

Phenotypic Variation of *Cocos nucifera* L. Stems and Its Implications for Population Genetics in Pesisir Barat Lampung

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ABSTRACT

Coconut (*Cocos nucifera* L.) plays a vital role in coastal ecosystems and local economies, yet its population diversity may be shaped by historical cultivation practices. This study evaluated stem phenotypic variation and its implications for population genetics in coconut populations of Pesisir Barat, Lampung. A total of 92 coconut trees were sampled using stratified purposive sampling across representative coastal sites. Three stem morphometric traits were measured following IPGRI (1995) descriptors, namely stem circumference at 1.5 m above ground (CS), stem circumference at 20 cm above the base (CB), and the height of the 11th internode from the ground surface (HS). Data were analyzed using descriptive statistics, coefficients of variation (CV), and Principal Component Analysis (PCA). Results indicated relatively limited phenotypic variation, with CS exhibiting the lowest variability (CV 9.87%), while CB and HS showed moderate variability (CV 15.35% and 16.75%, respectively). PCA revealed close clustering of individuals, with the first two principal components explaining 91.0% of the total phenotypic variation, indicating limited phenotypic differentiation within the population. The observed phenotypic homogeneity may partly reflect the historical legacy of the PRPTE program, which distributed relatively uniform planting material during 1982–1984. Although inferences regarding genetic diversity remain preliminary, the findings suggest constrained population-level differentiation and highlight the importance of integrating morphometric and molecular approaches to support germplasm management, breeding strategies, and long-term sustainability of *C. nucifera* in coastal ecosystems.

Keywords: *Cocos nucifera*, germplasm, PCA, phenotypic variation, population genetics

INTRODUCTION

Genetic erosion in long-established plantation systems often occurs silently, particularly when populations originate from historically uniform planting materials (Zapico et al., 2020). In perennial crops such as coconut, this hidden narrowing of diversity may remain undetected for decades, yet it can shape population resilience, constrain adaptive responses, and compromise the long-term sustainability of breeding resources (Henrietta, 2025). Coastal ecosystems represent transitional zones between terrestrial, marine, and intertidal

environments, characterized by unique community structures and complex ecological interactions (Elsani et al., 2023). These ecosystems play a vital role in sustaining biodiversity and supporting biological resources (Rajesh et al., 2021), including the cultivation of coconut (*C. nucifera* L.), one of the key agricultural commodities in Pesisir Barat Regency, Lampung. This concern is particularly relevant in Indonesian coastal plantation systems, where historical replanting programs have shaped present-day crop populations.

C. nucifera is a highly adaptable tropical crop that supports coastal livelihoods and regional economies, including approximately 6,368 ha of plantations in Pesisir Barat (Badan Pusat Statistik, 2024). However, many plantations are aging and experiencing declining productivity, highlighting the need for improved germplasm evaluation and long-term sustainability strategies (Kano-Nakata et al., 2024; Zainol et al., 2023). In many long-established plantations, declining productivity is often accompanied by reduced regeneration quality and increasing structural uniformity among cultivated populations. Under such conditions, phenotypic evaluation becomes increasingly important as an initial approach for identifying variation that may still persist within historically managed coconut stands.

Efforts to improve the productivity and sustainability of coconut cultivation depend heavily on germplasm evaluation and characterization. While prior studies have assessed the genetic performance of coconut germplasm, few have comprehensively analyzed morphological and agronomic traits across natural and cultivated populations (R. Zhang et al., 2021). Although *C. nucifera* is taxonomically monotypic, substantial intraspecific variation persists across natural and managed populations, providing a basis for germplasm differentiation (Arumugam & Hatta, 2022). Therefore, systematic evaluations using standardized morphological descriptors, such as those proposed by the International Plant Genetic Resources Institute (IPGRI) are critical for improving germplasm management strategies (IPGRI, 1995).

