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GENETIC VARIABILITY AND PARENT SELECTION IN MALAYSIAN DWARF COCONUTS USING REML, BLUP, AND MULTI-TRAIT INDICES

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SUMMARY

Coconut (*Cocos nucifera* L.) cultivation prevails in over 90 tropical countries. Dwarf coconut varieties from Asia-Pacific are prominent for their short stature, early flowering, and high yield. In Malaysia, coconut ranks as the fourth most important crop, yet production comes behind the demand due to rising industrial and household use. Improving dwarf cultivars is crucial to enhancing productivity and reducing imports. This study analyzed genotypic variability in three Malaysian recommended dwarf cultivars—Malayan Yellow Dwarf, Malayan Red Dwarf, and Pandan—to identify genotypes suitable for further development. Ninety mature palms (30 per cultivar) succeeded in their assessment for 10 phenotypic traits per palm. Such traits were nut yield (number of nuts per palm per year), palm height, girth at 20 cm and 150 cm aboveground levels, the number of female flowers, spadix length, largest unopened spathe length, the number of unopened spathes, length of 11 leaf scars, and the number of rachillas. The restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) were methods used to estimate variance components, and the multi-trait genotype-ideotype distance index (MGIDI) enabled the multi-trait selection. Significant genotypic variability was evident among coconut genotypes, with heritabilities at 69%–99% and repeatabilities at 68%–100%. Cluster and principal component analyses (PCA) distinguished the Pandan cultivar from MYD and MRD. PCA explained 83.5% of the variation (PC1: 40.8%; PC2: 18.9%), with the yield, palm height, and girth loading comprising PC1 and spathe and spadix lengths on PC2. The MGIDI identified four superior genotypes per cultivar, with yield gains up to 67% in MRD, 59% in MYD, and 34% in Pandan.

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Keywords: Dwarf coconut (*C. nucifera* L.) cultivars, inter and intra population variability, phenotypic traits, REML, BLUP, MGIDI, Cluster and PCA, yield gain

Key findings: The study revealed significant genetic variability within and among three dwarf coconut (*C. nucifera* L.) cultivars, with the highest heritability and repeatability supporting effective selection. Yield, palm height, and girth were the main traits driving genetic variability and offering practical targets for further improvement in coconut yield.

INTRODUCTION

The coconut (*Cocos nucifera* L.) cultivar classification has evolved a considerable genetic variability due to the species' extensive diversity. Past studies have used diverse classification systems based on centers of origin, palm and fruit morphology, and pollination modes, to name a few (Niral *et al*., 2021). Among all these, the morphological and growth-habit-based approaches proved more prominent and most widely used for simple, observable traits, not needing advanced training or specialized equipment. Using these criteria, coconuts entailed broad division into tall and dwarf types, typically further distinguished by geographic origin and fruit color for dwarfs (Niral *et al*., 2021).

Dwarf coconut characteristics include shorter stems, early flowering, and uniform fruit color within populations (Arhin *et al.*, 2023). Their short stature also eases harvesting, with their fruits highly valued as tender and producing more nuts per bunch (Perera, 2012). As a result, dwarf cultivars have become widely used as female parents in breeding programs to transfer precocity and high yield.

Moreover, dwarf coconuts play an important role in the global coconut industry. Cultivars, such as Nam Hom (Thailand), are precious for aromatic water, while Brazil's Green Dwarf, Malayan Dwarfs, etc., are costly for sweet and tender nuts, and Kalpasree shows resistance to root wilt disease (Rethinam and Krishnakumar, 2022).

Among global dwarf diversity, Malayan dwarf cultivars are distinct for precocity and favorable phenotypic traits. Their importance shines in their inclusion in the Coconut Genetic Resources Database of COGENT and their recommendation for breeding from a limited number of dwarf accessions, despite extensive documented diversity (Batugal and Bourdeix, 2005).

Malaysia, the center of origin of Malayan Dwarfs, achieved a coconut self-sufficiency ratio of 70% in 2023 (Ministry of Agriculture and Food Security, 2023). Nevertheless, rising demand for fresh coconuts and value-added products has increased imports (Dardak and Yon, 2021). Key industry challenges include limited improved planting material and harvesting constraints in tall palms (Arumugam and Hatta, 2022).

Although 16 coconut cultivars succeeded in their registration in Malaysia, only three dwarf types—Malayan Yellow Dwarf, Malayan Red Dwarf, and Pandan—have achieved formal recommendations (Rahman *et al*., 2018). Limited knowledge of inter- and intra-varietal variability within these dwarfs constrains breeding progress, highlighting the need to establish a genetic variability baseline.

Studies on coconut genetic variability and heritability are crucial for accelerating breeding and identifying elite genotypes with valuable traits. For example, Zhang *et al.* (2021) evaluated 16 traits in 17 germplasm accessions in Hainan, China, identifying two high-yielding, sweet-water dwarf varieties suitable for commercial production. Similarly, Subramanian *et al*. (2019) reported that selection based on genetic variability can improve first-generation coconut performance by 25%–35%, highlighting its role in enhancing yield and quality.

