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DECIPHERING MORPHOMETRIC RELATIONSHIPS OF ANACARDIACEAE (R. BR.) LINDL. IN BANGLADESH

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Abstract

The present study explored morphometric relationships among 24 species belonging to 14 genera of the family Anacardiaceae (R. Br.) Lindl. for the first time in Bangladesh, using a numerical systematic approach. A total of 33 vegetative and reproductive characters were analyzed through cluster analysis (CA) and principal component analysis (PCA). The UPGMA dendrogram revealed two major clades, comprising 18 and 6 species, respectively. In the first clade, *Mangifera indica* and *M. longipes* (tribe Anacardieae) exhibited the highest similarity, while in the second clade, the highest affinity was found between *Spondias dulcis* and *S. pinnata* (tribe Spondiadeae). PCA explained 85.70% cumulative variance across the first six principal components, with scatter and projection plots aligning with the cluster analysis results. These findings provide insights into the taxonomic relationships within Anacardiaceae in Bangladesh, aiding conservation strategies, particularly for threatened and medicinally important species, and serving as a foundation for future molecular phylogenetic endeavor.

Introduction

Anacardiaceae (R.Br.) Lindl. comprises approximately 70 genera and about 985 species distributed worldwide, representing a significant component of the tropical flora (Ariyarathne *et al.* 2020). These species are primarily found in tropical, subtropical, and temperate regions, with the Malaysian region recognized as the center of diversity (Ariyarathne *et al.* 2020, Mitchell *et al.* 2022). In Bangladesh, Anacardiaceae is represented by 24 species across 14 genera. The family is characterized by a diverse range of morphological traits, predominantly consisting of woody plants, including trees, shrubs, and lianas. Leaves are typically alternate, pinnate, or occasionally simple, often containing resinous ducts. Inflorescences are generally terminal or axillary, occurring as panicles, racemes, or cymes, with small, often unisexual, actinomorphic flowers. Flowers possess a five-parted perianth, with distinct or fused sepals and petals, and a variable number of stamens. Fruits are typically fleshy or fibrous, usually containing a single seed, and may feature resin canals (Ahmed *et al.* 2009, Pell *et al*. 2010). Anacardiaceae includes many economically important species in Bangladesh such as *Anacardium occidentale* L. (cashew), *Mangifera indica* L. (mango), *Spondias pinnata* (L. f.) Kurz (hog plum) etc., which are vital for food production, timber, and medicinal applications (Al-Snafi *et al*. 2021, Swathi and Lakshman 2022, Guerra *et al*. 2025). However, lesser-known species, including *Drimycarpus racemosus* (Roxb.) Hook. f. *ex* Marchand and *Semecarpus subpanduriformis* Wall. *ex* Hook. f., are increasingly threatened by habitat loss and overexploitation (Ahmed *et al.* 2009).

Morphometrics, integrates taxonomy with mathematical principles to quantify morphological variations and infer evolutionary relationships (Sneath and Sokal 1973, Bookstein 1991, Vieira *et al.* 2014). By evaluating character states and identifying numerical gaps between taxa,

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this approach provides a robust framework for species delimitation and systematic studies (Otte and Endler 1989). By analyzing key vegetative and reproductive traits, morphometric assessments help in recognizing cryptic species, resolving taxonomic ambiguities, and identifying conservation priorities. Moreover, integrating morphometric data with molecular phylogenetics offers a comprehensive approach for biodiversity assessment, thereby guiding policymakers and conservationists in the sustainable management of Anacardiaceae species in Bangladesh (Ahmed and Rahman 2024).

Despite the ecological and economic importance of Anacardiaceae, morphometric studies on this family remain largely unexplored in Bangladesh. To date, no attempt has been made to delineate the morphometric relationships among Anacardiaceae members in Bangladesh. Therefore, the present study aims to conduct a comprehensive morphometric assessment of Anacardiaceae to uncover their phenotypic variations and systematic relationships.

Materials and Methods

A total of 24 species belonging to 14 genera were analyzed using a combination of quantitative and qualitative morphological traits. Morphological data were gathered from both fresh samples and herbarium specimens stored at the Dhaka University Salar Khan Herbarium (DUSH) and the Bangladesh National Herbarium (DACB), following standard techniques (Hyland 1972, Alexiades 1996). All taxa included in the morphometric analysis are presented in Table 1.