Beyond univariate evaluation of individual morphological traits, multivariate approaches such as Principal Component Analysis (PCA) provide an analytical framework for resolving multivariate phenotypic structuring within plant populations (Li et al., 2023). By reducing complex variation into major axes of differentiation, PCA can reveal patterns of similarity, divergence, or clustering that may not be apparent from single-trait observations alone (Q. Zhang et al., 2020). In studies of germplasm characterization, this approach is particularly useful for supporting indirect inference regarding population-level organization and the potential consequences of historical planting uniformity (Civan et al., 2024). Therefore, integrating standardized morphometric descriptors with multivariate analysis offers a more robust basis for evaluating the phenotypic foundation of local *C. nucifera* populations, particularly when assessing historical plantation legacies in which phenotypic differentiation may be subtle rather than discrete.

A distinctive feature of coconut populations in Pesisir Barat is their historical origin. Most of the existing plantations were established through the Coconut Replanting and Rehabilitation Project (Proyek Peremajaan dan Rehabilitasi Tanaman Ekspor/PRPTE), a large-

scale program initiated by the Indonesian government between 1982 and 1984 (Kartolo, personal communication, April 5, 2025). Under this initiative, thousands of seedlings from selected mother trees were distributed to farmers with the objective of improving productivity and introducing high-quality planting materials. However, after four decades, the current phenotypic uniformity, or variability, among these populations can reveal crucial insights into the population-level organization of the original seedlings.

Phenotypic traits, particularly stem morphometric parameters, are closely linked to underlying genetic variation (Pangestu et al., 2023; Singh et al., 2023). Detecting low phenotypic diversity may suggest a narrow genetic base caused by the uniformity of government-supplied seedlings, whereas identifying significant variability could indicate greater underlying genetic heterogeneity despite the controlled seed distribution (Afful et al., 2024). Understanding these patterns is vital not only for reconstructing the genetic consequences of the PRPTE initiative but also for informing current breeding strategies, conservation efforts, and sustainable utilization of local coconut germplasm for future phytopharmaceutical innovation.

However, despite the historical significance of the PRPTE program, little is known about whether plantations established from government-distributed seedlings still retain detectable phenotypic signals of uniformity or divergence after four decades. This unresolved question represents a critical knowledge gap, particularly because such long-term planting legacies may shape both present population structure and future adaptive potential. To our knowledge, studies explicitly linking long-term government-distributed planting legacies, stem morphometric variation, and preliminary inference on population genetic implications in Indonesian coconut populations remain scarce. Therefore, this study aimed to evaluate stem phenotypic variation of local *C. nucifera* populations in Pesisir Barat Lampung using descriptive and multivariate morphometric analyses, as a preliminary approach to provide indirect inference regarding genetic diversity, assess the uniformity of historically distributed seedlings, and provide a foundation for conservation and breeding programs to enhance the long-term sustainability of coconut production.

METHOD

This study was conducted in the coastal region of Pesisir Barat Regency, Lampung Province, an area recognized as one of the primary centers of *C. nucifera* L. cultivation in Indonesia. Field sampling was conducted in April 2025 during the normal growing season to minimize seasonal effects on morphometric observations. Purposive sampling was chosen because the study specifically targeted historically established PRPTE-derived trees that met predefined inclusion criteria, making random sampling less suitable for addressing the study objective. To improve representativeness, sampling followed a stratified purposive approach across multiple coconut-growing coastal sites in Pesisir Barat Regency. Sampling locations were selected to capture variation in plantation distribution and environmental conditions typical of the coastal production landscape (Figure 1). Mature coconut trees presumed to

originate from the PRPTE planting period (approximately 41–43 years old) were selected using inclusion criteria consisting of healthy trunk condition, active productive status, and a minimum inter-tree distance of 20–30 m to reduce repeated sampling of immediately adjacent individuals and improve spatial independence among observations (Kartolo, personal communication, April 5, 2025).

