Research Article

ISAH Indian Journal of Arid Horticulture

Year 2025, Volume-7, Issue-1 (January - June)

Variability in date palm (*Phoenix dactylifera* L.) genotypes in Kachchh, India: a study on morphological and fruiting characteristics

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ARTICLE INFO

Received: 21 February 2025
Accepted: 07 April 2025

Keywords: Cluster analysis, date palm, genetic diversity, morphological traits, PCA

doi:10.48165/ijah.2025.7.1.4

ABSTRACT

This study investigates the morphological diversity among 38 date palm genotypes grown in Kachchh, India, using Principal Component Analysis (PCA) and Hierarchical Clustering. A dataset comprising 27 quantitative and qualitative traits were analysed. The correlation analysis revealed significant associations between key traits such as pulp thickness, fruit weight, and pulp-to-stone ratio, which are crucial for fruit quality improvement. PCA identified major traits contributing to morphological variability, with the first three principal components explaining over 52% of total variance. Hierarchical clustering grouped genotypes into four distinct clusters, demonstrating significant genetic diversity. The findings highlight the importance of fruit-related traits in genetic differentiation and provide a framework for breeding superior date palm genotypes.

Introduction

Date palm (*Phoenix dactylifera* L.) is one of the oldest fruit crops cultivated in arid and semi-arid regions of the world (Gros-Balthazard & Flowers, 2021). It plays a crucial role in the economy, food security, and cultural heritage in many Arabian countries, where it is a key commercial crop. India is a major importer of dates, but the Kachchh region of Gujarat has a significant genetic resource of date palm, estimated to have been introduced in the 16th-17th century CE (Baidiyavadra *et al.*, 2019). Despite its economic importance, studies on Indian date palm genetic diversity remain limited (Muralidharan *et al.*, 2019).

Morphological characterization is essential for genetic evaluation and breeding programs, helping in the identification of superior cultivars (Anonymous, 2005). Principal Component Analysis (PCA) and hierarchical clustering are advanced statistical tools that allow precise classification of genotypes. Correlation analysis further helps in understanding linkages among traits, facilitating informed breeding decisions (Ahmed *et al.*, 2011). This study aims to analyze morphological diversity in Kachchh date palm genotypes using these statistical tools.

Material and Methods

The study was conducted at the Date Palm Research Station, Sardarkrushinagar Dantiwada Agricultural University, Mundra-Kachchh, Gujarat India, during 2022-2023. The region has an arid climate with high temperatures and low rainfall, making it an ideal location for date palm cultivation. A total of 38 genotypes were selected comprising of local and exotic origin (Table 1).

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Table 1. List of date palm genotypes used in the study

S. No.	Genotypes	Indigenous/ exotic	S. No.	Genotype	Indigenous/ exotic
1	ADP-1	Indigenous	20	MDP-8	Indigenous
2	Barhee	Exotic	21	MDP-9	Indigenous
3	Bhugso	Indigenous	22	MDP-10	Indigenous
4	Dayri	Exotic	23	MDP-11	Indigenous
5	Gulchatti	Exotic	24	MDP-12	Indigenous
6	Halawy	Exotic	25	MDP-21	Indigenous
7	Hatemi	Exotic	26	MDP-22	Indigenous
8	Khadrawi	Exotic	27	Medjool	Exotic
9	Khalash	Exotic	28	Meznaz	Exotic
10	Khasab	Exotic	29	Panjab Red	Indigenous
11	Khuneji	Exotic	30	Ruziz	Exotic
12	Kotho	Indigenous	31	Saidy	Exotic
13	MDP-1	Indigenous	32	Samraan	Exotic
14	MDP-2	Indigenous	33	Sayar	Exotic
15	MDP-3	Indigenous	34	Sopari	Indigenous
16	MDP-4	Indigenous	35	Tayar	Exotic
17	MDP-5	Indigenous	36	Trofo	Indigenous
18	MDP-6	Indigenous	37	Zaglool	Exotic
19	MDP-7	Indigenous	38	Zahidi	Exotic

Morphological data collection

Morphological characterization was performed on 27 quantitative traits, which includes fruit characteristics (fruit length, fruit width, fruit weight, pulp thickness, pulp-to-stone ratio, and TSS (°Brix)), bunch characteristics (average bunch weight, number of strands per spathe, number of berries per strand, and strand length), leaf characteristics: leaf length, leaflet length, spine number, spine length, rachis length, and distance between spines) and seed characteristics (stone length, stone width, stone depth, and stone weight). Measurements were taken using standard horticultural procedures, including digital Vernier callipers, weighing scales, and manual counting as per the trait. Each genotype was evaluated based on at least three randomly selected trees, with three replicates per tree. Measurements were taken following the guidelines as proposed by Anonymous (2005) and DUS test guidelines of PPV&FRA (Anonymous, 2018) with necessary modifications.

