



RESEARCH ARTICLE

Evaluation of selected Andaman Tall coconut (*Cocos nucifera* L.) population for uniformity, stability and genetic variation using microsatellite markers

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Abstract

Tall coconut genotypes of Andaman were investigated using phenotypic traits and molecular marker analysis to determine genetic consistency. A set of 35 Andaman Tall coconut genotypes was subjected to molecular analysis using fourteen SSR primers. Uniform banding profiles were obtained with 10 out of 14 primers, while four primers exhibited polymorphism, indicating a relatively high level of genetic similarity with moderate genetic variation among the genotypes. Cluster analysis grouped the genotypes into three major clusters, with twelve genotypes in Cluster I, twenty-one in Cluster II and two in Cluster III. From the present study, it is inferred that seed nuts should preferably be collected from mother palms exhibiting consistent and stable phenotypic traits across seasons and from isolated or controlled pollination setups (*interse* mating), to maintain true-to-type progenies and preserve genetic uniformity. The findings of this study demonstrate that SSR-based molecular markers can serve as an effective tool for identifying genetically true-to-type mother palms for coconut varietal improvement programmes.

Keywords: Andaman; coconut; genetic diversity; microsatellites; morphometric studies; SSR markers

Introduction

The Andaman-Nicobar archipelago extends from the Arakan Yoma ranges of western Myanmar to Sumatra and is bounded by the Andaman Sea to the east and the Bay of Bengal to the west. The island chain, located about 1200 km southeast of mainland India, stretches over 700 km and covers an area of 8249 km². The region experiences a tropical climate with high humidity (79–89 %) and temperatures ranging from 21–33 °C. Nearly 80 % of the land area is under forest cover, supporting rich biodiversity. The undulating terrain and climate are highly suitable for plantation crops. Notably, the islands harbour diverse coconut accessions exhibiting unique traits such as beaked and horned fruits, persistent petioles, fused leaflets (plicata), soft endosperm (macapuno) and unbranched inflorescences (spicata) (1). Tall genotypes of Andaman are widely cultivated and valued for their large, attractive fruits and robust growth habit. The palms exhibit sturdy stems with a prominent basal bole and dark green leaves with intermediate drooping. Fruits are generally large and oblong, with a husk thickness of 2–3 cm; dehusked nuts are round to oval with a thick shell (> 4 mm) and kernel thickness (> 1.3 cm). Considerable variation in fruit colour exists within the population, ranging from dark green to light green or brown, though green shades predominate. These palms are

drought-hardy, tolerant to strong winds and comparatively late bearing. Copra content ranges from 180–250 g per nut, with about 65 % oil recovery and the annual yield varies from 50–150 nuts per palm depending on management. The cultivar also shows field tolerance to nematodes. Nuts are primarily used for copra and value-added products such as desiccated coconut and virgin coconut oil. The retention of varietal traits depends on genetic purity, which has been found to be positively associated with yield. Studies on genetic uniformity, whether based on morphological traits or molecular markers, are crucial for identifying genetically true-to-type mother palms for use in future breeding programmes.

Morphological characterisation is performed on a representative population of an accession using a standardised set of species-specific descriptors (2). Some traits are largely governed by genetics and remain stable across environments; these are referred to as constant characters and are highly heritable (3). In contrast, other traits are more susceptible to environmental influence, with their phenotypic expression resulting from the interaction between genotype and environment. Consequently, morphological markers have inherent limitations. These constraints associated with phenotype-based markers have driven the development and use of molecular markers.

In recent years, the use of molecular markers for varietal identification and purity assessment has gained significant importance (4). DNA-based markers can complement and in some cases potentially replace, traditional morphological and protein-based methods. These molecular approaches have proven effective in detecting genomic variations among cultivars and are increasingly utilised in cultivar identification as well as in the construction of genetic maps (5). Molecular markers such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), simple sequence repeats (SSR), inter-simple sequence repeats (ISSR) and single nucleotide polymorphisms (SNPs) have been widely employed in studies of genetic diversity and genetic mapping (6–11). For genetic uniformity assessment, amplified fragment length polymorphisms (AFLP) and SSR markers are most frequently used (12). SSR markers are particularly advantageous due to their high level of polymorphism and their derivation from specific chromosomal locations. The research focused on assessing the level of homogeneity and genetic consistency among 35 tall coconut palms belong to Andaman Tall population using molecular and morphological methods, with the objective of selecting suitable mother palms for use in crop improvement and breeding initiatives.

Materials and Methods

Plant material

In the present investigation, a total of thirty-five Andaman Tall coconut genotypes were used. Seed nuts were collected from identified high-yielding mother palms of tall genotypes located at Khurmadera, South Andaman (11°49'52.2" N, 92°39'31.1" E) (Fig.1) and seedlings were raised at World Coconut Germplasm Centre, Sipphihat Farm, ICAR–Central Island Agricultural Research Institute (CIARI), Andaman. A total of 330 palms were characterised morphologically as per the coconut descriptors (13) and 35 uniform coconut palms were selected for further evaluation. These 35 selected coconut palms were used for molecular characterisation in the present study.

