



Structure of a Coconut Tree (*Cocos nucifera* L.) BC1 Population according to Vegetative Growth Characteristics: Implications for Quantitative Trait Loci (QTL) Mapping

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Authors' contributions

This work was carried out in collaboration among all authors. Authors SD and AJSK conceived and planned the study, performed the statistical analyses, developed the experimental protocol, and drafted the first version of the manuscript. Author KAB contributed to the in-depth statistical analyses and critically revised the first version of the manuscript. Authors IAE and SDP contributed to the improvement, revision, and finalization of the manuscript. All authors read and approved the final manuscript.

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Abstract

This study aimed to characterise agro-morphological variability and assess the phenotypic structure of a BC1 coconut population (*Cocos nucifera* L.) as a basis for future quantitative trait loci (QTL) mapping analyses. A total of 186 BC1 progenies were evaluated using ten stem and leaf traits measured during the first nine months after planting. Principal component analysis (PCA), hierarchical cluster analysis (HCA), and discriminant factor analysis (DFA) revealed substantial phenotypic variability within the population. The first two PCA axes accounted for 81.5 % of the total variance, with the first axis being primarily associated with a vegetative growth gradient. Hierarchical cluster analysis distinguished three phenotypic groups that showed highly significant differences in all ten traits investigated ($p < 0.001$), indicating distinct phenotypic profiles within the BC1 population. Discriminant factor analysis confirmed this phenotypic structure, with 97.85 % of individuals correctly reclassified, demonstrating a high level of agreement between the clustering and discriminant approaches. The observed phenotypic differentiation provides valuable information for characterising the genetic material and identifying individuals or groups with contrasting vegetative growth traits. These findings provide a relevant phenotypic basis for integrating morphological and molecular data in subsequent genetic analyses and identifying genomic regions associated with vegetative growth traits in coconut. The results may contribute to the development of more effective strategies for genetic improvement and QTL mapping in coconut breeding programmes.

Keywords: *Cocos nucifera* L.; BC1 population; phenotypic variability; vegetative growth; QTL mapping.

1. Introduction

The coconut palm (*Cocos nucifera* L.) is one of the main perennial crops in tropical regions, playing a major economic, food, and industrial role for millions of coastal populations worldwide (Bourdeix *et al.*, 2005; Arumugam & Md Hatta, 2022). This species provides a wide range of derivative products used in the food, cosmetics and energy industries, thus reinforcing its strategic importance in tropical agricultural systems. In Côte d'Ivoire, the coconut palm is an essential cash crop for coastal communities, contributing significantly to agricultural income and food security (Assa *et al.*, 2006). A recent evaluation of coconut genotypes in Karnataka also documented differences in vegetative growth measurements among the genotypes studied (Jagadeesha *et al.*, 2026).

Despite its importance, the genetic improvement of coconut palms remains limited by several major biological constraints, notably their long juvenile growth phase, extended reproductive cycle and the low efficiency of selection based solely on phenotypic traits. Indeed, observed phenotypic performance does not always accurately reflect the true genetic value of individuals, which considerably slows down breeding programmes (Alemu *et al.*, 2024; Batugal *et al.*, 2005; Bourdeix *et al.*, 1997). These limitations have led to the development of new approaches, particularly quantitative trait loci (QTL) mapping, which makes it possible to identify genomic regions associated with agronomic traits of interest (Collard *et al.*, 2005; Grattapaglia *et al.*, 2024; Resende *et al.*, 2017; Xu & Crouch, 2008; Zhu, 2024) and to accelerate genetic progress through marker-assisted selection. A recent review of coconut biotechnology likewise identifies prolonged juvenile development and the genetic variability of seed-derived plants as challenges for conventional improvement (Radhika & Sujatha, 2025).

In recent years, significant progress has been achieved in coconut genomics, particularly through the construction of dense genetic maps based on SNP markers and the identification of QTLs associated with traits such as flowering, vegetative growth, and yield (Yang *et al.*, 2021; Grattapaglia *et al.*, 2024). For example, recent studies have highlighted the involvement of major genes in the control of flowering precocity in coconut, confirming the importance of genetic mapping approaches for the improvement of this species (Grattapaglia *et al.*, 2024). An assessment of worldwide coconut germplasm using microsatellite markers also documented genetic diversity and variation in vegetative characteristics among the accessions studied (Sudha *et al.*, 2023). A chromosome-scale genome assembly of the Chowghat Green Dwarf cultivar has provided an additional genomic resource for coconut research (Rajesh *et al.*, 2024). An SNP-based analysis of dwarf and tall coconut accessions also distinguished genetically differentiated groups, illustrating the value of population characterisation for subsequent genomic analyses (da Silva *et al.*, 2024).

However, the effectiveness of QTL mapping is highly dependent on the quality and structure of the populations used. Backcross populations (BC1) are widely used for the genetic analysis of quantitative traits because they allow the segregation of QTL alleles to be studied in a largely controlled genetic background, thus facilitating their detection and validation (Hospital, 2005; Marcotuli *et al.*, 2025; Semagn *et al.*, 2010). However, to our knowledge, no study has comprehensively evaluated the suitability of using these populations for QTL mapping in coconut, particularly using phenotypic descriptors from the early vegetative growth phase.

