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GENETIC DIVERGENCE IN *LEUCAENA* VARIETIES USING NON- HIERARCHICAL EUCLIDEAN ANALYSIS

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Nature and magnitude of genetic divergence was assessed in 49 varieties of *Leucaena* using non-hierarchical cluster analysis for morphological and biomass traits. The population was grouped into 9 clusters. Maximum number of genotypes figured in clusters I and IX, four in 11, and VI and one each in IV and VIII. Intra-cluster distance was found maximum for the cluster VI(2.01). Inter-cluster diversity was found maximum between clusters VI and V(11.69) and minimum between cluster III and IX (1.87). The geographical diversity was not related to genetic diversity. Clusters with small statistical distance were considered less diverse than those with large distances.

Key words : *Leucaena*, genetic divergence, cluster analysis, geographical diversity

Leucaena's which are known as "Alfa alfa of Tropics" are among the most versatile of tropical trees. They belong to the sub-family Mimosidae of family Leguminosae. As a leguminous plant native to the "New World", they have been long introduced to other tropical and sub tropical countries owing to its multifarious uses. Few tropical trees matched *Leucaena's* ability to grow fast, provide nutritious fodder, fuel wood, green manure and other useful products. This also helps in preventing the erosion and is used as a nurse crop, shade crop and wind breaks in plantations.

The more diverse the parents, within over all limits of fitness, the greater are the chances of obtaining higher amounts of heterotic expression in F1's and broad spectrum of variability in segregating generations. The use of Mahalanobis's D2 statistics for estimating genetic divergence have been emphasized by many workers in many agricultural crops, but such studies in forestry are very limited. Among tree crops it has been used by Burley *et al* (1971) in *Eucalyptus camaldulensis*, Khosla *et al* (1979) in *Populus ciliata*, Pandey *et al* (1977) in *Bauhinia variegata*. Recently non-hierarchical euclidean cluster analysis derives the attention to overcome the limitations of Mahalanobis D2 statistic suggested by Beale (1969) and Sparks (1973). Garg and Gautam (1997) have attempted this method in wheat germplasm to identify the rust and powdery mildew resistant stock. The present investigation was aimed at ascertaining the nature and magnitude of genetic diversity present in a set of 49 *Leucaena* species/varieties.

MATERIALS AND METHODS

Seeds of different species/varieties of *Leucaena* were procured from CFI Oxford, University of Hawaii, IGFRI Jhansi, PAU Ludhiana and CCS HAU, Hisar. Before sowing, the seeds were mechanically scarified by nicking the rounded end of the seed and soaked in cold water over night. The seeds were sown (after mixing with pure Rhizobium culture Agro forester TM, Tropical Seeds, Holualoa, HI96725 USA) in complete randomised block design with three replications. The spacing between and within the rows was kept 30 cm and 10 cm, respectively in one meter bed. Data on ten competitive plants was subjected to statistical analysis vis- a-vis non-hierarchical *euclidean* analysis. Seedlings per replications were randomly selected excluding the border ones. The observations were recorded on the selected individuals for morphological and biomass traits viz; germination, seedling height, collar diameter, inter-nodal length, number of nodes, number of leaves, leaf area, shoot and root fresh and dry weight. Mean data was recorded as suggested by Beale (1969) and Spark (1973).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences in variety means for all the eleven characters under study which indicated that there existed a considerable inherent difference between these genotypes. Non-hierarchical euclidean cluster analysis proved useful for estimating the genetic divergence in 49 *Leucaena* genotypes which were grouped into 9 clusters (Table 1). The grouping indicated considerable amount of genetic diversity in the germplasm. Maximum species/varieties were in cluster 111 involving 12 genotypes followed by cluster II and VI had 44 each and cluster IV and VIII possessed one each. The table under reference revealed that some varieties from different locations are accommodated in the same cluster (K-636 Hawaii, K-8 Hisar and K-340 Jhansi) and thus indicated their close affinity. On the other hand varieties developed from the same area like K-39 Jhansi, CS 10-Jhansi were distributed to different clusters. These results show that geographical diversity may not necessarily be related to genetic diversity. These findings are in general agreement with the results obtained by Murty and Arunachalam (1966), Bhatt (1970) and Tewari (1970) in different agricultural crops; Pandey *et al* (1995) and Chauhan *et al* (1997) in forest tree species.