DNA extraction from leaves

Genomic DNA was extracted from spindle leaves following a standardised protocol (14). Approximately 1 g of spindle leaf tissue was chopped into small pieces, frozen in a pre-chilled mortar using liquid nitrogen and ground into a fine powder. About 0.25 g of polyvinylpyrrolidone (PVPP, MW 400000) was added to the powdered tissue, mixed thoroughly and transferred to a centrifuge

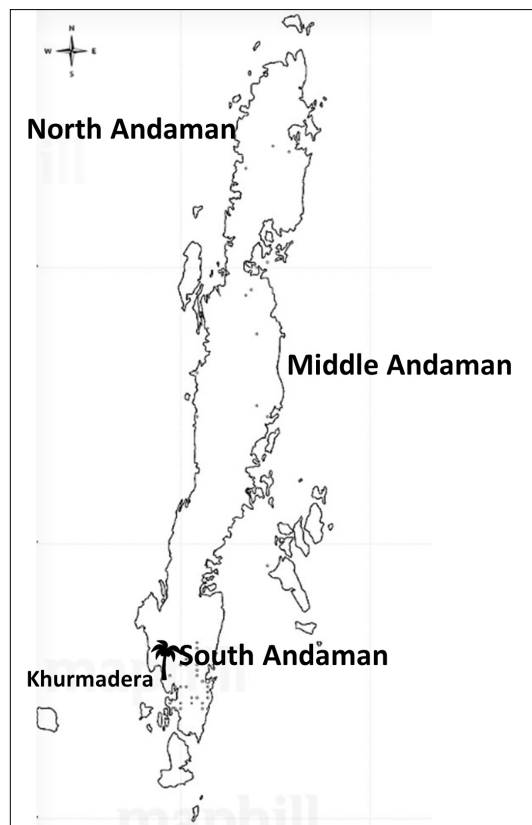


Fig. 1. Location of the mother palm of Andaman Tall genotypes used in the study.

tube containing 4.5 mL of preheated extraction buffer. To this, 0.5 mL of 10 % SDS and 50 μ L of β -mercaptoethanol were added and the mixture was incubated at 65 °C for 1 hr with intermittent mixing. After incubation, 3 mL of a 24:1 (v/v) chloroform:isoamyl alcohol mixture was added and gently inverted for 15 min before centrifugation at 12000 rpm for 10 min at 4 °C. The aqueous phase was carefully transferred to a new tube and two-thirds of its volume of ice-cold ethanol was added to precipitate DNA. The DNA was collected in a 1.5 mL microtube after incubation at 4 °C for 30 min. The DNA pellet was washed three times with 70 % ethanol, air-dried and finally dissolved in 0.5 mL of TE buffer. The quality and integrity of the extracted genomic DNA were assessed by running it on 0.8 % agarose gel stained with ethidium bromide and visualised using a gel documentation system (Bio-Rad, USA).

DNA amplification and SSR marker genotyping

A total of fourteen SSR primer pairs were employed in the study. The primer sequences and associated details are presented in Table 1. Primers showing polymorphism were selected for further analyses.

Table 1. Primer sequences, annealing temperatures and allele size ranges of SSR markers used in the study

Sl. No.	Primers	Sequence (5'–3')		Annealing temperature (°C)	Allele size (bp)
		Forward	Reverse		
1	CnCir A3	AATCTAAATCTACGAAAGCA	AATAATGTGAAAAAGCAAAG	52	120–180
2	CnCir A9	AATGTTTGTGCTTTGTGCGTGTGT	TCCTTATTTTCTTCCCTTCCTCA	59	131–139
3	CnCir B6	GAGTGTGTGAGCCAGCAT	ATTGTTACAGTCTTCCA	58	218–232
4	CnCir B12	GCTCTTCAGTCTTTCTCAA	CTGTATGCCAATTTTCTA	56	150–220
5	CnCir C3	AGAAAGCTGAGAGGGAGATT	GTGGGGCATGAAAAGTAAC	58	180–220
6	CnCir C7	ATAGCATATGGTTTTCCT	TGCTCCAGCGTTCATCTA	58	100–160
7	CnCir C12	ATACCACAGGCTAACAT	AACCAGAGACATTGAA	54	140–200
8	CnCir E2	TCGCTGATGAATGCTTGCT	GGGGCTGAGGGATAAACC	55	190–285
9	CnCir E10	TGGGTTCATTCTTCTCTCATC	GCTCTTTAGGGTTCGTTTCTTAG	57	218–229
10	CnCir E12	TCACGCAAAAGATAAAACC	ATGGAGATGGAAGAAAGG	58	162–174
11	CnCir F2	GGTCTCTCTCCCTCTTATCTAAC	CGACGACCCAAACTGAAC	58	206–262
12	CnCir G11	AATATCTCCAAAATCATCGAAAG	TCATCCACACCTCCTCT	58	196–208
13	CnCir H4	TTAGATCTCCTCCCAAAG	ATCGAAAGAACAGTCACG	54	109–141
14	CnCir H7	GAGATGGCATAACACCTA	TGCTGAAGCAAAAGAGTA	58	130–166

