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GENETIC DIVERGENCE IN MULBERRY GERMPLASM

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The analysis of variance for nine characters of 124 accessions of mulberry (*Morus* L.) germplasm indicated the significant differences due to genotypes, seasons and their interactions. The heritability coefficients for fresh weight of leaves, internode length and plant height were high (> 0.7). The 124 accessions were grouped into 11 clusters, indicating the existence of considerable diversity. Maximum number of genotypes were included in cluster I (114) and other clusters contained one genotype each. The genetic diversity and geographical distribution were not related. Fresh weight of leaves, plant height, lamina-petiole ratio by weight and internode length were the most potential characters contributing to the total genetic divergence. Intra-cluster D^2 values were 0-4.95 and inter-cluster 2.963-17.24. The cluster IX and cluster XI were highly divergent. Highest mean performance was observed for more number of characters in cluster XI, followed by cluster IV. The inter-cluster divergence was also more between these two clusters (14.341) and accessions from these clusters can be used as promising parents, for varietal improvement through hybridization.

Key words: Mulberry, germplasm, divergence, cluster analysis

Mulberry (*Morus* L.) is the most important component of the sericulture industry as its leaf is the sole food source of the silkworm (*Bombyx mori* L.). Since area of mulberry cultivation is spreading to different climatic conditions in the country, it is imperative to emphasize the need to develop superior as well as location-specific mulberry cultivars. To cater to these demands, large scale long-ranging breeding programmes are necessary. As a back up, an adequately conserved broad genetic base of mulberry and its systematic evaluation for various desirable characters is a prerequisite.

For the choice of diverse parents, and their utilization in hybridization programmes, multivariate analysis by Mahalanobis D^2 statistics has been extensively used in quantifying the degree of genetic divergence among parents in numerous crops (Bartual *et al.*, 1985). It appears that relatively little information is available on mulberry (Susheelamma *et al.*, 1997). The present study was undertaken to measure the genetic diversity among mulberry genotypes to identify the suitable parents for hybridization, for its improvement.

MATERIALS AND METHODS

The 124 mulberry genotypes evaluated were acquired by field collections, genetic exchange and through visiting scientists. These genotypes were maintained in the field genebank (Mallikarjunappa *et al.*, 1995). Data were recorded on propagation parameters like sprouting and rooting of cuttings, growth and yield parameters like plant height, number of branches per plant, internode length, fresh weight of 100 leaves, lamina-petiole ratio by weight and quality parameters like leaf water

content and leaf water loss at six hours after harvest (from five plants per accession), for nine trials covering different seasons, from 1989-1994.

The mean values were subjected for analyses of variance. Multivariate analysis was carried out using Mahalanobis D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into different clusters following the Tocher's method as described by Rao (1952). The relative contribution of different characters towards divergence was estimated.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences between the genotypes and the environments (seasons) for all the nine characters, indicating the existence of genetic variability in the genotypes studied. Heritability coefficients indicated that characters like fresh weight of leaf, internode length and plant height were highly heritable (> 0.7) and rooting, number of branches per plant and lamina-petiole ratio by weight were having moderate heritability of 0.61-0.63 (Table 1).

Based on the relative magnitude of D^2 values, the 124 genotypes were grouped into 11 clusters (Table 2). The maximum genotypes (114) were included in cluster I. Whereas, clusters II to XI were unique with only single genotype each. The grouping pattern indicated that the clusters were heterogenous with respect to geographical origin of the genotypes. It indicated that the genotypes from different geographic regions, do not necessarily give good recombinants, and therefore genotypes should be evaluated on the basis of their individual merit and genetic diversity (Joshi and Rana, 1997). According to Murty and Arunachalam (1966), the genetic drift and selection in different environments could cause greater diversity than the geographic distance.

The intra-cluster divergence was zero for all the clusters except cluster I (4.95). Minimum inter-cluster distance was observed between cluster III and cluster V (2.963), followed by cluster V and cluster VII (3.754), indicating the close relationship among these clusters (Table 3). Maximum inter-cluster distance was found between cluster IX and cluster XI (17.24). This indicated that the genotypes included in these clusters had maximum divergence (Sardana et al., 1998). These clusters were followed by cluster VI and Cluster XI (14.961) and cluster IV and cluster XI (14.341).

The contribution of different characters towards genetic divergence was calculated by using Mahalanobis D^2 divergence (Table 1). The character fresh weight of leaf contributed maximum (35.85%), followed by plant height (15.57%), lamina-petiole ratio by weight (15.38%), internode length (13.30%) and rooting (10.12%). The least contribution was from leaf water content (0.18%), followed by leaf water loss (0.37%). The potent variables such as fresh weight of leaves, plant height, lamina- petiole ratio by weight, internode length and rooting can be given greater importance in selection of potential parents for hybridization.

