were strongly associated with fruit size traits. Small-fruited types, including BMA, BMB, BMC (Bukit Mertajam, Penang), and ME (Merlimau, Malacca), clustered at the positive end of PC1. Late-harvesting and morphologically distinct accessions, represented by KK (Kubang Kerian, Kelantan) and BPC (Batu Pahat, Johor), were located far along PC2. The remaining accessions, including BE (Beseri, Perlis); CHA, CHB (Chuping, Perlis); BA (Baling, Kedah); BK (Bukit Kor, Terengganu); KB (Kuala Berang, Terengganu); AG (Alor Gajah, Melaka); JE

(Jenjarom, Selangor); SB (Sungai Buloh, Selangor); BPA, BPB, BPD (Batu Pahat, Johor), were clustered near the origin, indicating intermediate morphological profiles. Among these, the PP (Pasir Puteh, Kelantan) accession occupied a central position, reflecting its intermediate fruit size and reproductive traits. Its proximity to the origin indicates that PP does not exhibit extreme phenotypes but instead represents a balanced genotype, linking large-fruited and medium-fruited groups (Figures 1 & 2). These results confirm that fruit size descriptors (PC1) and harvest timing/seed traits (PC2) were the major dimensions structuring diversity in Malaysian *M. cochinchinensis* accessions.

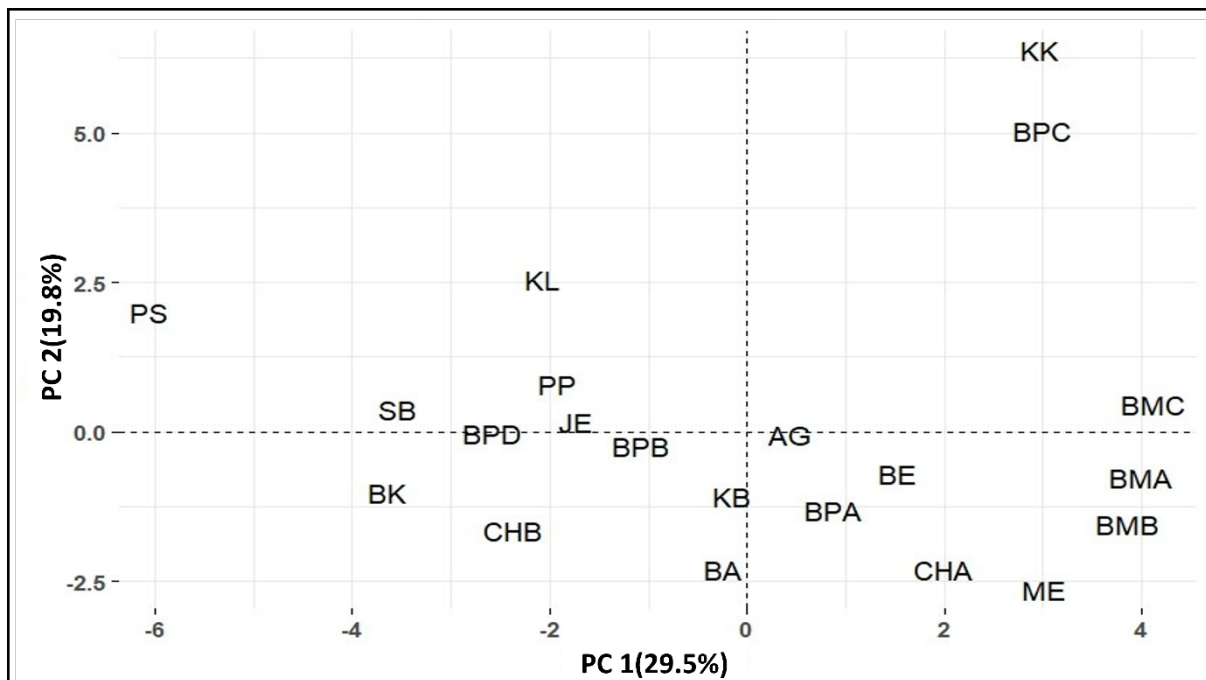


Figure 1. Principal Component Analysis (PCA) scatter plot of 21 *M. cochinchinensis* accessions