Biometrical tools, such as restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP), allow precise estimation of genetic variance. The REML separates environmental from genetic effects, providing accurate estimates of genetic variance and better insight into population structure (Lourenço *et al.*, 2017). The cluster analysis and the principal component analysis (PCA) reduce complex trait data to key dimensions, revealing patterns of diversity essential for selection (Mohammadi and Prasanna, 2003). Traditional selection indices often fail to balance multiple traits, whereas the multi-trait genotype-ideotype distance index (MGIDI) integrates all traits into a single metric, supporting more efficient and balanced selection decisions (Debnath *et al.*, 2024).

Therefore, this study aimed to evaluate genotypic variability within and among the three recommended dwarf cultivars and identify superior parental genotypes, employing REML, PCA, and the MGIDI index to guide efficient selection for future hybrid development.

MATERIALS AND METHODS

Breeding material and study site

Coconut (*C. nucifera* L.) genotypes totaling 90 reached evaluation, comprising 30 individual genotypes each from the three dwarf coconut cultivars, viz., Malayan Yellow Dwarf (MYD), Malayan Red Dwarf (MRD), and Pandan from the breeding plots of the Department of Agriculture in Perak. The sample size of 30 genotypes per cultivar, as selected, relied on the recommendation in the Standardization Manual for Coconut Research (Baudouin and Labouisse, 1996), ensuring a 5% significance level and 95% confidence interval. The coconut MRD population comprised the genotypes G01 to G30, the MYD consisted of G31 to G60, and Pandan included G61 to G90. Assessments proceeded during three distinct climatic periods: the inter-monsoonal period in May 2022, the southwest monsoon in September 2022, and the northeast monsoon in December 2022.

The coconut genotypes underwent evaluation at Pusat Pertanian in Lekir, Perak (4.1379° N, 100.7320° E). Meteorological data from Jabatan Meteorologi Malaysia indicated rainfall totals of 72.4 mm in May, 96.8 mm in September, and 299.0 mm in December, with corresponding mean temperatures of 28.7 °C, 27.6 °C, and 26.6 °C, respectively. The MYD and MRD palms commenced planting in 2014, with the Pandan palms already planted in 2006. The age difference among the varieties is unlikely to be a confounding factor, as dwarf coconuts generally reach vegetative and reproductive stability by 6–8 years after planting (Nampoothiri and Parthasarathy, 2018). Moreover, the phenotypic traits evaluated are structurally stable after physiological maturity and are reliable indicators of genetic variability among coconut varieties (Sin *et al.*, 2024).

Phenotypic traits

The field data recorded occurred on 10 phenotypic traits, including the number of nuts per palm per year (yield), palm height, girth at 20 and 150 cm above the ground level, and the number of female flowers per palm. Other traits were spadix length per palm, the biggest unopened spathe length per palm, the length of 11 leaf scars per palm, the number of unopened spathes per palm, and the number of rachillas per palm.

All the data collection followed the guidelines outlined in the Standardization Manual for Coconut Research and the International Plant Genetic Resources Descriptors for Coconut (IPGRI, 1995). Yield estimation followed a modified PCA-based method (Magat, 1995). Assuming regular bunch emission and stable fruit set in mature palms, the nut load of the three oldest bunches served as a representative of annual fruiting. Total nut counts from these bunches incurred averaging across assessments and scaling to 12 months to estimate annual yield, calculated as:

Estimated number of nuts per palm =

$$\Sigma\left(\left(\bar{y}_1 + \bar{y}_2 + \bar{y}_3\right) / 3\right) x\ 12)$$

Where $\bar{y}i$ represents the average yield per palm per count.

Determining the number of female flowers and rachillas per palm continued by averaging counts from three freshly opened inflorescences. Palm height per palm's measurement came straight from the ground to the base directly below the crown in meters using a 3-in-1 laser range finder. The lengths of 11 leaf scars and the girth, spathe, and spadix entailed measurement in centimeters using a measuring tape from the average lengths of three freshly opened inflorescences per palm at every data gathering of the three seasons.

Experimental design and statistical analysis

The conduct of the experiment used a randomized complete block design, with the assessment period treated as the replication. Data collected resulted from across three climatic periods: inter-monsoonal (May 2022), southwest monsoon (September 2022), and northeast monsoon (December 2022), which served as replications for the analysis.

Variance components and heritability estimations used the inti R package (v0.6.7; Lozano-Isla, 2024) implemented in R (v4.4.3; R Core Team, 2024), fitting a linear mixed model with genotypes as random effects and replications as fixed effects using REML. Replications sustained modelling as fixed effects as they corresponded to specific, non-random assessment periods.

$$yij = \mu + \alpha i + gj + \varepsilon ij$$

Where μ: overall mean (fixed), αi: fixed effect of replication I, gj: random effect of genotype j, and εij: residual.