PCR reactions were carried out in a 20 µL volume, comprising 35 ng of genomic DNA, 0.2 µM each of forward and reverse primers (Sigma), 0.1 µL of 10 mM dNTPs (MBI Fermentas), 2 µL of 10× PCR buffer (10 mM Tris-HCl, pH 9.0; 50 mM KCl; 1.5 mM MgCl₂; 0.01 % gelatin) and 0.5 µL of Taq DNA polymerase (3 U/µL; Genei Laboratories Pvt. Ltd., India). The reaction mixtures were briefly centrifuged to ensure proper mixing and then aliquoted into 20 µL thin-walled clear PCR tubes. PCR was performed under the following conditions: an initial denaturation at 94 °C for 2 min, followed by 39 cycles of 94 °C for 1 min, annealing at primer-specific temperatures for 1 min and 72 °C for 1 min 30 sec, with a final extension at 72 °C for 10 min. Amplified products were analysed using the DNA 500 kit on a MultiNA microchip electrophoresis system (MCE-202, Shimadzu). The MultiNA software (MultiNA Control Software and Data Analysis Software MultiNA Viewer; Shimadzu) was used for automated peak size detection in the electropherograms.

Data analysis

Alleles were scored individually by comparison with a 25 bp molecular ladder. For the 35 microsatellite loci, the observed number of alleles, effective number of alleles and Shannon's information index were calculated using GDA software (Genetic Data Analysis) (15). Cluster analysis was performed on the similarity matrix using the unweighted pair group method with arithmetic averages (UPGMA) and the resulting phenogram was constructed. Additionally, principal coordinate analysis (PCoA) based on pairwise genetic distances among coconut germplasm was carried out. F-statistics for the 35 loci were estimated using GenAEx version 6.2 (16). For the morphological traits, mean values were calculated and variability parameters, including standard deviation (SD) and coefficient of variation (CV), were estimated using Microsoft Excel. These statistical measures were used to assess variation and to compare genotypic performance.

Results and Discussion

Molecular markers are considered as powerful technique for examining and classifying various genetic resources (17). In the present study, 14 SSR primer pairs were used to detect polymorphism and determine the extent of genetic diversity of 35 palms of tall accessions from the Andaman Islands.

A total of 525 alleles were identified across all loci, with the number of alleles per locus ranging from 2.0–4.3 and an average of 2.7 alleles per locus (Table 2) (Fig. 2). At each locus, the number of alleles observed was high, which indicates that the SSRs have the capacity to detect high polymorphism. Earlier studies also correspond well with these results (18–23).

Shannon's information index is a valuable tool for quantifying the polymorphic nature of the loci (24). The mean Shannon's information index of 0.77 in the Andaman populations indicates that there is moderate genetic diversity in the population.

F_{ST} represents the fraction of total genetic variance that is present within a subpopulation relative to the overall genetic variance, with values ranging from 0 to 1. In the present study, moderate F_{ST} value of 0.1 indicated that the populations are sharing their genetic material through high levels of breeding (Table 3). An F_{ST} value of zero suggests no differentiation in allele frequencies among the subpopulations.

F_{IS}, the inbreeding coefficient, represents the proportion of genetic variance within a subpopulation that is attributable to individual deviation. The Andaman population recorded the lowest F_{IS} value, indicating that the set of subpopulations, as a whole, has an excess of heterozygotes (25). In a population with moderate genetic diversity, F_{IS} values are generally expected to be close to zero (-0.1 to +0.1), indicating near-random mating. However, in cross-pollinated species such as coconut, particularly tall types, negative F_{IS} values are commonly observed due to the predominance of outcrossing and protandrous flowering behaviour. The negative mean F_{IS} observed in the present study therefore reflects excess heterozygosity arising from natural cross-pollination and genetic admixture within the population.

The average observed heterozygosity (0.635) was greater than the expected heterozygosity across the population. The observed heterozygosity in the present study is comparable to values reported in coconut using SSR markers, which range from 0.42 to 0.66, indicating that the Andaman Tall accessions fall within the higher range of genetic variability (26–30). However, compared to earlier studies that reported higher allelic richness and polymorphic information content (PIC) values (21, 22), the present population shows relatively moderate allelic diversity, possibly due

Table 3. F-statistics for the 10 microsatellite loci

Locus	F _{IS}	F _{IT}	F _{ST}	PIC
CnCirE10	0.175	0.234	0.072	0.379
CnCirE12	-0.781	-0.760	0.012	0.393
CnCirE2	-0.478	-0.203	0.186	0.333
CnCirH4	0.911	0.939	0.308	0.397
CnCirG11	-1.000	-1.000	0.001	0.255
CnCirB6	-0.515	-0.443	0.048	0.379
CnCirC3	-0.343	-0.209	0.100	0.285
CnCirF2	-0.159	0.051	0.181	0.335
CnCirA9	-0.070	0.000	0.066	0.352
CnCirH7	-0.282	-0.257	0.020	0.463
Mean	-0.254	-0.165	0.100	0.357
SE	0.168	0.170	0.031	