This study aims to highlight the morphological variability and structure of a BC1 population based on descriptors of the early vegetative growth phase. The results will provide a phenotypic database necessary for future genetic analyses, incorporating molecular data for QTL detection.

2. Materials and Methods

2.1 Study Site

The study was conducted at the Marc Delorme Research Station of the National Center for Agronomic Research (CNRA), located in Port-Bouët, in the Abidjan district, on the southern coast of Côte d'Ivoire, approximately 12 km from the Abidjan–Grand-Bassam Road. This station is situated between 5°14' and 5°35' North latitude and 3°54' and 3°55' West longitude. Average annual temperatures there vary from 24.6 to 27.6 °C, with a maximum in March (27.2 °C), a minimum in August (24.1 °C), and an annual average close to 25 °C. The average monthly sunshine duration is approximately 182.17 hours, with seasonal variations linked to rainfall patterns, providing favourable conditions for the physiological processes of the coconut palm.

2.2 Plant Material

The plant material consisted of 186 seedlings grown from germinating nuts obtained during the 4th and 5th harvest rounds of progeny resulting from backcrosses between intervarietal hybrid coconut palms [Malaysian Yellow Dwarf (NJM) x Great West African (GOA)] and Malaysian Yellow Dwarf coconut palms.

2.3 Experimental Design

The trial was conducted on experimental plot No. 122 at the Marc Delorme research station using a block design. The BC1 population was subdivided into two distinct blocks corresponding to the origin of the seedlings:

- **Block 1:** seedlings grown from nuts obtained during the 4th harvest of the BC1 progeny;

- **Block 2:** seedlings grown from nuts obtained during the 5th harvest of the BC1 progeny.

Each block was arranged in rows and columns, with uniform spacing of 10 m between seedlings to minimise competition. Additional seedlings grown from nuts obtained during the 3rd, 4th, and 5th harvests of the BC1 progeny were planted along the edge of the experimental plot and used as guard trees. Plants of the Malaysian Yellow Dwarf (NJM) variety and of the PB 121⁺ hybrid, resulting from a cross between the Malaysian Yellow Dwarf and Great West African (GOA) varieties, were also included in the experiment as reference cultivars (Fig. 1).

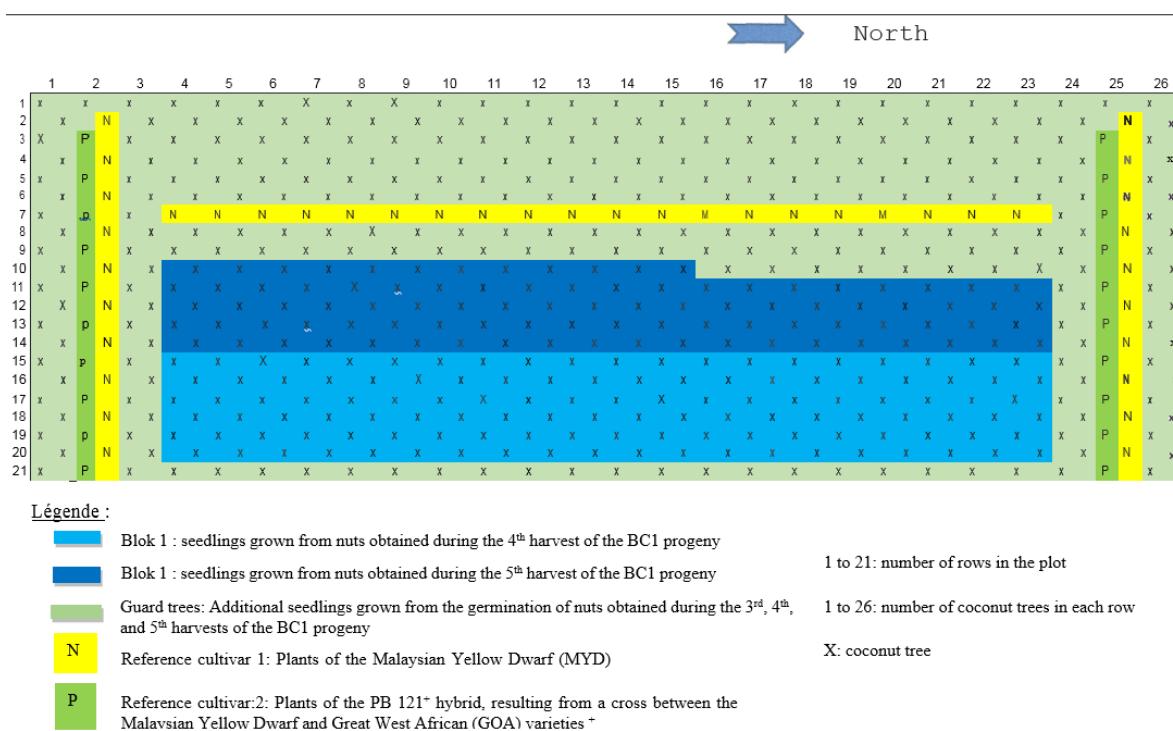


Fig. 1. Experimental design for the assessment of phenotypic traits in the studied coconut tree BC1 population

2.4 Data Collection

Ten (10) morphological descriptors of the trunk and leaves (Table 1) were measured six months after planting the coconut seedlings. The data were collected three times, over a period of 9 months, at regular three-month intervals.

