

BIODIVERSITY AMONG INDIAN JUJUBE (*ZIZIPHUS MAURITIANA* LAMK.) GENOTYPES FOR POWDERY MILDEW AND OTHER TRAITS

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Abstract. Indian ber (*Ziziphus mauritiana* Lamk.) is one of the most ancient fruits indigenous to India. It grows throughout the tropical, sub-tropical and arid regions. There is little information available on the genetic diversity of this important underutilized fruit crop. The reduction of genetic variability makes the crop vulnerable to diseases and other adverse factors. Morphological variation among thirty five important ber genotypes collected from different parts of India were studied at CCS Haryana Agricultural University, Hisar, India, during 2005-2006. Ten morphological traits viz., powdery mildew, leaf length, leaf breadth, leaf area, fruit weight, fruit length, fruit breadth, stone weight, stone length, stone breadth were recorded and data analyzed by using Mahalanobis's D^2 Statistic using Tocher's method. All the genotypes were classified into VII distinct clusters. Cluster I was the largest with nine genotypes followed by cluster IV (six genotypes). Clusters VI and VII were the most divergent with an inter cluster distance of 5.162. This suggests that the parents for hybridization could be selected especially for powdery mildew resistance (Sanori No. 5, Noki and Mirchia) and smaller stone size (Illaichi and Kishmish) from these diverse clusters, in order to develop useful disease resistant and smaller stone size breeding material for Indian jujube.

Key words: *Ziziphus*, biodiversity, India, powdery mildew, resistance

INTRODUCTION

Indian jujube is an important fruit crop, grown in the tropical, sub-tropical and arid regions of world. It belongs to family *Rhamnaceae*. The ripe fruits are mostly consumed raw but they can also be prepared candid, dried and powder. The leaves can be consumed by camels, goats, cattle and are nutritive. Nutritionally, the ripe fruit is richer than apple in protein, phosphorus, calcium, carotene and vitamin C (Bal and Mann, 1978). Ripe fruit provides 20.9 Kcal per 100 g pulp. It is rich source of ascorbic acid 70-165 mg/100 g pulp and contains 70 IU vitamin A. The plants remain dormant during summer (May and June) in northern Indian states to reduce the moisture loss. Powdery mildew *Oidium erythroides* f. *zhizhyphi* Fr. causes varying degree of losses in ber in different parts of the world. The commercial cultivars like Gola, Kaithli, Umran, Laddu, Kala Gola etc. are most susceptible to powdery mildew under high input management conditions rendering the entire produce unmarketable (Pardeep and Jambhale, 2001). Hence, an effort was made to identify genotypes, which are source of resistance to powdery mildew in *Ziziphus* for initiating resistance breeding programme. There are many methods, such as Mahalanobis's D^2 Statistic described (Rao, 1952) to represent variation. Although D^2 Statistics is a quantitative measure of genetic divergence, but the clustering pattern of the genotypes is arbitrary (Saran *et al.*, 2006). In the present study, genotypes were subjected to non-hierarchical Euclidean cluster

analysis to overcome the limitations of D² Statistics. The information on the nature and degree of genetic diversity could be helpful for further improvement through hybridization.

MATERIAL AND METHODS

Location and site characteristics: The present investigations were carried out at the experimental orchard of CCS Haryana Agricultural University, Hisar, India, during 2005-2006. This place is located (at latitude 29.10°N and longitudes 75.46°E) at an altitude of 215.2 m above sea, about 165 km west of New Delhi, the capital of India. Though the wild trees of this species are found up to 1650 m, the commercial cultivation of this crop extends only up to 1000 m height with the summers quite hot and dry.

Plant materials: Genotypes for ber fruit were introduced from different parts of India. Thirty five ber accessions (Table 1) were selected for the present studies. The morphological traits, such as powdery mildew, leaf length, leaf breath, leaf area, fruit weight, fruit length, fruit breath, stone weight, stone length and stone breath were determined.