Statistical analysis

A comprehensive statistical analysis was conducted to evaluate the morphological diversity among the genotypes. Correlation analysis was based on Pearson's correlation coefficients were determined to assess relationships between traits. Principal component analysis (PCA) was performed to identify major sources of variation and to reduce the dimensionality of the dataset. The first few principal components explaining the highest variance were selected for further analysis. Hierarchical cluster analysis was conducted using Ward's method based on Euclidean distances to construct a dendrogram illustrating genetic relationships.

All statistical analyses were conducted using R (randomforest, ggplot2, ggpubr, corrplot and lattice libraries). Data visualization, including heatmaps and dendrograms, was used to enhance the interpretability of results.

Results and Discussion

Correlation analysis

The correlation of different characters is presented in Fig. 1. The correlation matrix revealed significant relationships between several morphological traits. Notably, pulp thickness exhibits a strong positive correlation with fruit weight (r = 0.86), indicating that thicker pulp significantly contributes to heavier fruits. This trait is crucial for enhancing fruit quality in breeding programs (Ahmed *et al.*, 2023). Similarly, the pulp-to-stone ratio correlates positively with fruit weight (r = 0.80), suggesting that genotypes with heavier fruits generally possess a higher pulp-to-stone ratio, which is desirable for consumer preferences and market value (Alahyane *et al.*, 2022).

Other important positive correlations include fruit width and fruit weight (r = 0.68), showing that larger fruit dimensions contribute to overall fruit mass (Baidiyavadra *et al.*, 2019). The relationship between TSS (°Brix) and pulp thickness (r = 0.61) suggests that thicker pulp enhances the sweetness and overall quality of the fruit. Moreover, strand-related traits, such as the length of strand and the number of berries per strand (r = 0.45), highlight the longer strand may accommodate higher number of berries and can play role in determining fruit production potential (Jaradat & Zaid, 2004). In seed characters, stone length and stone diameter (r = 0.76) shows uniformity in stone dimensions, which could influence seed viability and market traits (Elhoumaizi *et al.*, 2002).