2.5 Statistical Analyses

Descriptive statistics (range, median, means, standard deviations, and coefficients of variation) of phenotypic traits were calculated, and histograms of their values were constructed to assess their distributions in the BC1 progeny. The structure of the BC1 progeny, based on variability in agro-morphological traits, was evaluated using principal component analysis (PCA) and hierarchical clustering analysis (HCA). The relevance of the classification was assessed by a discriminant analysis (DA) carried out using the factorial coordinates of the coconut trees obtained from the PCA. All statistical analyses were performed using version 4.5.1 of the R statistical software.

Table 1. Agro-morphological descriptors used to characterize the coconut trees BC 1 population

No.	Codes	Descriptors	Measurement methods
1	TruCir	Trunk circumference	The circumference at the base of the plant stem, corresponds to the circumference of the ring between the roots and the stem. It is determined using a measuring tape graduated in centimeters.
2	LeafNu	Leaf Number	The number of leaves is obtained by counting.
3	TruHei	Trunk Height	The plant's height is measured from the ground to the tip of the last leaf on the trunk, that is, the youngest frond. This is done using a measuring tape graduated in centimeters.
4	RacLen	Rachis Length	The rachis length is the length of the leaf blade. It is measured using a measuring tape graduated in centimeters.
5	PetLen	Petiole Length	The petiole length is the distance between the point where the frond attaches to the trunk and the first leaflet. It is measured using a measuring tape graduated in centimeters.
6	PetWid	Petiole Width	The petiole width is the distance between the lateral edges of the petiole. It is measured in centimeters at the junction of the petiole and the leaf blade using calipers.
7	LealLen	Leaflet Length	The length of the leaflet is measured across four leaflets selected from the center of the palm (two leaflets on each side). This is the distance between the point where the leaflet attaches to the rachis and the tip of the leaflet, measured with a metal measuring tape graduated in centimeters.
8	LealWid	Leaflet Width	The width of the leaflet is measured across four leaflets selected from the center of the palm (two leaflets on each side). This is the distance between the lateral edges of the leaflet, measured with a metal measuring tape graduated in centimeters.
9	LealNu	leaflet Number	The number of leaflets is obtained by counting.
10	LgLLen	Longest leaf length	It corresponds to the distance between the point where the leaflet attaches to the trunk and the tip of the leaf. The measurement is performed using a measuring tape graduated in centimeters.

3. Results

3.1 Descriptive Statistics and Distribution of Agro-morphological Traits in the BC1 Progeny

The values of all the analysed phenotypic traits exhibited a normal distribution in the BC1 progeny, with coefficients of variation ranging from 0.2 for length, width, and number of leaflets to 0.4 for number of leaves and trunk circumference (Table 2). The traits exhibited an overall balanced Gaussian distribution (Fig. 2), as indicated by the close mean and median values (Table 2).

3.2 Structure of Phenotypic Diversity in the BC1 population according to Principal Component Analysis

The data collected on the 10 agro-morphological traits in the BC1 population were suitable for principal component analysis (PCA). Indeed, the mean KMO (Kaiser-Meyer-Olkin) index was 0.91 across all traits, with individual values ranging from 0.87 to 0.95. Furthermore, Bartlett's sphericity test was highly significant (p -value = 0.000). The PCA effectively summarised the phenotypic variability within the BC1 population along the first two factorial components, which explained 81.5% of the total variance, with 72.5 % for component 1 and 9 % for component 2.

Component 1 is strongly correlated with coconut tree growth traits, namely Trunk circumference (TruCir), Trunk height (TruHei), Rachis length (RacLen), Petiole length (PetLen), Petiole width (PetWid), Leaflet length (LealLen), Leaflet width (LealWid), Number of leaflets (LealNu), and Length of the longest leaf (LgLLen). This factorial component reflects a gradient of vegetative vigour within the BC1 population. Component 2 is primarily associated with the number of leaves (LeafNu). That component reflects a gradient of leaf emission capacity within the B1 population (Table 3).

Projecting the BC1 population onto the factorial space defined by components 1 and 2 revealed three groups of coconut trees, distinguished primarily along component 1 (Fig. 3). Group 1 comprises the coconut trees located on the negative side of component 1. They have the lowest values for the growth traits correlated with that component. The coconut trees in groups 2 and 3 are located on the positive side of component 1. However, the coconut trees in group 3 are distinguished by the highest trait values, while those in group 2 have values intermediate between those of groups 1 and 3.

