Journal of Applied Horticulture, 26(4): 480-486, 2024
https://doi.org/10.37855/jah.2024.v26i04.91
Journal of Applied Horticulture
ISSN: 0972-1045

Genetic diversity and correlation analysis of Indian date palm (*Phoenix sylvestris* Roxb.): Insights into an underutilized native fruit crop

Prahlad Deb*, Madhu Kumar, Pradipto Kumar Mukherjee and Agniva Halder

*Department of Horticulture and Postharvest Technology, Institute of Agriculture, Visva-Bharati, Sriniketan - 731236, West Bengal. *E-mail: debprld@yahoo.com*

Abstract

Indian date palm (*Phoenix sylvestris* Roxb.) is one of the important nutritious, naturally abundant, potentially underutilized rain-fed fruit of the western dry tract of West Bengal available in the natural vegetation. Considering the diversity of the crop under this region, the present study aimed to study genetic diversity using multivariate analysis based on fruit physico-chemical and antioxidative properties of fifteen wild date palm accessions (P-1 to P-15) from natural vegetation of different locations from Bolpur Sriniketan Block under the Birbhum district during the year 2022 and 2023. The Indian date palm accessions exhibited wide ranges of variation in different fruit physico-chemical and antioxidative properties. The significant and high positive correlation of fruit weight with fruit size (length, diameter), pulp weight, seed weight, seed length and seed diameter were noted within Indian date palm accessions. A fairly positive correlation was observed between fruit weight, spadix girth, TSS, and total sugar. Similarly, fruit diameter was positively correlated with spadix girth, TSS, total sugar and reducing sugar. Pulp weight had a high positive correlation with TSS and total sugar. UPGMA clustering of date palm accessions has shown three major clusters. The eigenvalue and Eigenvector have exhibited five major principal components, of which the first principal component (PC1) contributed a maximum of 49.5% towards total variability. Bi-Plot also confirms the variability and the association of different characteristics within Indian date palm accessions.

Key words: Correlation, PCA, HCA, Bi-Plot, *Phoenix sylvestris* Roxb.

Introduction

The wild date palm (*Phoenix sylvestris* Roxb.) is the most prevalent minor or underutilized fruit plant in arid and desert regions. Belonging to the palm family Palmae, it originated around the Persian Gulf and has been available in natural vegetation since ancient times in India, Africa, and Spain (Tengberg, 2014). It grows naturally along roadsides, in households, forests, and barren lands in India, serving as a common food source for impoverished communities, particularly among tribal forest populations. Due to its low pulp content and large seeds, it is mainly used to produce "Neera", a traditional drink (Sharma and Murlidhar, 2021). Nevertheless, ripe fruits are highly valued by poor villagers, tribal communities, and forest dwellers, providing essential nutrition and fulfilling local fruit demands (Kumar *et al.*, 2024).

The date fruit is an oblong, terete, one-seeded berry with a fleshy pericarp and a membranous endocarp (Salomón *et al.*, 2021). This fruit is rich in various carbohydrates (fructose and glucose), proteins (such as thiamine, riboflavin, niacin, and folic acid), vitamins, minerals, and dietary fibers (Ioannis, 2010). It also has significant amounts of minerals like calcium, iron, potassium, phosphorus, magnesium, selenium, copper and other micronutrients (Aljaloud *et al.*, 2020). Additionally, it is rich in different phenolics with more significant antioxidant activity, making it a potent source of bioactive agents (Al-Shwyeh, 2019). Various processed and value-added products, such as sugar, starch, vinegar, juice, and toffees, are also derived from this fruit (Salomón *et al.*, 2021; Ashraf and Hamidi, 2011).

Phoenix sylvestris is found throughout India, especially in the plains of Andhra Pradesh, Gujarat, Karnataka, Madhya Pradesh, Maharashtra, West Bengal, Odisha, Assam (Al-Alawi *et al.*, 2017). The Western Dry tract of West Bengal, including districts like Birbhum, Bankura, West Burdwan, and Purulia, holds significant potential for expanding the cultivation of these rain-fed fruit crops with a substantial population of wild types serving as natural resources for local people. However, only a few reports are there with respect to Indian date palms (Kumar *et al.*, 2024). Thus, the present research focused on the morpho-biochemical and antioxidative characterization of selected wild date palm genotypes, followed by their genetic diversity analysis.

Materials and methods

The study involved selecting fifteen wild date palm genotypes from a preliminary study of thirty diverset ypes, all aged between 20 and 25 years, from various villages within the Bopur Sriniketan Block of Birbhum district, West Bengal. The GPS coordinates of each date palm plant were recorded using a handheld Garmin GPS 12H device (Table 1). Fully mature and ripe bunchs of fruits from each genotype were brought to the laboratory at the Department of Horticulture and Post-harvest Technology, Institute of Agriculture, Visva-Bharati, Sriniketan, West Bengal, India for recording the following observations:

Fruit physical characters: The fruit morphological characteristics of selected date palm plants were recorded as per the descriptors from the Protection of Plant Varieties and Farmers Rights Authority (PPV &FRA) of India. Observations included bunch

diameter (using a vernier caliper), number of bunches, fruits, and spikelets spathe diameter, number of spikes per bunch, berries per spike, fruit length, diameter and seed length and diameter were measured using a vernier caliper. Fruit weight and seed weight were measured using a pan balance.