Table 1

List of Indian jujube genotypes

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	Gola Gurgaon	13.	Popular Gola	25.	Mundia Murhara
2.	Chonchal	14.	Laddu	26.	Chuhara
3.	Kathaphal	15.	Noki	27.	Thornless
4.	Dandan	16.	Safeda Rohtak	28.	Ziziphus mauritiana elongate
5.	Sandhura Narnaul	17.	Z.G.-3	29.	Sanori No. 5
6.	Illaichi	18.	Sanori No. 1	30.	Golar
7.	Banarasi Karka	19.	Kaithali	31.	Sua
8.	Triloki No. 1	20.	Narikali	32.	Seo
9.	Kala Viola	21.	Gola Gurgaon-2	33.	Illaichi Jhajjar
10.	Sanori No. 3	22.	Katha Gurgaon	34.	Kishmish
11.	Safeda Selection	23.	Katha Rajasthan	35.	Mirchia
12.	B.S.-2	24.	Umran		

Experimental design: Thirty five genotypes of *Ziziphus mauritiana* (Table 1) were studied for ten morphological characters as listed in Table 2. The selected genotypes planted at 8 m x 8 m spacing in RBD with three representative plants of twenty five year age, having uniform training and pruning budded on *Ziziphus rotundifolia* root stock contributed as experimental plant material.

Data collection: Ten morphological traits (Table 2) were observed during 2005-06.

Table 2

Morphological traits used in biodiversity evaluation

Sr. No.	Morphological traits	Unit	Measured by
1.	Powdery mildew	%	counting
2.	Leaf length	cm	Verniers calliper
3.	Leaf breath	cm	Verniers calliper
4.	Leaf area	Square cm	Leaf aera meter
5.	Fruit weight	g	Electronic balance
6.	Fruit length	cm	Verniers calliper
7.	Fruit breath	cm	Verniers calliper
8.	Stone weight	g	Electronic balance
9.	Stone length	cm	Verniers calliper
10.	Stone breath	cm	Verniers calliper

Data were again collected at harvesting for 10 traits as mentioned in plant materials. From the analysis of variance and covariance, the error variance and covariance values were subjected to multivariate analysis. The original correlated variables (x's) were first transformed into uncorrelated ones (Y's as linear function of X's) and then D^2 values were worked out. Pivotal condensation method was used to computer inverse matrix of the error dispersion matrix. The generalized distance function (D^2) between the two genotypes is simply the sum of squares of differences in Y's i.e.

$$D^2_{1,2} = \sum_{i=1}^P (Y_{1i} - Y_{2i})^2$$

$$D^2_p = \sum_{i=1}^P \sum_{j=1}^P (W_{ij} - d_i d_j)$$

where D^2_p is the D^2 -value between the variables on the basis of P characters, W_{ij} is the inverse matrix of the pooled common dispersion obtained from error matrix, 'd' is the difference in mean value for the characters of respective genotypes as indicated by i and j.

Diverse between any two populations was obtained as sum of squares of difference in the values of corresponding entries using D^2 statistic. Based on the D value, the entire germplasm was classified into distinct clusters, grouping together the less divergent genotypes according to Tocher's method. Dendogram and pairwise dissimilarities according to Euclidean Square distance.

RESULTS AND DISCUSSION

The significant values of mean sum of squares from the analysis of variance (Table 3) revealed the presence of significant variability among the genotypes for all the characters investigated. But such analysis is unable to tell anything about the extent of genetic diversity.