Table 2. Descriptive statistics of phenotypic traits measured in the BC1 population of coconut trees

Traits Statistics	LeafNu	TruCir	TruHei	RacLen	PetLen	PetWid	LealLen	LealWid	LealNu	LgLLen
Minimum	1	9.9	38	37	21	0.9	23.9	1.3	27	72
Maximum	8	59	292	172.3	171.5	3	76.6	3.2	62	337
Range	7	49.1	254	135.3	150.5	2.1	52.7	1.9	35	265
Median	3	23.25	125	90.5	62	1.6	49	2	41	176
Mean	3.3	25.3	132.5	95.6	65.3	1.7	49.4	2.1	41.9	182.9
Standard deviation	1.3	10.8	38.3	25.3	20.5	0.5	10	0.4	7.1	47.3
Coefficient of variation	0.4	0.4	0.3	0.3	0.3	0.3	0.2	0.2	0.2	0.3

Legend: LeafNu: Number of leaves, TruCir: Trunk circumference, TruHei: Trunk height, RacLen: Rachis length, PetLen: Petiole length, PetWid: Petiole width, LealLen: Leaflet length, LealWid: Leaflet width, LealNu: Number of leaflets, LgLLen: Length of the longest leaf

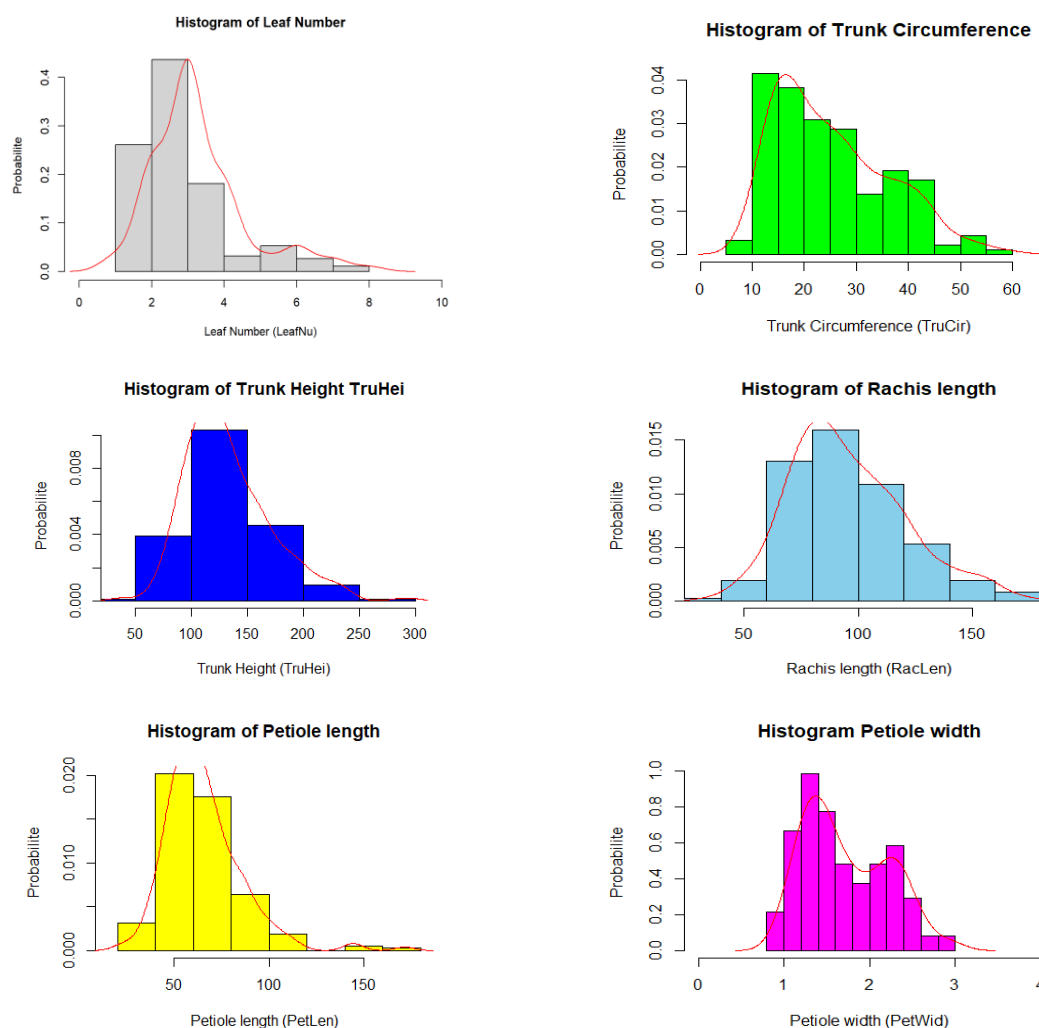
Table 3. Characteristics of components 1 and 2 of the principal component analysis

Eigenvalues and percentages of variance explained		
Eigenvalues	Comp. 1	Comp. 2
Explained variances (%)	72.5	9
Cumulative explained variances (%)	72.5	81.5
Correlation coefficients with agro-morphological characteristics		
Agro-morphological characteristics	LeafNu	0.41
	TruCir	0.87
	TruHei	0.84
	RacLen	0.94
	PetLen	0.78
	PetWid	0.89
	LealLen	0.91
	LealWid	0.91
	LealNu	0.86
	LgLLen	0.96
		0.84
		-0.16
		-0.19
		-0.08
		-0.30
		0.09
		-0.04
		0.03
		0.04
		-0.13

Legend: LeafNu: Number of leaves, TruCir: Trunk circumference, TruHei: Trunk height, RacLen: Rachis length, PetLen: Petiole length, PetWid: Petiole width, LealLen: Leaflet length, LealWid: Leaflet width, LealNu: Number of leaflets, LgLLen: Length of the longest leaf

3.3 Structure of the BC1 Coconut Tree Population, Revealed by Hierarchical Ascending Classification

The hierarchical classification, performed using the factorial coordinates of the coconut trees obtained from the PCA, revealed three phenotypic groups, G1, G2, and G3, containing 92, 64, and 30 individuals, respectively (Fig. 4).