Table 1. Clustering pattern of 49 species/varieties on the basis of genetic divergence

Cluster number	Number of genotypes	Name of species/varieties
I	5	*L. salvadorensis* (ID)-34/88), *L.macrophylla nelsonii, L. salvadorensis* (ID-36/88), *L.hybrid* (ID-1/95), *L.trichodes*
II	4	*L.collinii* (ID-52/88), *L. pallida* (137/94), *L. salvadorensis* (36/88), *L. shannonii magnifica*
III	12	*L. pulverulentax L. leucocephala* (-75), *L. pulverulenta (22/86), L. leucocephla* (k-Ludhiana), *L. leucocephala* (S-22), *L. leucocephala* (K-8,Jhansi), *L. salvadorensis* (17/86), *L. leucocephala* (K-29, Jhansi), *L. leucocephala* (K-636, Jhansi), *L. leucocephalax L.diversifolia* (K-743A, Ludhiana), *L.diversifolia* (45/87), *L. leucocephala* (K-39, Jhansi)
IV	1	*L. esculenta paniculata* (52/87)
V	7	*L. pulverulanta* (84/87), *L. leucocephalax L. pulverulenta* (K-340, Ludhiana), *L. diversifolia* (83/92), *L. lempirana and L. multicapitulata*
VI	4	*L. diversifolia* (K-784, Jhansi), *L. esculenta paniculata* (79/92), *L. lanceolata and L. pulverulenta* (83/87)
VII	10	*L. collinsii* (51/88), *L. leucocephala* (S-10, Jhansi), *L. collinsii* (18/84), *L. leucocephala* (K-601, Jhansi), *L. leucocephala* (K-8, Hissar), *L. leucocephala* (K-340, Jhansi), *L. leucocephala* (K- 636, Hawaii), *L. leucocephala* (nauni), *L. leucocephala var EL Salvadorensis* (Jhansi), *and L. leucocephala* (34/92)
VIII	1	*L. leucocephala esculenta* (47.87)
IX	5	*Leucaena hybrid* (K-636 × K-156 < Hawaii), *L. leucocephala* (S-24, Jhansi), *L. leucocephala* (K-636, Ludhiana), *L. diversifolia* (83/92) *and L. collinsii* (56/88)

Intra and inter-cluster distances are presented in table 2. This provided an index of genetic diversity among and within the cluster. The intra-cluster

Table 2. Inter and intra cluster distances in 49 *Leucaena* species/varieties

	I	II	III	IV	V	VI	VII	VIII	IX
I	1.74								
II	2.77	1.74							
III	3.47	4.87	1.65						
IV	9.35	7.18	10.37	0.00					
V	3.12	5.14	2.78	11.69	1.60				
VI	2.68	3.18	4.32	7.73	4.73	2.01			
VII	3.41	3.90	2.13	8.53	4.40	3.66	1.70		
VIII	7.82	6.01	9.13	2.52	10.35	4.30	7.23	0.00	
IX	2.20	4.18	1.87	10.31	2.26	3.51	2.87	9.03	1.30

value ranged from 0.00 (cluster VIII) to 2.01 (cluster VI). Maximum inter cluster distance (11.69) was found between cluster V and IV, suggesting wide diversity between the groups. The crosses between the genotypes from these clusters may give putative transgressive segregants. On the other hand, minimum distances occurred between cluster IX and IV (1.87) indicating the close relationship.

The intermediate value was recorded between cluster II and VI (6.01). The species/varieties included in these clusters were not as much diverse as in cluster V and IV but may be of high yielding potential. The genetic diversity among the parents to be included in hybridization programme has been greatly emphasized in agricultural crops. Therefore, during the selection of parents in forest tree species inter-cluster distances must be taken into consideration.

The comparison of cluster means for 11 characters are appended in table 3. It is apparent from the table that different characters showed considerable

Table 3. Cluster mean for 9 clusters of 49 *Leucaena* species/varieties

Character	I	II	III	IV	V	VI	VII	VIII	IX
Germination	36.67	35.21	37.17	51.67	26.07	35.42	46.75	62.50	27.67
Seedling height	77.26	98.97	59.87	140.9	36.49	75.14	83.63	117.5	65.89
Collar diameter	6.41	6.20	4.81	8.90	3.98	6.32	6.06	10.01	5.69
Inter nodal length	5.74	7.12	3.84	8.28	4.23	5.23	4.95	7.74	4.12
No. of nodes	15.36	16.97	19.34	22.47	15.92	15.85	20.37	20.37	16.57
No. of leaves	14.65	16.75	18.83	22.53	15.32	15.39	19.90	20.60	16.15
Leaf area	69.77	76.92	37.61	114.0	56.20	83.93	46.80	123.3	38.95
Shoot fresh weight	53.19	96.57	39.68	146.3	41.20	62.24	48.17	122.1	41.63
Shoot dry weight	28.19	45.21	16.83	70.56	18.68	33.43	24.18	56.18	22.92
Root fresh weight	7.27	8.25	7.86	20.74	4.80	14.06	9.95	19.11	7.36
Root dry weight	4.67	5.47	4.79	12.64	3.11	8.46	5.58	10.15	5.11

differences between the clusters. Maximum field germination was observed for cluster VIII followed by cluster VII. Seedling height, inter nodal length, no. of nodes, no. of leaves, shoot and root fresh and dry weight was found maximum for cluster IV followed by cluster VIII, Collar diameter and leaf area were recorded highest for cluster VIII followed by cluster IV. Among the 9 clusters, cluster IV and cluster VIII recorded the highest values. The crossing programme involving genotypes from these clusters could help in obtaining the wide spectrum of variability for the above mentioned characters in the subsequent generations.

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