Fruit size and weight have repeatedly been identified as the most discriminating descriptors. Yadav *et al.* (2024) reported that fruit weight and seed number were the primary traits distinguishing among *Momordica dioica* accessions. Our findings similarly highlight fruit size traits as the dominant contributors to PC1, separating large-fruited accessions from small-fruited ones. In Malaysia, it was observed that agromorphological differentiation among *M. cochinchinensis* accessions was largely driven

by fruit dimensions and reproductive characteristics (Mohd Khairi & Othman, 2023). The present PCA analysis confirms this, with reproductive descriptors contributing strongly to PC2. Sunny *et al.* (2023) highlighted the importance of flowering and fruiting periods and seed characteristics in differentiating plant populations. Consistent with these findings, our analysis identified harvesting time and seed-related traits as key contributors to accession separation along PC2.

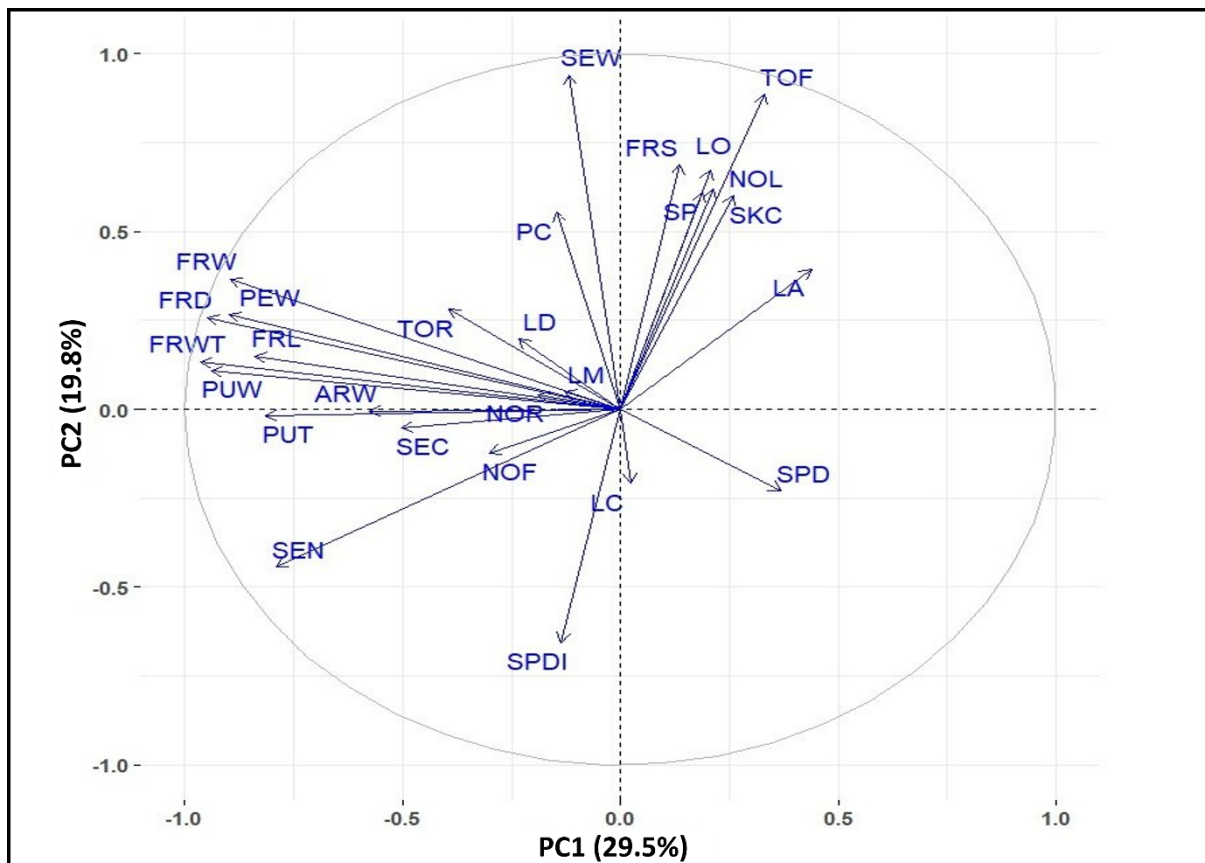


Figure 2. Principal component analysis (PCA) biplot of 27 agromorphological traits in *M. cochinchinensis* accessions

Clustering Analysis

Hierarchical clustering utilising UPGMA based on the Gower distance corroborated the patterns observed in PCA. The dendrogram separated the 21 *M. cochinchinensis* accessions into five clusters at a cut height of about 0.293, supported by a strong cophenetic correlation ($r = 0.831$) and moderate partitioning (silhouette $k = 2: 0.323$; $k = 5: 0.287$) (Rodrigues *et al.*, 1998; Odong *et al.*, 2011).