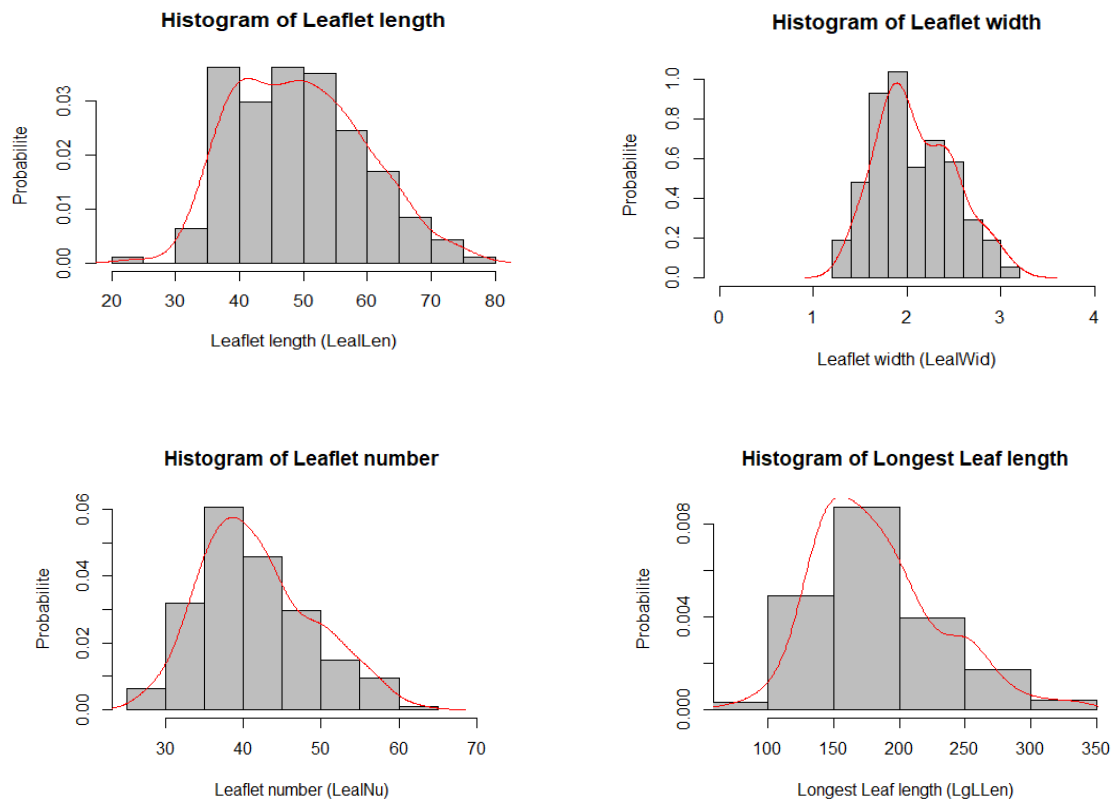


Fig. 2. Histogram of ten quantitative traits within the BC1 population of coconut trees

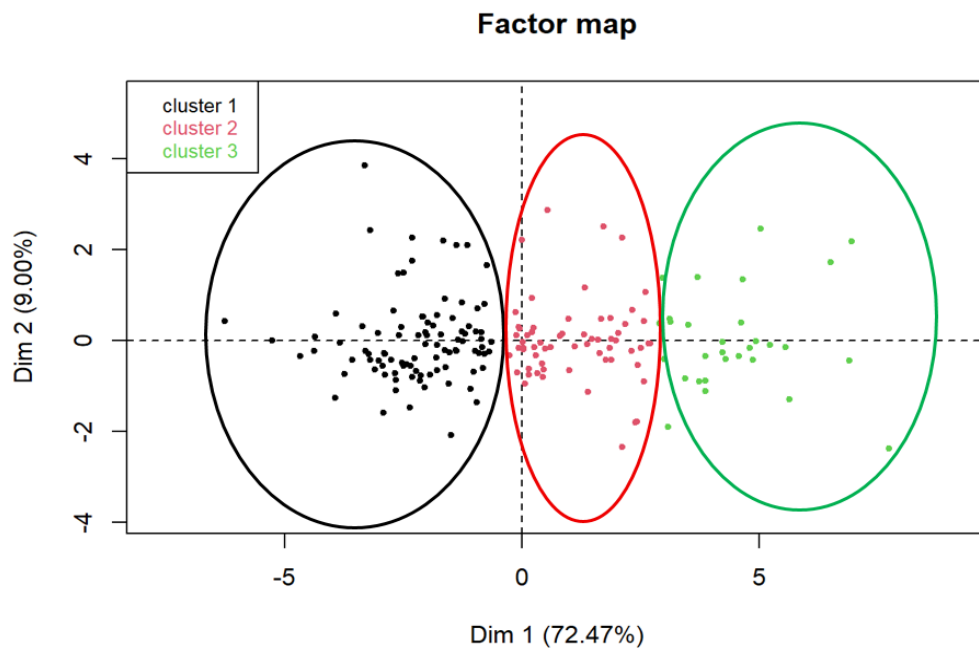


Fig. 3. Distribution of coconut trees into three groups in the factorial space defined by components 1 and 2 of the principal component analysis

Analysis of variance (ANOVA) revealed a highly significant group effect on each of the 10 evaluated agro-morphological traits ($p < 0.001$). The Newman-Keuls multiple comparisons test revealed significant differences in mean group values for each trait, indicating that each group has a specific phenotypic profile (Table 4).

