

Genetic Evaluation of *Leucaena* genotypes in Bundelkhand Region of Central India

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Introduction

During the 1970s and 1980s, *Leucaena* was known as the “miracle tree” native to Central America and Mexico, because of its worldwide success as a long-lived and highly nutritious forage tree. It is estimated to cover 2-5 million ha area worldwide. The genus *Leucaena* is one of the most widely grown tropical fodder trees and is the subject of extensive research. This is mainly due to its long life span; high productivity even under regular defoliation; its adaptation to wide climatic and edaphic tolerances; excellent palatability and digestibility and many uses including wood for timber and fuel wood. The species possesses enormous wealth of variability and great potential for economic yield which attract the breeders in utilizing the species in hybridization. A logical way to start any breeding programme is to survey the variations present in the germplasm. Precise information on the nature and degree of genetic divergence in respect of important traits is a prerequisite for undertaking meaningful breeding programme towards the improvement and conservation of a species.

Further an investigation into the nature and degree of divergence among populations will be useful in understanding the course of evolution and for classifying the tree population into groups based on the diversity, particularly when they are overlapping in one more characters. Therefore, the present study was conducted to estimate genetic divergence among different germplasm of genus *Leucaena*.

Materials and Methods

Leucaena research was extensively carried out by Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, where germplasms were evaluated and selection were carried out for characters such as biomass yield, psyllid resistant, forage quality and quantity. Later a field evaluation trial was carried out at experimental farm of ICAR-CAFRI, Jhansi. For the trial, twenty five germplasm of *Leucaena* were collected from IGFRI, Jhansi. The germplasm consisted of five species namely *Leucaena diversifolia*, *L. shannoni*, *L. lanceolata*, *L. collinsii* and *L. leucocephala* and one hybrid (*L. shannoni* x *L. leucocephala*). Seedling of different germplasms were planted at 3 x 3m spacing with three replications during 2007-2008. At the age of nine years all these accessions were recorded for tree height and diameter at breast height (dbh). For estimating tree biomass and volume, published equations were used. In the case of *Leucaena*, timber weight ($W = (339.913 * D^2h) - 15.513$ kg/tree) and volume per tree ($V = (0.345714 * D^2h) - 0.0157482$ m³) were estimated by using the equations developed by Dhanda *et al.* 2006. The genetic divergence was estimated by using hierarchical Euclidean cluster analysis (SPSS version 16). The genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were calculated using GENERES statistical package.



Fig 1: Germplasm evaluation of *Leucaena* at CAFRI, Jhansi

Results and Discussion

Growth performance of germplasm: The observation on morphological growth traits viz., plant height, dbh, volume and biomass pertaining to 25 germplasm are presented in Table 1. The analysis of variance revealed significant differences among all the germplasm. As far as tree height is concerned it was found maximum in *L. leucocephala* S-18 (14.57m) and minimum in *L. leucocephala* S-23 (10.12m). The dbh ranged from 0.081m (*L. leucocephala* S-24) to 0.188 m (*L. leucocephala* S-18). The maximum volume and biomass was recorded in *L. leucocephala* S-18 (0.166 m³ and 163.35 kg/tree) and minimum was observed in *L. leucocephala* S-24.

Table 1: Growth performance of various *Leucaena* germplasms

Accession Name	Accession No	Source*	Height (m)	Diameter (m)	Volume (m ³)	Biomass (kg/tree)	
<i>L. diversifolia</i> -504	1	OFI, UK	12.10	0.136	0.065	63.54	
<i>L. diversifolia</i> - 83/92	2		10.33	0.086	0.011	11.09	
<i>L. diversifolia</i> -46/87	3		10.87	0.103	0.028	27.39	
<i>L. shannoni</i> -22/83	4	University of Hawaii, USA	12.82	0.184	0.136	133.30	
<i>L. lanceolata</i>	5	CSIRO, Australia	11.53	0.122	0.045	44.40	
<i>L. lanceolata</i> -49/37	6		10.50	0.124	0.062	60.52	
<i>L. collinsii</i> -18/84	7	DoA, USA	11.40	0.115	0.037	35.99	
<i>L. collinsii</i> -56/88	8		12.70	0.113	0.041	40.09	
<i>L. collinsii</i> - 15/83	9		10.72	0.116	0.034	33.53	
<i>L. shannoni</i> X <i>L. leucocephala</i>	10	-	13.63	0.132	0.070	68.90	
<i>L. leucocephala</i> S-1	11	IGFRI, India	14.00	0.139	0.079	77.98	
<i>L. leucocephala</i> S-4	13		11.27	0.114	0.037	36.62	
<i>L. leucocephala</i> S-6	14		13.77	0.142	0.081	79.54	
<i>L. leucocephala</i> S-7	15		12.43	0.109	0.037	36.80	
<i>L. leucocephala</i> S-10	17		11.50	0.087	0.014	14.07	
<i>L. leucocephala</i> S-11	18		13.63	0.132	0.072	70.35	
<i>L. leucocephala</i> S-12	19		14.43	0.150	0.097	95.58	
<i>L. leucocephala</i> S-13	20		12.33	0.123	0.051	50.39	
<i>L. leucocephala</i> S-14	21		11.47	0.099	0.024	23.74	
<i>L. leucocephala</i> S-15	22		12.70	0.152	0.089	87.12	
<i>L. leucocephala</i> S-18	23		14.57	0.188	0.166	163.35	
<i>L. leucocephala</i> S-23	25		10.12	0.091	0.013	12.97	
<i>L. leucocephala</i> S-24	26		11.30	0.081	0.010	9.71	
<i>L. leucocephala</i> IGFRI-23-1	27		12.77	0.126	0.055	54.31	
<i>L. leucocephala</i> K-217	34		-	11.87	0.113	0.038	37.29
Grand mean				12.19	0.123	0.055	54.74
CD (0.01%)				2.61	0.052	0.074	73.16
SEd			0.97	0.020	0.028	27.27	