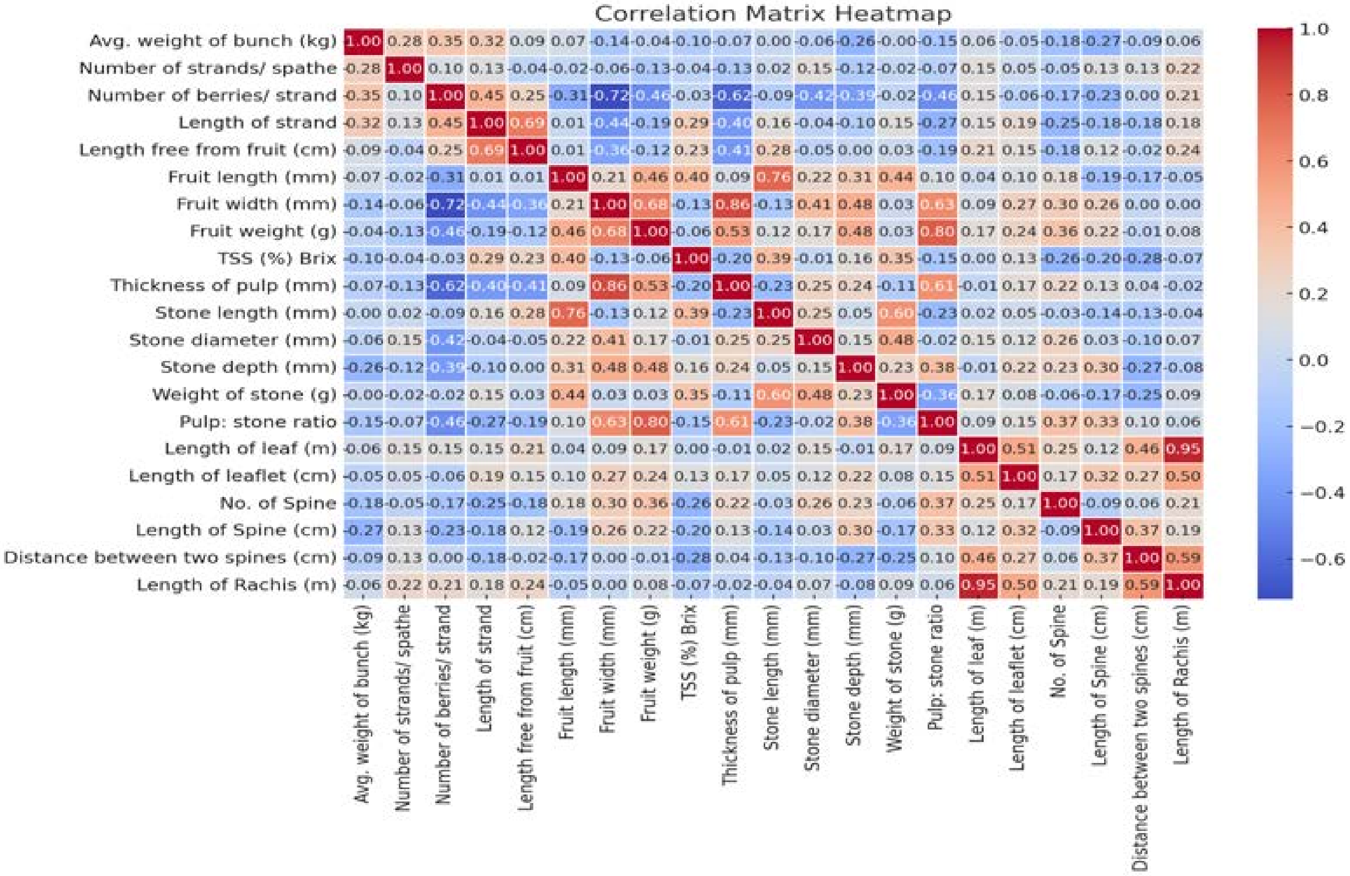

Fig. 1. Correlation matrix of different date palm characters

Conversely, some traits show negative correlations. The number of berries per strand shows a negative correlation with fruit weight (r = -0.46), suggesting that a higher number of berries can reduce the size of individual fruits, likely due to resource competition. Similarly, the length free from fruit is negatively correlated with the number of berries per strand (r = -0.42), implying that strands with more berries efficiently utilize their length for fruiting. Another negative correlation exists between the distance between spines and the number of spines (r = -0.30), where more compact spines are associated with shorter distances (Bedjaoui & Benbouza, 2020).

Traits such as the length of the leaf and length of rachis exhibit weak or negligible correlations with most other traits, indicating their limited direct influence on yield or fruit quality. These findings suggest that while some traits are critical for breeding efforts, others may be less impactful on the overall performance of genotypes (Ahmed *et al.*, 2011).

Principal component analysis (PCA)

The scree plot for principal component analysis is illustrated in Fig. 2 and details presented in Table 2 explaining the variance of each principal component (PC). The first principal component (PC1) accounts for the largest proportion of variance, followed by a sequential decrease in variance for subsequent components. In this analysis, PC1 explains 22.92% of the variance, while PC2 and PC3 explain 15.04% and 14.56%, respectively. The first three principal components collectively account for over 52% of the total variance, which is sufficient to capture the majority of the dataset's variability. The elbow in the scree plot, occurring at PC3, suggests that additional components contribute marginally to the total variance, making it reasonable to focus on the first three components for further analysis. Similar trends in PCA variance distribution have been reported in previous studies, where the first three PCs explained 50–60% of the total variation in date palm genotypes (Ahmed *et al.*, 2011; Bedjaoui & Benbouza, 2020)