A total of 33 morphological characters were scored. The characters were encoded into a binary data matrix to facilitate numerical analysis. For species unavailable in fresh conditions, character states were inferred from relevant taxonomic literature (Ahmed *et al.* 2009, Uddin and Hassan 2018).

The dataset was compiled and formatted using NTedit (Version 1.2), and all analyses were performed using NTSYS-pc (Version 2.10e) (Rohlf 2012). A similarity matrix was constructed using the Simple Matching Coefficient. Cluster analysis was conducted using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) to identify phenetic relationships among species. The Sequential, Agglomerative, Hierarchical, and Nested Clustering (SAHN) module was used to generate a dendrogram illustrating species affinities. To explore patterns of morphological variation, Principal Component Analysis (PCA) was performed using the Ordination module and Eigen package (Ahmed and Rahman 2024).

Results and Discussion

The study revealed 33 characters from 24 species of the family Anacardiaceae including both vegetative and reproductive traits. All 24 species were represented by codes, as shown in Table 1, and their binary character states were presented in Table 2.

Cluster analysis (CA) revealed two major clades in the UPGMA dendrogram (Fig. 1). The major clade 1 comprised 18 species from 10 genera: *Anacardium, Mangifera, Semecarpus, Swintonia, Bouea, Buchanania, Drimycarpus, Holigarna, Gluta* and *Nothopegia*. The close affinity between *Anacardium* and *Mangifera* supports their strong genetic relatedness within the family, consistent with a recent chloroplast genome-based phylogenetic study, in which *Anacardium* was grouped with the *Mangifera* taxa keeping 100% bootstrap support (Mao *et al.* 2025). Similarly, all *Semecarpus* species formed a subclade that reinforces their phylogenetic proximity. This congruence between morphometric analysis and phylogenetic studies further validates the reliability of numerical taxonomy in resolving systematic relationships within the family Anacardiaceae (Simo-Droissart *et al.* 2013).

Table 1. List of species of Anacardiaceae with their codes and vouchers used in the present investigation.