3.4 Structure of the BC1 Coconut-tree Population, Revealed by the Discriminant Analysis

The discriminant analysis confirmed the coconut-tree groups identified by hierarchical ascending classification (Table 5) with 97.87 % accuracy. The first two discriminant functions explained 100% of the groups' variability, with the first (LD1) and the second (LD2) canonical functions accounting for 97.43 % and 2.57 % of the discriminant variance, respectively. The Wilks' λ test revealed that 6 of the 10 agro-morphological traits significantly discriminated the coconut-tree groups ($p < 0.05$). These were the length of the longest leaf (LgLLen), petiole width (PetWid), leaflet width (LealWid), petiole length (PetLen), trunk circumference (TruCir) and number of leaflets (LealNu) (Table 6). Petiole width and leaflet width are the most discriminating traits, with the absolute values of their coefficients in the first two canonical functions being the highest (Table 7). The centroids of the coconut-tree groups are clearly distinct (Fig. 5).

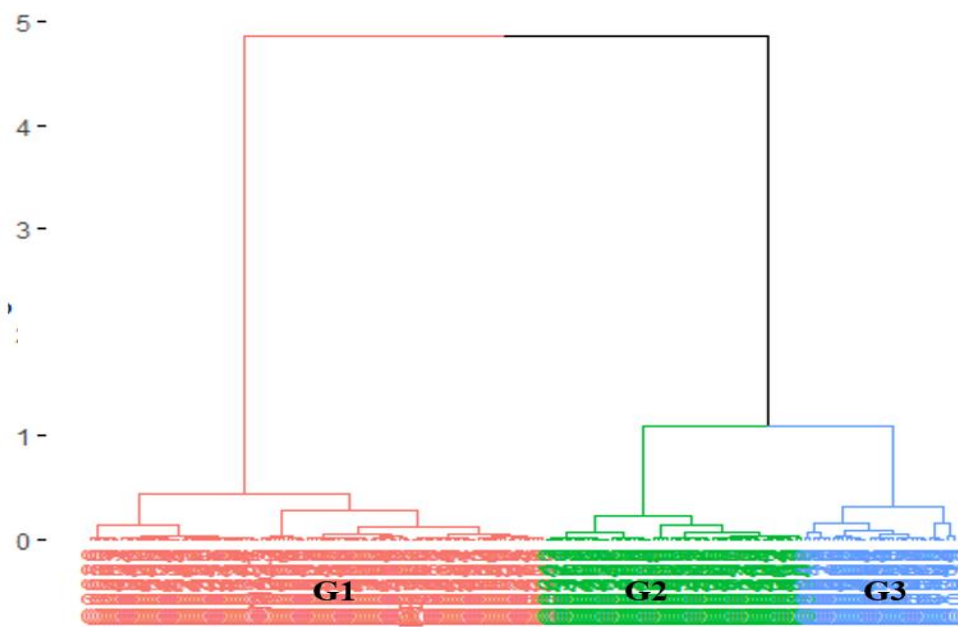


Fig. 4. Dendrogram of the coconut tree BC1 population obtained by hierarchical ascending classification

Table 4. Results of the Newman-Keuls test comparing mean values of the coconut groups in the BC1 population, for each agro-morphological descriptor

Traits	Group G1	Group G2	Group G3	P-value
TruCir	17.54 ± 6.10 a	29.08 ± 6.10 b	41.81 ± 6.10 c	< 0,001
TruHei	108.14 ± 25.21 a	142.14 ± 25.21 b	187.70 ± 25.21 c	< 0,001
RacLen	76.72 ± 13.41 a	104.32 ± 13.41 b	136.26 ± 13.41 c	< 0,001
PetLen	52.19 ± 14.69 a	72.04 ± 14.69 b	91.31 ± 14.69 c	< 0,001
PetWid	1.34 ± 0.26 a	1.98 ± 0.26 b	2.43 ± 0.26 c	< 0,001
LealLen	41.78 ± 5.43 a	53.42 ± 5.43 b	64.35 ± 5.43 c	< 0,001
LealWid	1.78 ± 0.22 a	2.31 ± 0.22 b	2.68 ± 0.22 c	< 0,001
LgLLen	36.85 ± 4.28 a	44.41 ± 4.28 b	52.33 ± 4.28 c	< 0,001
NbrFeu	2.88 ± 1.25 a	3.42 ± 1.25 b	4.20 ± 1.25 c	< 0,001
LealNu	147.46 ± 23.81 a	197.93 ± 23.81 b	261.30 ± 23.81 c	< 0,001

For each agro-morphological trait, mean values followed by the same letter are not significantly different, according to the Newman-Keuls test at a 5% p-value level