Cluster I comprised BPC (Batu Pahat, Johor) and KK (Kubang Kerian, Kelantan), characterised by high PC2 scores, late-harvesting (130 ± 13.19 days), and distinct morphology (average fruit weight: 446.5 ± 51.61 g; length: 14.93 ± 0.75 cm; width: 12.11 ± 0.11 cm). Cluster II contained KL (Kuala Lipis, Pahang), PS (Pokok Sena, Kedah), representing large-fruited elite accessions with the highest fruit biomass (average fruit weight 981.8 ± 195.9 g; length: 17.4 ± 1.69 cm; width: 16.13 ± 2.07 cm).

Cluster III was represented solely by PP (Pasir Puteh, Kelantan), reflecting its unique intermediate position bridging elite and generalist groups (average fruit weight: 582.33 g; length: 14.33 cm; width: 13.33 cm). Cluster IV included BMC, BMA, BMB (Bukit Mertajam, Penang), and ME (Merlimau, Malacca), which had the smallest fruits and formed a tight group (average fruit weight: 366 ± 15.9 g; length: 12.79 ± 0.86 cm; width: 10.2 ± 0.27 cm). Cluster V grouped BE (Beseri, Perlis); CHA, CHB (Chuping, Perlis); BA (Baling, Kedah); BK (Bukit Kor, Terengganu); KB (Kuala Berang, Terengganu); AG (Alor Gajah, Malacca); JE (Jenjarom, Selangor); SB (Sungai Buloh, Selangor); BPA, BPB, BPD (Batu Pahat, Johor) accessions, that exhibited intermediate fruit size (average fruit weight 538.0 ± 80.7 g; length: 16 ± 0.85 cm; width: 11.52 ± 0.31 cm) and heterogeneous morphological profiles (Figure 3). Cluster robustness was further validated by bootstrap analysis (UPGMA, $k = 5$). Jaccard support values indicated high stability for Cluster II (0.951), Cluster III (0.859), and Cluster I (0.819), while Cluster IV showed moderate stability (0.771) and Cluster V was the

least stable (0.608) (Table 7). These results suggest that clusters with extreme phenotypes (e.g., large-fruited KL, Kuala Lipis, Pahang, and PS, Pokok Sena, Kedah; small-fruited BMA,

BMB, BMC, Bukit Mertajam, Penang, and ME, Merlimau, Malacca) were more consistently resolved, whereas heterogeneous groups (e.g., Cluster V) exhibit weaker support.