The use of the likelihood ratio test (LRT) evaluated the random effects of the model, with its significance tested by the chi-square (X^2) test using Plant Breeding Tools version 1.4 by the International Rice Research Institute. For cluster analysis, the study utilized packages cluster, ape, and stats in R (v4.4.3). Gower's coefficient of dissimilarity metric between the 90 palms gained computation, as shown in the equation below, to generate a dendrogram.

Gower's general Coefficient of Dissimilarity $d_{\text{Gower }(x,\, y)}$:

$$d_{Gower(x,y)} = 1 - [\Sigma^{m}_{i=1} = S_i W_i / \Sigma^{m}_{i=1} W_i]$$

Where $Si = 1 \; if \; xi = yi$ (binary or quantitative data), $Si = 0 \; if \; xi \neq yi$ (binary or quantitative data), $Si = 1 - |xi - yi| \; / \; Ri$ (quantitative data), $Wi = 1 \; if \; xi$ can be compared to yi, and $Wi = 0 \; if \; xi$ cannot be compared to yi.

Before cluster analysis, multicollinearity assessment ensued using the variance inflation factor (VIF) method with the aid of the lm () function in R (v4.4.3).

$VIFj=1/1-R^2j$

Where R^2j: R-squared from regressing predictor xj on all the other predictors, VIF = 1 → No multicollinearity, and VIF > 5 or 10 → High multicollinearity (rule-of-thumb thresholds).

Conducting principal component analysis (PCA) employed the Prcomp function in R (v4.4.3).

The selection of superior coconut genotypes, as performed, used the multi-trait genotype–ideotype distance index (MGIDI) utilizing the R Package 'metan' version 1.18.0.

RESULTS

Variance inflation factor (VIF) and inter-varietal variations

All the evaluated traits had variance inflation factor (VIF) values below the threshold of 5, indicating no multicollinearity among the traits. Therefore, retention of all traits occurred for analysis to assess inter- and intra-varietal variability in the coconut (*C. nucifera* L.).

Cluster analysis grouped all the coconut genotypes into four clusters, clearly separating the dwarf cultivar Pandan from the MRD and MYD populations. Cluster 1 contained seven MRD genotypes characterized by the highest fruit numbers and superior phenotypic values. In cluster 2, it included nine MYDs and one MRD (G04) genotype, with the MYD genotypes showing superior fruit counts and G04 recording the most unopened spathes,