Table 1. Location details of various wild date palm genotypes selected for the present study

Date palm genotypes	Geographical location	
	Latitude	Longitude
P-1	23.669758	87.661211
P-2	23.674586	87.660483
P-3	23.674676	87.660475
P-4	23.673152	87.658335
P-5	23.668926	87.666253
P-6	23.669736	87.666602
P-7	23.668617	87.666534
P-8	23.668558	87.666504
P-9	23.669756	87.670360
P-10	23.669755	87.670367
P-11	23.666056	87.672337
P-12	23.667112	87.672284
P-13	23.668212	87.662464
P-14	23.667924	87.662468
P-15	23.666339	87.673272

Fruit biochemical characters: Total soluble solids (TSS) content was recorded by digital refractometer (0-65°B, Konika Minolta, Japan) and expressed in °Brix. Total acidity was determined by titrating five mL of juice (from 5g of pulp) mixed with 2-3 drops of phenolphthalein indicator and against 0.1 N NaOH (Rangana, 1986). Total sugar was determined using the AOAC method (1990), which involved acid hydrolysis of sugar and neutralization by NaOH in the presence of phenolphthalein as an indicator, followed by titration against Fehling's solution. Juice filtrate was titrated against Fehling's solution to a brick-red precipitate to determine the reducing sugar (Lane and Eynon, 1923). Ascorbic acid was quantified using the indophenol dye method (Rangana, 1986). The scavenging capacity of free radicals (RSA) was measured using the DPPH assay (Brand-Williams *et al.*, 1995) using a double-beam UV-Visible spectrophotometer (LABMAN, LUV2000T, India).

Statistical analysis: The data were examined using descriptive statistics and analysis of variance, following the method proposed by Ronald A. Fisher (Gomez and Gomez, 1984) to test the significance of the differences between them. The fruit morphological and biochemical data were investigated with the statistical software SPSS (Statistical Package for Social Sciences, IBM SPSS Version 27) for correlation and principal component analysis. Bi-plot analyses and dendrograms were constructed using R-Studio Version 2022.

Results and discussion

The mean, range, coefficient of variation and standard error of the mean of different parameters studied on various Indian date palm accessions are presented in Table 2.

Correlation estimation: The correlation coefficient for important yield attributes and fruit biochemical parameters of Indian date palm accessions is presented in Table 3. The significant high positive correlation between fruit weight and fruit length (0.948), fruit diameter (0.957), pulp weight (0.954), seed weight (0.954), seed length (0.983) and seed diameter (0.958) were noted in the present study. Similarly, fruit length was highly positively correlated with fruit diameter (0.969), pulp weight (0.909), seed weight (0.900), seed length (0.944), seed diameter (0.871) and cap diameter (0.866). Similarly, fruit diameter exhibited a high positive correlation with pulp weight (0.940), seed weight (0.886), seed length (0.941) and seed diameter (0.889) and pulp weight had a high positive correlation with seed weight (0.820), seed length (0.974), and seed diameter (0.983). Seed length was highly positively correlated with seed diameter (0.961) and cap diameter (0.845). At the same time, fairly high positive correlation was found for fruit weight with spadix girth (0.604), TSS (0.536), and total sugar (0.544). Similarly, fruit length had a considerable high positive correlation with spadix girth (0.666), TSS (0.653), total sugar (0.660) and reducing sugar (0.532). Similarly, fruit diameter was positively correlated with spadix girth (0.550), TSS (0.622), total sugar (0.621) and reducing sugar (0.552) and pulp weight was fairly high correlation with TSS (0.524) and total sugar. Seed weight had fairly high positive correlation with cap diameter (0.788) spadix girth (0.657). Similarly, seed length was positively correlated with spadix girth (0.614), TSS (0.543), and total sugar (0.546). Seed diameter had shown a high positive correlation with cap diameter (0.773) and spadix girth (0.541) and cap diameter was also correlated with TSS (0.601) and total sugar (0.567).

Table 2. Mean, range, coefficient of variation and standard error of mean of different parameters of various Indian date palm accessions

Characteristics	Mean	Range	CV (%)	SEm
NOB	11.06	3.02 – 27.15	25.88	1.65
NOF	354.1	58.09 – 645.25	13.07	22.32
NOS	63.26	28.32 – 89.35	21.65	2.22
NOFS	24.73	9.65 – 34.54	16.32	1.64
SG	22.50	14.73 - 33.24	19.88	1.22
FL	25.04	23.2 - 28.65	11.32	0.39
FD	12.76	11.66 - 16.15	10.57	0.28
FW	2.19	1.53 - 3.91	25.11	0.11
PW	1.18	0.8 - 1.7	9.82	0.07
SW	1.01	0.7-1.94	13.94	0.05
SL	18.08	16.9 - 21.8	16.43	0.41
SD	8.93	8.03 -11.15	12.91	0.21
CL	3.38	2.87 - 3.69	17.04	0.08
CD	6.64	6.03 - 7.88	13.16	0.16
TSS	34.03	31.3 - 36.6	8.36	0.92
TA	0.84	0.56 - 1.13	12.45	0.07
TS	38.97	35.9 - 41.4	11.63	0.89
RS	32.02	29.5 - 34.93	14.22	0.81
AA	3.35	2.3 - 4.41	9.73	0.10
AO	82.19	52.38 - 97.54	21.48	1.34

No. of bunches/tree: NOB; No. of fruits /bunch: NOF; No. of spikelet/ bunch: NOS; No. of fruits/spikelet: NOFS; Spadix girth (cm): SG; Fruit length (mm): FL; Fruit diameter (mm): FD; Fruit weight (g): FW; Pulp weight (g): PW; Seed weight (g): SW; Seed length (mm): SL; Seed diameter (mm): SD; Cap length (mm): CL; Cap diameter (mm): CD; TSS (Brix) TSS; Titrable Acidity (%): TA; Total sugar (%): TS; Reducing sugar (%): RS; Ascorbic Acid (mg/100g): AA; Antioxidant (%DPPH): AO

The significant high negative correlation of fruit weight was found with the number of fruits per spikelet (-0.679), fruit length with the number of fruits per spikelet (-0.647) and fruit diameter with the number of spikelets (-0.669) and cap length (-0.572) and similarly pulp weight is correlated with cap length (-0.573). Seed weight was associated with the number of fruits per spikelet (-0.544), and seed length was correlated with the number of fruits per spikelet (-0.619), and the number of fruits per spikelet was

Table 3. The correlation coefficient (Pearson, n) for important yield attributes and fruit biochemical parameters of date palm (*Phoenix sylvestris*) genotypes.