Table 3

Analysis of variance

Source of replication	d.f.	Powdery mildew	Leaf length	Leaf breath	Leaf area	Fruit weight	Fruit length	Fruit breath	Stone weight	Stone length	Stone breath
Replication	2	50.25	0.53	1.5	10.87	0.47	0.01	0.01	0.00	0.17	0.01
Treatment	34	1490.42	213.2	2.17	197.3	52.97	2.17	0.32	0.16	0.93	0.06
Error	68	72.12	22.73	0.14	6.83	0.61	0.01	0.00	0.00	0.02	0.00
CV (%)		19.56	6.28	7.57	9.28	5.64	2.34	1.94	9.93	5.72	8.08

To overcome this problem and simultaneously to quantify genetic divergence between any two genotypes or groups of genotypes, the thirty five ber genotypes were grouped into seven clusters on the basis of their relative magnitude of D^2 values, in such a way that the D^2 values within the cluster had been lower than those belonging to different clusters. The distribution pattern of genotypes in different clusters is presented in Table 4. It revealed that with unweighted pair group using arithmetic mean (Mahalanobis Euclidean Square Distance) cluster analysis, the 35 ber genotypes fell into 7 clusters. The first cluster comprised of 9 germplasm, while second cluster comprised of six genotypes, cluster fifty and eighth comprise 4 each, while third, fourth and sixth containing 3, 7 and 2 respectively. Likewise dissimilarities of ber genotypes according to Squared Euclidean Distance showed that

genotypes Safeda Selection, Laddu, Umran, Katha Rajasthan, Sua and Dandan were close to each other. A maximum dissimilarity was observed between genotypes Mirchia, Golar of group six and Illaichi, Illaichi Jhajjar and Kishmish of group seven as given in both the diagrams (Figure 1 - Standard Euclidean and Figure 2 - Euclidean Distance).

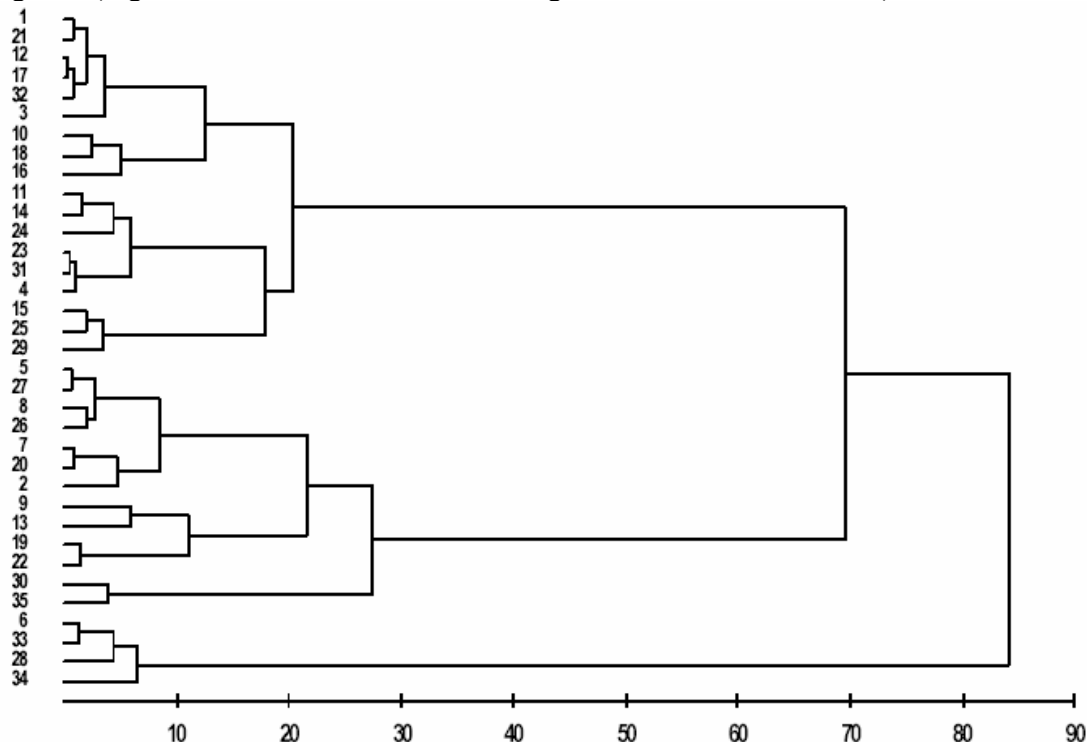


Figure 1. Ward's Minimum Variance Dendrogram; Standardized Euclidean² Distance

The intra and inter-cluster average D^2 values are depicted in Table 5. Intra cluster distance ranged from 2.300 (II) to 2.835 (VII). The inter-cluster distance varied from 0.17 or 2.300 (between I and II) to 5.690 or 7.944 (between cluster VI and VII).