*Gupta and Roy (2009)

Genetic parameter

The results on genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance for morphometric traits under field condition are presented in Table 2. The genotypic coefficient of variations for tree height and dbh was 9.01 % and 18.83 % respectively, which falls under the category of lower GCV (<20 %). The lowest PCV (13.28 %) was recorded for height (20%) and medium PCV (27.06 %) in dbh (20-30%). The volume and biomass registered highest GCV and PCV values (>30 %) over dbh and height. The extent of variability was measured by GCV and PCV which provides information about relative amount of variation in different characters. In the present study, GCV was found to be low magnitude than PCV for all traits which indicates that these traits are influenced by the environmental factors.

Table 2: Genetic estimates of morphological traits

Traits	GCV (%)	PCV (%)	Heritability	Genetic advance
Height	9.01	13.28	0.46	12.59
Diameter	18.83	27.07	0.48	26.98
Volume	58.36	84.40	0.48	83.14
Biomass	58.49	84.52	0.48	83.38

For all the four traits medium heritability was observed (0.3- 0.6). The high degree of genetic advance as per cent of mean was observed for volume (83.14) and biomass (83.38), whereas dbh and height comes under low degree of genetic advance (<30). In the present study the high heritability with high genetic gain was observed for volume and biomass, so it could be a reliable indicator for further tree improvement programme and it indicates that such characters are controlled by additive gene action. Selection of high biomass producing germplasms will lead way to selection of high fodder producing germplasms. The findings of current study are in line with Chavan and Keerthika (2013) in *Leucaena leucocephala*.

Cluster Analysis

Cluster analysis is an important tool in tree breeding for estimating genetic divergence. The application of D² clustering technique in *Leucaena* genetic resources resolved in the twenty five genotypes into three clusters (Fig 2). Cluster I had the maximum number of 13 germplasm followed by in cluster II (10 germplasm) and cluster III (2 germplasm). In the present investigation, some clusters included genotypes of different species and locations. It could be seen that the genotypes from different locations grouped together to form a single major cluster as evident in cluster I and therefore the pattern of divergence was not depend on the geographic locations. These findings were in agreement with the results of Aslam *et al.* (2011) in *Pinus wallichiana* and Chavan and Keerthika (2013) in *Leucaena leucocephala* and suggested that all the genotypes from a given area may not necessarily form a single cluster. Thus, the pattern of divergence is not dependent on the geographical nearness of the genotypes and such a pattern could be attributed to differences in the genetic make-up of the otherwise co-occurring genotypes.

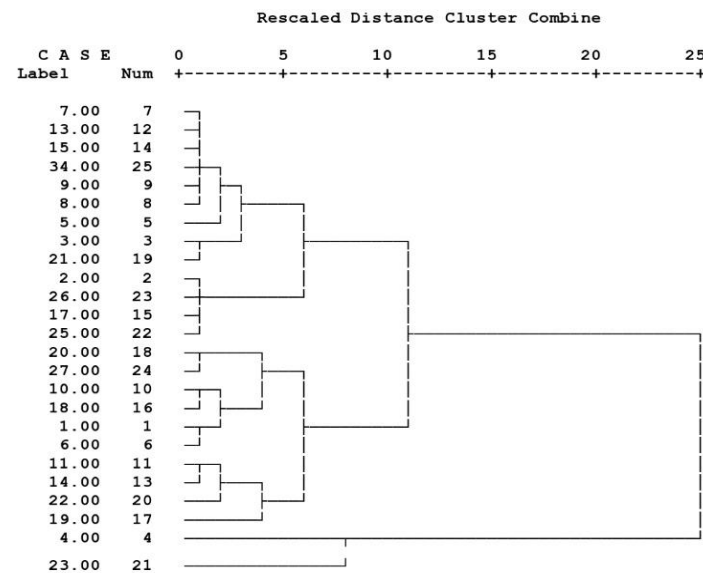


Fig 2: Dendrogram of twenty five leucaena germplasms

Conclusion

This miracle tree of tropics has wide potential in meeting the fodder requirements in developing countries with large livestock populations. From the current study, *L. leucocephala* S-18 recorded superiority in terms of growth characteristics and this germplasm can be exploited for future tree fodder improvement programmes. The genetic knowledge of tree species will be helpful to propagators, breeders and tree improvement specialists in maximizing the quality and productivity of the fodder plantation to meet the market demand over a time. Adoption of *Leucaena* has been lower than expected. Its benefits need to be demonstrated on farms. This versatile plant can be exploited in many ways to make farming systems more productive and sustainable in both developing and developed countries.

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