Variables	NOB	NOF	NOS	NOFS	SG	FL	FD	FW	PW	SW	SL	SD	CL	CD	TSS	TA	TS	RS	AA
NOB	1.00																		
NOF	0.41	1.00																	
NOS	0.38	0.49	1.00																
NOFS	-0.01	0.47	-0.05	1.00															
SG	0.12	0.00	0.56	-0.20	1.00														
FL	0.19	-0.06	0.42	-0.65	0.67	1.00													
FD	0.24	-0.02	0.41	-0.67	0.55	0.97	1.00												
FW	0.10	-0.12	0.40	-0.68	0.60	0.95	0.96	1.00											
PW	0.10	-0.24	0.33	-0.75	0.50	0.91	0.94	0.95	1.00										
SW	0.09	-0.01	0.43	-0.54	0.66	0.90	0.89	0.95	0.82	1.00									
SL	0.11	0.01	0.46	-0.62	0.61	0.94	0.94	0.98	0.90	0.97	1.00								
SD	0.06	-0.08	0.34	-0.60	0.54	0.87	0.89	0.96	0.85	0.98	0.96	1.00							
CL	-0.44	-0.14	-0.31	0.36	-0.22	-0.47	-0.57	-0.48	-0.57	-0.34	-0.41	-0.36	1.00						
CD	0.28	-0.01	0.50	-0.56	0.50	0.87	0.84	0.83	0.80	0.79	0.85	0.77	-0.20	1.00					
TSS	0.27	-0.19	-0.02	-0.65	0.25	0.65	0.62	0.54	0.52	0.50	0.54	0.49	-0.12	0.60	1.00				
TA	-0.27	-0.03	-0.09	-0.43	0.10	0.25	0.23	0.24	0.28	0.18	0.23	0.18	-0.19	0.05	0.22	1.00			
TS	0.21	-0.25	-0.03	-0.62	0.29	0.66	0.62	0.54	0.53	0.51	0.55	0.50	-0.11	0.57	0.98	0.18	1.00		
RS	0.35	-0.29	-0.19	-0.71	0.05	0.53	0.55	0.44	0.49	0.36	0.40	0.39	-0.28	0.48	0.92	0.19	0.88	1.00	
AA	0.29	-0.01	-0.12	0.10	0.01	0.05	0.02	0.02	0.06	-0.02	0.01	-0.01	-0.05	0.11	-0.18	0.08	-0.22	-0.14	1.00
AO	-0.15	-0.18	-0.01	0.01	0.44	0.29	0.28	0.39	0.28	0.47	0.37	0.47	-0.11	0.02	0.07	-0.10	0.20	-0.07	-0.07

correlated with TSS (-0.653), total sugar (-0.616) and reducing sugar (-0.707).

Debabeche *et al.* (2022) evaluated twenty-six Algerian local date palm varieties and reported a positive correlation between fruit weight and size and seed length. A positive correlation was noted between fruit diameter and fruit weight, and a negative correlation was noted between seed/fruit length and mass ratios. Alrashidi *et al.* (2023) reported an almost identical correlation pattern in date varieties grown in Saudi Arabia. A positive correlation between fruit weight and most of the other fruit size parameters was also noted by Allam *et al.* (2021). Ahmad *et al.* (2023) found that the pulp weight had a strong relationship with fruit weight, length and diameter. An inviolable positive correlation has also been found among antioxidant capacity, antioxidant activity, and total phenolic content. Thus the correlation studies of different fruit morphological and biochemical parameters reported by different scientists aline with the findings of present experiment, although the differences might be due to the species variation.

Hierarchical cluster analysis (HCA) of Indian date palm accessions: Agglomeration schedule based on the least dissimilarity coefficient (DC) to make the cluster is presented in Table 4. According to the agglomeration schedule, P-10 and P-14 exhibited a minimum DC (249.855). The next combination was of P-11 with P-13 (with DC=352.621). P-5 combined with P-9 in the third stage with DC=457.422. After that, at the fourth stage, P-4 combined with P-10 with DC=695.533. In the next stage *i.e.*, fifth, the cluster of P-7 combined with P-9 recorded DC=758.418. Similarly, DC=1625.472 was noted in the sixth stage, where P-8 was combined with P-11. Then, accession P-12 was combined with P-15 and DC=2025.974 at the seventh stage. At the next P-3 combined with P-8, a DC of 2100.409 was found at stage eight. The combination of P-4 with P-13 noted a DC=3380.748 at stage nine. At the tenth stage, DC of 4203.583 was recorded, and P-16 was combined with P-12. Similarly, date palm genotype P-2 and P-5 noted a DC of 7047.924 at stage eleven. At the next, P-1 combined with P-3 showed a DC of 17527.410 at stage twelve. The combination of P-2 with P-14 noted DC of 30752.896 at stage thirteen. At stage fourteen, the highest DC (146324.642) was noted between the genotypes P-7 and P-6. The current findings demonstrated that good combing potential across genotypes was not biased by geographical specificity, where the genotypes were chosen. The most remarkable dissimilarity in the proximity matrix was observed between 'P-1 and P-6', followed by 'P-1 and P-2', 'P-1 and P-3', 'P-2 and P-3', 'P-2 and P-6', and 'P-2 and P-8'. Overall, the proximity table indicates that genotypes P-6, P-12 and P-15 are substantially more distant from most other genotypes.