Table 4

Classification of ber genotypes in different clusters

Cluster	No. of genotypes	Name of genotype
I	9	Gola Gurgaon-3, Gola Gurgaon-2, Bawal Selection-2, Z.G.-3, Seo, Kathaphal, Sanori No. 3, Sanori No. 1, Safeda Rohtak
II	6	Safeda Selection, Laddu, Umran, Katha Rajasthan, Sua, Dandan
III	3	Noki, Mundia Murhara, Sanori No. 5
IV	7	Sandhura Narnaul, Thornless, Triloki No. 1, Chhuhara, Banarasi Karka, Narikali, Chanchal
V	4	Kala Gola, Popular Gola, Kaithali, Katha Gurgaon
VI	2	Golar, Mirchia
VII	4	Illaichi, Illaichi Jhajjar, Z.M. elongate, Kishmish

The inter cluster average D^2 values were higher than any intra cluster D^2 values. In the present investigation, the maximum genetic diversity was observed in between cluster VI and VII followed by cluster III and VII, which is indicative of getting more heterotic F1's and promising segregants in the subsequent segregating generations if the genotypes possessing maximum genetic distances are involved in hybridization programme.

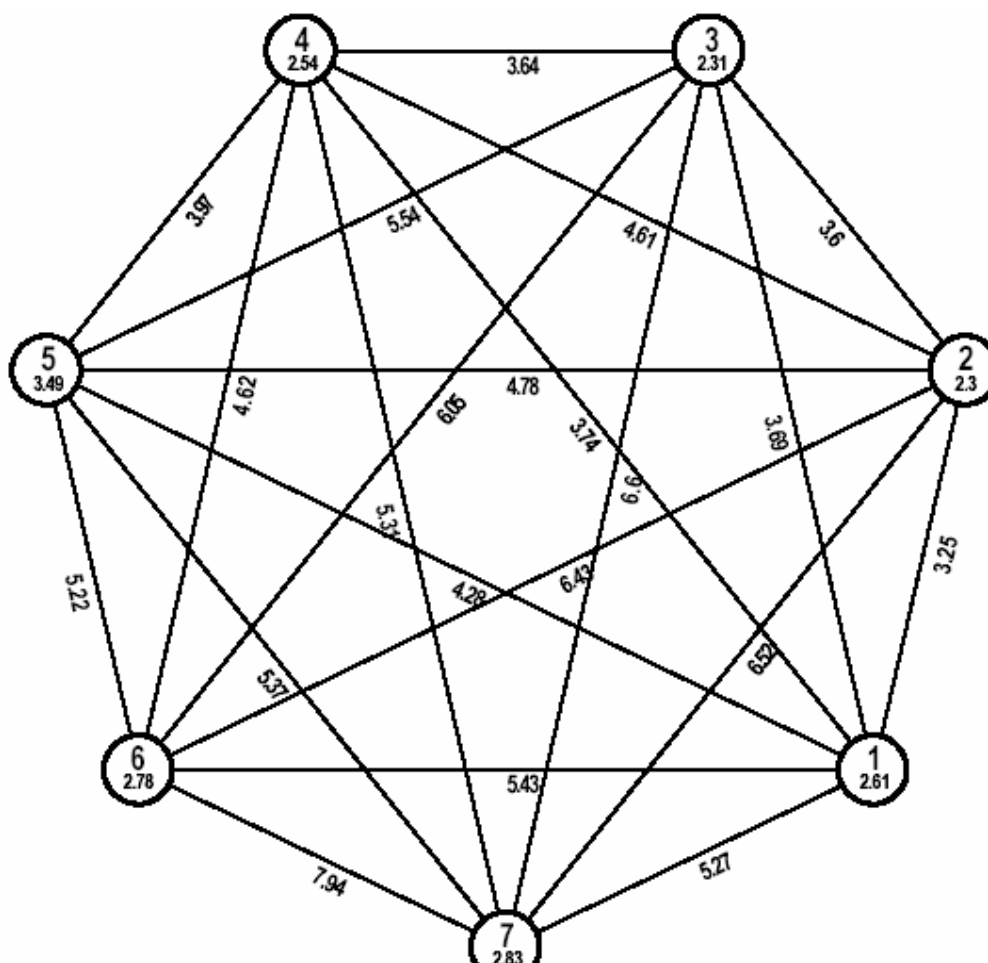


Figure 2. Euclidean Distance (Not to the Scale)

Table 5

Intra (diagonal) and inter cluster D^2 (average) values among ber genotypes

Cluster	I	II	III	IV	V	VI	VII
I	2.606	3.252	3.690	3.737	4.276	5.433	5.265
II		2.300	3.598	4.608	4.781	6.432	6.517
III			2.312	3.637	5.539	6.047	6.596
IV				2.535	3.972	4.625	5.311
V					3.485	5.219	5.365
VI						2.782	7.944
VII	-	-	-	-	-	-	2.835

The cluster mean values of different traits under study are presented in Table 6. The cluster means for different traits were reflections of genetic differences among the clusters. The clusters showed differences with each other for one or more traits.

