

Full Length Research Paper

Genetic variation for physicochemical characteristics in Lehsua (*Cordia myxa* L.)

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The experiments were carried out to study the genetic variation in Lehsua (*Cordia myxa* L.) in Thar desert of Rajasthan, India. The variability parameters were studied for physicochemical characters in 15 provenance of Lehsua. The genetic variation was recorded for fruits per cluster, fruit diameter, pulp:seed ratio, fruit weight and total soluble solids (TSS). Most of the characters especially fruits per cluster, fruit weight, fruit diameter and TSS had high heritability and genetic advance as percentage of mean indicating that these to be more under genetic control. The large extent of variation observed in them can be exploited for genetic improvement of this species.

Key words: Lehsua, provenances, heritability, genetic advance, phenotypic coefficient of variation, genotypic coefficient of variation.

INTRODUCTION

Lehsua or Gonda or Indian cherry (*Cordia myxa* L.) is an underutilized fruit that grows throughout India in arid and semi-arid regions. Besides India, it is also found in Myanmar, Egypt, Sri Lanka and tropical Australia (McCann, 1985). Lehsua belongs to family Boraginaceae, probably originated in India. The plant is medium sized tree, and can tolerate drought and moderate shade. Yet, it is not grown in orchards and grows in wild state in wastelands along farm boundaries or on road side. The tree also are seen on farm lands as scattered solitary tree. Green mature fruits are utilized for making good quality 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. They are also used in diseases of the chest and urinary passage (Anon., 1940). The fruit pulp is used as birdlime. The kernels are used for curing ringworm

(McCann, 1985). Fruits are rich source of carbohydrates, phosphorus and contain 40 mg/100 g of ascorbic acid (Pareek and Sharma, 1993).

Study of variation is the first step for any breeding programme. Effective tree breeding depends on an understanding of tree variation in nature and preserving such variation for future use. Vavilov (1951) was the first who realized that a wide range of variability in any crop provided a better chance of selection of desirable types. Most successful tree improvement programmes are those in which proper provenance or provenances are used (Zobel and Talbert, 1984). The morphological and physiological traits exhibit a significant amount of genetic variation both within and between plant populations (Stern and Roche, 1974). The objective of the present study was to assess the natural variation in Lehsua for important physicochemical traits so as to select the best plant material for multiplication or for future use in

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breeding programme.

MATERIALS AND METHODS

Study sites and sampling design

A pilot survey of population of *C. myxa* L. in Thar desert of Rajasthan State of India was undertaken to identify the sites, where this species occurs in the wild state. The sampling procedure includes delineation of the whole area, under the species into a number of sites depending upon the aspect variation in morphological characters. In this way, 15 sites were selected in 5 districts of Rajasthan namely, Ajmer (Bagolye, Gahnehra, Devnagar), Jodhpur (Sagari farm, Chopasani, Doli), Pali (Sadri, Ranawas, Sojat), Jalore (Santhu, Sura, Sharath) and Barmer (Siwana, Karna, Rawatsar).

Observations recorded

Three natural occurring trees of *C. myxa* having approximately the same age, height and diameter were selected within each site as per the methods adopted by Dumitriu-Tataranu (1970). These trees were marked for recording the collection of fruits for recording observations on different physicochemical characteristics.

Fruits/cluster was calculated by counting the total number of fruits in each cluster, in a tagged shoot. Twenty (20) fruits from each of the selected trees were collected depending upon their direction, that is, 5 from north, 5 from south, 5 from east and 5 from west and mixed together. Fruit weight was recorded with the help of a pan balance with sensitivity of 1 mg. Weight of 20 fruits was divided by total number of fruits to get the average fruit weight. Fruit diameter of these selected 20 fruits were measured in cm using Vernier caliper and averaged.

Pulp weight of randomly selected 20 fruits per tree was estimated by deducting stone weight from the total fruit weight. Then pulp weight was divided by stone weight to calculate pulp:seed ratio and average was worked out. Total soluble solids (TSS) and acidity was calculated as method described by AOAC (1990).

Statistical analysis

The data obtained were subjected to analysis of variance using randomized block design as described by Panse and Sukhatme (1995). The 15 sites were considered as treatment and the individual tree at each site was taken as the replication. The statistical analysis for each parameter was carried out on mean values.

$$\sigma^2 g \text{ (Genotypic variance)} = \frac{(\text{Mean S.S. due to treatment} - \text{Error mean square})}{\text{Number of replications}}$$

$$\sigma^2 p \text{ (Phenotypic variance)} = (\sigma^2 g + \sigma^2 e),$$

Where $\sigma^2 e$ is the error variance for a trait.