Table 2. Diversity statistics for the 10 SSR markers

Locus	No. of different alleles (N _a)	No. of effective alleles (N _e)	Shannon's information index (I)	uHe
CnCirE10	2.00	1.860	0.648	0.509
CnCirE12	2.667	2.301	0.878	0.630
CnCirE2	4.333	3.318	1.222	0.738
CnCirH4	2.00	1.595	0.476	0.324
CnCirG11	2.00	2.00	0.693	0.567
CnCirB6	3.333	2.115	0.844	0.565
CnCirC3	3.667	2.848	1.152	0.731
CnCirF2	2.667	1.629	0.592	0.428
CnCirA9	2.333	1.896	0.702	0.509
CnCirH7	2.00	1.483	0.496	0.366
Mean	2.700	2.105	0.770	0.537
SE	0.296	0.208	0.095	0.056

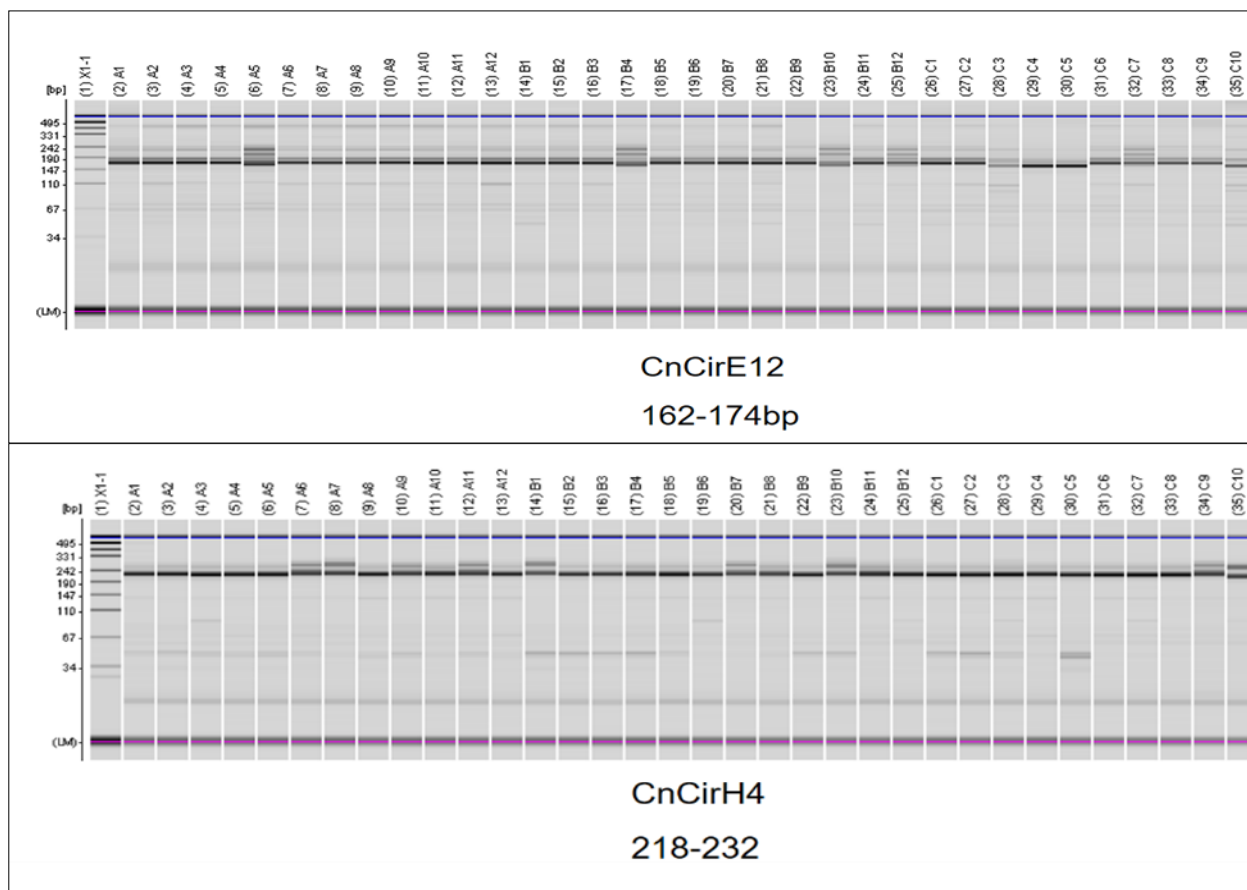


Fig. 2. Gel images of marker locus CnCirE12 and CnCirH4.

to its geographic isolation (Table 4). Additionally, the higher mean observed heterozygosity value is typical of plant species with an outcrossing mating system (31). In most accessions, the observed heterozygosity exceeded the expected heterozygosity, suggesting an effect of breaking isolation. This could be due to the greater allelic polymorphism present in these populations. The involvement of farmers in the sharing and preservation of coconut genetic resources may also be one of the reasons (19). Similarly, genetic diversity and population structure in *Dalbergia odorifera* were evaluated in a previous study (32). A total of 77 alleles were detected across 19 microsatellite markers in the database, with PIC values ranging from 0.03–0.66. The observed heterozygosity was 0.33, while the expected heterozygosity and Shannon's information index were 0.38 and 0.65 respectively. Among the groups, expected heterozygosity varied from 0.30 (RP3) to 0.38 (RP4).