Clustering through Ward's Minimum Variance Method grouped fifteen date palm accessions into three clusters (Table 5 and Fig. 1). Out of all the clusters, cluster I had the maximum number genotypes (8) P-1, P-3, P-8, P-11, P-13, P-4, P-10 and P-14. After that, cluster II included four accessions, namely, P-2, P-5, P-9 and P-7. Finally, cluster III is composed of three accessions *viz.* P-6, P-12 and P-15.

These findings are supported by an investigation by Khalilia *et al.* (2022) on date palm (*Phoenix dactylifera*) cultivars, where the dendrogram showed two main clusters. Cluster I included all of the six cultivars, and the remaining cultivars were grouped in a second large cluster, which exhibited two sub-clusters. In a study by Alrashidi *et al.* (2023) four main clusters were detected at distance matrix height 8 out of which the first cluster consisted only one, the second cluster consisted of nine date palm accessions, the third cluster with five and fourth cluster with three accessions. Jamil *et al.* (2020) found three major clusters of date

Table 4. Agglomeration schedule of different clusters based on qualitative traits

Stage	Cluster 1	Cluster 2	Coefficients
1	10	14	249.855
2	11	13	352.621
3	5	7	457.422
4	4	10	695.533
5	7	9	758.418
6	8	11	1625.472
7	12	15	2025.974
8	3	8	2100.409
9	4	13	3380.748
10	6	12	4203.583
11	2	5	7047.924
12	1	3	17527.410
13	2	14	30752.896
14	7	8	146324.642

Table 5. Clusters for characterization of different date palm genotypes using Ward's minimum variance method on squared Euclidean distance based on similarity matrix

Cluster	No. of genotypes	Genotypes
I	8	P-1, P-3, P-8, P-11, P-13, P-4, P-10, P-14
II	4	P-2, P-5, P-9, P-7
III	3	P-6, P-12, P-15

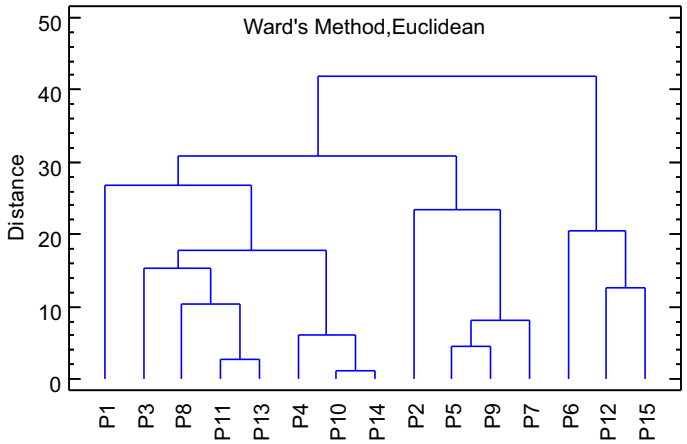

Fig. 1. Dendrogram through Ward's minimum variance method based on Euclidian distance for date palm genotypes

palm accessions: the first cluster formed with three genotypes, the second with seven genotypes, and the third with three date palm genotypes. UPGMA cluster study of date palm varieties was reported by Ibrahimi *et al.* (2023) with seven clusters, of which three were major. Dendogram of date palm accessions based on RAPD markers have been grouped into two UPGMA clusters as reported by Bahraminejad and Mohammadinejad (2015). Five major clusters with twenty-two date palm accessions were reported by Al-Harrasi *et al.* (2014) based on antioxidant activity under Oman conditions. Khierallah *et al.* (2011) have also reported 4 clusters of Iraqi date palms. RAPD-based genetic divergence analysis of date palm varieties has been classified into six major clusters (UPGMA) by Sedra *et al.* (1998). Hammami *et al.* (2024) also found variations in clusters of date palm varieties under different irrigation and salinity regimes. Thus all these findings are similar to the recent experiment and the variation in numbers of clusters as well as number of genotypes in a single cluster might be due to species variation and the total number of accessions under study.

Principal Component Analysis (PCA): In the current experiment, PCA was used to create fewer new variables. The characters contributing to the total variation for each principal axis are presented in Table 6. From the Scree plot representation (Fig. 2) for the optimum number of components in association with quantitative characters of date palm genotypes**,** it is revealed that 05 (five) Principal Components may be able to describe the whole scenario in a variation way with minimal information reduction. The principal component analysis of fifteen date palm accessions according to Eigenvalues (Eigen root) and eigenvectors, five Eigenvalue (Eigen root), eigenvectors and variance proportion is presented in Table 6. The first five components in the PCA analysis with Eigenvalues (Eigen root) contributed more than one to 85.3 % of the total variability among the genotypes evaluated for different quantitative traits. The first principal component (PC1), with an eigenvalue of 3.148, contributed a maximum *i.e.*, of 49.5% towards total variability, followed by PC2 with an Eigenvalue of 1.641, accounting for 13.4% of the total variability. Consequently, PC3, PC4 lastly PC5 with Eigen values1.395, 1.172, and 1.066 contributed 9.7%, 6.8%and 5.6%, respectively.

The PC1 revealed the highest positive association with the number of fruits per spikelet (0.233) followed by the number of fruits per bunch (0.037), whereas the highly negative association with fruit length content (-0.309) followed by fruit weight (-0.308), fruit diameter (-0.308), and seed length (-0.304). The PC2 expressed a high positive association with reducing sugar (0.402) and significant negative association with number of spikelet per bunch (-0.440) followed by average number of fruits per bunch (-0.380) and number of fruit per spikelet (-0.281). PC3 exhibited the highest pragmatic association with the number of bunch per tree (0.601), followed by the number of fruits per bunch (0.343) and reducing sugar (0.284). On the contrary, a high dismissive association was revealed with antioxidant (-0.420) followed by cap length (-0.203) and seed diameter (-0.160). A considerable positive association was observed between titrable acidity (0.527), ascorbic acid (0.470), and pulp weight (0.191), with the same positive loading in PC4. An elevated negative consortium was observed with cap length (-0.343), antioxidant (-0.293) and, total sugar (-0.287), *etc.* PC5 denoted raised positive association with ascorbic acid (0.648), titrable acidity (0.410) and antioxidant activity (0.323) and on the contrary high negative alliance was noted with the number of bunches per tree (-0.307), spikelet per bunch (-0.306) and fruits per bunch (-0.303).