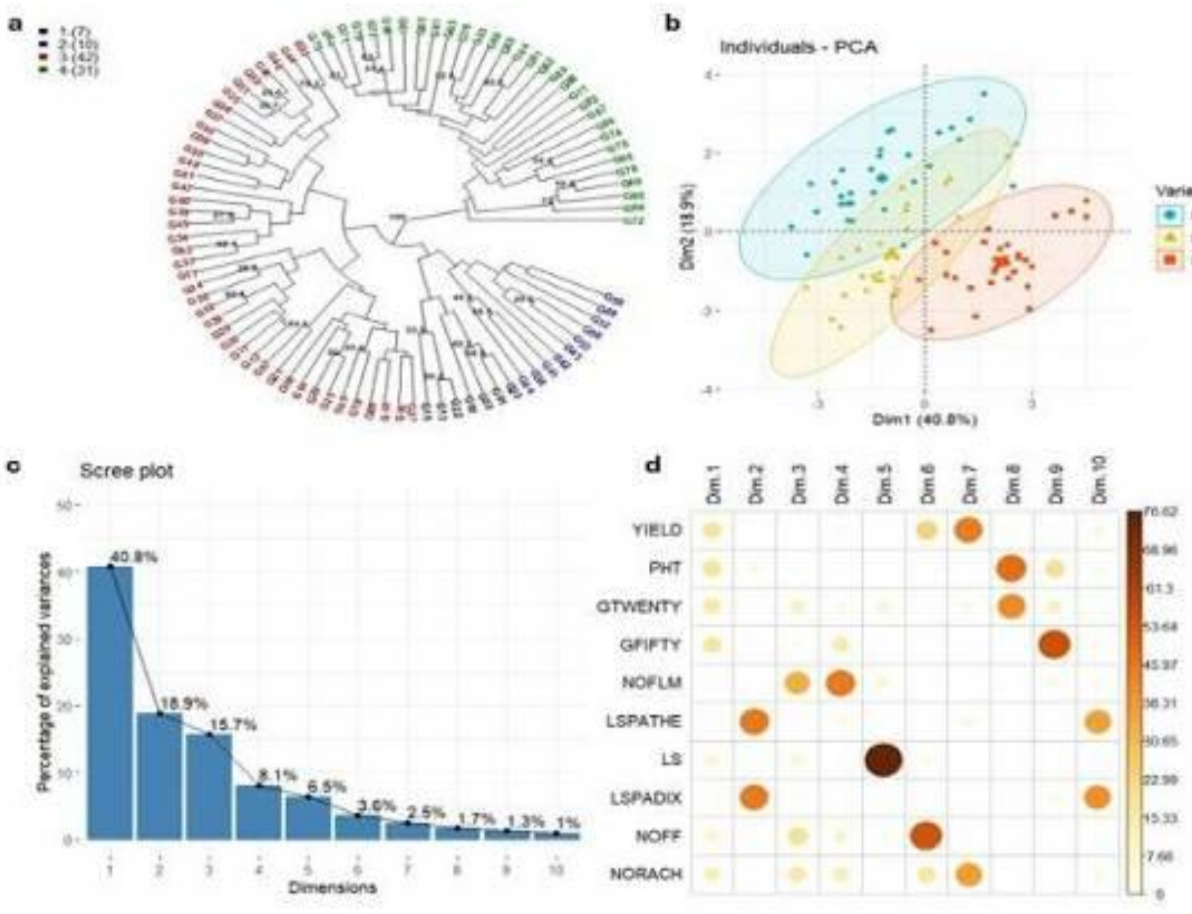

Figure 1. Inter-varietal variation and traits contribution in three dwarf coconut cultivars. a) UPGMA dendrogram of 90 genotypes (G01–G30 = MRD, G31–G60 = MYD, G61–G90 = Pandan) based on 10 phenotypic traits, b) PCA biplot showing clustering of the 90 palms, c) Scree plot of variance explained by the 10 principal components, and d) PCA biplot highlighting trait contribution to each principal components.

female flowers, and rachilla among the MRD genotypes. The largest group was cluster 3; it comprised 42 coconut genotypes (21 MRDs and 21 MYDs) characterized by low to moderate phenotypic trait values. Cluster 4 had dominance of the dwarf cultivar Pandan, with one MRD (G06) that exhibited the lowest spathe length among the MRD genotypes, reinforcing the phenotypic distinctiveness of Pandan (Figure 1a).

The PCA reduced dimensionality while retaining most variation, revealing three main cultivar-based groups and partial overlap between the MYD and MRD genotypes, consistent with cluster analysis (Figure 1b). The first four components explained 83.5% of the total variation, with PC1 (40.8%) considerably influenced by the traits of yield, plant height, and girth at 20 and 150 cm, while PC2 (18.9%) emerged as primarily associated with spathe and spadix lengths (Figures 1c, 1d).

Intra-varietal variability and traits potential

For the evaluated phenotypic traits, the variance components, genetic parameters, and likelihood ratio test (LRT) values appear in Table 1. The LRTs, based on BLUPs with random genotype and fixed replication effects, revealed significant genotypic variations within

Table 1. Estimates of variance components and genetic parameters in three dwarf coconut cultivars.

Traits	Vg	Ve	Vp	R	H^2p	H^2c	LRT
1a: Malayan red dwarf population							
Yield	3863.03	53.77	3880.96	0.99	0.99	0.99	81.95***
Pht	0.19	0.00	0.19	0.99	0.99	0.99	283.33***
No.spathe	0.09	0.13	0.14	0.68	0.68	0.66	13.44***
L.spathe	12.21	4.83	13.82	0.88	0.87	0.87	45.69***
L.spadix	7.47	1.03	7.81	0.96	0.95	0.94	45.38***
No.ff	51.36	2.01	52.03	0.99	0.98	0.95	81.03***
No.rach	15.96	0.73	16.20	0.99	0.99	0.96	119.47***
1b: Malayan yellow dwarf population							
Yield	3599.60	59.02	3619.27	0.99	0.99	0.98	125.63***
Pht(m)	0.19	0.00	0.19	1.00	1.00	0.99	261.35***
No.spathe	0.19	0.06	0.21	0.90	0.90	0.87	41.65***
L.spathe	21.01	1.77	21.60	0.97	0.97	0.95	107.90***
L.spadix	9.82	1.10	10.19	0.96	0.95	0.95	72.71***
No.ff	49.63	17.73	55.53	0.89	0.90	0.86	36.22***
No.rach	11.64	1.73	12.22	0.95	0.95	0.92	68.74***
1c: Pandan population							
Yield	3432.30	1303.98	3866.96	0.89	0.88	0.85	21.27***
Pht	0.08	0.00	0.08	0.99	0.99	0.97	135.67***
No.spathe	0.00	0.00	0.00	0.00	0.00	0.00	4.07*
L.spathe	4.91	6.06	6.94	0.71	0.71	0.69	15.90***
L.spadix	5.68	2.16	6.40	0.89	0.87	0.87	43.96***
No.ff	69.99	28.05	79.34	0.88	0.89	0.86	32.50***
No.rach	6.86	5.42	8.67	0.79	0.79	0.76	21.81***