The genotypic and phenotypic coefficients of variation were calculated by standard statistical procedures using the formula as suggested by Burton and Devane (1953) and Johnson et al. (1955). Heritability in broad sense was calculated by the formula given by Hanson et al. (1956) and was multiplied by 100 (Lush, 1940) to get percentage as shown below:

$$\text{Heritability (h}^2\text{)} = \frac{\sigma^2 g \times 100}{\sigma^2 p}$$

The expected genetic advance was calculated as suggested by Johnson et al. (1955).

$$\text{Genetic advance} = (h^2) \cdot (k) \cdot (\sigma^2 p)$$

Where, h^2 = heritability (broad sense); k = 2.06 (selection differential at 5% selection intensity); $\sigma^2 p$ = phenotypic standard deviation.

$$\text{Genetic advance as percentage of mean} = \frac{\text{GA} \times 100}{\text{Grand mean}}$$

RESULTS AND DISCUSSION

Mean fruits per cluster on pooled data basis varied from 7.17 to 17.50 with mean value of 12.70. S_1 provenance gave the highest mean fruits per cluster (17.50) which was statistically at par with S_6 and S_5 provenances. Minimum mean fruits per cluster (7.17) were recorded for S_8 provenance which was statistically at par with S_4 . Fruits per cluster recorded the highest value for coefficient of variation (12.30%). S_6 provenance gave the highest mean fruit diameter of 3.20 cm during both years of study followed by S_4 with diameter of 3.00 cm. Minimum fruit diameter of 2.26 cm was recorded for S_{13} provenance. Fruit diameter ranged between 2.26 and 3.20 cm with mean value of 2.60 cm and 8.17% coefficient of variation (Table 1). The ratio of pulp to seed was found to be between 2.20 and 2.99 (Table 1). S_5 provenance gave the highest mean pulp:seed ratio (2.99) during both years of study, which was statistically at par with S_4 , S_2 and S_3 . S_{15} provenance recorded the lowest value of 2.20 for pulp:seed ratio. Coefficient of variation for pulp:seed ratio was 10.37%. Fruit weight was observed to be maximum among the fruits collected from S_5 provenance with mean value of 17.55 g followed by S_4 and S_8 provenances. The lowest value of 11.38 g was recorded for S_{13} provenance which was statistically at par with S_{15} and S_7 . The fruit weight varied between 11.38 and 17.55 g with mean value of 15.16 g and contributed 9.05% coefficient of variation. It is evident from the data presented in Table 2 that TSS varied between 5.78 and 7.58° B with mean value of 6.71 and noticed 8.41% coefficient of variation. Maximum acidity was recorded from S_2 , S_7 and S_8 provenances with same value of 0.11%, while the lowest value of 0.08% was recorded from S_{15} provenance. The acidity varied between 0.08 and 0.11% with mean value of 0.096% and contributed 8.59% coefficient of variation. Fruits per cluster recorded the maximum phenotypic and genotypic variances of 19.43 and 16.99 followed by fruit weight, that is, 10.78 and 8.90, respectively (Table 2).

The increase in fruit size might be due to the enhanced synthesis of carbohydrates and water uptake and their movement into the fruits of capsicum (Miniraj and Shanmugavelu, 1987). The increase in fruit size might also been due to an enlargement of the cells in the fleshy part of the prunes fruits as have been observed by

Table 1. Extent of variation in physicochemical characteristics of *C. myxa* tree.

Code	Provenance	Fruits/cluster	Fruit diameter (cm)	Pulp: seed ratio	Fruit weight (g)	TSS (%)	Acidity (%)
S ₁	Bagolye	17.50	2.55	2.57	16.65	6.98	0.09
S ₂	Gahnehra	15.00	2.64	2.73	17005	6.25	0.11
S ₃	Devnagar	12.50	2.77	2.73	16.90	6.95	0.09
S ₄	Sagari Farm	8.83	3.00	2.80	17.45	7.33	0.09
S ₅	Chopasani	15.67	2.72	2.99	17.55	7.58	0.09
S ₆	Doli	17.33	3.20	2.61	16.55	7.52	0.09
S ₇	Sadri	10.17	2.37	2.34	12.20	5.90	0.11
S ₈	Ranawas	7.17	2.52	2.28	17.45	5.90	0.11
S ₉	Sojat	13.17	2.71	2.30	13.72	5.78	0.10
S ₁₀	Santhu	10.00	2.51	2.65	16.30	6.68	0.10
S ₁₁	Sura	14.00	2.36	2.49	13.70	6.68	0.10
S ₁₂	Sharath	13.83	2.47	2.58	14.09	6.50	0.10
S ₁₃	Siwana	12.33	2.26	2.25	11.38	7.05	0.09
S ₁₄	Karna	12.00	2.56	2.34	14.20	6.75	0.09
S ₁₅	Rawatsar	11.00	2.32	2.20	12.13	6.80	0.08
CD (P = 0.05)		1.839	0.249	0.308	1.616	0.665	0.01
Range		7.17-17.50	2.26-3.20	2.20-2.99	11.38-17.55	5.78-7.58	0.08-0.11
Mean		12.70	2.60	2.52	15.16	6.71	0.10
CV (%)		12.30	8.17	10.37	9.05	8.41	8.59