Sl. No.	Species	Code	Vouchers
1	*Anacardium occidentale* L.	AnOc	Chattogram: Pamua Range Office, Lohagara thana, 20 Apr 1996, Khan *et al.* K.9248 (DACB); Cumilla: Kotbari, 29 Nov 2023, Hasan *et al.* MSH-41, (DUSH).
2	*Bouea oppositifolia* (Roxb.) Meisn	BoOp	Cox's Bazar: Signal Hill, 24.12.1944, Sinclair 3866 (DACB); Mymensingh: Hasan, MSH-32, (DUSH).
3	*Buchanania lancifolia* Roxb.	BuLc	Rangamati: Islam KKI-2110 (DACB); Cox's Bazar: Ukhiya, 21 Mar 1989, Alam *et al.*, 6308 (BFRIH).
4	*Buchanania lanzan* Spreng.	BuLz	Inferred from literature.
5	*Buchanania sessifolia* Blume	BuSe	Rangamati: Kaptai, 08 Nov 2003, Uddin N-2023 (DACB).
6	*Drimycarpus racemosus* (Roxb.) Hook.f.	DrRa	Bandarban: Islam KKI-2977 (DACB); Rangamati: Sitapahar West, 26 Apr 1997, Huq *et al.* 10482 (DACB).
7	*Gluta elegans* (Wall.) Kurz	GuEl	Cox's Bazar: Chainda, 1 May 1970, Banik (BFRIH).
8	*Holigarna caustica* (Dennist.) Oken	HoCa	Habiganj: Adampur, 16 Apr 2000, Khan *et al.* K.10460 (DACB); Cox's Bazar: Bangabandhu Safari Park, 17 Apr 2017, Kabir *et al.* N-4513 (DACB).
9	*Holigarna kurzii* King.	HoKu	Cox's Bazar: Madhabpur Forest, 13 Apr 1997, Huq *et al.* 10727 (DACB).
10	*Lannea coromandelica* (Houtt.) Merr.	LaCo	Dhaka: Hasan, MSH-67, (DUSH); Tangail: Madhabpur Forest, 13 Apr 1997, Huq *et al.* 10454 (DACB).
11	*Mangifera indica* L.	MaIn	Chapai Nawabganj: Hasan, MSH-76, (DUSH); Chattogram: Chittagong University Campus, 29 Aug 2016, Tajul *et al.* TOK-0252 (DACB).
12	*Mangifera longipes* Griff.	MaLo	Khagrachhari: Kowser *et al.* KH-1781 (DACB); Cox's Bazar: Dulahazra Safari Park, Chokoria, 17 Apr 2004, Uddin N-2315 (DACB).
13	*Mangifera sylvatica* Roxb.	MaSy	Chattogram: Boroitoli, Baniarchara,Chokoria, 09 May 1994, Huq *et al.* H. 10379 (DACB); Boraitala, 22 May 1997, Mia 3795 (DACB).
14	*Nothopegia acuminata* J. Sinclair	NoAc	Bandarban: Poly Forest Range, Ruma, 23 Jan 2017, Hossain *et al.* IH-3486 (DACB).
15	*Pegia nitida* Colebr.	PeNi	Chattogram: Moniruzzaman *et al.* MAK-7769 (DACB); Bandarban: Rowanchari Forest Range, 19 Mar 2018, Islam *et al.* MSI7234 (DACB).
16	*Semecarpus anacardium* Linn. f.	SeAn	Tangail: Madhupur, 29 Jun 1969, Mansur 80 (DUSH); Hasan, MSH-33, (DUSH).
17	*Semecarpus nigroviridis* Thwaites	SeNi	Inferred from literature.
18	*Semecarpus prainii* King.	SePa	Rangamati: Kaptai, 23 Mar 2010, Uddin N-4172 (DACB).
19	*Semecarpus subpanduriformis* Wall. ex Hook.f.	SeSu	Inferred from literature.
20	*Spondias dulcis* Parkinson	SpDu	Khagrachhari: Miaschuri, Bigitola Range, Mohalchuri, 27 Sep 2016, Kowser *et al.* KH-728 (DACB); Dhaka: Hasan, MSH-03, (DUSH).
21	*Spondias pinnata* (L.) Kurz	SpPi	Dhaka: Ramna, Kalibari, 05 Mar 1964, Muhammad 103 (DUSH); Tangail: Madhupur, 30 Jun 1969, Moiz 249 (DUSH).
22	*Swintonia floribunda* Griff.	SwFl	Chattogram: Hazarikhil (west), 31 Oct 1987, Huq *et al.* H.8631 (DACB). Cox's Bazar: Natyan Pahar behind forest rest house, Teknaf thana, 12 Feb 1993, Khan *et al.* K.8975 (DACB).
23	*Toxicodendron khasianum* (Hook.f.) Kuntze	ToKa	Moulvibazar: Lawachara, Sreemangal, 11 May 2009, Uddin, N-3585 (DACB).
24	*Toxicodendron succedaneum* (L.) Kuntze	ToSu	Inferred from literature.

Table 2. Characters and encoded binary states used in the present investigation.

Sl.	Characters	Character states
1	Habit	Shrub (0), Tree (1).
2	Bark texture	Smooth (0), Rough, cracked or fissured (1).
3	Bark color	Light brown, brown or grayish brown (0), Others (1).
4	Leaf type	Simple (0), Compound (1).
5	Leaf arrangement	Spiral (0), Opposite or alternate (1).
6	Leaf habit	Deciduous (0), Evergreen or semi-evergreen (1).
7	Leaf structure	Unifoliate (0), Paripinnate or imparipinnate (1).
8	Leaf shape	Elliptic-oblong, oblong-lanceolate or elliptic lanceolate (0), Others (1).
9	Leaf size (cm)	Avg. length < 21 (0), Avg. length ≥ 21 (1).
10	Leaflets number	< 5 (0), ≥ 5 (1).
11	Petiole hairiness	Glabrous (0), Pubescent (1).
12	Petiole size (cm)	Avg. size < 4.0 (0), Avg. size ≥ 4.0 (1).
13	Inflorescence type	Terminal and axillary (0), Others (1).
14	Inflorescence hairiness	Glabrous (0), Pubescent (1).
15	Inflorescence size (cm)	Avg. size < 15.0 (0), Avg. size ≥ 15.0 (1).
16	Flower sex	Unisexual (0), Bisexual (1).
17	Flower state	Incomplete (0), Complete (1).
18	Flower merosity	Tetramerous (0), Pentamerous (1).
19	Flower hairiness	Glabrous (0), Pubescent (1).
20	Pedicel presence	Absent (0), Present (1).
21	Pedicel hairiness	Glabrous (0), Pubescent (1).
22	Calyx shape	Ovate (0), Others (1).
23	Calyx lobes	4 (0), 5 (1).
24	Calyx lobe size (cm)	Avg. size < 0.14 (0), Avg. size ≥ 0.14 (1).
25	Calyx hairiness	Glabrous (0), Pubescent (1).
26	Calyx persistence	Deciduous (0), Persistent (1).
27	Corolla lobes	4 (0), 5 (1).
28	Corolla shape	Elliptic or lanceolate (0), Others (1).
29	Petal size (cm)	Avg. length < 0.18 (0), Avg. length ≥ 0.18 (1).
30	Petal hairiness	Glabrous (0), Pubescent (1).
31	Stamens number	Avg. no. < 8 (0), Avg. no. 8 or ≥ 8 (1).
32	Stamens state	Free (0), Fused (1).
33	Stamen size (cm)	Avg. size < 0.19 (0), Avg. size ≥ 0.19 (1).