*** statistical significance at $P \leq 0.001$ for the likelihood ratio test (lrt); vg = genetic variance, ve = environmental variance, vp = phenotypic variance, *r* = repeatability, H^2p = heritability based on BLUES, H^2c = heritability based on BLUPS; yield = number of fruits per palm per year, pht = plant height (m), no.spathe = number of un-opened spathes per palm, l.spathe = length of biggest unopened spathe (cm), l.spadix = length of spadix (cm), no.ff = number of female flowers per palm, and no.rach = number of rachilla per palm.

all three coconut cultivars, confirming substantial intra-population variability. The coconut yield consistently showed the highest genotypic, phenotypic, and environmental variances, and the genotypic values range from 3432.30 (Pandan) to 3863.00 (MRD) and phenotypic values from 3619.27 (MYD) to 3866.96 (Pandan). Environmental variance was highest in the cultivar Pandan (1303.98), while the lowest was in the cultivar MRD (53.77). In contrast, the traits of plant height and the number of unopened spathes displayed the lowest variances, and the cultivar Pandan showed complete uniformity for unopened spathes across the sampling dates (Tables 1a-c).

The differences between the genotypic and phenotypic variances were generally small, and environmental contributions were negligible, except in yield. Consequently, broad-sense heritability (H^2c from BLUPs; H^2p from BLUEs) and repeatability (R) were high for most traits, indicating considerable genetic control and effective selection potential. However, an exception was unopened spathes in the cultivar Pandan, which showed zero heritability and repeatability. Following Resende's classification, most of the traits were notable with the highest heritability category ($H^2 \geq 0.60$). Among LRT values, the plant height resulted in the highest values across the populations (283.33 in MRD, 261.35 in MYD, and 135.67 in Pandan). Meanwhile, the lowest LRT values emerged for the trait of unopened spathes in cultivars Pandan (4.07) and MRD (13.44) and for the trait of female flowers in the cultivar MYD.

Parent selection

The multi-trait genotype–ideotype distance index (MGIDI) with the values of factor

Table 2. Factorial loadings, communalities, and uniqueness in three dwarf coconut cultivars.

No.	Traits	FA1	FA2	FA3	communality	Uniqueness
2a: Malayan yellow dwarf population						
1	Yield	-0.81	0.4	0.21	0.86	0.14
2	Pht	-0.83	0.28	-0.31	0.86	0.14
3	G@20	-0.84	-0.04	0.04	0.71	0.29
4	G@150	-0.33	0.5	0.49	0.6	0.4
5	No.Spathe	0.17	0.82	-0.12	0.72	0.28
6	Lspathe	-0.4	0.86	0.13	0.92	0.08
7	Ls	0.1	-0.08	0.89	0.8	0.2
8	Lspadix	-0.54	0.74	0.13	0.86	0.14
9	Noff	-0.43	0.68	-0.11	0.65	0.35
10	Norach	-0.89	0.3	0.01	0.89	0.11
Mean					0.787	0.213
2b: Pandan population						
1	Yield	-0.63	-0.19	0.48	0.66	0.34
2	Pht	-0.79	-0.07	0.21	0.68	0.32
3	G@20	-0.72	-0.1	-0.06	0.53	0.47
4	G@150	-0.78	-0.21	-0.03	0.66	0.34
5	No.Spathe	0.14	-0.86	-0.2	0.79	0.21
6	Lspathe	-0.14	-0.8	-0.09	0.81	0.19
7	Ls	-0.7	-0.05	0.27	0.56	0.44
8	Lspadix	-0.29	-0.8	0.27	0.79	0.21
9	Noff	0.08	0.03	0.84	0.71	0.29
10	Norach	-0.36	0.08	0.74	0.68	0.32
Mean					0.687	0.313
2c: Malayan red dwarf population						
1	Yield	-0.81	-0.23	0.71	0.29	
2	Pht	-0.86	-0.14	0.76	0.24	
3	G@20	-0.24	-0.84	0.77	0.23	
4	G@150	-0.09	-0.94	0.88	0.12	
5	No.Spathe	-0.14	-0.84	0.72	0.28	
6	Lspathe	-0.54	-0.47	0.51	0.49	
7	Ls	-0.7	0.03	0.49	0.51	
8	Lspadix	-0.7	-0.3	0.58	0.42	
9	Noff	-0.79	-0.32	0.72	0.28	
10	Norach	-0.78	-0.12	0.62	0.38	
Mean				0.676	0.324	

Yield = number of fruits per palm per year, pht = plant height (m), g@20 = girth at 20 cm aboveground, g@150 = girth at 150 cm aboveground, no.spathe = number of un-opened spathes per palm, l.spathe = length of biggest unopened spathe (cm), ls = length of 11 leaf scars (cm), l.spadix = length of spadix (cm), no.ff = number of female flowers per palm, and no.rach = number of rachilla per palm.

loadings, communalities, and uniqueness is available in Table 2. In coconut cultivars MYD and Pandan, all the traits sustained grouping in three factors, while in the cultivar MRD, a structuring in two factors arose. For the cultivar MYD, defining factor 1 (FA1) was by the traits of rachilla number, plant height, girth (20 and 150 cm), and yield; factor 2 was by the traits of unopened spathes, spathe length, and spadix length; and factor 3 was only by the variable, leaf scar length (Table 2a). Regarding the cultivar Pandan, FA1 showed an association with growth and yield traits, FA2 with unopened spathes and spathe and spadix lengths, and FA3 with female flowers and rachilla (Table 2b). In the coconut cultivar MRD, almost all traits succeeded in loading onto FA1, except the traits of girth and unopened spathes, while these three traits dominated FA2 (Table 2c). Communalities were the highest across populations (68%–79%), indicating reliable factor structures.