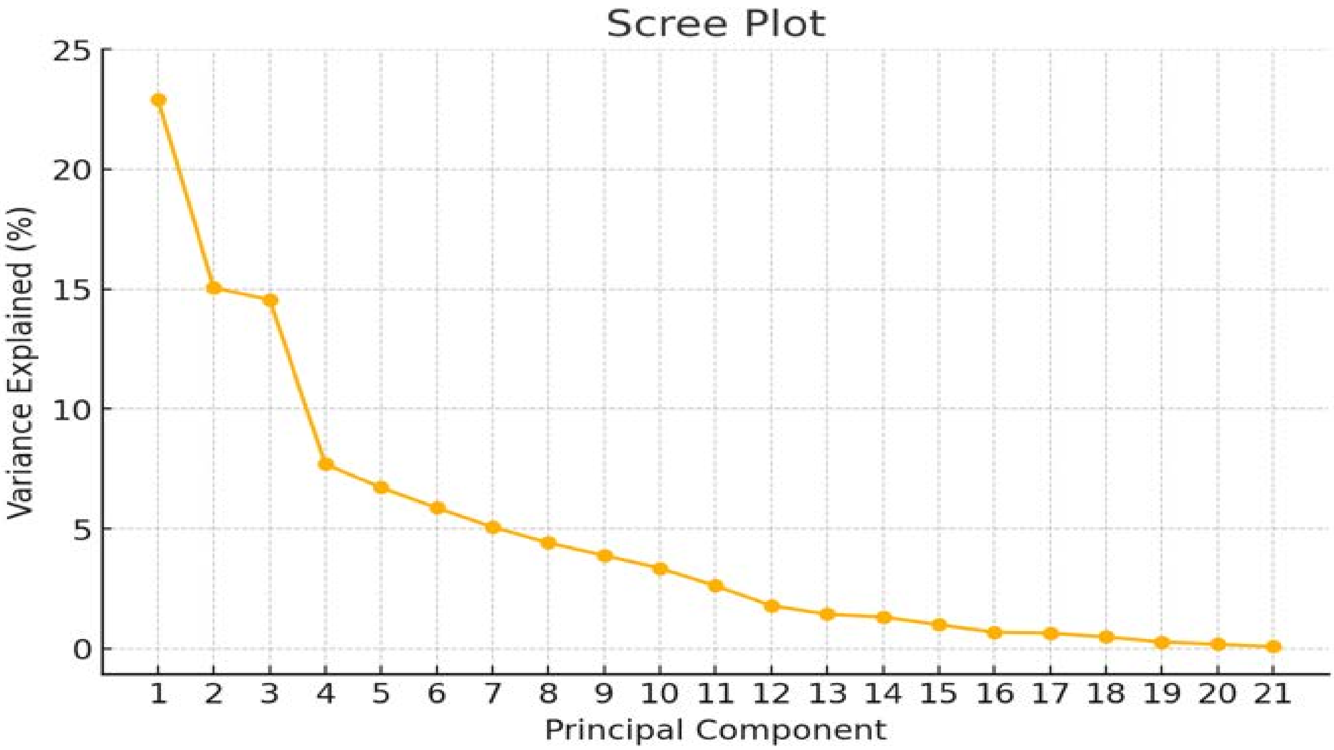

Fig. 2. Scree plot of principal components

Table 2. Eigen value and variance of principal components

Principal component	Eigenvalue	Variance explained (%)
PC1	4.94	22.92
PC2	3.24	15.04
PC3	3.14	14.56
PC4	1.66	7.69
PC5	1.45	6.71
PC6	1.27	5.87
PC7	1.09	5.07
PC8	0.95	4.41
PC9	0.84	3.88
PC10	0.72	3.35
PC11	0.56	2.62
PC12	0.39	1.79
PC13	0.31	1.43
PC14	0.28	1.32
PC15	0.21	0.99
PC16	0.15	0.68
PC17	0.14	0.64
PC18	0.10	0.48
PC19	0.06	0.28
PC20	0.04	0.18
PC21	0.02	0.08

The results of the Principal Component Analysis (PCA) and scree plot provide valuable insights into the morphological diversity of the 38 date palm genotypes. The scree plot indicates that the first three principal components (PCs) explain a substantial proportion of the total variance, accounting for over 52%. PC1 contributes the largest share (approximately 23%), dominated by traits such as fruit weight, pulp thickness, and stone dimensions. These findings emphasize the importance of fruit-related characteristics in defining variability among genotypes, which aligns with the findings of Simozrag *et al.* (2016), who reported that fruit traits like pulp weight and flesh-to-seed ratio had the highest influence on PC1. Similarly, studies by El-Kadri *et al.* (2019) and Ahmed *et al.* (2023) have demonstrated that reproductive traits play a dominant role in PCA-based differentiation of date palm genotypes.