Buchanania (tribe Rhoideae) demonstrated a close relationship with *Bouea* (tribe Spondiadeae) within major clade 1 (Fig. 1), despite belonging to different tribes of the family Anacardiaceae. This unexpected clustering may be attributed to morphological convergence, where similar ecological pressures have led to shared phenotypic traits between these genera. Additionally, the retention of ancestral characteristics might have contributed to their grouping, as certain morphological traits can persist across evolutionary lineages despite phylogenetic divergence. Since morphometric analyses primarily rely on phenetic similarities, they may not always reflect phylogenetic relationships derived from molecular data. Environmental factors, such as habitat and climatic conditions, may also have influenced the observed morphological similarities (Simo-Droissart *et al*. 2016).

Table 3. Similarity matrix of 24 species of Anacardiaceae showing morphometric affinities.

Spp.	AnOc	BoOp	BuLc	BuLz	BuSe	DrRa	GuEl	HoCa	HoKu	LaCo	MaIn	MaLo	MaSy	NoAc	PeNi	SeAn	SeNi	SePa	SeSu	SpDu	SpPi	SwFl	ToKa	ToSu
AnOc	1																							
BoOp	0.67	1																						
BuLc	0.73	0.70	1																					
BuLz	0.76	0.67	0.79	1																				
BuSe	0.70	0.67	0.79	0.76	1																			
DrRa	0.72	0.70	0.70	0.61	0.61																			
GuEl	0.52	0.54	0.49	0.46	0.52	0.55	1																	
HoCa	0.54	0.58	0.52	0.55	0.67	0.64	0.55	1																
HoKu	0.64	0.61	0.67	0.64	0.69	0.79	0.58	0.85	1															
LaCo	0.39	0.42	0.49	0.46	0.52	0.42	0.46	0.37	0.46	1														
MaIn	0.82	0.54	0.67	0.64	0.64	0.67	0.58	0.49	0.58	0.52	1													
MaLo	0.85	0.58	0.69	0.67	0.67	0.69	0.67	0.46	0.61	0.42	0.91	1												
MaSy	0.69	0.49	0.67	0.58	0.52	0.61	0.58	0.49	0.58	0.39	0.88	0.85	1											
NoAc	0.58	0.67	0.55	0.46	0.46	0.73	0.76	0.55	0.64	0.39	0.52	0.54	0.46	1										
PeNi	0.39	0.49	0.55	0.64	0.58	0.42	0.21	0.61	0.52	0.52	0.46	0.36	0.46	0.33	1									
SeAn	0.68	0.61	0.61	0.69	0.76	0.61	0.39	0.61	0.58	0.58	0.69	0.67	0.58	0.39	0.58	1								
SeNi	0.79	0.64	0.58	0.61	0.67	0.69	0.49	0.64	0.67	0.42	0.79	0.76	0.67	0.55	0.49	0.79	1							
SePa	0.76	0.73	0.72	0.69	0.76	0.73	0.46	0.79	0.82	0.46	0.69	0.67	0.64	0.52	0.64	0.76	0.85	1						
SeSu	0.73	0.69	0.69	0.61	0.79	0.64	0.49	0.64	0.67	0.54	0.79	0.76	0.67	0.49	0.49	0.79	0.82	0.79	1					
SpDu	0.52	0.42	0.49	0.52	0.58	0.55	0.46	0.49	0.46	0.51	0.64	0.61	0.64	0.39	0.64	0.52	0.55	0.52	0.55	1				
SpPi	0.58	0.36	0.55	0.52	0.52	0.55	0.39	0.43	0.46	0.58	0.69	0.67	0.69	0.39	0.64	0.52	0.55	0.52	0.55	0.94	1			
SwFl	0.61	0.58	0.69	0.61	0.67	0.64	0.73	0.64	0.67	0.30	0.67	0.76	0.79	0.55	0.49	0.55	0.64	0.67	0.64	0.67	0.61	1		
ToKa	0.52	0.42	0.55	0.46	0.46	0.73	0.39	0.49	0.58	0.58	0.46	0.49	0.52	0.52	0.52	0.52	0.55	0.58	0.49	0.64	0.64	0.49	1	
ToSu	0.52	0.36	0.55	0.39	0.46	0.67	0.52	0.49	0.58	0.64	0.58	0.55	0.64	0.46	0.46	0.52	0.55	0.58	0.49	0.64	0.64	0.61	0.82	1