Similar results were reported using 30 microsatellite markers, where a total of 100 alleles were identified, with an average of 3.37 alleles per locus (33). The inbreeding coefficients (FIS) were estimated for the three morphological groups: Tall-like (TL), Dwarf-

like (DL) and Mixed group (M)—based on mean gene diversity and heterozygosity values. The DL group showed the highest FIS value, indicating a high level of homozygosity within the DL population, in line with the typical situation in dwarf coconuts. The TL group had the greatest FIS and the M group had a value that was nearly as high as TL, indicating relatively high levels of heterozygosity in these morphological categories.

Earlier research documented a mean of 5.32 alleles per locus with an observed heterozygosity of 0.443 (21) and 13.7 alleles per locus with observed heterozygosity of 0.46, expected heterozygosity of 0.53, PIC value of 0.85 and FST of 0.17 (22), indicating that SSR markers are capable of detecting a high level of polymorphism.

The fixation indices exhibited notable variation across loci, highlighting differences in locus-specific genetic behaviour among the SSR markers. The fixation index (*f*) corresponds to Wright's inbreeding coefficient (FIS), with both measures showing consistent trends. Loci such as CnCirE12, CnCirE2, CnCirG11 and CnCirB6 displayed negative FIS values, indicating an excess of heterozygotes, whereas CnCirH4 showed a high positive FIS (0.911), reflecting

Table 4. Observed heterozygosity (H_o), expected heterozygosity (H_e) and fixation index (*f*) for the tall coconut accessions of Andaman using SSR primers

Locus	Observed heterozygosity (H_o)	Expected heterozygosity (H_e)	Fixation index (<i>f</i>)
CnCirE10	0.376	0.457	0.133
CnCirE12	1.0	0.561	-0.792
CnCirE2	0.984	0.666	-0.536
CnCirH4	0.027	0.314	0.916
CnCirG11	1.0	0.5	-1.0
CnCirB6	0.773	0.511	-0.494
CnCirC3	0.869	0.647	-0.346
CnCirF2	0.424	0.366	0.040
CnCirA9	0.488	0.456	-0.056
CnCirH7	0.408	0.319	-0.262
Mean	0.635	0.480	-0.292
SE	0.118	0.049	0.162

heterozygote deficiency, possibly due to factors such as null alleles, selection, or population sub-structuring (34, 35).

The F_{ST} values also demonstrated locus-wise variation, ranging from negligible levels (e.g., CnCirG11: 0.001; CnCirE12: 0.012) to comparatively higher values (e.g., CnCirH4: 0.308; CnCirF2: 0.181), indicating differential contributions of loci to genetic structuring. While some loci appear relatively conserved, others contribute more prominently to genetic differentiation within the population. The mean F_{ST} value (0.100) reflects a moderate level of differentiation, consistent with patterns reported in perennial, cross-pollinated species (36). Comparable trends have also been documented in coconut using SSR markers (26, 27).

UPGMA clustering was used to create a dendrogram. The Andaman Tall populations were divided into three main groups. Cluster I was made up of twelve Andaman Tall palms, including Andaman 1, Andaman 9, Andaman 10, Andaman 33, Andaman 7, Andaman 11, Andaman 19, Andaman 22, Andaman 5, Andaman 21, Andaman 14 and Andaman 24, indicating a subset of genotypes with relatively closer genetic affinity, suggesting a shared genetic background or possible common ancestry. Cluster II comprised 21 populations, including Andaman 2, Andaman 6, Andaman 28, Andaman 32, Andaman 27, Andaman 34, Andaman 29, Andaman 30, Andaman 31, Andaman 3, Andaman 15, Andaman 25, Andaman 4, Andaman 17, Andaman 8, Andaman 12, Andaman 13, Andaman 20, Andaman 35, Andaman 16 and Andaman 18. Cluster II, comprising the majority of the accessions, exhibited comparatively broader dispersion within the cluster, indicating moderate genetic variability among these palms. Andaman 23 and Andaman 26 grouped together to form Cluster III (Fig. 3). This cluster was distinctly separated, suggesting a relatively higher degree of divergence from the rest of the population.

The occurrence of both tightly grouped and dispersed genotypes within clusters indicates that, although the palms were selected for morphological uniformity, such traits may not fully capture the underlying genetic variation. This is consistent with the nature of coconut as a highly cross-pollinated species, in which gene flow and recombination contribute to genetic heterogeneity even within phenotypically similar populations.

The presence of polymorphism detected by SSR markers further supports this observation, reflecting moderate levels of genetic diversity among the selected palms. The clustering pattern may also be influenced by selection pressure for economically important traits such as fruit size, shape, husk thickness and copra content, which could lead to phenotypic convergence despite underlying genetic differences. This indicates a recent process of population differentiation, suggesting that only a few generations have elapsed since divergence from their ancestral populations (21).

Morphological characters

The morphological traits of the tall coconut genotypes from Andaman are presented in Table 5. Analysis of various morphological parameters in this study indicates that Andaman Tall coconuts exhibit a robust growth habit. The length of the inflorescence and the number of female flowers are important factors influencing both the yield and quality of the fruits (33). Careful measurement and assessment of these inflorescence traits can serve as valuable germplasm resources and contribute to the development of high-yielding and superior-quality coconut varieties.