PC2, which explains 15% of the variance, is influenced by bunch-related traits like bunch weight and strand length, reflecting the structural contribution of reproductive traits to overall variability. A similar contribution of bunch-related traits to PC2 was also noted by Raza *et al.* (2020) and Alahyane *et al.* (2022), indicating the significant role of inflorescence characters in morphological differentiation. PC3, contributing 14% of the variance, highlights the role of leaflet and rachis traits, are relevant for morphological classification. Previous studies have also reported that leaflet dimensions, rachis width, and petiole length significantly contribute to the later PCs in PCA analyses of date palm diversity (Hammadi *et al.*, 2009; Ennouri *et al.*, 2018).

The PCA scatter plot (Fig. 3) further elucidates the relationships among the genotypes. Genotypes such as Dayri and Panjab Red are clustered in the upper-right quadrant, indicating shared traits such as larger fruit weight and thicker pulp, making them potential candidates for breeding programs focused on improving fruit quality. Similar clustering patterns have been observed in previous studies, where high fruit weight and pulp content led to distinct groupings in PCA projections (Elsafy *et al.*, 2015; Alrashidi *et al.*, 2023). Conversely, genotypes such as MDP-6 and Khasab, located in the lower-left quadrant, exhibit unique morphological traits, which can be valuable for enhancing genetic diversity in hybridization efforts. Clustering of morphologically unique genotypes based on PCA has also been reported by Ahmed *et al.* (2011) and Raza *et al.* (2020), supporting the role of this technique in identifying genetically diverse accessions. Intermediate genotypes like MDP-2 and MDP-7, situated near the origin, display balanced traits without extremes, suggesting their adaptability for multiple purposes. Similar observations were made by El-Kadri *et al.* (2019), where intermediate genotypes showed stable performance across different environments.

Overall, the PCA results underscore the importance of fruit-related traits in genetic differentiation while showcasing the potential of structural and leaf-related traits to enhance diversity. These findings are consistent with prior reports highlighting the dominance of fruit size, pulp thickness, and inflorescence traits in determining the morphological variation of date palms (Simozrag *et al.*, 2016; Ahmed *et al.*, 2023).