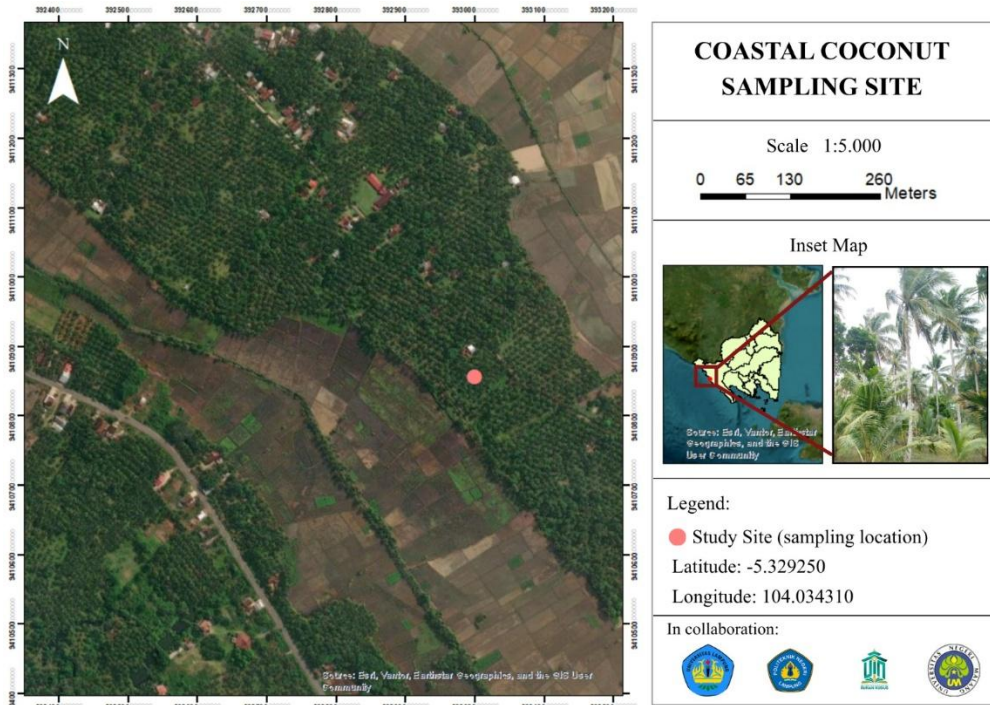


Figure 1. Location of sampling in coastal sites in Pesisir Barat Regency.

A total of 92 individual coconut trees were selected from different sites within the study area to capture potential variation within the population. The sample size was considered adequate for exploratory morphometric analysis because it captured phenotypic variation across multiple representative sites. It also provided sufficient observations relative to the limited number of variables included in the multivariate analysis. Phenotypic observations focused on three key stem morphometric parameters adapted from the *Descriptors for Coconut* published by the IPGRI (1995), namely the circumference of the stem at 1.5 meters above the ground (CS), the circumference at 20 cm above the base (CB), and the height of the 11th internode from the ground surface (HS). All measurements were conducted directly in the field using a flexible measuring tape to ensure consistency and accuracy across individual observations. Each morphometric variable was measured in triplicate for each sampled individual, and the mean value was used for analysis to minimize random measurement error. All observations were conducted by the same observer following IPGRI (1995) descriptors to reduce inter-observer variability. Repeated measurements were performed when discrepancies exceeded 5%.

Morphometric data were summarized using descriptive statistics, including mean, standard deviation, and coefficient of variation (CV), to quantify phenotypic variability among individuals. Coefficients of variation were used as a relative measure of trait dispersion to compare phenotypic variability among morphometric parameters. PCA was performed using standardized (z-score transformed) morphometric data based on the correlation matrix to account for differences in measurement scales among variables. Principal components with eigenvalues >1 were retained for interpretation following the Kaiser criterion. Statistical analyses, including descriptive statistics and PCA, were conducted in R version 4.5.2 using base statistical functions and the factoextra package for multivariate visualization.

RESULTS AND DISCUSSION

Stem morphometric variation was evaluated using three key descriptors (CS, CB, and HS) to characterize phenotypic structure within the sampled *C. nucifera* population. Together, these parameters provide a basis for assessing population-level uniformity, environmental influence on trait expression, and their possible implications for historical planting legacies. The sampled populations were distributed across coastal plantation areas in Pesisir Barat Regency characterized by sandy soils, open coastal exposure, and long-established coconut cultivation systems presumed to originate from the PRPTE planting period. Representative field conditions and plantation structure of the sampled populations are presented in Figure 2.



Figure 2. Representative field conditions of sampled *C. nucifera* populations in Pesisir Barat Regency, Lampung: (A) coastal agroecosystem landscape surrounding the coconut plantations and (B) vegetation structure and mature coconut stands within the sampled plantation area.