The PC1 exhibited a negative association with the greater part of the traits under study except for the count of fruits per spikelet and ascorbic acid. The PC2 disclosed a negative association with

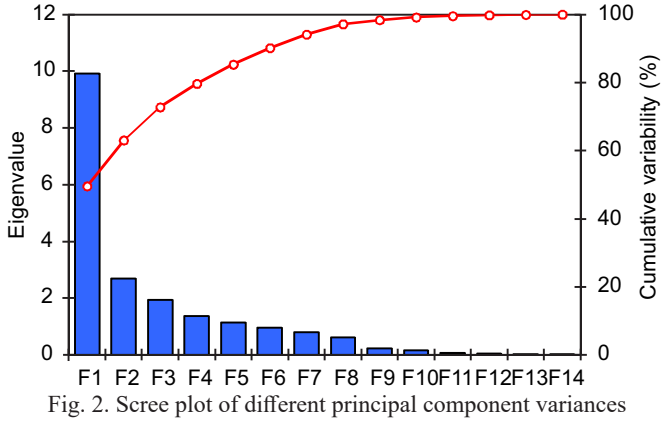

Fig. 2. Scree plot of different principal component variances

Table 6. Eigen root and cumulative percentage of variation for different major principal components (PCs) among date palm (*Phoenix sylvestris* Roxb.) genotypes

Characters	PC1	PC2	PC3	PC4	PC5
NOB	-0.068	-0.146	0.601	-0.063	0.307
	(0.046)	(0.057)	(0.706)	(0.006)	(0.107)
NOF	0.037	-0.380	0.343	-0.062	-0.303
	(0.014)	(0.390)	(0.230)	(0.005)	(0.105)
NOS	-0.122	-0.440	0.170	-0.114	-0.306
	(0.148)	(0.524)	(0.057)	(0.018)	(0.107)
NOFS	0.233	-0.281	0.011	-0.223	0.127
	(0.542)	(0.213)	(0.000)	(0.069)	(0.019)
SG	-0.192	-0.250	-0.147	-0.175	0.022
	(0.369)	(0.169)	(0.042)	(0.042)	(0.001)
FL	-0.308	-0.075	-0.111	0.062	0.016
	(0.952)	(0.007)	(0.000)	(0.001)	(0.000)
FD	-0.309	-0.050	0.001	0.020	0.011
	(0.945)	(0.008)	(0.003)	(0.006)	(0.000)
FW	-0.308	-0.052	0.035	0.064	0.002
	(0.941)	(0.016)	(0.024)	(0.005)	(0.000)
PW	-0.295	-0.009	-0.072	0.191	0.031
	(0.866)	(0.000)	(0.010)	(0.050)	(0.001)
SW	-0.292	-0.131	-0.144	-0.071	0.005
	(0.847)	(0.047)	(0.041)	(0.007)	(0.000)
SL	-0.304	-0.113	-0.089	0.010	-0.032
	(0.917)	(0.035)	(0.016)	(0.000)	(0.001)
SD	-0.290	-0.087	-0.160	-0.018	0.040
	(0.835)	(0.021)	(0.050)	(0.000)	(0.002)
CL	-0.150	0.138	-0.203	-0.343	-0.000
	(0.225)	(0.051)	(0.081)	(0.162)	(0.000)
CD	-0.272	-0.064	0.118	-0.047	0.031
	(0.734)	(0.011)	(0.027)	(0.003)	(0.001)
TSS	-0.224	0.331	0.207	-0.230	-0.027
	(0.497)	(0.295)	(0.084)	(0.073)	(0.001)
TA	-0.224	0.324	0.135	-0.287	0.009
	(0.066)	(0.060)	(0.025)	(0.382)	(0.192)
TS	-0.193	0.402	0.284	-0.075	0.048
	(0.498)	(0.284)	(0.036)	(0.114)	(0.000)
RS	0.006	-0.117	0.090	0.470	0.648
	(0.370)	(0.437)	(0.158)	(0.008)	(0.003)
AA	-0.101	-0.108	-0.420	-0.293	0.323
	(0.000)	(0.037)	(0.016)	(0.304)	(0.479)
AO	-0.081	0.149	-0.113	0.527	0.410
	(0.101)	(0.032)	(0.344)	(0.119)	(0.119)

Values in parentheses are squared cosine of the variables and bold correspond for each variable to the factor for which the squared cosine is the largest and good representation on the components

most of the characteristics under omitting TSS, sugar and acidity. PC3 showed nearly equal negative and positive association with the quantitative traits of date palms under study. The PC4 expressed the most negative association of the traits under study except for fruit weight, length, diameter, pulp weight, seed length, ascorbic acid, and titrable acidity. The PC5 manifested the positive consortium with a more significant part of the traits, barring seed length, cap length, fruits per bunch, spikelet per bunch and TSS. Conversely, the PC1 had a negative union with 70.00% of the genotypes. In comparison, PC2 revealed a negative association with 75.00% of the accessions, and PC3 was the same, with slightly less than 50.00% of the accessions (*i.e.*, 11 numbers of genotypes).

Table 6 also exhibits the squared cosine of the variables to the factor for which the squared cosine is the most significant representation of the components. A high value of squares cosine variables resembles a good representation of the respective component. The variables like the number of fruits per spikelet, spadix girth, fruit length, fruit diameter, fruit weight, pulp weight, seed weight, seed length, seed diameter, cap diameter, TSS and total sugar possessed high squared cosine values and have a good representation of first principal component (PC1). Second principal component (PC2) was better represented by a number of fruits per bunch, the number of spikelet per bunch and reducing sugar while third principal component (PC3) by the number of bunches per tree and antioxidant activity; the fourth principal component (PC4) by titrable acidity and fifth principal component (PC5) by ascorbic acid content.