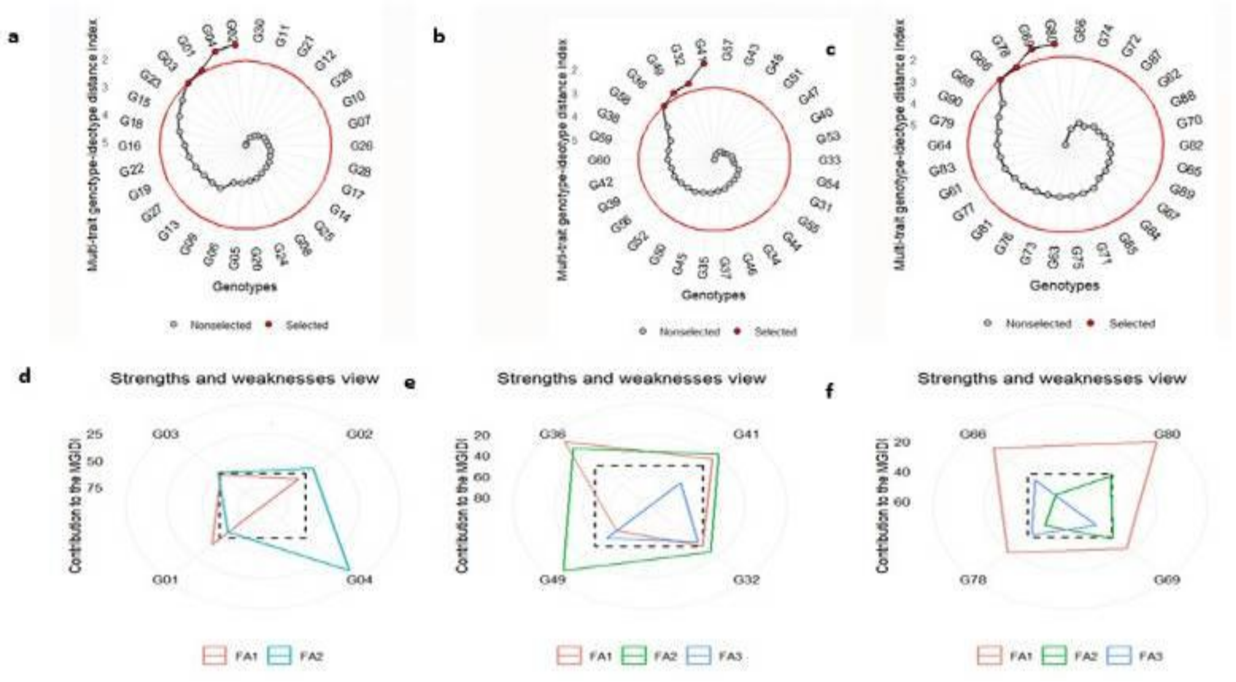

Figure 2. Top-performing genotypes in three dwarf coconut cultivars and their strengths and weaknesses based on MGIDI factors. a) Selected genotypes in the MRD population, b) Selected genotypes in the MYD population, c) Selected genotypes in the Pandan population, d) MGIDI factors influencing MRD genotypes, e) MGIDI factors influencing MYD genotypes, and f) MGIDI factors influencing Pandan genotypes.

The MGIDI identified four superior genotypes per coconut cultivar (Figures 2a-2c), and the selected genotype means surpassed the population means, revealing positive selection differentials (SD%) and selection gains (SG%) (Tables 3a-c). Yield showed the greatest improvement, with SD% up to 71.2% and SG% up to 67.2% in the cultivar MRD, while the trait of unopened spathes in the cultivar Pandan had the lowest gains (SD% = 1.2% and SG% = 0.57%; Table 3c). In the cultivar MYD, yield gains reached 59.5% (SD%) and 58.5% (SG%) (Table 3b). The selected coconut genotypes were G01–G04 (MRD) (Figure 2a), G41, G32, G49, G36 (MYD) (Figure 2b), and G80, G69, G78, and G66 (Pandan) (Figure 2c). Cumulative selection gains were the highest in the cultivar MRD (194.61), followed by MYD (160.67) and Pandan (81.45), and yield contribution expressed the most improvement across populations (Tables 3a-3c).