The Circumference of the Stem at 1.5 Meters above the Ground (CS)

CS was used as a primary morphometric parameter to assess phenotypic variation within the sampled *Cocos nucifera* population in Pesisir Barat, Lampung (Figure 1). As a structural trait closely related to long-term growth patterns, the distribution of CS offers an initial basis for evaluating the degree of phenotypic uniformity or variability among individuals, while also providing preliminary insight into the potential consequences of historically standardized planting material associated with the PRPTE program. This parameter is particularly useful for identifying overall growth consistency in long-established coconut plantations managed under relatively similar cultivation histories.

The histogram revealed that most individuals are concentrated within an intermediate range of stem circumference values, particularly around 85–100 cm, with a clear peak near 90–95 cm. This pattern suggests substantial similarity in stem dimensions among sampled individuals, reflecting a strong tendency toward phenotypic homogeneity. The distribution is moderately right-skewed, with only a few individuals exhibiting larger circumference values above 110 cm and very few extreme observations approaching 120–130 cm, suggesting the presence of limited outliers rather than broad morphological divergence. This relatively narrow spread is consistent with the low coefficient of variation observed for CS (9.87%), reinforcing the interpretation that stem circumference at 1.5 m exhibits low phenotypic variability within the population and may reflect a relatively homogeneous phenotypic foundation associated with historically shared planting material.

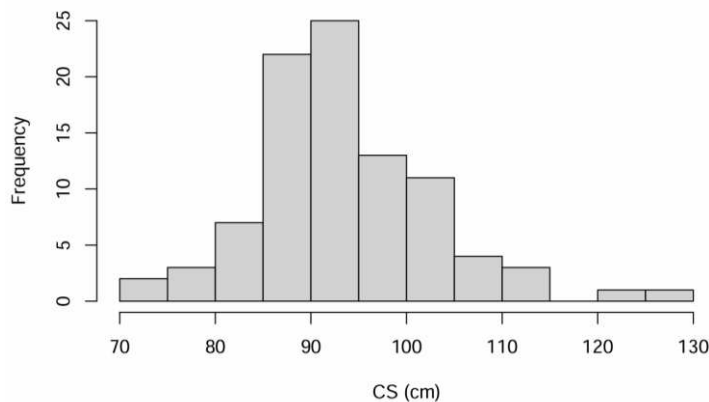


Figure 3. Frequency distribution of CS in sampled *Cocos nucifera* individuals.

This pattern reflects a strong tendency toward phenotypic homogeneity within the population (Pillay, 2024). One plausible explanation for this consistency is the historical implementation of the PRPTE in the 1980s, during which standardized, high-quality seedlings were distributed to farmers. Consequently, the similarity in stem circumference among individuals may partly reflect the historical use of relatively uniform planting material (Hori et al., 2022).

The limited range of stem circumference variation may indicate constrained phenotypic differentiation within the sampled population (Pecetti et al., 2023). Since phenotypic traits, such as stem morphometry, are partially determined by underlying genetic composition, the observed uniformity may reflect limited phenotypic differentiation and could potentially be associated with genetic similarity, although molecular evidence is required for confirmation (Andersson & Purugganan, 2022). While this homogeneity may have contributed to uniform plantation productivity in the short term, it also highlights potential long-term vulnerabilities. A population with limited genetic variability may have reduced adaptive capacity when facing environmental stressors, pests, or diseases (Kumar et al., 2022). Therefore, the results emphasize the need to integrate phenotypic assessments with molecular genetic analyses in future studies to better characterize population structure and ensure the resilience of local coconut germplasm (Uddin et al., 2024).

From an applied perspective, the stable stem circumference at 1.5 meters provides a simple yet informative morphological reference for monitoring vegetative growth performance in field conditions. The consistency of this parameter suggests its suitability as a standardized measurement for field-based evaluations of coconut plantations, particularly in assessing growth uniformity within populations established from government-supplied seedlings. Beyond agricultural monitoring, these findings also have implications for broader resource management strategies (Feng et al., 2024). Ensuring the sustainability of *C. nucifera* production requires not only evaluating productivity but also maintaining sufficient genetic diversity to support long-term adaptability.