Legend: LeafNu: Number of leaves, TruCir: Trunk circumference, TruHei: Trunk height, RacLen: Rachis length, PetLen: Petiole length, PetWid: Petiole width, LealLen: Leaflet length, LealWid: Leaflet width, LealNu: Number of leaflets, LgLLen: Length of the longest leaf

Table 5. Classification matrix of coconut trees obtained by hierarchical clustering and discriminant analysis

	Groupe I	Groupe II	Groupe III	Total
Groupe I	92	0	0	92
Groupe II	1	62	1	64
Groupe III	0	2	28	30
Total	93	64	29	

Rows: classifications determined by the Hierarchical Clustering; Columns: classifications obtained from the Discriminant Analysis

Table 6. Results of Wilk's lambda test determining the relevant agro-morphological traits for discriminating coconut tree groups in the BC1population

Variables	Wilks.lambda	F.statistics.overall	p.value.overall	F.statistics.diff	p.value.diff
LgLLen	0,25	281,21	8,10E-57	281,21	8,10E-57
PetWid	0,17	133,47	2,58E-70	44,77	2,22E-16
LealWid	0,16	92,78	2,02E-70	5,33	5,63E-03
PetLen	0,15	73,17	4,16E-71	6,40	2,07E-03
TruCir	0,14	60,62	3,43E-71	4,67	1,06E-02
LealNu	0,13	51,97	4,69E-71	3,94	2,11E-02

Legend: LeafNu: Number of leaves, TruCir: Trunk circumference, TruHei: Trunk height, RacLen: Rachis length, PetLen: Petiole length, PetWid: Petiole width, LealLen: Leaflet length, LealWid: Leaflet width, LealNu: Number of leaflets, LgLLen: Length of the longest leaf

Table 7. Coefficients of each of the analysed coconut tree agro-morphological characteristics in the canonical discriminant functions LD1 and LD2

Traits	LD1	LD2
LeafNu	0.042	0.073
TruCir	0.032	0.084
TruHei	0.000	0.004
RacLen	0.009	0.022
PetLen	0.020	-0.036
PetWid	1.281	-2.152
LealLen	0.021	-0.035
LealWid	0.822	-3.198
LgLLen	0.053	-0.022
LealNu	0.007	0.039

Legend: LeafNu: Number of leaves, TruCir: Trunk circumference, TruHei: Trunk height, RacLen: Rachis length, PetLen: Petiole length, PetWid: Petiole width, LealLen: Leaflet length, LealWid: Leaflet width, LealNu: Number of leaflets, LgLLen: Length of the longest leaf

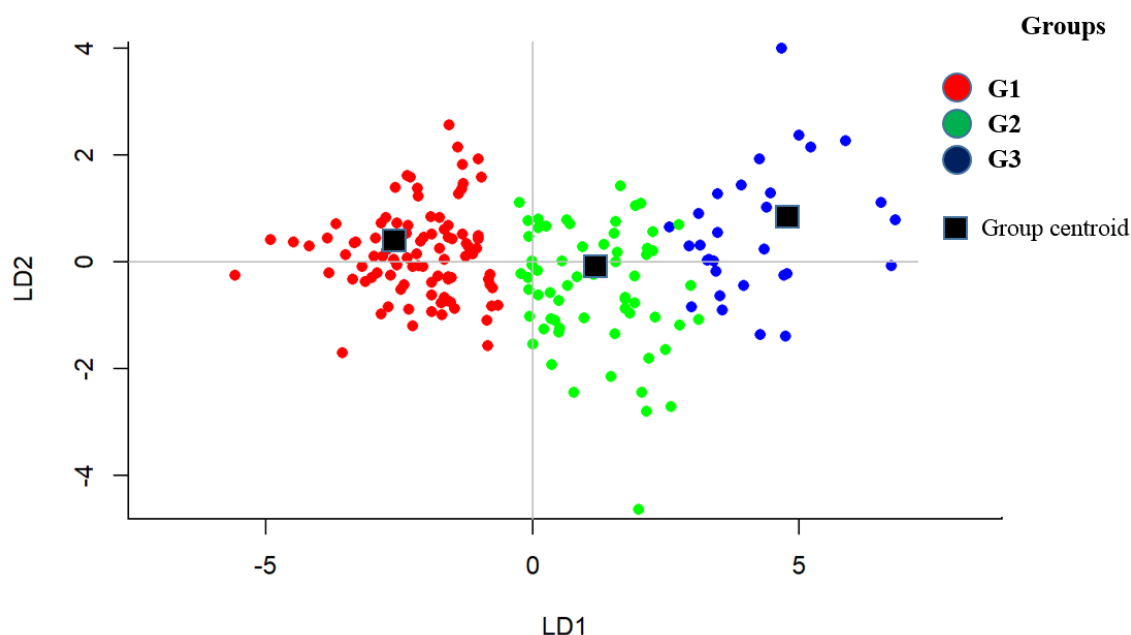


Fig. 5. Projection of coconut palm groups and their centroids onto the plane defined by the first two discriminant functions (LD1 and LD2)

4. Discussion

The ten studied agro-morphological traits exhibited Gaussian distributions, differing from the two distinct phenotypic classes expected for a trait under monogenic control in a backcross progeny. These continuous phenotypic distributions are consistent with the quantitative nature of the traits potentially controlled by multiple genes with cumulative effects, alongside possible environmental influences. Furthermore, they align with the reproductive modes of the Malayan Yellow Dwarf (MYD) coconut, which is self-pollinating with a residual outcrossing rate of 5 % (Bourdeix, 1988) and the West African Tall coconut, which is not strictly outcrossing (Foale *et al.*, 2020). Indeed, molecular studies have shown that, owing to higher outcrossing rates, Tall-type

coconut palms exhibit significantly higher levels of heterozygosity and genetic diversity than Dwarf-type palms (Perera, 2005; Perera *et al.*, 2001; Riangwong *et al.*, 2020).

