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Short Communication

Genetic diversity in germplasm of mulberry (*Morus* spp.) on root proliferation

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Exploitation of heterosis is considered as an outstanding success of plant breeding. The magnitude of heterosis gained by the hybrids largely depends on the genetic divergence between the parents. This information facilitates the breeders in selection of parents for crossing and development of hybrids. The genetic diversity of the parents is not always related with the geographical diversity [1]. Assessment of genetic divergence for parents' selection is necessary for which statistical procedures, such as, D^2 statistics and nonhierarchical Euclidean cluster analysis [2, 3] is considered. Development of superior varieties with higher survival is one of the important factors in mulberry breeding. In sericulture, mulberry (*Morus* spp.) plays the key role due to the monophagous habit of the silkworm (*Bombyx mori* L.) where production and quality of silk largely depend on the quality of mulberry. Vegetative nature of mulberry propagation allows perpetuation of the characters once it is introduced through crossing. In vegetative propagated plants, rooting ability is the most important criteria, since a well developed root system determines the utilization of nutrients from the soil for growth and development [4]. As a large number of indigenous and exotic mulberry germplasm accessions are available, study of genetic divergence of the parents are necessary to identify genetically diverse genotypes with higher adaptability for selection and utilization in breeding programme.

Fifty-six indigenous and 29 exotic mulberry accessions collected from 12 different countries, maintained in the germplasm bank (GPB) at Central Sericultural Research and Training Institute, Berhampore West Bengal, India (24°6'N and 88°15'E) were studied. The experiment was conducted during 2000-2001 in the polythene tube condition with three replications. Stem cuttings of each accession were planted in the polythene tube and nurtured. On 90th day of cutting plantation, plants were gently removed from the soil and root proliferations *viz.*, number of roots, root length, fresh and dry weight of roots, root hair zone and root volume were recorded. Data were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic [2] and the accessions were grouped into different clusters following Tocher's method of cluster formation [5].

The analysis of variance showed significant difference among the accessions irrespective of their country of origin. Using Tocher's procedure, the accessions were grouped into 6 clusters. Among these, cluster I was the largest and consists 66 accessions followed by cluster II with 10 accessions and cluster III with 6 accessions. Clusters IV, V and VI were unique, since each had only one accession (Table 1). The random distribution of the accessions was evident from cluster I having maximum number with diverse distribution. The grouping pattern did not show any relationship between genetic divergence and geographic diversity [6]. The inclusion of accessions of different origin together in the same cluster indicated the ancestral relationship among the accessions. Average inter-cluster divergence among the accessions showed highest value (77.26) between the clusters IV and VI followed by clusters II and V (72.70), clusters I and V (66.85), clusters V and VI (66.18) and clusters III and IV (65.71) whereas the least value (29.42) was observed between the clusters I and III (Table 2).

The data on intra- and inter-cluster distances are given in Table 3. The D^2 values among 85 accessions revealed that cluster III showed minimum intracluster distance (3.40), which indicate that the accessions within the cluster were similar. While cluster II showed maximum D^2 value (3.74) followed by cluster I (3.70). Maximum inter-cluster distance (8.79) was observed between cluster IV and VI and minimum between cluster I and III. High values of D^2 indicate genetic divergence among the accessions and least value showed close affinity among the accessions of the clusters. However in all the cases, inter-cluster distances were greater than the intra-cluster distance indicating the degree of genetic diversity present among the accessions of different clusters. The average cluster means of six characters revealed that only one accession placed in cluster V was highest in fresh weight of root (12.21 g), root volume (39.67 ml) and root hair zone (5.61 cm) but moderate in length of root (38.67 cm) and number (14.22). The accession Matigara white of cluster IV was highest in root length (60.44 cm). The average number of roots (22) was highest in the accessions of cluster II.

Table 1. Distribution of 85 mulberry germplasm accessions in different clusters based on D^2 values

Clusters	Accessions	Origin/country	Number of accessions
I	**Indigenous**	India	45
	Kajli, Ber-A, Ber-20, *M. indica* (x), CSRS-2, Assambola, Kolitha-7, Kolitha-8, Kolitha-9, Dudhia red, Dudhia white, Bishnupur-4, Bishnupur-9, Tollygunge, Bush malda-A, Bush malda-B, Matigata black, Tista valley, Kurseong, Sujanpur, Sultanpur, KPG-1, KPG-2, Kanva-2, MS-1, MS-5, *M. indica* (HP), Sujanpur-5, RFS-175, OPH-1, Ace-105, Nagaland local, Kaliakotai, Golaghat, Jatinuni, Punjab local, MS-6, Mysore local, Almora local, Kakpillai, FGDTR-9, MS-8, Jodhpur, S 1635		
	Exotic		
	China black-B, China white	China	21
	Kokuso-13	Japan	
	Philippine	Philippine	
	Burma-8, Mandalaya, Thailand (unlobed), Monla-1, Monlai, Molai	Burma	
	Bogura-4, Shrim-2, Shrim-5, Shrim-8	Bangladesh	
	M. australis	Australia	
	Calabresa, Fernandodias	Paraguay	
	M. multicaulis	Russia	
	M. rotandiloba, Multicaulis	France	
	M. nigra	Indonesia	
II	**Indigenous**		
	M. indica black, MR-1, Surat	India	3
	Exotic		
	Italian mulberry	Italy	7
	Okinowaso	Japan	
	Australia	Australia	
	Cyprus	Greece	
	Muroso	Paraguay	
	Thailand (lobed)	Burma	
	M. cathyana	Indonesia	
III	Ber-B,Ber-6,Kolitha-3,Black cherry,MS-7,MS-9	India	6
IV	Matigara white	India	1
V	VI	India	1
VI	Bogura-1	Bangladesh	1

Table 2. Average intra and inter-cluster values of D^2 among different clusters in mulberry

Cluster	I	II	III	IV	V	VI
I	13.69					
	(3.70)					
II	42.21	14.00				
	(6.50)	(3.74)				
III	29.43	43.26	11.59			
	(5.43)	(6.58)	(3.40)			
IV	37.76	50.75	65.71	0.00		
	(6.15)	(7.12)	(8.11)	(0.00)		
V	66.85	72.70	47.55	60.26	0.00	
	(8.18)	(8.53)	(6.90)	(7.76)	(0.00)	
VI	47.35	58.34	31.96	77.26	66.18	0.00
	(6.88)	(7.64)	(5.65)	(8.79)	(8.14)	(0.00)

Antiqued values are intra-cluster distances; D^2 values are in parenthesis

Table 3. Cluster mean of different root characters

Cluster	Number of roots	Length of root (cm)	Fresh wt. of root (g)	Root volume (ml)	Root hair zone (cm)	Dry wt. of root (g)
I	12.47	26.72	3.46	16.24	3.96	3.17
II	22.48	27.47	3.97	15.45	4.32	2.38
III	7.5	19.31	4.51	13.22	3.21	1.97
IV	16.78	60.44	3.87	24.33	3.49	25.77
V	14.22	38.67	12.21	39.67	5.61	3.09
VI	11.89	27.89	5.93	13.11	4.83	2.32

It can be concluded that while selecting the accessions as parents in breeding for obtaining potential hybrids, the parents of distant clusters with higher genetic divergence in root characters may be used to create high adaptability.

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