The Circumference at 20 cm Above the Base (CB)

CB was used as a complementary morphometric parameter to evaluate variation in basal stem development within the sampled *Cocos nucifera* population. Unlike stem circumference measured at 1.5 m, the basal portion of the trunk is more likely to reflect localized environmental influences, particularly soil-related factors such as texture, compaction, moisture availability, and nutrient conditions near the root zone (Figure 2). Therefore, the distribution of CB provides an important basis for assessing whether phenotypic variability in basal growth is broader than that observed in upper stem morphology, while also offering insight into how environmental heterogeneity may interact with historically shared planting material in shaping population-level phenotypic expression.

The histogram revealed that most individuals are concentrated within an intermediate range of basal stem circumference values, particularly around 120–160 cm, with a peak frequency near 125–145 cm. Compared with CS, the distribution of CB appears broader and more dispersed, indicating greater phenotypic variability in basal stem development. The distribution also indicated a moderate right-skew, with a limited number of individuals extending toward larger circumference values above 170 cm and only a few extreme observations approaching 190–200 cm. This wider spread suggests that environmental influences may contribute more strongly to variability at the stem base than in the upper stem

region. The pattern is consistent with the moderate coefficient of variation recorded for CB (15.35%), supporting the interpretation that basal stem morphology exhibits moderate phenotypic variability while still maintaining an overall tendency toward population-level structural uniformity. This variation suggests that environmental factors, particularly edaphic conditions such as soil composition, compaction, and moisture availability, may have a stronger influence on stem development near the base than at higher points along the trunk (Langstroff et al., 2022).

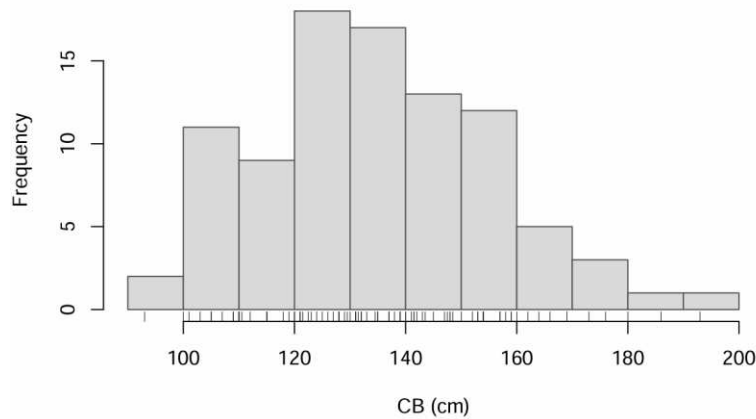


Figure 4. Frequency distribution of CB in sampled *Cocos nucifera* populations.

The broader distribution observed in CB highlights the potential role of phenotypic plasticity in the sampled populations. This may explain why CB exhibited a higher coefficient of variation than CS. Because the lower part of the stem is more directly affected by soil conditions, individual differences in root access to nutrients, water retention, and salinity tolerance may contribute to the variability detected. These findings indicate that the ability of certain trees to adapt to localized environmental heterogeneity could lead to subtle phenotypic divergence within an otherwise genetically uniform population (Zeltinš et al., 2018). This environmental influence on stem morphology demonstrates how phenotypic traits can integrate both genetic and ecological components, underscoring the importance of considering habitat-specific factors when evaluating morphological variation in *C. nucifera* populations (Bruggisser et al., 2020).

From a genetic perspective, the observed variability in CB, compared to the more stable distribution of CS, provides valuable insights into the interaction between genotype and environment. Although the historical PRPTE supplied relatively uniform seedlings, differences in edaphic conditions appear to have introduced localized morphological divergence (Yazgi & Degirmencioglu, 2007). Understanding this relationship is critical for designing effective management strategies for coconut plantations in coastal ecosystems, where soil heterogeneity is common. Furthermore, the inclusion of CB measurements alongside other morphological traits enhances the robustness of phenotypic assessments, providing baseline information for

integrating molecular genetic studies in future research to evaluate adaptive capacity, optimize germplasm conservation, and support sustainable coconut production.