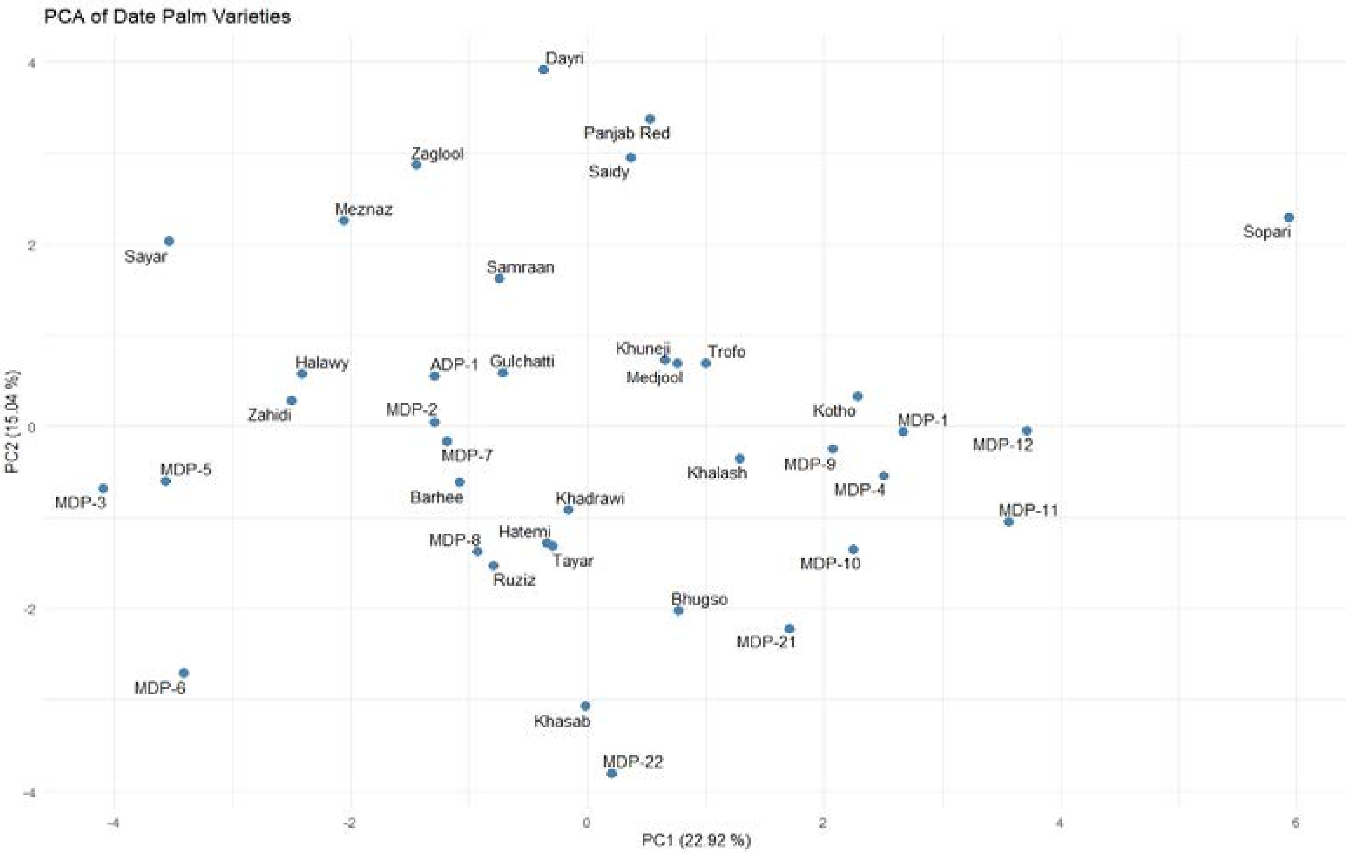

Fig. 3. Principal component analysis of date palm variability

Hierarchical cluster Aalysis

The hierarchical clustering dendrogram provides a clear representation of the morphological relationships among the 38 date palm genotypes. Based on the dendrogram, the genotypes were grouped into four distinct clusters, reflecting their phenotypic similarities and differences. Each cluster represents a group of genotypes that share key morphological traits, making them potential candidates for specific breeding strategies. Similar hierarchical clustering results have been reported in earlier studies, where genotypes were consistently grouped into clusters based on reproductive and vegetative traits (Ahmed *et al.*, 2011; Raza *et al.*, 2020).

The first cluster, which includes genotypes such as Bhugso, Barhee, MDP-6, etc. is characterized by genotypes with unique fruit-related and bunch characteristics. A similar clustering of genotypes based on fruit-related traits was observed by Ennouri *et al.* (2018), where cluster formation reflected significant variations in pulp thickness and fruit weight. This group may include genotypes suitable for hybridization programs aimed at enhancing traits like fruit quality and bunch size. The second cluster includes widely spaced genotypes such as Dayri, Zaglool, Panjab Red, etc.

which appear to be morphologically distinct based on their fruit characters. The third cluster, containing genotypes such as Khuneji, Tayar, Khadravi, etc. groups genotypes with characters like rachis length and leaf morphology. The fourth cluster, with genotypes such as Sopari, MDP-11, MDP-9, etc. is characterized by distinctive features such as fruit dimensions and high pulp-to-stone ratios. These traits make this group particularly attractive for commercial cultivation due to their potential marketability, similar grouping aligns with observations made by Simozrag *et al.* (2016) and Alrashidi *et al.* (2023).