Table 2. Variance and coefficient of variability in physicochemical characteristics of *C. myxa* tree.

Character	Variances		Coefficient of variation (%)	
	Phenotypic	Genotypic	Phenotypic	Genotypic
Fruits/cluster	19.43	16.99	25.96	22.87
Fruit diameter	0.172	0.127	12.48	9.43
Pulp: seed ratio	0.155	0.087	13.49	8.63
Fruit weight	10.78	8.90	16.27	13.52
TSS	0.853	0.535	11.81	8.30
Acidity	0.00018	0.00017	11.68	7.90

Tukey and Young (1939). Hendrickson and Veihmeyer (1934) reported that the prune fruits affected by lack of available moisture during the fruit growing season, remained small even with subsequent irrigation. Further increase in fruit size and weight with the increase in soil moisture content may be attributed to greater vegetative growth under wettest condition, which indicates role of environment in which fruit plant grows. Significant variation was recorded for fruits per cluster. This is one of the important parameters which related to the fruit yield. High pulp:seed ratio is an indicator of good quality fruit. Significant variation for this trait was noticed among provenances. Increase in fruit TSS might be associated with increased translocation of organic assimilates from leaves to hormonal stimulation (Kriedemann, 1968). Various factors such as hormonal stimulation of

translocation of assimilate (Davies and Wareing, 1965) and alteration of skins may contribute to depression or enhancement of acid content in fruits.

Acidity recorded the minimum value of 11.68 and 7.90 for phenotypic and genotypic coefficient of variation. Fruits per cluster recorded highest value of 77.60% heritability and 41.50% for genetic advance as percentage of mean, whereas the minimum value of 40.90% for heritability was registered for pulp:seed ratio (Table 3). Variation refers to the observable differences in individual for a particular trait. These differences may be partly due to genotypic factor and partly due to environmental effects. The combined reflections of both factors are the phenotypic effect. For the proper utilization of observed variation in a species, it is pre-requisite to know the extent of variation; and also that

Table 3. Estimates of genetic parameters for physicochemical characteristics of *C. myxa* tree.

Character	Heritability (%)	Genetic advance (%)	Genetic advance as percentage of mean
Fruits/cluster	77.60	5.27	41.50
Fruit diameter	57.10	0.38	14.64
Pulp: seed ratio	40.90	0.29	11.50
Fruit weight	69.00	3.51	23.16
TSS	49.30	0.51	23.16
Acidity	45.80	0.01	10.40

whether it is due to the genetic or the environmental factors. Hence, information on variability among the desirable parameters and their correlation is vital for any breeding programme (Johnson et al., 1955). Therefore, a species exhibiting a wide range of variability (in terms of parameters value and high standard deviation, variance, coefficient of variation and genotypic coefficient of variation) offer ample scope for undertaking screening for the desired traits.

The observed variation in a character is partly composed of genetic (heritable) variation and partly of non-heritable. The proportion of total variation, which is due to genetic differences, is termed as the heritability in broad sense (Lush, 1937). Heritability provides a measure of genetic variation upon which all the possibilities of changing the genetic composition of the species depend. Genetic advance refers to the improvement in the mean genotypic values of the selected cultivars over the populations. The genetic coefficient of variation indicates the range and magnitude of genetic variability existing between the characters, whereas the observed variation in a group of individual is known as phenotypic coefficient of variation. In the present investigation, the result obtained for the different characters with regard to the variability parameters indicates that value have a wide range depicting the presence of good amount of variation. Those characters having high heritability coupled with high genetic advance as percentage of mean indicates that the improvement in these traits can be made through direct selection. In the present study, the characters like fruits per cluster, fruit weight, fruit diameter and TSS showed high heritability coupled with high genetic advance. The traits having lower range suggested limited variability in the population and need to generate more variability for improvement.

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