The Height of the 11th Internode from the Ground Surface (HS)

HS was used as a morphometric indicator of vertical growth stability within the sampled *C. nucifera* population (Figure 3). This trait was selected because internode height reflects long-term vegetative development and is associated with stem elongation patterns shaped by both genetic regulation and environmental conditions. Compared with stem circumference traits, HS provides a complementary perspective on structural growth by capturing variation in vertical development rather than radial expansion. Therefore, the distribution of HS offers an important basis for assessing the degree of phenotypic consistency in growth architecture among individuals established from historically shared planting material. Evaluating the HS distribution enables an assessment of phenotypic consistency within the population and provides a reference point for monitoring long-term growth dynamics in plantations established during the PRPTE project (Scherdel et al., 2016).

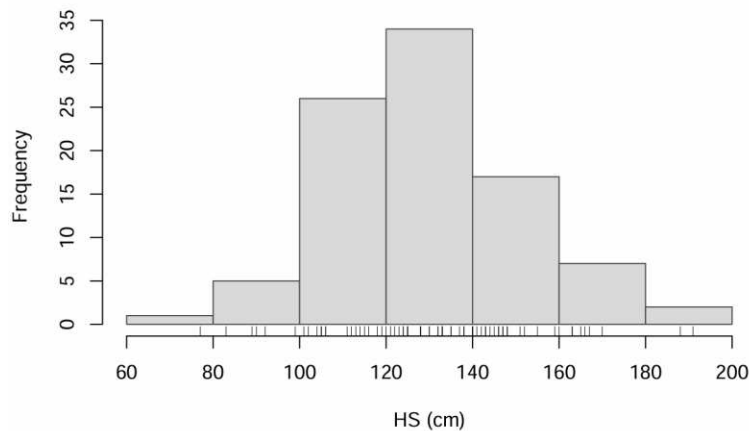


Figure 5. Frequency distribution of HS in sampled *Cocos nucifera* individuals.

The histogram shows that most individuals are concentrated within an intermediate range of internode height values, particularly around 110–150 cm, with a clear peak near 120–140 cm. This distribution indicates that the majority of sampled trees exhibit relatively similar patterns of vertical growth, suggesting a general tendency toward phenotypic stability. The distribution indicated moderate spread, with relatively few individuals occupying lower values below 90 cm or higher values approaching 180–200 cm, indicating limited extreme observations. Although the spread is slightly broader than that observed for CS, the overall clustering remains compact, supporting the interpretation of moderate but controlled phenotypic variability. This pattern is consistent with the coefficient of variation recorded for

HS (16.75%), which indicates moderate variation while still reflecting a structurally uniform population likely shaped by a relatively homogeneous planting background.

The overall stability in HS measurements reflects a relatively narrow phenotypic range, which may be consistent with constrained phenotypic differentiation and may reflect a relatively narrow genetic foundation. Since internode elongation is strongly influenced by genotype, the observed uniformity supports the hypothesis that plantations established through the PRPTE relied on seedlings derived from a relatively homogeneous genetic pool (R. Zhang et al., 2020). While this uniformity can be advantageous for achieving standardized plantation performance, it also raises concerns about reduced adaptability to future environmental challenges, such as salinity stress, changing climatic conditions, and pest outbreaks (Gouveia et al., 2020). Integrating morphological assessments with molecular studies would provide a deeper understanding of the population's genetic structure and inform strategies for sustaining productivity in coastal environments (Davis et al., 2018; Parvizi et al., 2022a).

From a practical perspective, the 11th internode height serves as a key reference parameter for monitoring long-term vegetative growth and supporting germplasm enrichment strategies (Madić et al., 2016). Maintaining records of this parameter over time allows for the detection of shifts in vertical growth performance, which can be critical for identifying potential changes in environmental conditions or plantation health. Furthermore, understanding the degree of phenotypic stability assists in selecting suitable genotypes for breeding and conservation programs aimed at sustaining coconut production in coastal regions.