Andaman Tall palms are vigorous, with a height of about 759.3 cm and a distinct bole. The length of the leaflet-bearing portion is around 576.3 cm, with a strong petiole. Each leaf has 398.2 leaflets, which are 230.2 cm long and 6.0 cm wide. It is predominantly cross-pollinated, as there is a distinct gap between the male and female phases. The fruit weight is around 720 g. The nut has a thick kernel and a thin shell. The copra content is 160.4 g per nut, with a nut yield of 98.8 per palm per year. It produces 2.7 tonnes of copra per hectare. Variability measures, including SD and CV, for the morphological parameters of Andaman Tall coconuts fell within the accepted range for stable coconut varieties.

Various fruit component characters also showed robustness. This was evident in traits such as fruit size and weight, kernel thickness, shell weight and copra content. Husk thickness was reflected in the ratio of husk to whole fruit weight. The values of SD and CV for the nut characteristics were within the acceptable range for a stable variety.

Table 5. Morphological characterisation of the Andaman Tall coconut

Sl. No.	Parameters	Mean	SD	CV (%)
1.	Crown shape	Circular		
2.	Presence of bole	Present		
3.	Plant height (cm)	759.3	167.37	22.04
4.	Girth of trunk (cm) at base	144.5	6.85	4.74
5.	Total number of leaves	29.2	3.53	12.09
6.	Length of petiole (cm)	141.2	10.58	7.49
7.	Length of leaflet bearing portion (cm)	576.3	35.83	6.22
8.	Number of leaflets	398.2	7.74	1.94
9.	Length of leaflet (cm)	230.2	15.39	6.69
10.	Breadth of leaflet (cm)	6.0	1.08	18.00
11.	Number of leaf scars in 1m length	25.0	6.13	24.52
12.	Length of single internodes (cm)	5.9	1.2	20.34
13.	Length of inflorescence (cm)	131.7	12.65	9.61
14.	Length of spikelet bearing portion (cm)	45.8	4.00	8.73
15.	Length of stalk (m)	53.0	10.05	18.96
16.	Length of spikelet (cm)	39.5	6.26	15.85
17.	Number of spikelets in the inflorescence	32.5	4.41	13.57
18.	Number of female flowers /inflorescence	29.2	6.06	20.75
19.	Number of bunches on the crown	12.8	1.05	8.20
20.	Length of fruit (cm)	29.3	2.48	8.46
21.	Breadth of fruit (cm)	15.6	1.17	7.50
22.	Weight of fruit (g)	720	361.88	50.26
23.	Thickness of husk (cm)	3.0	0.13	4.33
24.	Thickness of kernel (cm)	1.3	0.08	6.15
25.	Weight of copra (g)	160.4	9.06	5.65

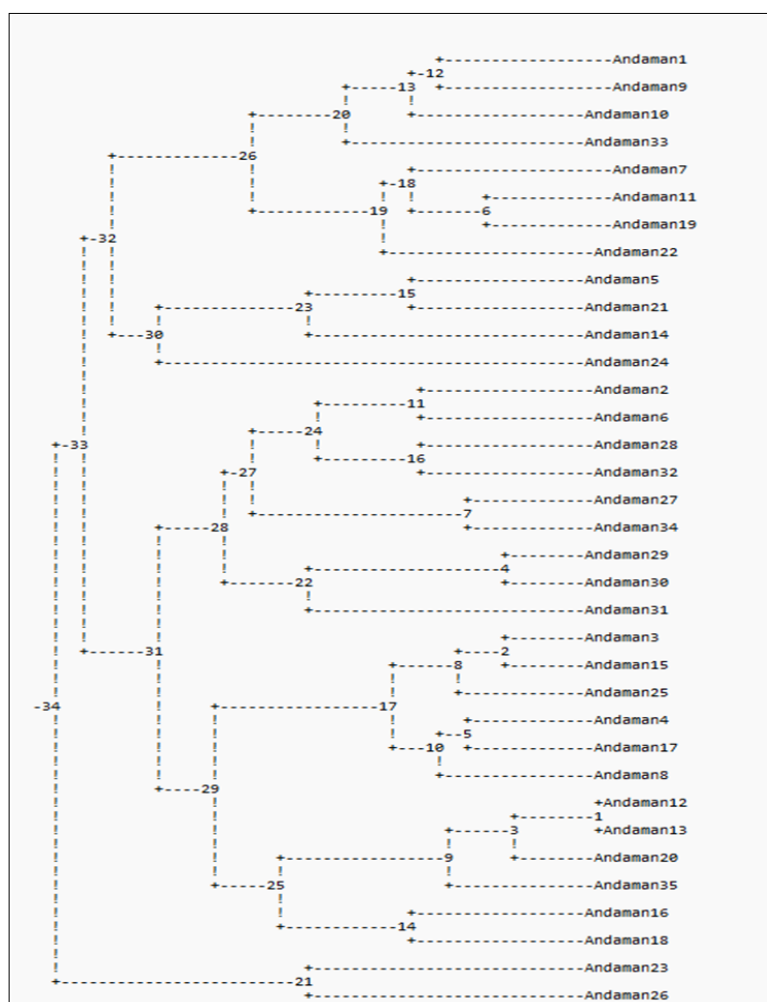


Fig. 3. Dendrogram based on genetic similarities discriminated all the coconut genotypes.