The contribution of different variables for the variances of major principal components is presented in Table 7. It is clear from the data that variables like the number of fruits per spikelet, fruit length, fruit diameter, fruit weight, pulp weight, seed weight, seed length, seed diameter, cap diameter TSS and total sugar have very high contributions to creating variation by first principal component (PC1). The number of fruits per bunch, number of spikelets per bunch, number of fruits per spikelet, spadix girth, TSS, total sugar and reducing sugar have exhibited significant contributions for variance by the second principal component. A number of bunches per tree created the more significant variation by the third principal component (PC3), number of fruits per bunch and reducing sugar. Similarly, variables like cap length, TSS, acidity, total sugar, ascorbic acid content and antioxidant content have shared the maximum for variance of fourth principal component (PC4). The variance of the fifth principal component was contributed mainly by the number of bunches per tree, number of fruits per bunch, number of spikelets per bunch, titrabale acidity, ascorbic acid content and antioxidant content.

Scoring and loading PCA Bi-Plot: Component scores of date palm (2D Editor Plot) and loading of quantitative characters were presented in Fig. 3 and Fig. 4, respectively. The scoring Bi-Plot exhibited the close association of date palm accessions like P-1, P-3, P-4, P-8, P-10, P-13 and P-14 are in the fourth quadrant (distant from PC1 but closer to PC2), which is also supported by

Table 7. Contribution of different variables in different major principal components (PCs) among date palm genotypes

Variables	PC1	PC2	PC3	PC4	PC5
NOB	0.464	2.132	36.212	0.407	9.438
NOF	0.142	14.492	11.791	0.397	9.226
NOS	1.494	19.438	2.919	1.303	9.372
NOFS	5.469	7.914	0.013	5.004	1.635
SG	3.722	6.273	2.168	3.076	0.051
FL	9.604	0.251	0.000	0.043	0.014
FD	9.528	0.279	0.129	0.412	0.000
FW	9.495	0.576	1.234	0.394	0.026
PW	8.740	0.010	0.524	3.651	0.097
SW	8.546	1.742	2.084	0.507	0.003
SL	9.245	1.281	0.802	0.012	0.107
SD	8.420	0.762	2.583	0.034	0.160
CL	2.269	1.905	4.137	11.810	0.000
CD	7.401	0.413	1.406	0.227	0.100
TSS	5.018	10.970	4.309	5.310	0.078
TA	0.664	2.233	1.277	27.787	16.863
TS	5.023	10.551	1.834	8.288	0.009
RS	3.729	16.230	8.084	0.576	0.231
AA	0.004	1.371	0.817	22.126	42.107
AO	1.022	1.179	17.676	8.639	10.483

the cluster analysis of the date palm accessions. Accessions like P-2, P-5, P-7, and P-9 are closely associated and placed in the third quadrant (closer to both the PCs). P-6 seems as outlier as it is in the outer border of the second quadrant. P-12 and P-15 are more distant accessions and are placed in the first quadrant. Conversely, the first quadrant of the loading Bi-plot comprised the number of bunches per tree, number of spike, spadix girth, seed diameter, seed weight, fruit weight, pulp weight, antioxidant content and two only accessions (P-12, P-15). The second quadrant is loaded with four characteristics (reducing sugar, total sugar, TSS, and titrable acidity) and comprises only one accession *i.e.*, P-6. The third quadrant is composed of only one character (cap length) and four accessions (P-2, P-5, P-7 and P-9). Out of the remaining three characters (ascorbic acid, fruits per spikelet and fruits per bunch), ascorbic acid was placed on the border of the first and fourth quadrants. It showed the remaining seven accessions, namely P-1, P-3, P-4, P-8, P-10, P-13 and P-14.

Hamad *et al.* (2015) reported two principal components (PC1 and PC2) accounting for 49.6% of the cumulative variance. The Bi-Plot of the PCA characters expressed well distribution within the quadrants and association of the characters with the date palm accessions. These outcomes of the principal component study

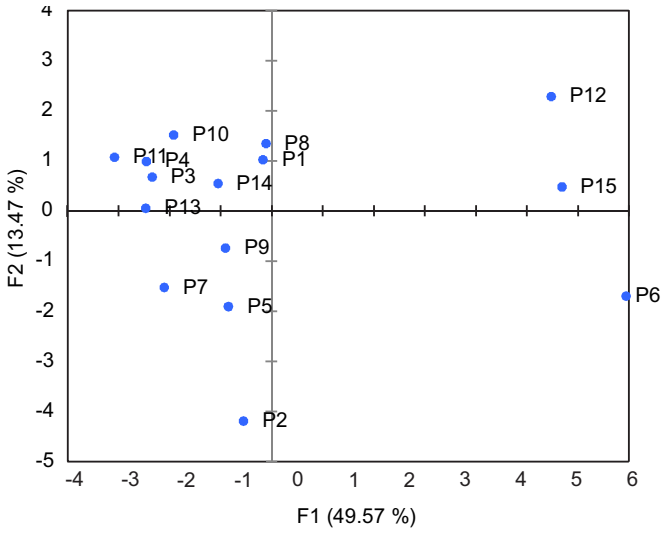

Fig. 3. Scoring Bi-Plot representation of date palm accessions in association with various qualitative traits