The trait contributions to genotype performance across the three coconut cultivars are illustrative of Figures 2d-2f. Narrower, pointed factor projections revealed the considerable traits' influence. In the cultivar MYD, FA1 traits mainly shaped genotypes G36 and G41, while the genotypes G49 and G36 reflected FA2, and G49, G41, and G32 reflected FA3 (Figure 2e). In the cultivar Pandan, the genotypes G80 and G66 gave an association with FA1 traits, G80 and G69 with FA2, and genotypes G66, G69, and G78 with FA3 (Figure 2f). For the coconut cultivar MRD, the genotypes G01, G02, and G03 gained influences mainly from FA1 traits, while the genotypes G04 and G03 reflected FA2 effects (Figure 2d).

Table 3. Multi-trait selection index metrics in three dwarf coconut cultivars.

No.	Traits	Xo	Xs	SD	SD%	H2	SG	SG%
3a: Malayan red dwarf population								
1	Yield	141	242	101	71.2	0.944	95.0	67.2
2	Pht	2.46	3.10	0.65	26.3	0.99	0.644	26.2
3	L.spathe	71.6	75.5	3.93	5.49	0.879	3.46	4.83
4	Ls	28.9	34.0	5.13	17.8	1.00	5.13	17.8
5	L.spadix	61.0	63.2	2.20	3.60	0.878	1.93	3.16
6	No.ff	25.2	34.2	9.00	35.7	0.944	8.49	33.7
7	No.rach	34.6	39.8	5.18	15.0	0.973	5.04	14.6
8	g@20	81.8	91.7	9.92	12.1	1.00	9.92	12.1
9	g@150	68.6	74.6	5.97	8.70	1.00	5.97	8.70
10	No.spathe	3.08	3.36	0.29	9.31	0.679	0.194	6.32
Σ								194.61
3b: Malayan yellow dwarf population								
1	Yield	169	270	101	59.9	0.976	98.8	58.5
2	Pht	2.73	3.12	0.397	14.6	0.998	0.397	14.5
3	L.spathe	67.4	75.2	7.84	11.6	0.967	7.58	11.2
4	Ls	27.3	29.7	2.37	8.66	0.975	2.31	8.45
5	L.spadix	54.4	60.1	5.71	10.5	0.934	5.34	9.81
6	No.ff	30.4	36.8	6.42	21.1	0.846	5.43	17.8
7	No.rach	38.2	43.3	5.17	13.5	0.928	4.80	12.6
8	g@20	72.0	78.3	6.25	8.68	1.00	6.25	8.68
9	g@150	68.2	75.0	6.82	10.0	1.00	6.82	10.0
10	No.spathe	3.79	4.19	0.399	10.5	0.866	0.346	9.13
Σ								160.67
3c: Pandan population								
1	Yield	225	325	99.8	44.3	0.760	75.8	33.7
2	Pht	5.34	5.54	0.202	3.79	0.980	0.198	3.72
3	L.spathe	65.8	67.6	1.87	2.84	0.709	1.32	2.01
4	Ls	31.7	34.7	3.05	9.62	1.00	3.05	9.62
5	L.spadix	56.7	60.7	4.08	7.19	0.873	3.56	6.28
6	No.ff	32.3	35.2	2.88	8.92	0.829	2.39	7.40
7	No.rach	39.0	41.2	2.20	5.64	0.764	1.68	4.31
8	g@20	96.9	104	7.05	7.28	0.986	6.95	7.18
9	g@150	81.8	87.3	5.45	6.66	1.00	5.45	6.66
10	No.spathe	3.41	3.45	0.0416	1.22	0.468	0.0195	0.571
Σ								81.45

(X_o) = Original Mean, (X_s) = Selected Mean, (SD) = Selection Differential, (SD%) = Selection Differential Percentage, (H^2) = Heritability, (SG) = Selection Gain, and (SG%) = Selection Gain Percentage; Yield = Number of fruits per palm per year, Pht = Plant height (m), g@20 = Girth at 20 cm aboveground, g@150 = Girth at 150 cm aboveground, No.spathe = Number of un-opened spathes per palm, L.spathe = Length of biggest unopened spathe (cm), Ls -= Length of 11 leaf scars (cm), L.spadix = Length of spadix (cm), No.ff = Number of female flowers per palm, and No.rach = Number of rachilla per palm.

DISCUSSION

This study established genotypic variability among 90 genotypes that belong to three dwarf coconut (*C. nucifera* L.) cultivars. Cluster analysis grouped the cultivar Pandan separately, underscoring its phenotypic distinctiveness, while the two coconut cultivars, MRD and MYD, showed partial overlap, which may be because of some environmental influence on visible traits rather than true genetic mixing (Evgenidis *et al*., 2011).