Conclusion

The morphometric and molecular investigation of 35 Andaman Tall coconut genotypes using 14 SSR markers revealed a relatively consistent genetic background with moderate levels of genetic diversity, as evidenced by monomorphic banding with 10 primers alongside polymorphism at other loci. Cluster analysis grouped the genotypes into three major clusters, reflecting genetic structuring within the population rather than complete uniformity. These findings highlight the importance of selecting seed nuts from phenotypically consistent mother palms across seasons, preferably maintained under isolated or controlled pollination conditions, to ensure greater uniformity in the progeny.

The SSR profiles demonstrate their utility for varietal identification and for supporting the selection of genetically consistent mother palms. Therefore, integrating SSR-based screening into selection protocols can improve the genetic fidelity and stability of coconut planting material. Overall, the combination of morphometric evaluation and molecular characterisation indicates that the Andaman Tall population possesses relative stability with detectable genetic variation, making it a valuable resource for breeding and improvement programmes.

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Authors' contributions

MKR, RS, JBA and IJS designed the research. JBA and VD performed the experimental work in the field. RS and MKR performed the laboratory analysis. MKR performed the statistical analysis. RS and JBA prepared the manuscript. RS, MKR, JBA and IJS reviewed the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

1. Arunachalam V, Jerard BA, Elangovan M, Ratnambal MJ, Dhanapal R, Rizal S, et al. Unexploited diversity in coconut palm (*Cocos nucifera* L.). *Plant Genet Resour Newsl.* 2001;127:39–43.
2. Benjamin P, Cesar O, Rigoberto H, Alba M, Daniel D, Mariano M, et al. Module 4: Germplasm conservation. 2008.
3. Deborah A, Karamura D. Numerical taxonomic studies of the East African highland bananas in Uganda. PhD [thesis]. Reading (UK): University of Reading; 1998.
4. Zhang J, Jiang Y, Wang Y, Guo Y, Long H, Deng G, et al. Molecular markers and cytogenetics to characterize a wheat-*Dasypyrum villosum* 3V(3D) substitution line conferring resistance to stripe rust. *PLoS One.* 2018;13(8):e0202033. <https://doi.org/10.1371/journal.pone.0202033>