Species codes as in Table 1.

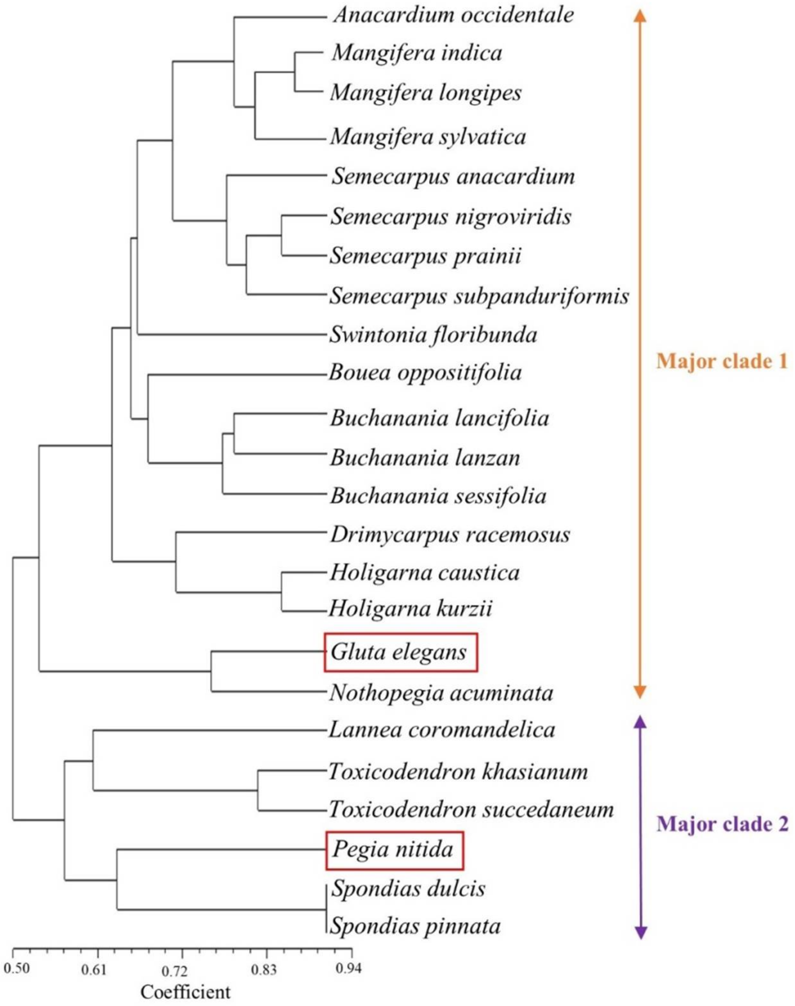

Fig. 1. UPGMA dendrogram showing inter-specific relationships of the Anacardiaceae taxa based on the Simple Matching coefficient.