Cluster VI had minimum powdery mildew (22.83%), maximum leaf length (12.63 cm), leaf breadth (6.35 cm), leaf area (45.72 cm), fruit weight (19.59 g), fruit length (4.83 cm). Cluster II had highest cluster mean value for fruit breadth (3.05 cm), while cluster VII has lowest stone weight (0.32 g), stone length (1.40 cm) and stone breadth (0.67 cm). The cluster VI and VII performed outstanding on the basis of better cluster means for most of the characters.

Table 6

Cluster-wise mean values of 10 traits in ber genotypes

Sr. No.	Cluster	Powdery mildew (%)	Leaf length (cm)	Leaf breath (cm)	Leaf area (cm ²)	Fruit weight (g)	Fruit length (cm)	Fruit breath (cm)	Stone weight (g)	Stone length (cm)	Stone breath (cm)
1.	I	34.29	9.00	4.81	26.88	13.59	3.48	2.79	0.82	2.05	0.93
2.	II	67.77	8.02	4.18	20.64	17.35	3.59	3.05	0.84	2.11	0.95
3.	III	27.00	7.86	3.76	18.00	16.85	4.61	2.74	0.87	2.85	0.79
4.	IV	34.812	9.67	4.89	30.42	13.63	4.56	2.49	0.61	2.82	0.69
5.	V	77.41	9.80	5.90	37.08	13.12	3.74	2.65	0.52	2.20	0.75
6.	VI	22.83	12.63	6.35	45.72	19.59	4.83	2.93	0.87	3.09	0.78
7.	VII	31.08	9.30	4.90	28.18	4.85	2.24	2.00	0.32	1.40	0.67

DISCUSSION AND CONCLUSIONS

In this study, genotypes were grouped in seven clusters. The cluster I possessed maximum number of genotypes (nine) followed by cluster IV (seven) while minimum was in cluster VI (two). The genetic divergence had little relationship with the geographic distance as observed by the random pattern of distribution of genotypes into various clusters. Likewise, genotypes from different sources were grouped in the same cluster, thus suggesting that geographical diversity does not necessarily represent genetic diversity. The findings of the present study are supported by Saran et al. (2006) and Rai et al. (2002).