Table 7. Validation and stability statistics for UPGMA clustering of *M. cochinchinensis* accessions

Analysis	Statistic	Value
Clustering (UPGMA)	Cophenetic correlation (r)	0.831
Clustering (UPGMA)	Silhouette width (k=2)	0.323
Clustering (UPGMA)	Silhouette width (k=5)	0.287
Clustering (UPGMA)	Cut height (k=5)	0.293
Bootstrap (UPGMA, k=5)	Jaccard stability C1	0.819
Bootstrap (UPGMA, k=5)	Jaccard stability C2	0.951
Bootstrap (UPGMA, k=5)	Jaccard stability C3	0.859
Bootstrap (UPGMA, k=5)	Jaccard stability C4	0.771
Bootstrap (UPGMA, k=5)	Jaccard stability C5	0.608

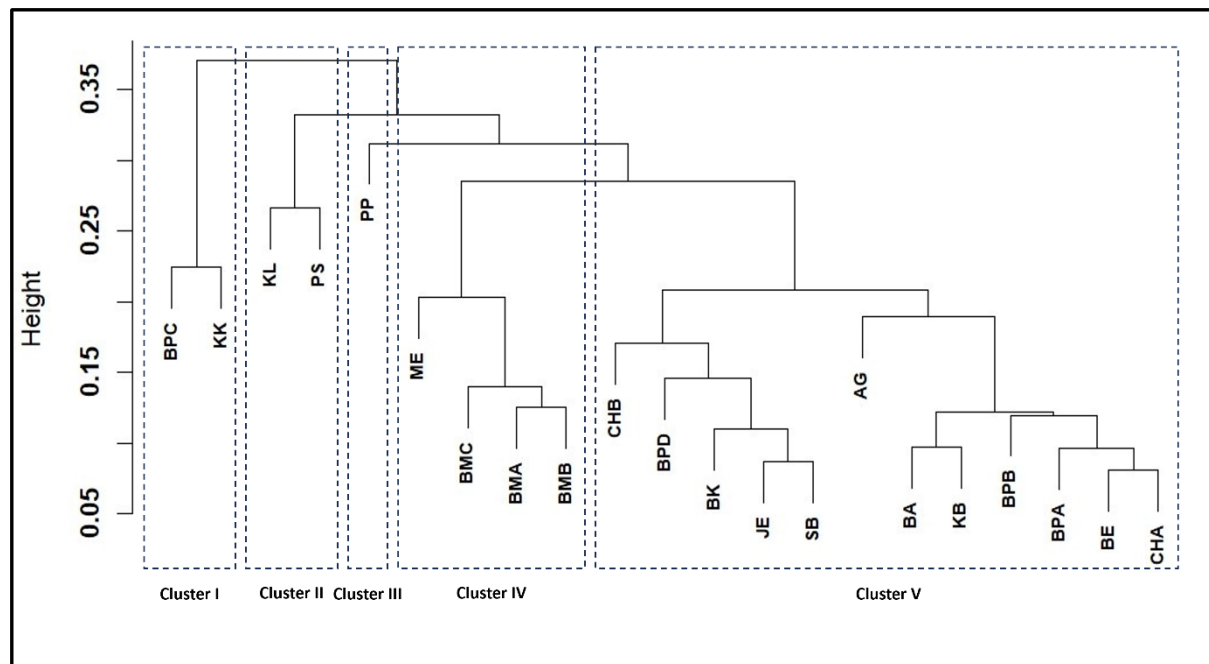


Figure 3. UPGMA dendrogram of 21 *M. cochinchinensis* accessions based on Gower distance

These findings align with earlier studies reporting fruit size and weight as the most discriminating descriptors in *M. cochinchinensis* (Othman & Mohd Khairi, 2023; Abdul Rahman et al., 2024). The Mantel test revealed no significant association between agromorphological variation and geographical origin ($r = -0.025$, $p = 0.854$), indicating that diversity in *M. cochinchinensis* is not geographically structured. This likely reflects traditional farmer practices of exchanging planting materials (Thorn et al., 2020) and the predominance of vegetative propagation, which