The second major clade included six species from four genera: *Lannea* (tribe Spondiadeae), *Toxicodendron* (tribe Anacardieae), *Pegia* (tribe Spondiadeae), and *Spondias* (tribe Spondiadeae) (Fig. 1). Despite belonging to different tribes, species of these genera grouped together in a distinct clade, suggesting that, although they are phylogenetically distant, they share certain phenotypic traits contributing to their morphological similarity. This clustering may be attributed to convergent evolution, where similar ecological pressures or adaptive traits lead to analogous features across unrelated lineages (Simo-Droissart *et al.* 2013, 2016).

The similarity matrix revealed values ranging from 0.21 to 0.94, reflecting varying degrees of morphological similarity among the examined species. These values offer insight into the phenetic affinities and potential taxonomic relationships within Anacardiaceae (Table 3). The highest similarity (0.94) was observed between *Spondias dulcis* and *S. pinnata*, indicating a strong morphological resemblance. This finding suggests that these species share highly conserved traits, likely influenced by similar evolutionary pressures and ecological adaptations (Ahmed and Rahman 2024). Their similarities in leaf morphology, fruit characteristics, and growth habits support their close taxonomic relationship within the genus *Spondias*. In the genus *Buchanania*, three species, namely *B. lancifolia*, *B. lanzan*, and *B. sessifolia* exhibited relatively high similarity values, ranging between 0.76 and 0.79, indicating a strong morphological coherence within the genus, likely due to shared adaptive traits and evolutionary lineage. Similarly, three *Mangifera* species, viz. *M. indica*, *M. longipes*, and *M. sylvatica* also demonstrated high similarity values (0.85–0.91), reinforcing their close phenetic relationship. The strong clustering within *Mangifera* is likely attributable to common fruit characters, floral morphology, and leaf arrangements, which are key taxonomic indicators of the genus. In contrast, *Pegia nitida* exhibited the lowest similarity value (0.21) with *Gluta elegans*. This low resemblance suggests that *Pegia* may have undergone significant evolutionary divergence, leading to morphological differentiation from other taxa in Anacardiaceae. Likewise, species within the genus *Toxicodendron*, including *T. khasianum* and *T. succedaneum*, exhibited moderate similarity values (0.36-0.73) with other genera. The observed differences in *Toxicodendron* may be attributed to its leaf structures and fruit morphology, which set it apart from closely related taxa.

The clustering patterns revealed by the similarity matrix align to some extent with the established taxonomic classifications, while also highlighting areas for potential re-evaluation. The high phenetic affinity within *Mangifera* and *Buchanania* supports strong intrageneric cohesion, whereas lower similarity values for *Pegia* and *Toxicodendron* suggest broader evolutionary divergence. Although *Mangifera* and *Buchanania* were placed in separate subclades, their inclusion within the same tribe (Anacardieae) and the first major clade supports their close evolutionary relationship.

Principal Component Analysis (PCA) was performed to assess the contribution of different variables in explaining the total variance within the dataset. The eigenvalues, the percentage of variance explained by each principal component (PC), and cumulative variance are presented in Table 4. The results indicated that the first principal component (PC1) had the highest eigenvalue of 14.68, accounting for 61.16% of the total variance. This suggests that PC1 is the most influential component in explaining the variability within the dataset. The second principal component (PC2) contributed 6.82% of the variance, increasing the cumulative variance explained to 67.98%. The third (PC3) and fourth (PC4) components added 5.60% and 5.34% of the variance, respectively, bringing the cumulative variance to 78.92% (Table 4).

A significant portion of the variance (85.70%) was observed in first six principal components (PC1–PC6), indicating that these components contained most of the critical information in the dataset. The variance contribution from subsequent components gradually decreased, with PC7 to PC10 collectively accounting for 93.89% of the total variance. Beyond PC10, the eigenvalues dropped below 0.40, with each component contributing less than 2% to the overall variance. The last few components (PC20–PC24) contributed negligible variance, with PC24 having an eigenvalue of 0 and presenting only 0.01% of the total variance. These findings confirm that the latter components hold minimal significance in explaining variability. The dominance of the first few principal components suggests that a small subset of features primarily drives the observed variation. This finding is particularly important, as it implies that dimensionality reduction techniques can be effectively employed without significant information loss. Moreover, by focusing on the first few components, computational efficiency can be improved while maintaining meaningful interpretations of the dataset. Collectively, the first six principal components are sufficient to describe the majority of the variation within the dataset, making them the most relevant for further analysis. These results highlight the effectiveness of PCA in identifying key patterns and reducing the complexity of multidimensional data (Sharma and Pandit 2011, Shandalya *et al.* 2025).