The pronounced distinctiveness of the Pandan cultivar relative to MYD and MRD can be due to both morphological and inherent biochemical differences. Pandan displayed a unique characteristic of 2-acetyl-1-pyrroline, the compound responsible for its quality pandan aroma, which is present in both vegetative tissues and nut water, setting it apart from other dwarf coconut cultivars. In contrast, MYD and MRD are primarily remarkable by pigmentation traits, with MYD exhibiting yellow and MRD reddish-orange petioles, inflorescences, and fruits. Additionally, MYD is highly homozygous, whereas MRD exhibits lower homozygosity and greater phenotypic variability, likely contributing to their partial overlap in multivariate analyses. These fundamental genetic and morphological distinctions may explain the consistent separation of Pandan in the cluster analysis and support its classification as a phenotypically and genetically distinct dwarf cultivar.

The PCA supported these results, with the palms generally clustering within their respective cultivars. The traits of yield, plant height, and the girth (at 20 and 150 cm) emerged as the considerable contributors to genetic variability; therefore, these coconut traits tended to be key drivers of genetic diversity for breeding. Reports of similar findings resulted in Malaysian dwarf coconuts (Sin *et al*., 2024) and in other studies across the multiple dwarf populations using UPGMA and REML (Sobral *et al.*, 2019). Molecular marker studies further confirmed the varietal distinctiveness, including differences among the Malayan dwarfs (Meerow *et al.*, 2003).

Intra-varietal variability among the coconut genotypes was also significant. The REML and LRT indices revealed the observed differences were largely genetic, not environmental (Li and Cui, 2016). The small differences between genotypic and phenotypic variances, coupled with high heritability and repeatability for most traits, suggested considerable genetic control and the potential for efficient selection. The traits of girth at 20 cm, girth at 150 cm, and the length of leaf scar exhibited 100% heritability and repeatability, reflecting their remarkable stability across seasonal replications. This pattern aligns with the growth physiology of coconut palms, which lack a vascular cambium and, therefore, do not undergo secondary thickening. Determining stem girth in coconut is primarily by early primary thickening and remains essentially constant once reaching physiological maturity (Kuo-Huang et al., 2004). As a result, these traits bore strong genetic control, with minimal environmental influence, making them reliable descriptors for selection.

For unopened spathes in the cultivar Pandan, although the estimated variance was approximately zero, the significant LRT reflects the conservative nature of variance component testing in generalized mixed models. It further indicates the presence of meaningful, albeit small, genotypic variability for this trait (Social Science Computing Cooperative, 2016).

For a perennial like the coconut, the revealed genetic control is particularly valuable, as it may facilitate early selection and reduce the time and resources required for breeding (Gonçalves et al., 2013). These results align with earlier reports of intra-population variability in Sri Lankan yellow dwarf (Kamaral et al., 2016) and the Gudanjali dwarf in India (Niral et al., 2007). They are also consistent with previous research showing the highest heritability for yield and growth traits in dwarf coconut genotypes (Sivakumar et al., 2020).

The MGIDI analysis recognized the genotype evaluation by grouping correlated traits into factors, minimizing redundancy, and weighing economically important traits (Debnath *et al.*, 2024). In coconut cultivars MYD and Pandan, the yield showed a consistent association with vegetative vigor traits, while reproductive traits clustered differently across the populations. In the cultivar MRD, most traits loaded onto a single factor, indicating greater interdependence. The cultivar MYD recorded the highest communality (79%), reflecting more stable trait relationships. The MGIDI identified four superior genotypes in each coconut cultivar, and these promising genotypes excelled the population means and showed positive selection differentials and genetic gains. The coconut yield exhibited the greatest improvement, particularly in the cultivar MRD, where selection gains reached 67.2%.

The MGIDI prioritized the traits of yield, palm height, girth, rachilla, and female flowers, which emerged as crucial for coconut improvement and industry relevance. Higher yield directly enhanced the economic returns; shorter palms lower harvesting costs; girth provides stability; and reproductive traits improve pollination and fruit set. By integrating multiple traits into a single index, MGIDI ensures balanced progress and avoids trade-offs common in single-trait selection. These results appeared consistent with earlier coconut studies that used phenotypic trait-based selection (Zhang *et al.*, 2021) and also received support from similar application of MGIDI in rice (Pallavi *et al.*, 2024). Overall, the integration of cluster analysis, PCA, REML, and MGIDI highlighted the genotypic variability and breeding potential of Malaysia’s dwarf coconut populations, providing a genetic base for targeted hybrid development.

CONCLUSIONS

The study revealed significant inter- and intra-varietal genotypic variability among the populations of three recommended cultivars of dwarf coconuts (*C. nucifera* L.). Cluster analysis, PCA, and REML effectively characterized the coconut population structure and identified the key sources of variation. The traits of yield, palm height, and girth (at 20 and 150 cm) were the main contributors to variability, which were identified as important breeding criteria. Heritability and repeatability estimates disclosed that much of the variation was genetic, causing passage to the next generation, enabling selection. Using the MGIDI, four superior parent palms succeeded in their identification in each coconut cultivar, providing valuable material for developing high-yielding dwarf coconut hybrids to support Malaysia’s coconut industry.

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