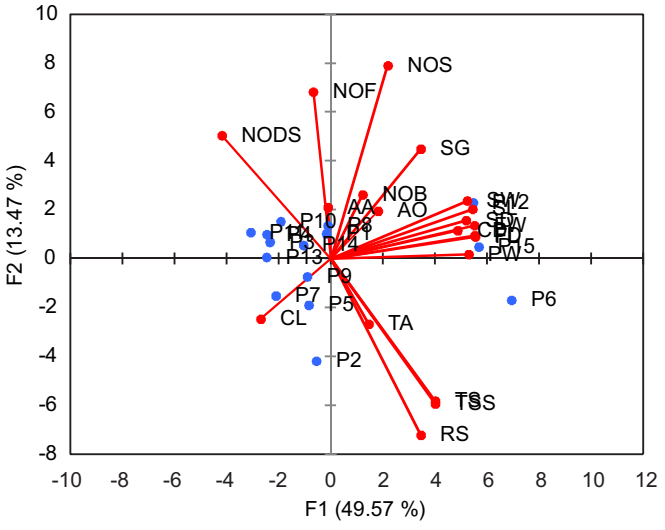

Fig. 4. Loading Bi-Plot representation of date palm accessions in association with various qualitative traits

partially agree with the most recent investigation results of Ahmad *et al.* (2023). Khierallah *et al.* (2011) analyzed PCA based on twenty-two SSR loci contributing 57% of the total variation and the PCA Bi-plot exhibited three date palm accessions in the first quadrant, eleven in the second quadrants, six in the third quadrant and eight accessions in the fourth quadrant. In an experiment, four paramount principal components were found by Khierallah and Azhar (2016), representing 73.12% of the total variance and they found nine accessions in the first quadrant of PCA Bi-Plot, ten in the second quadrant, twelve in third quadrant and eight accessions in the fourth quadrant. Hamza *et al.* (2014) studied the quantitative traits loaded on the PC1, which accounted for 31.13% of total variation and PC2 accounted for 23.91 % of the total dissimilarity. Bi-plot analysis of fifty date palm cultivars has been done by Ahmad *et al.* (2023) based on two major principal components with a maximum variability of 57.82%. Principal component analysis for the observed variability between the date palm genotypes by Elboghdady *et al.* (2022) revealed that the first and second components (PC1 and PC2) exhibited 55.75 % ve association.

The biometric analysis of fifteen locally selected date palm genotypes revealed significant genetic diversity, with physical fruit characteristics showing more genetic stability than biochemical traits. UPGMA clustering grouped the genotypes into three main clusters, while principal component analysis identified five key components, with the first component contributing 49.5% of the total variability. The bi-plot further confirmed variability and associations among traits in Indian date palm accessions.

References

Ahmad, R., H.M. Ali, A. Lisek, W.F.A. Mosa, S. Ercisli and M.A. Anjum, 2023. Correlation among some phenological and biochemical traits in date palm (*Phoenix dactylifera* L.) germplasm. *Front. Plant Sci.*, 14: 1118069. http://doi.org/10.3389/fpls.2023.1118069.

Al-Alawi, R.A., J.H. Al-Mashiqri, J.S.M. Al-Nadabi, B.I. Al-Shihi and Y. Baqi, 2017. Date palm tree (*Phoenix dactylifera* L.): natural products and therapeutic options. *Front. Plant Sci.,* 8: 845. http://doi.org/10.3389/fpls.2017.00845.

Al-Harrasi, A., N.U. Rehman, J. Hussain, A.L. Khan, A. Al-Rawahi, S.A. Gilani, M. Al-Broumi and L. Ali, 2014. Nutritional assessment and antioxidant analysis of 22 date palm (*Phoenix dactylifera*) varieties growing in Sultanate of Oman. *Asian Pacific J. Tropic. Med.*, 7(Suppl 1):S591-S598. http://doi.org/10.1016/S1995-7645(14)60294-7.

Aljaloud, S., H. Colleran and S. Ibrahim, 2020. Nutritional value of date fruits and potential use in nutritional bars for athletes. *Food Nutri. Sci.,* 11: 463-480. http://doi.org/10.4236/fns.2020.116034.

Allam, A., K. Djafri, M. Bergouia, E. Khemissat, M. Tama and B. Taleb, 2021. Morphological and physicochemical characterization of date palm cultivars from Ghardaïa (Southeast Algeria). *J. Appl. Life Sci. Env.*, 1(185): 12-24. https://doi.org/10.46909/journalalse-2021-0.

Alrashidi, A.H.M., A. Jamal, M.J. Alam, L. Gzara, N. Haddaji, N. Kachout, A. Abdelgadir, R. Badraoui and S. Elkahoui, 2023. Characterization of palm date varieties (*Phoenix dactylifera* L.) growing in Saudi Arabia: Phenotypic diversity in Saudi Arabia: Phenotypic diversity estimated by fruit and seed trait. *Notul. Bot. HortiAgrobot. Cluj-Napoca*, 51(1): 12996. http://doi.org/10.15835/nbha51112996

Al-Shwyeh, H.A. 2019. Date Palm (*Phoenix dactylifera* L.) fruit as potential antioxidant and antimicrobial agents. *J. Pharmacol. Biol. Sci.*, 11(1): 1-11. http://doi.org/10.4103/jpbs.JPBS_168_18.

AOAC (Association of Official Analytical Chemists) 1990. *Official Methods of Analysis* Vol-I (15th Edition) Ed: Kenneth Helrich, AOAC, Virginia, pp:83.

Ashraf, V.Z. and E.Z. Hamidi, 2011. Date and date processing: a review. *Food Rev. Int.*, 27: 101-133. http://doi.org/10.1080/87559129.2010.535231.

Bahraminejad, A. and G. Mohammadi-Nejad, 2015. Genetic diversity analysis of date palm (*Phoenix dactylifera* L.) genotypes using RAPD markers. *Ann. Res. Rev. Biol.*, 5(1):41-47.