Table 4. Eigen value and cumulative variance recorded during PCA analysis.

Sl. No.	Eigen value	Eigen value (%)	Cumulative (%)	Sl. No.	Eigen value	Eigen value (%)	Cumulative (%)
1	14.68	61.16	61.16	13	0.19	0.80	96.91
2	1.64	6.82	67.98	14	0.15	0.64	97.55
3	1.34	5.60	73.58	15	0.15	0.62	98.16
4	1.28	5.34	78.92	16	0.10	0.44	98.60
5	0.84	3.51	82.43	17	0.09	0.37	98.97
6	0.78	3.27	85.70	18	0.08	0.33	99.30
7	0.67	2.81	88.51	19	0.07	0.28	99.58
8	0.54	2.27	90.77	20	0.05	0.20	99.78
9	0.39	1.61	92.38	21	0.03	0.14	99.92
10	0.36	1.51	93.89	22	0.01	0.05	99.96
11	0.32	1.35	95.24	23	0.01	0.03	99.99
12	0.21	0.87	96.10	24	0.00	0.01	100

The 2D scatter diagram represents the distribution and clustering of 24 species of the family Anacardiaceae (Fig. 2), revealing two distinct major clades, similar to the grouping observed in the UPGMA dendrogram (Fig. 1). This visualization provides valuable insights into the relationships among the species within the family.

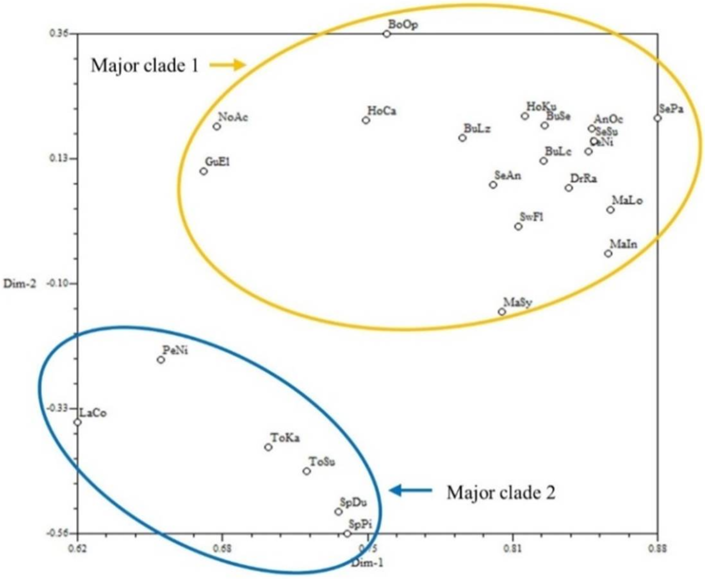

Fig. 2. Scatter diagram showing the relationships of the taxa within Anacardiaceae. The species codes are denoted in Table 1.

Major clade 1 included species from the genera *Anacardium*, *Bouea*, *Buchanania*, *Drimycarpus*, *Gluta*, *Holigarna*, *Mangifera*, *Nothopegia*, *Semecarpus*, and *Swintonia*. The close association of *Anacardium occidentale* with *Mangifera indica* aligned well with the grouping found in the UPGMA dendrogram. Similarly, the grouping of *Buchanania* species, i.e. *B. lancifolia*, *B. lanzan* and *B. sessifolia* reflects their genetic proximity, suggesting that shared phenotypic traits contribute to their clustering and further reinforce their taxonomic relationship. Major clade 2 also exhibited a pattern very similar to that of the UPGMA analysis. The 2D scatter plot further reinforces the reliability of PCA in capturing the key morphological characters driving species differentiation. Additionally, species positioned at the periphery of clusters indicate potential morphological divergence, emphasizing the need for further taxonomic investigation.