The first principal component of the PCA explained 72.5 % of the total phenotypic variance in the BC1 progeny. This component is strongly correlated with nine growth traits of coconut tree leaves and stems. These results indicate that phenotypic diversity in the BC1 population is primarily linked to a vegetative growth gradient. The leaves and stems thus appear to exhibit generally synchronous growth dynamics, explaining their strong contribution to defining the first principal component. Strong positive correlations between the phenotypic values of several of these traits support this hypothesis.

The continuous distribution of phenotypic trait values does not allow direct determination of the homozygous or heterozygous state of coconut trees at the loci controlling these traits. Determining the population's genotypic structure requires informative molecular markers. This step is crucial for establishing allele segregation patterns at marker loci and enabling QTL mapping. Given the varying heterozygosity levels in Tall and Dwarf coconut varieties, the double pseudo-testcross strategy is a viable option for genotyping the BC1 progeny. This approach was developed for progenies from two heterozygous parents and enables the construction of genetic linkage maps based on informative genetic markers of each parent. It is particularly well-suited to perennial species for which generating homozygous lines is difficult or extremely time-consuming (Grattapaglia & Sederoff, 1994).

Applying the "double pseudo-testcross" strategy to an F2 population derived from a cross between "Tall" and "Dwarf" coconut palms enabled the construction of a high-density genetic linkage map based on 3,714 SNP markers (Grattapaglia *et al.*, 2024). This map covers 16 linkage groups, corresponding to the haploid chromosome number of coconut gametes. Additionally, a major QTL associated with early flowering was mapped. These results demonstrate the value of combining phenotypic and molecular data to identify genomic regions associated with traits of interest in coconut. Regarding the BC1 progeny examined in this study, Yang *et al.* (2021) genotyped 216 individuals and obtained 8,402 SNP markers. These markers allowed for the development of a genetic map that also comprised 16 linkage groups. This genomic characterisation complements the phenotypic characterisation presented in this study. Consequently, the phenotypic data can be combined with the existing molecular data to investigate the genomic regions controlling variation in the analysed traits.

PCA, AHC, and DA analyses identified three phenotypic groups of coconut trees within the BC1 progeny: G1, G2 and G3, comprising 92, 64, and 30 individuals, respectively. This structure suggests an alternative genotyping approach for mapping the QTLs involved in the expression of the traits under study. Groups G1 and G3, which contain coconut palms located at the two extremes of the Gaussian distribution curves for phenotypic values, could be used for selective genotyping (Ćeran *et al.*, 2024). This approach reduces the number of individuals to be genotyped while emphasising the phenotypic contrast between groups, and also enables the detection of QTLs with major effects on trait expression (Darvasi & Soller, 1992). However, excluding the intermediate group G2 results in a loss of information and risks limiting the precision of estimates regarding QTL effects and positions. Thus, selective genotyping of coconut trees in groups G1 and G3 could serve as a first step toward identifying candidate genomic regions, although the resulting marker-trait associations would need to be validated across the entire BC1 population. Such validation would confirm the associated markers and refine the estimation of their effects. In this regard, the 8,402 SNP markers previously identified by Yang *et al.* (2021) provide a solid foundation for mapping the QTLs associated with the agro-morphological traits under study.

5. Conclusion

The study revealed significant agro-morphological variability among coconut palms in the BC1 progeny derived from an initial cross between Malayan Yellow Dwarf (MYD) and West African Tall (GOA⁺) varieties. PCA and HCA identified three phenotypic groups, differentiated primarily along a vegetative growth gradient. The Wilks' lambda test and the confirmation of the coconut tree groupings with 97.87% accuracy by discriminant analysis (DA) underscore the suitability of the traits used to characterise this population. Despite the Gaussian distribution of phenotypic data within the BC1 progeny, these data can effectively be combined with molecular marker data to map the QTLs involved in the expression of vegetative growth traits. Such markers could be obtained using the double pseudo-testcross strategy or through selective genotyping of coconut trees located at the tails of the Gaussian distribution.

6. Limitations

This study characterised 186 BC1 coconut individuals from two harvest-derived blocks at a single research station, using ten vegetative descriptors measured during early growth. Consequently, the findings reflect phenotypic variation within this specific population and observation period, potentially limiting their generalisability to other environments, genetic backgrounds and developmental stages. Environmental and block-related influences were not explicitly separated from the observed phenotypic variation. Furthermore, molecular marker-trait associations were not evaluated. Future investigations should incorporate assessments across different environments and developmental stages, alongside molecular analyses, to clarify the genetic basis of the observed vegetative traits.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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