Brand-Williams, W., M.E. Cuvelier and C. Berset, 1995. Use of a free radical method to evaluate antioxidant activity, *LWT - Food Sci. Tech.*, 28(1): 25-30. https://doi.org/10.1016/S0023-6438(95)80008-5.

Debabeche, K., A. Bouafia and A. Bencheikh, 2023. Phenotypic diversity of date palm varieties (*Phoenix dactylifera* L.) from southwest Algeria estimated by fruit characteristics. *Acta Agri. Sloven.*, 119(1): 1–10. Http://doi.org/10.14720/aas.2023.119.1.2611

Elboghdady, A., A.H. Gomma, A.M. Hamed and A.M. Abdallatif, 2023. Assessment of phenotypic diversity of some date palm male genotypes growing under Egyptian conditions. *Revist. Brasil. Frutic.*, v.45, e-896. https://dx.doi.org/10.1590/0100-29452023896.

Gomez, K.A. and A.A. Gomez, 1984. *Statistical Procedures for Agricultural Research,* John Willey & Sons, Canada, pp: 187-240.

Hamad, I., H. Abd-Elgawad, S. Al-Jaouni, G. Zinta, H. Asard, S. Hassan, M. Hegab, N. Hagagy and S. Selim, 2015. Metabolic analysis of various date palm fruit (*Phoenix dactylifera* L.) cultivars from Saudi Arabia to assess their nutritional quality. *Molecules*, 20: 13620-13641. http://doi.org/10.3390/molecules200813620.

Hammami, Z., H. Mahmoudi, A. Al-Janaahi and R.K. Singh, 2024. Evaluation of date palm fruits quality under different irrigation water salinity levels compared to the fruit available in the market. *Front. Sust. Food Syst.*, 7: 1322350. http://doi.org/10.3389/fsufs.2023.1322350.

Hamza, A.M., A. Collins, S.G. Ado, C.E. Ikuenobe, C.D. Ataga and J.O. Odewale, 2014. Proximate compositions evaluation and viability among cultivars of date palm (*Phoenix dactylifera* L.) in Nigeria. *Int. J. Plant Soil Sci.*, 3(3): 248-259.

Ibrahimi, M., N. Brhadda, R. Ziri, M. Fokar, D. Iraqi, F. Gaboun, M. Labhilili, A. Habach, R. Meziani, J. Elfadile, A. Abdelwahd and G. Diria, 2023. Analysis of genetic diversity and population structure of Moroccan date palm (*Phoenix dactylifera* L.) using SSR and DAMD molecular markers. *J. Genet. Eng. Biotechnol.*, 21: 66. https://doi.org/10.1186/s43141-023-00516-7.

Ioannis S.A., 2010. Carbohydrates (Chapter 14), In: Irradiation of Food Commodities, Eds: Ioannis S. Arvanitoyannis, Academic Press, pp: 561-605. https://doi.org/10.1016/B978-0-12-374718-1.10014-8.

Jamil, S., R. Shahzad, S. Kanwal, E. Yasmeen, S.U. Rahman and M.Z. Iqbal, 2020. DNA fingerprinting and population structure of date palm varieties grown in Punjab, Pakistan using Simple Sequence Repeat markers. *Int. J. Agric. Biol.*, 23(5): 943-950. http://doi.org/10.17957/IJAB/15.1373

Khalilia, W.M., R. Abuamsha, N. Alqaddi and A. Omari, 2022. Phenotypic characterization of local date palm cultivars at Jericho in Palestinian Jordan Valley District. *Ind. J. Sci. Tech.*, 15(20): 989-1000. https://doi.org/10.17485/IJST/v15i20.2381.

Khierallah, H.S.M. and H.D. Azhar, 2016. Study of genetic diversity of Iraqi date palms using some morphological markers. *Int. J. Curr. Microbiol. Appl. Sci.*, 5(3): 317-327. http://dx.doi.org/10.20546/ijcmas.2016.503.039

Khierallah, H.S.M., S.M. Bader, M. Baum and A. Hamwieh, 2011. Genetic diversity of Iraqi date palms revealed by microsatellite polymorphism. *J. Eur. Soc. Hort. Sci.*, 136(4): 282-287.

Kumar, M., P. Deb and P.K. Mukherjee, 2024. Fruit physicochemical and antioxidant properties of wild date palm (*Phoenix sylvestris* Roxb.) accessions under the western part of West Bengal. *J. Appl. Hort.*, 26(1): 15-20. https://doi.org/10.37855/jah.2024.v26i01.03.

Lane, J.H. and L. Eynon, 1923. Methods for determination of reducing and non-reducing sugars. *J. Sci.*, 42: 32-37.

Ranganna, S., 1986. *Handbook of Analysis and Quality Control of Fruit and Vegetable Products*. 2nd Edition, Tata McGrow-Hill Education, New York.

Salomón, T.R., R. Krueger, J.P.G. Vázquez, R.V. Angulo, C.V. Angulo, N.O. Uribe, J.A.S. Uribe and L.S. Sandoval, 2021. Date palm pollen: features, production, extraction and pollination methods. *Agron.*, 11: 504. https://doi.org/10.3390/agronomy11030504.

Sedra, My Hassan, Philippe Lashermes, Pierre Trouslot and Marie-Christine Combes, 1998. Identification and genetic diversity analysis of date palm (*Phoenix dactylifera* L.) varieties from Morocco using RAPD markers." *Euphytica* 103(1): 75-82.

Sharma, A. and M. Murlidhar, 2021. An update on uses, benefits and potential application of Neera. *J. Nutri. Food Proc.*, 4(8): 1-18. http://doi.org/10.31579/2637-8914/072.

Tengberg, M., 2014. Date Palm: Origins and development. In: *Encyclopedia of Global Archaeology*, Ed: Smith, C., Springer, New York, https://doi.org/10.1007/978-1-4419-0465-2_2175.

Received: September, 2024; Revised: September, 2024; Accepted: October, 2024