The three-dimensional vector projection plot also depicted two major clades, consistent with the UPGMA dendrogram and the 2D scatter plot (Fig. 3). The distribution of the 18 species in the first major clade closely mirrored that of the 2D scatter plot, reinforcing the robustness of the clustering pattern. Similarly, the second major clade showed congruence in the arrangement and positioning of six species. This alignment across multiple analytical approaches highlights the reliability of morphometric methods in assessing phenetic relationships and underscores the significance of PCA in capturing morphological variations within the family Anacardiaceae.

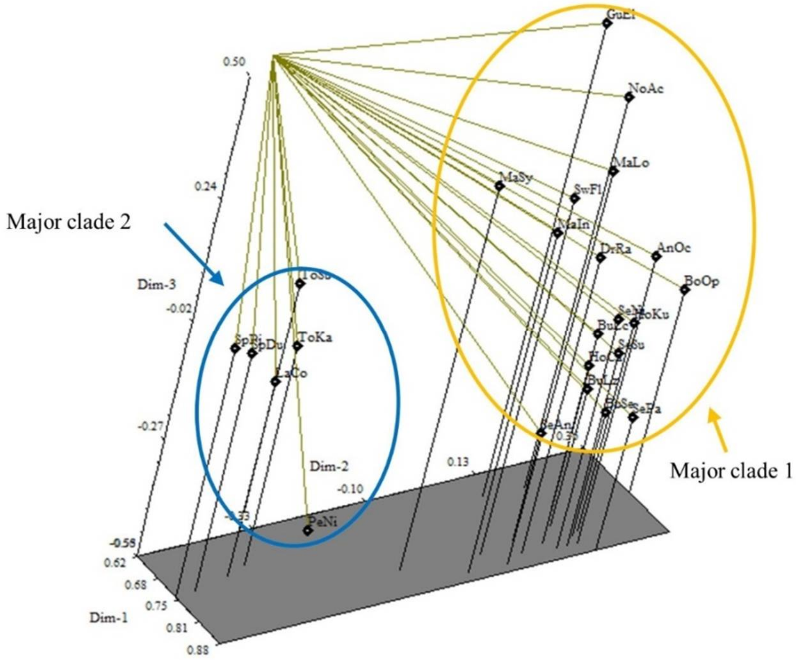

Fig. 3. Three-dimensional vector projection plot of PCA based on the first two principal components, illustrating major clustering patterns among Anacardiaceae taxa. The species codes are denoted in Table 1.

The combined use of Cluster Analysis (CA) and PCA provided a comprehensive assessment of morphological variation within Anacardiaceae. CA effectively grouped taxa based on phenotypic similarities, revealing distinct clusters that aligned with taxonomic relationships. While some genera formed expected clusters, others grouped unexpectedly, suggesting possible convergent evolution or shared ecological adaptations. PCA identified key morphological traits driving species differentiation, with the first few components explaining the majority of the variance. The clustering patterns observed in the 2D scatter plot and 3D vector projection closely mirrored those in the UPGMA analysis, reinforcing the reliability of the analyses. The integration of these multivariate methods minimized subjectivity in taxonomy, offering a robust framework for species delimitation and evolutionary insights within Anacardiaceae. The application of CA and PCA analyses in this study aligns with previous studies comparing UPGMA and PCA in *Tibouchina hatschbachii* and *T. marumbiensis*, where both methods demonstrated congruent results, reinforcing their reliability in morphometric analysis (Maia and Goldenberg 2019). Furthermore, the successful application of UPGMA clustering in delineating morphometric relationships among *Desmodium* and *Senna* species in Bangladesh supports its validity (Rahman and Rahman 2012, Rahman *et al.* 2013). Very recently, a study on the subfamily Byttnerioideae reaffirmed the utility of CA and PCA in resolving morphometric relationships, further highlighting their robustness in taxonomic research (Ahmed and Rahman 2024).

The present investigation provides the first comprehensive morphometric assessment of the family Anacardiaceae in Bangladesh, highlighting the taxonomic relationships among 24 species across 14 genera. The strong congruence between CA and PCA clustering reinforces the reliability of numerical systematics in species delimitation and affinity assessment. The identification of distinct clusters and high similarity values among certain taxa offer valuable insights for taxonomic classification and conservation efforts. These findings establish an important baseline for future molecular phylogenetic studies and enhance the systematic understanding of this ecologically and economically important plant family.

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