



## Genetic divergence in Lehsua (*Cordia myxa* Roxb.)

B. L. Nagar and M. S. Fageria<sup>1</sup>

Department of Horticulture, S. K. N. College of Agriculture, Jobner 303 329

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Lehsua or Gonda or Indian Cherry (*Cordia myxa* Roxb.) is a minor fruit that grows throughout India in arid and semi-arid regions. Green mature fruits are utilized for making good quality of the pickle and vegetable purpose while nutritive ripe fruits have mucilage and may be used for fresh consumption and liquor. The fruits are used as medicine, astringent, anthelmintic, diuretic, demulcent and expectorant. Genotypes are essential in order to develop superior recombinants/ varieties [1]. In chilli, the genetic divergence among parents was estimated by Mahalanobis  $D^2$  statistics; later these divergent parents were used for hybridization [1]. Keeping all facts in view the present study was initiated to estimate the genetic divergence present in a set of 15 provenances of lehsua.

The investigation was carried out during 2001-02 and 2002-03 in 15 provenances of lehsua selected from five major lehsua growing districts of Rajasthan. The experiment was conducted in randomized block design with three replications. The plants were having age of 10 years. The genetic diversity among the genotypes was worked out using Mahalanobis  $D^2$ -statistics as described by Rao [2]. On the basis of the magnitude of  $D^2$  values, Tochers method as described by Rao [2] was employed to group the genotypes into different clusters.

Pooled analysis of variance revealed significant mean square estimates for all the characters indicating sufficient diversity among genotypes. Based on divergence and magnitude of  $D^2$  values, 15 provenances were grouped in to six clusters (Table 1). The distribution of different genotypes revealed that cluster I having maximum number of genotypes (7), cluster II, cluster III and cluster IV had two genotypes each whereas, clusters V and VI, both having one genotypes each. The genotypes had distributed randomly in different clusters irrespective of geographic origin. Further, the grouping of genotypes did not show any relationship between genetic divergence and geographic diversity.

**Table 1.** Clustering pattern of lehsua genotypes in differed clusters and their place of acclimatization (Based on two years pooled mean)

Cluster No.	Number of accessions	Constituent genotypes	Place of acclimatization
I	7	Bagolye, Devnagar, Chopasani, Doli, Sojat, Sura, Sharath	Ajmer, Jodhpur, Pali, Jalore
II	2	Sagarifarm, Santhu	Jodhpur, Jalore
III	2	Sadri, Rawatsar	Pali, Barmer
IV	2	Siwana, Karna	Barmer
V	1	Ranawas	Pali
VI	1	Gahnehra	Ajmer

The same observations were also reported by earlier workers [3, 4]. The genetic drift and selection in different environments could cause greater diversity than geographic distance [5].

The inter-cluster and intra-cluster distance of 15 genotypes is presented in table 2. Maximum intra-cluster distance observed in cluster III ( $D^2 = 27.76$ ) while minimum in cluster I. Maximum inter cluster distance

**Table 2.** Average inter- and intra-cluster (Diagonal)  $D^2$  and D (in parenthesis) values for different lehsua provenances (pooled mean of 2001-02 and 2002-03)

Clusters No.	I	II	III	IV	V	VI
I	15.29 (3.91)	28.22 (5.31)	39.58 (6.32)	29.39 (5.42)	17.22 (4.15)	28.22 (5.31)
II		17.58 (4.19)	44.89 (6.70)	39.11 (6.25)	28.44 (5.33)	8.79 (2.96)
III			27.76 (5.27)	24.16 (4.91)	38.33 (6.19)	44.89 (6.70)
IV				0.00 (0.00)	31.26 (5.59)	39.11 (6.25)
V					20.96 (4.58)	28.44 (5.33)
VI						17.58 (4.19)

<sup>1</sup>Present address: Department of Horticulture, Agricultural Research Station, Durgapura, Jaipur 302 018

observed between cluster III and VI, II and III which can be expected to exert high heterotic effect in the hybrids when crossed and consequently may generate desirable segregants. The minimum inter-cluster distance observed was between cluster II and VI. The cluster II and VI were characterized by the highest fruit weight, tallest plant, maximum fruit diameter and pulp : seed ratio with minimum fruits per cluster. On the contrary, cluster IV showed the minimum plant spread and fruit weight (Table 2). The contribution of individual character towards divergence is presented in Table 3. Leaf width showed no contribution towards the genetic diversity. The characters like fruit weight (32.38%) followed by fruits per cluster (23.81%) and plant height (10.48) contributed maximum towards genetic divergence.

**Table 3.** Cluster mean of various characters in lehsua (pooled mean of 2001-02 and 2002-03)

Characters	Clusters						Contribution towards divergence %
	I	II	III	IV	V	VI	
Plant height (m)	7.26	7.32	7.30	7.08	6.39	7.32	10.48
Plant spread (m <sup>2</sup> )	50.72	43.13	60.50	38.94	46.21	43.13	4.76
Fruits/cluster	14.86	9.42	10.59	12.33	12.39	9.42	23.81
Fruit diameter (cm)	2.59	2.76	2.32	2.26	2.24	2.76	9.52
Pulp: seed ratio	2.61	2.73	2.27	2.25	2.19	2.73	2.86
T.S.S. (° Brix)	6.86	7.01	6.35	7.05	5.80	7.01	3.81
Acidity (%)	0.094	0.095	0.095	0.090	0.082	0.095	2.86
Leaf length (cm)	13.95	14.69	14.54	15.43	12.14	14.69	9.52
Leaf width (cm)	12.56	12.69	13.33	13.97	10.81	12.69	0.00
Fruit weight (g)	15.59	16.88	12.17	11.38	13.45	16.88	32.28

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