The existence of diversity among the genotypes was also supported by the considerable amount of variation in cluster means for different characters (Table 3). Cluster XI ranked first for plant height (197.73), fresh weight of leaf (909.01) and internode length (8.04). cluster X recorded the highest value for rooting (56.33). Cluster VIII has shown highest value for lamina-petiole ratio by weight (14.70), whereas cluster IV consisted the highest value for number of branches per plant (30.78). Since the inter- cluster distance between cluster IX and cluster XI has been the highest, the maximum number of mean values for the characters was found to be only three, viz., plant height, internode length and the fresh weight of leaves. The inter-cluster distance between clusters VI and XI has been the second highest, the number of characters with higher mean values were again found to be above mentioned three

Table 1. Mean squares from analysis of variance for nine characters, heritability and contribution of different characters to the diversity in mulberry

Character	Mean	Trials (d.f. 8)	Genotypes (d.f. 123)	Error (d.f. 984)	Heritability (h^2)	Contribution (%)
Plant height (cm)	173.9	49971.01**	14113.63**	618.78	0.7079	15.57
No. of branches/plant	21.42	2093.71**	415.11**	27.39	0.6113	7.78
Internode length (cm)	4.56	3.87**	5.65**	0.19	0.7538	13.3
Fresh wt. of 100 leaves (g)	412.53	68582.49**	194668.09**	4938.75	0.8102	35.85
Lamina-petiole ratio by wt. (%)	8.37	39.89**	19.46**	1.24	0.6203	15.38
Leaf water content (%)	74.57	66.94**	30.60**	8.54	0.2229	0.18
Leaf water loss (%)	12.65	309.02*	70.98**	18.57	0.2388	0.37
Sprouting (%)	65.64	25633.94**	3570.43**	698.84	0.3135	1.46
Rooting (%)	31.35	12427.70**	4134.99**	245.80	0.6374	10.12

Table 2. Distribution of 124 mulberry genotypes in 11 clusters based on D^2 values

Cluster	No. of genotypes	Genotypes with origin
I	114	Indigenous-78
		Exotic - 46 (from 7 countries)
II	1	Ooshima (Japan)
III	1	Rymenokuwa (Japan)
IV	1	*M. multicaulis* (China)
V	1	Daimyo Nishiki (Japan)
VI	1	Tokiyutaka (Japan)
VII	1	Acc. no. 246 (Japan)
VIII	1	Chigimikawa (Japan)
IX	1	Acc. no. 175 (Japan)
X	1	Cemeintero (venenzuela)
XI	1	*M. laeviqata* (India)

Table 3. Average intra- (in bold) and inter-cluster values of D^2 in 11 clusters of mulberry germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**4.95**	6.737	7.782	6.412	8.712	8.054	9.345	7.953	10.516	8.516	12.008
II		**0**	4.591	9.917	4.737	4.178	5.131	6.695	6.514	8.246	11.621
III			**0**	11.693	2.963	6.464	3.913	8.036	8.955	6.05	9.562
IV				**0**	12.483	10.543	13.302	8.359	12.719	11.707	14.341
V					**0**	6.47	3.754	8.368	8.281	6.417	10.557
VI						0	4.827	7.625	3.98	11.149	14.961
VII							**0**	9.433	6.564	9.175	13.159
VIII								**0**	0.946	9.821	11.255
IX									**0**	13.47	17.24
X										**0**	6.186
XI											**0**

Table 4. Cluster mean values for nine characters in mulberry

Character	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
Plant height (cm)	179.54	90.60	120.72	196.90	67.44	65.03	70.11	87.38	27.10	173.33	197.73
No. of branches/plant	22.30	7.22	13.33	30.78	8.79	8.57	5.56	9.89	3.22	13.22	13.22
Internode length (cm)	4.60	3.79	4.21	4.66	4.02	2.16	2.82	4.30	1.10	6.40	8.04
Fesh wt. of 100 leaves (g)	398.35	466.00	760.87	141.06	745.62	416.10	722.14	376.32	355.44	848.34	909.01
Lamina-petiole ratio by wt. (%)	8.27	7.83	8.49	10.72	8.54	8.83	7.81	14.70	7.69	8.53	11.16
Leaf water content (%)	74.61	73.46	77.51	70.21	75.50	74.98	77.82	73.74	66.24	76.67	75.15
Leaf water loss (%)	12.71	12.54	9.35	22.43	8.09	15.44	7.50	15.48	11.65	8.78	8.43
Sprouting (%)	67.90	13.49	34.26	67.44	45.10	28.45	54.85	29.43	31.09	66.50	28.59
Rooting (%)	32.80	1.27	0.56	45.83	28.44	3.81	5.60	4.64	1.67	56.44	0.00

characters. Further, the inter-cluster distance between cluster IV and cluster IX was found to be third highest and the number of characters with higher mean values were found to be four, viz., number of branches per plant, in addition to above mentioned characters. Also, the characters with second higher mean values were found to be more between these two clusters. Hence, genotypes of the cluster XI (Accn. no. 181) and cluster IV (Accn. no. 188), would be the better parents for hybridization programmes (Singh *et al.*, 1998). In addition, the genotypes with outstanding mean performance from the other clusters could also be involved as potential parents in interspecific hybridization, for developing superior mulberry cultivation.

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