Principal Component Analysis (PCA)

PCA was performed to evaluate the multivariate phenotypic structure of the sampled *Cocos nucifera* population based on three stem morphometric traits, namely stem circumference at 1.5 m above ground (CS), stem circumference at 20 cm above the base (CB), and the height of the 11th internode (HS) (Figure 4). Unlike univariate frequency distributions, PCA provides an integrated assessment of how these traits collectively contribute to phenotypic differentiation among individuals (Cao et al., 2025). By reducing multidimensional variation into principal axes, this analysis allows identification of the major sources of phenotypic variation while simultaneously assessing whether the sampled population exhibits clear structuring or a tendency toward overall homogeneity.

The PCA results showed that the first two principal components explained 91.0% of the total phenotypic variation, with PC1 accounting for 60.67% and PC2 accounting for 30.33%, indicating that the major structure of variation was effectively captured by these two axes and demonstrating strong explanatory power of the first two components. The ordination plot showed a close clustering of individuals without clear separation into distinct phenotypic groups, suggesting limited phenotypic differentiation across the sampled population. PC1 was primarily associated with variation in stem circumference traits, particularly CS and CB, whereas PC2 was strongly influenced by HS, indicating that vertical growth contributed a distinct dimension of variability relative to radial stem development. This pattern is consistent

with the low to moderate coefficients of variation observed for the three traits and supports the interpretation of relatively homogeneous phenotypic structure within the sampled coconut population.

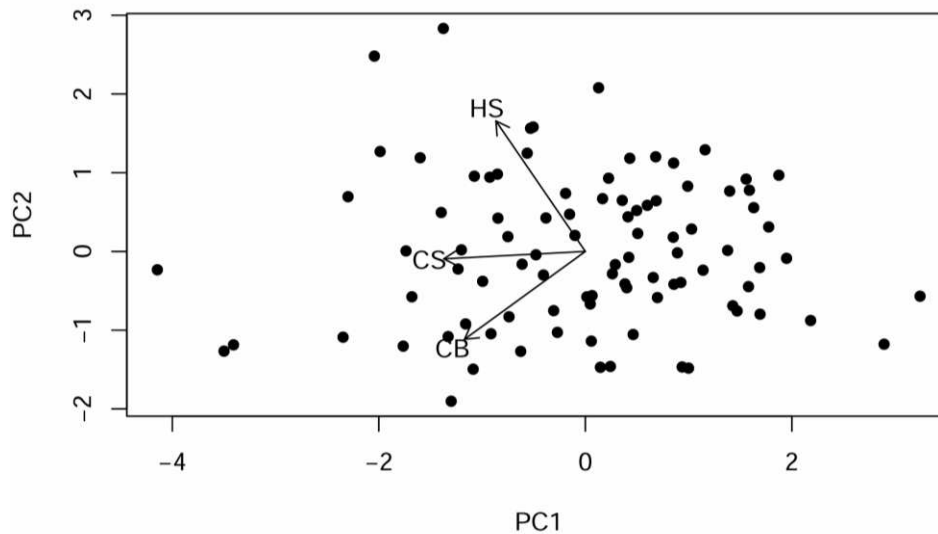


Figure 6. PCA ordination plot showing phenotypic structuring of 92 *Cocos nucifera* individuals based on stem morphometric traits. The first two principal components explained 91.0% of the total phenotypic variation.

The close clustering of individuals in the PCA ordination suggests that the sampled coconut population shares a relatively narrow multivariate phenotypic foundation. In population-level morphometric studies, the absence of distinct group separation is often interpreted as evidence of limited divergence among individuals, particularly when combined with modest trait-level variability (Gonul et al., 2025). In this case, the concentration of individuals around the central ordination space indicates that variation exists, but does not form discrete phenotypic subgroups. Such a pattern is compatible with a population established from historically related planting material, where shared ancestry may have constrained broad phenotypic differentiation over time.

The loading pattern further suggests that stem circumference traits (CS and CB) contribute strongly to the major axis of variation, whereas internode height (HS) represents a distinct but related dimension of growth variability. This distinction implies that radial stem development and vertical growth may respond somewhat differently to developmental or environmental influences, even within a relatively uniform population (Lambers & Oliveira, 2019; Liu et al., 2021). The stronger alignment between CS and CB is biologically reasonable, as both traits reflect structural growth of the stem and may be influenced by overlapping physiological processes. In contrast, the separation of HS along PC2 indicates that vertical

growth contributes an additional dimension of phenotypic organization, although not sufficient to generate clear population subdivision.