5. Lai K, Lorenc MT, Lee HC, Berkman PJ, Bayer PE, Visendi P, et al. Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. *Plant Biotechnol J*. 2015;13(1):97–104. <https://doi.org/10.1111/pbi.12240>
6. Tanksley SD, Young ND, Paterson AH, Bonierbale MW. RFLP mapping in plant breeding: new tools for an old science. *Nat Biotechnol*. 1989;7:257–64. <https://doi.org/10.1038/nbt0389-257>
7. Lynch M, Milligan BG. Analysis of population genetic structure with RAPD markers. *Mol Ecol*. 1994;3:91–9. <https://doi.org/10.1111/j.1365-294X.1994.tb00109.x>
8. Akkaya MS, Bhagwat AA, Cregan PB. Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics*. 1992;132:1131–9. <https://doi.org/10.1093/genetics/132.4.1131>
9. Reddy MP, Sarla N, Siddiq EA. Inter simple sequence repeat (ISSR) polymorphism and its application in plant breeding. *Euphytica*. 2002;128:9–17. <https://doi.org/10.1023/A:1020691618797>
10. Jorde LB, Watkins WS, Bamshad MJ, Dixon ME, Ricker CE, Seielstad MT, et al. The distribution of human genetic diversity: a comparison of mitochondrial, autosomal and Y-chromosome data. *Am J Hum Genet*. 2000;66(3):979–88. <https://doi.org/10.1086/302825>
11. Goldstein JA, Blaisdell JA, Limdi NA. A potentially deleterious new CYP2C9 polymorphism identified in an African American patient with major hemorrhage on warfarin therapy. *Blood Cells Mol Dis*. 2009;42(2):155–8. <https://doi.org/10.1016/j.bcmd.2008.10.011>
12. Jamali SH, Cockram J, Hickey LT. Insights into deployment of DNA markers in plant variety protection and registration. *Theor Appl Genet*. 2019;132:1911–29. <https://doi.org/10.1007/s00122-019-03348-7>
13. Ratnambal MJ, Nair MK, Muraliedharan K, Kumaran PM, Bhaskara Rao EVV, Pillai RV. Coconut descriptors. Kasaragod: CPCRI; 1995.
14. Rajesh MK, Jerard BA, Preethi P, Thomas RJ, Fayas TP, Rachana KE, et al. Development of a RAPD-derived SCAR marker associated with tall-type palm trait in coconut. *Sci Hortic*. 2013;150:312–6. <https://doi.org/10.1016/j.scienta.2012.11.023>
15. Lewis PO, Zaykin D. Genetic Data Analysis (GDA): computer program for the analysis of allelic data. Version 1.1 (d16c). Storrs (CT): University of Connecticut; 2002.
16. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 3rd ed. New Delhi: ICAR; 1969.
17. Zavinton F, Adoukonou-Sagbadja H, Keilwagen J, Lehnert H, Ordon F, Perovic D. Genetic diversity and population structure in Beninese pigeon pea (*Cajanus cajan*) landraces revealed by SSR and genome-wide SNP markers. *Genet Resour Crop Evol*. 2020;67(1):191–208. <https://doi.org/10.1007/s10722-019-00864-9>
18. Teulat B, Aldam C, Trehin R, Lebrun P, Barker JHA, Arnold GM, et al. Analysis of genetic diversity in coconut (*Cocos nucifera* L.) populations using SSR and AFLP markers. *Theor Appl Genet*. 2000;100(5):764–71. <https://doi.org/10.1007/s001220051350>
19. Perera L, Russell JR, Provan J, Powell W. Levels and distribution of genetic diversity of coconut (*Cocos nucifera* L. var. typica) from Sri Lanka assessed by microsatellite markers. *Euphytica*. 2001;122(2):381–9. <https://doi.org/10.1023/A:1012987224319>
20. Rajesh MK, Nagarajan P, Jerard BA, Arunachalam V, Dhanapal R. Microsatellite variability of coconut genotypes from Andaman and Nicobar Islands. *Curr Sci*. 2008;94:12.
21. Ribeiro FE, Baudouin L, Lebrun P, Chaves LJ, Brondani C, Zucchi MI, et al. Population structure of Brazilian tall coconut (*Cocos nucifera* L.) by microsatellite markers. *Genet Mol Biol*. 2010;33(4):696–702. <https://doi.org/10.1590/S1415-47572010005000077>
22. Geethanjali S, Rukmani JA, Rajakumar D, Kadirvel P, Viswanathan PL. Genetic diversity, population structure and association analysis in coconut (*Cocos nucifera* L.) using SSR markers. *Plant Genet Resour*. 2018;16(2):156–68. <https://doi.org/10.1017/S1479262117000119>
23. Preethi P, Rahman S, Naganeeswaran S, Sabana AA, Gangaraj KP, Jerard BA, et al. Development of EST-SSR markers for genetic diversity analysis in coconut. *Mol Biol Rep*. 2020;47(12):9385–97. <https://doi.org/10.1007/s11033-020-05981-8>
24. Loiola CM, Azevedo AON, Diniz LE, Aragao WM, Azevedo CDDO, Santos PHA, et al. Genetic relationships among tall coconut palm accessions of ICG-LAC using microsatellite markers. *PLoS One*. 2016;11(3):e0151309. <https://doi.org/10.1371/journal.pone.0151309>
25. Martinez RT, Baudouin L, Berger A, Dollet M. Characterization of genetic diversity in tall coconut of the Dominican Republic using microsatellite markers. *Tree Genet Genomes*. 2010;6:73–81. <https://doi.org/10.1007/s11295-009-0229-6>
26. Rivera R, Edwards KJ, Barker JHA, Arnold GM, Ayad G, Hodgkin T, et al. Isolation and characterization of polymorphic microsatellites in *Cocos nucifera* L. *Genome*. 1999;42:668–75. <https://doi.org/10.1139/g98-170>
27. Perera L, Russell JR, Provan J, Powell W. Microsatellite DNA markers for evaluating genetic diversity of coconut. *Genome*. 2000;43(1):15–21. <https://doi.org/10.1139/g99-079>
28. Meerow AW, Wisser RJ, Brown SJ, Kuhn DN, Schnell RJ, Broschat TK. Analysis of genetic diversity and population structure within Florida coconut germplasm using microsatellite markers. *Theor Appl Genet*. 2003;106(4):715–26. <https://doi.org/10.1007/s00122-002-1121-z>
29. Devakumar K, Jayadev K, Rajesh MK, Chandrasekhar A, Manimekalai R, Kumaran PM, et al. Assessment of genetic diversity of Indian coconut accessions using microsatellite markers. *Plant Genet Resour Newsl*. 2006;145:38–45.
30. Hamrick JL, Godt MJW. Allozyme diversity in plant species. In: Brown AHD, Clegg MT, Kahler AL, Weir BS, editors. *Plant population genetics, breeding and genetic resources*. Sunderland (MA): Sinauer Associates; 1989. p. 43–63.
31. Liu FM, Zhang NN, Liu XJ, Yang ZJ, Jia HY, Xu DP. Genetic diversity and population structure of *Dalbergia odorifera* using microsatellite markers. *Genes*. 2019;10(4):281. <https://doi.org/10.3390/genes10040281>
32. Perera KC, Chandrika, Perera KLN, Dasanayaka N. Genetic diversity of Sri Lanka yellow dwarf coconut as revealed by microsatellite markers. *Trop Agric Res*. 2013;26(1):131. <https://doi.org/10.4038/tar.v26i1.8078>
33. Feng ML, Li J, Tang LX. Correlation analysis between climatic factors and flowering and pollination characteristics of aromatic coconut. *Southwest China J Agric Sci*. 2015;28(4):1780–3.
34. Wright S. The interpretation of population structure by F-statistics with special regard to systems of mating. *Evolution*. 1965;19:395–420. <https://doi.org/10.1111/j.1558-5646.1965.tb01731.x>
35. Weir BS, Cockerham CC. Estimating F-statistics for the analysis of population structure. *Evolution*. 1984;38:1358–70. <https://doi.org/10.1111/j.1558-5646.1984.tb05657.x>
36. Hartl DL, Clark AG. Principles of population genetics. 3rd ed. Sunderland (MA): Sinauer Associates; 1997.

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