Table 7

Diverse and superior genotypes selected from different clusters

Genotypes	Cluster	Characters/traits
Sanori No. 5, Noki, M. Murhara	III	Powdery mildew
Mirchia, Golar	VI	Powdery mildew tolerance, fruit weight, leaf area etc.
Kishmish, Illaichi, Illaichi Jhajjar	VII	Stone size (length and breath)

In the present investigation, the highest genetic distance among genotypes existed between cluster VI and VII (7.944) followed by cluster VII and VII (6.596). Among these clusters, only cluster VI had lowest cluster mean values for powdery mildew and highest for leaf and fruit traits, while cluster VII also had lowest cluster value for stone traits. Powdery mildew tolerance (22.83%), maximum size of leaf (45.72), fruit weight (19.59 g) and related traits to yield and lowest stone values like stone weight (0.32 g), stone length (1.40 cm) and stone breath (0.67 cm) are very important in choosing parents for cross combinations likely to generate the highest possible variability for various economic traits in ber genotypes, for yield and contributing traits (Saran et al., 2006).

Genetic divergence using Mahalanobis's D^2 Statistic was studied in a population of 35 ber genotypes. The genotypes differed significantly for ten traits studied and grouped into seven clusters based on similarities of D^2 values. Maximum inter cluster distance (7.944) was observed between cluster VI and VII. The parents for hybridization could be selected on the basis of their greater inter-cluster distance for isolating useful recombinations in the next generation. Therefore, to improve various characters like powdery mildew tolerance, fruit size (larger) and smaller stone size in ber diverse genotypes like Illaichi, Mirchia, Kishmish, etc. (Table 7), they can be utilized for hybridization programme as well as for introducing their useful traits in the commercial ber cultivars.

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REZUMAT

BIODIVERSITATEA EXISTENTĂ ÎNTRE DIFERITE GENOTIPURI DE *Ziziphus mauritiana* Lamk. DIN INDIA PENTRU REZISTENȚA LA FĂINARE ȘI ALTE CARACTERISTICI DE INTERES

Ziziphus mauritiana Lamk. este una dintre cele mai vechi specii fructifere indigene în India, crescând în regiunile tropicale, subtropicale și aride ale țării.

Există relative puține informații disponibile referitoare la diversitatea genetică a acestei importante specii fructifere, dar cu un potențial insuficient exploatat. Reducerea variabilității genetice în cadrul speciei induce riscul vulnerabilității plantelor la atacul agenților patogeni și a diverșilor factori adversi. Variabilitatea morfologică existentă între 35 de genotipuri valoroase de *Ziziphus* colecționate din diferite părți ale Indiei a fost studiată la Universitate Agricolă CCS Haryana, Hisar, India, în perioada 2005-2006. Zece caractere morfologice, respective comportarea la fâinare, lungimea frunzelor, lățimea frunzelor, suprafața frunzelor, greutatea frunzelor, greutatea fructelor, lungimea fructelor, lățimea fructelor, greutatea semințelor, lungimea semințelor, lățimea semințelor au fost urmărite și analizate statistic prin testul D^2 Mahalanobis, folosindu-se metoda Tocher. Toate genotipurile au fost clasificate în VII grupe sau "ciorchini" (clusters) distincți. Grupa I a cuprins cele mai mult genotipuri (nouă), aceasta fiind urmată de grupa IV, cu șase genotipuri. Grupele VI și VII au prezentat cea mai amplă divergență a genotipurilor în interior, distanța inter-cluster de 5.162 sugerând că pot fi selecționate unele genotipuri utile pentru ameliorarea speciei. Astfel de genotipuri pot fi utilizate ca genitori, în hibridări artificiale, în vederea obținerii de descendenți rezistenți la fâinare (ex. Sanori No. 5, Noki and Mirchia), sau cu mărime mică a sâmburilor (Illaichi and Kishmish).