The PCA pattern also provides indirect support for the historical influence of the PRPTE program on present-day population structure. Because the sampled trees are presumed to derive largely from standardized seedlings distributed during the 1982–1984 planting period, the observed phenotypic clustering may reflect the long-term legacy of relatively uniform planting material. Although environmental heterogeneity in coastal ecosystems may introduce modest variation, the absence of pronounced multivariate separation suggests that such effects have not generated strong divergence within the population (Morales et al., 2026; Parvizi et al., 2022b). This interpretation is further supported by the coefficient of variation values, which indicate low variation for CS and moderate variation for CB and HS, collectively pointing to constrained rather than extensive phenotypic diversification.

From a population genetics perspective, these results should be interpreted as preliminary but informative. Although phenotypic similarity does not directly confirm low genetic diversity, the combination of limited multivariate differentiation, moderate trait variability, and historical planting uniformity may suggest a relatively narrow genetic foundation (Swarup et al., 2021; Wang et al., 2023; J. Zhang et al., 2024; Zhao et al., 2026). Such conditions could have implications for adaptive capacity, particularly under future pressures such as salinity stress, pest outbreaks, or climatic instability in coastal production systems. At the same time, the modest spread observed in the ordination indicates that some level of phenotypic variability persists, which may represent valuable standing variation for conservation and future breeding efforts (Mable, 2019). These findings therefore reinforce the importance of integrating morphometric evidence with molecular approaches to more fully characterize population genetic structure and long-term resilience.

Implications for Population Genetics

The relatively limited variation observed across stem morphometric traits, together with the close clustering identified in the PCA ordination, suggests that the sampled *C. nucifera* populations exhibit a tendency toward phenotypic homogeneity. This pattern may partly reflect the historical legacy of the PRPTE program, in which standardized seedlings derived from selected mother trees were widely distributed across plantations in Pesisir Barat. Although phenotypic similarity does not directly confirm low genetic diversity, the observed uniformity may indicate constrained population-level differentiation and could be consistent with a relatively narrow genetic foundation (Khoury et al., 2022; Ma et al., 2020; O'Hara et al., 2026). These interpretations should, however, be viewed as preliminary because they are based on phenotypic rather than molecular evidence.

From an ecological and adaptive perspective, such phenotypic homogeneity may have implications for long-term resilience, particularly in coastal production systems exposed to salinity fluctuations, climatic instability, pest outbreaks, and other environmental stressors (De Battisti, 2021; Yadav et al., 2024). Populations with limited standing variation may possess

reduced capacity to respond to changing conditions, potentially affecting both productivity and persistence over time (Thurman et al., 2020). At the same time, the moderate variation detected in CB and HS suggests that some degree of phenotypic variability remains within the population, which may represent valuable material for germplasm enrichment, conservation planning, and future breeding efforts aimed at strengthening adaptive capacity (Thakur et al., 2024).

These findings highlight the importance of integrating morphometric evidence with molecular approaches to more fully evaluate population genetic structure in historically established coconut plantations. Analyses based on DNA markers, population genetic parameters, or genomic tools will be necessary to verify whether the phenotypic patterns observed here correspond to underlying genetic uniformity or whether hidden genetic variation remains undetected by morphology alone (Zimmerman et al., 2020). Such integration would provide a stronger foundation for germplasm management strategies designed to balance plantation productivity, genetic resilience, and long-term sustainability of *C. nucifera* cultivation in Pesisir Barat.

CONCLUSION

This study demonstrates that *C. nucifera* populations in Pesisir Barat exhibit relatively limited phenotypic variation in stem morphometric traits, with a general tendency toward phenotypic homogeneity supported by low to moderate coefficients of variation and close clustering in PCA ordination. This study provides the first morphometric baseline for evaluating phenotypic structure of PRPTE-derived coconut populations in Pesisir Barat and offers a foundation for future molecular assessments and germplasm management programs. Although these interpretations remain preliminary because they are based on phenotypic rather than molecular evidence, the findings provide baseline information for germplasm management and indicate the need for molecular studies to verify genetic structure and support long-term resilience and sustainability of coconut cultivation in coastal ecosystems.

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