maintains identical genetic material across regions. Together with insect-mediated pollination and natural hybridisation, these factors contribute to genetic homogenisation across Peninsular Malaysia. Similar farmer-driven patterns have been reported in cassava (*Manihot esculenta*) (Rabbi et al., 2015), watermelon (*Citrullus lanatus*) (Huh et al., 2014), and barley (*Hordeum vulgare*) (Gadissa et al., 2021). While such interconnectedness may reflect a shared ancestral pool (Stankiewicz et al., 2001), other studies have shown regional clustering in *M. cochinchinensis* (Wimalasiri et

al., 2016; Toan *et al.*, 2018). Thus, agromorphological descriptors remain valuable for capturing diversity, particularly when complemented by molecular approaches (Salgotra & Chauhan, 2023).

These findings demonstrate substantial agromorphological variation within Malaysian *M. cochinchinensis*, with fruit biomass and reproductive traits emerging as the principal axes of diversity. Large-fruited, high-yielding accessions such as KL (Kuala Lipis, Pahang) and PS (Pokok Sena, Kedah) represent valuable accessions for breeding programmes aimed at improving yield and consumer appeal, while small-fruited accessions, including BMA, BMB, BMC (Bukit Mertajam, Penang) and ME (Merlimau, Malacca), may serve as reservoirs of adaptive traits suited to niche uses. The distinct separation of KK (Kubang Kerian, Kelantan) and BPC (Batu Pahat, Johor), alongside the intermediate but strategically placed PP (Pasir Puteh, Kelantan), illustrates the importance of conserving accessions from varied eco-geographical regions, as both divergent and bridging types contribute unique value for breeding programmes. Multivariate analyses (PCA and UPGMA clustering) effectively distinguished distinct groups with traits desirable for cultivation and breeding, providing essential baseline data on agromorphological diversity, identifying promising accessions with high-yielding and resilient characteristics, and informing germplasm conservation and future domestication efforts.

CONCLUSION

This study demonstrated substantial agromorphological variation among *M. cochinchinensis* accessions cultivated in Peninsular Malaysia. Fruit biomass traits and yield-associated as well as phenological traits emerged as the principal axes of diversity, as revealed by PCA and UPGMA clustering. These analyses consistently separated the accessions into biologically meaningful groups and provided robust baseline data for future crop improvement and conservation planning.

Specific accession-level insights offer actionable recommendations. Large-fruited, high-yielding accessions, such as PS (Pokok Sena, Kedah) and KL (Kuala Lipis, Pahang), should be prioritised in breeding programs

targeting yield improvement and consumer appeal. Small-fruited accessions from BMA, BMB, BMC (Bukit Mertajam, Penang) and ME (Merlimau, Malacca) formed a genetically stable cluster and represent reservoirs of adaptive alleles that may contribute to resilience or niche market applications. Divergent accessions such as KK (Kubang Kerian, Kelantan) and BPC (Batu Pahat, Johor), with unique harvesting patterns, should be conserved as distinct germplasm resources to safeguard rare reproductive traits. Importantly, the intermediate but strategically positioned PP (Pasir Puteh, Kelantan) accession links elite large-fruited types with more generalist profiles, making it a valuable bridging genotype for introgression and the development of balanced cultivars.

The absence of significant geographic structuring highlights the role of farmer-mediated exchange and vegetative propagation in shaping diversity. While such practices promote genetic mixing, they also emphasise the need for structured conservation to maintain rare and extreme phenotypes. Future research should integrate molecular marker data with agromorphological evaluations, broaden sampling across Malaysia, including Sabah and Sarawak regions, and develop preliminary selection indices that capture agronomic productivity (fruit biomass, pulp and aril yield), reproductive efficiency (flowering synchrony, fruit harvesting time), and adaptive traits relevant for both conservation and breeding. Such integrative approaches will validate the present findings and strengthen strategies for domestication, germplasm management, and breeding. Taken together, this study provides the first comprehensive, statistically validated baseline for Malaysian *M. cochinchinensis* diversity and translates it into concrete recommendations for breeding, conservation, and sustainable utilisation.

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