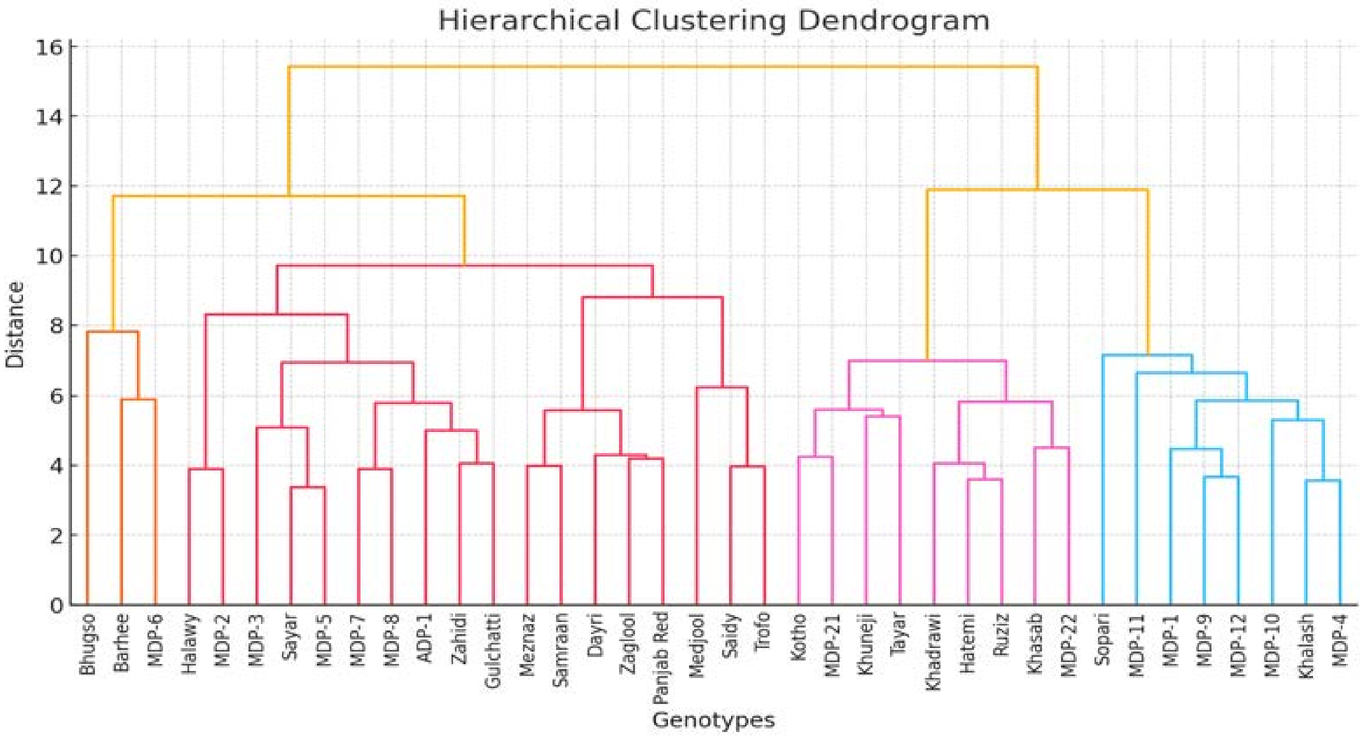

Fig. 4. Hierarchical clustering of date palm genotypes

The clustering results also align well with the PCA findings, which emphasize the importance of traits like fruit weight, pulp thickness, and strand length in defining variability. The dendrogram reinforces the diversity present in the genotypes and highlights clusters with significant potential for targeted breeding.

The PCA results align with the hierarchical clustering findings, where distinct groups of genotypes were identified based on morphological similarities. The grouping and separation observed in the PCA scatter plot validate the diversity among the studied genotypes, highlighting specific trait-based clusters that can inform targeted breeding and conservation strategies. Previous studies using both PCA and cluster analysis have confirmed that genotype groupings based on fruit and vegetative traits are consistent with traditional classification systems (Bedjaoui & Benbouza, 2020; Ahmed *et al.*, 2023).

In conclusion, the hierarchical clustering results provide a robust framework for understanding the genetic and phenotypic diversity of date palm genotypes. These findings can be directly applied to breeding programs aimed at improving fruit yield, quality, and adaptability. The identification of distinct clusters underscores the potential for leveraging genetic diversity to address specific breeding objectives, ensuring long-term sustainability in date palm cultivation (Raza *et al.*, 2020; Bedjaoui & Benbouza, 2020).

Conclusion

This study highlights the morphological diversity among date palm genotypes using PCA and hierarchical clustering. The findings confirm that fruit-related traits significantly contribute to genetic differentiation, and hierarchical clustering effectively groups genotypes based on shared attributes. These insights are valuable for breeding programs and conservation efforts aimed at maintaining genetic diversity in date palm cultivation.

Acknowledgements

The authors are grateful to the authorities of university and AICRP on AZF, Bikaner for providing the fund and other necessary facilities to conduct this research.

Conflict of Interest

The authors have no conflict of interest.

Data Sharing

All relevant data are within the manuscript.

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