Indian J. Genet., **62**(1): 52-54 (2002)

Genetic divergence in mulberry (*Morus* spp.)

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(Received: December 1998; Revised: January 2000; Accepted: November 2001)

Abstract

Genetic divergence among 98 mulberry (*Morus* spp.) genotypes (63 exotic, 35 indigenous) of different eco-geographic origin was assessed using Mahalanobis D^2 statistics. The total genotypes were grouped into seven clusters. Maximum number of genotypes were grouped in cluster III (19), IV (19), II (16), IV (16), VII (13) and V (12), respectively. Cluster I had only 3 exotic genotypes. All the clusters having both the exotic and indigenous genotypes except cluster I. The genotypes falling in cluster III had the maximum divergence followed by cluster I and II. The maximum and minimum divergence were revealed between cluster I and VI and between cluster V and VI, respectively. The cluster I and VI showed higher and lower mean values for most of the characters. So, mulberry crop improvement programme may be tried with the genotypes of divergent clusters for better heterotic effects.

Key words : Mulberry, exotic genotypes, indigenous genotypes, genetic divergence

Introduction

Mulberry is the sole food of silkworm (*Bombyx mori* L.). The plants are mainly grown for its foliage and breeding of mulberry are directed towards higher foliage production. To meet this objective, genetically diverse parents are required which could produce high heterotic effects with more variability in segregating generations. Till date, mulberry breeding has mainly confined to include indigenous genotypes to evolve improved variety. The available exotic genotypes collected from different eco-geographic origin has not been properly exploited to create variability for more production. The genetic diversity among mulberry genotypes have been reported by several authors [1,2,3]. But the information was based on limited parameters and genotypes. So, the present study was carried out to assess the genetic divergence among the genotypes using Mahalanobis D^2 statistics and to select the suitable genotypes for further utilization in breeding programme.

Materials and methods

The study was carried out at CSR&TI, Berhampore, West Bengal, during 1993-1995. The mulberry genotypes were maintained as high bush, spacing 1.5 m × 1.5m with once annual pruning. Recommended agronomic practices were followed to maintain the plantation. Each genotype represented by a row of 5 plants. Growth parameters were recorded after 90 days of pruning of 5 plants and the plant attained 5 years when data was recorded. Leaf moisture and moisture retention capacity in harvestsed leaves were calculated following the standard procedure.

The observation on 11 parameters i.e., Moisture %, moisture retention capacity %, laminar index %, nodal distance, 100 leaves dry wt., lenticel/sq.cm. no. of buds sprouted, days to sprout, biomass wt., growth rate at 90 days and no. of twigs/plant were recorded from all 5 plants. The statistical analysis was carried out using Mahalanobis D^2 method [4] and the genotypes were grouped into different clusters following Tocher's method as described by Rao [5].

Results and discussion

The mulberry genotypes representing different eco-geographic origins are presented in Table 1. Based on divergence and magnitude of D^2 values, 98 genotypes were grouped into 7 clusters (Table 2). The distribution of different genotypes revealed that cluster III and IV having maximum number of genotypes. Cluster II and VI, both having 16 genotypes each. The clusters VI and V had 13 and 12 genotypes, respectively. The cluster I had only 3 exotic genotypes. The genotypes had distributed randomly in different clusters irrespective of geographic origin. Further, the grouping of genotypes did not show any relationship between genetic divergence and geographic diversity. The same observations were also reported by several authors (1, 2,3,7). The genetic drift and selection in different environments could cause greater diversity than geographic distance [6].

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Table 1. Eco-geographical distribution of 98 mulberry genotypes

Country name	No. of genotypes	%
Afganistan	01	1.02
Australia	01	1.02
Bangladesh	02	2.04
Burma (Myanmar)	03	3.06
Canada	01	1.02
China	02	2.04
Egypt	01	1.02
France	03	3.06
Greece	01	1.02
Hungary	01	1.02
India	35	35.71
Italy	07	7.14
Japan	33	33.67
Philippine	01	1.02
Portugal	02	2.04
Russia	01	1.02
Spain	01	1.02
Turkey	01	1.02
USA	01	1.02
Total	98	100.00

The intercluster and intracluster distances of 98 genotypes presented in Table 3. Maximum intracluster distance observed in cluster III and minimum in cluster V. Maximum intercluster distance observed between cluster I and VI followed by Cluster I and V and I and III, respectively. The minimum intercluster distance observed between cluster V and VI. The cluster wise mean values (Table 4) showed cluster I had maximum values in all the characters except days to sprout, growth rate at 90 days and internodal distance. The cluster VI having lower mean values in all the characters, except internodal distance and growth rate at 90 days.

The contribution of individual character towards divergence is presented in Table 4. Nodal distance, lenticel/sq. cm and growth rateat 90 days showed no contribution towards the genetic diversity. The characters like 100 leaves dry wt. (41.41%) followed by no. of buds sprouted (41.43%) and twig no./plant (14.83%) contributed maximum towards genetic divergence. Other characters have contributed very less towards divergence.

The success of hybridization depends on the genetic diversity among the parents. The cluster I and VI showed maximum divergence. It is expected that hybridization between the genotypes of these two divergent clusters will lead to high heterotic effects with better segregants. Thus, it may be concluded that for developing better variety, crosses between the genotypes of divergent clusters may be tried.

Table 2. Distribution of 98 mulberry genotypes in different clusters

Cluster	Exotic	Indigenous	Total
I	Seijuro, Kanmasori, Goshoerami	-	03
II	Sukakuchi, Moretiana, Okinowa, KNG, Ankara, *M. alba* L, Sidseguwa, Ichinose, *M. rubra*, Ichehei, Kosen, China black A, Burma- 8, Lemoncina	Kolitha-7, Kolitha-9	16
III	Italian mulberry, Hungarian, Oshima, Bogura1, Artificial, Aoroso, Atucanidia, Lisbon	Kajli, Ber A, Ber-20, Ber-6, Ber-4, Assambola, *M. Indica*-X, Lloyos, Ber-B, Assamjati, Ber-39	19
IV	Senmatso, Ensutakasuke, Rokokuyoso, Cyprus, Cattaneo, Simanochi, Kairo-roso, Asiyoke, Tomeiso, Rosteli, Rotundiloba, Tagawase, Madrid Spain, Rohachi, Moretti Seringe	Nan-nayapati, Kolitha-8, Tista Valley, Ber-4	19
V	Kenmochi, *M. alba* Rangoon, Roso, Kairo-Akita, Kurimato, Sosuke	Black Cherry, Mirganj, Bush Malda-A, Bush Malda-B, Matigara White, Sujanpur	12
VI	China Black-B, Sterile, Wasemidori, *M. ihou* Seringe, Kabul	Kolitha-8, Kurseong, CSRS-II, Matigara Black, Sultanpur, Bishnupur-9, CSRS-I, Dudhia Red, Takdah, Tollygunge, KPG-I	16
VII	Akagi, Rosodilombardi, Okinowa, Egypt Cairo, *M. multicaulis*, Mandalaya, Obowase, Tushimakowa, Multicaulis, Mizusawa, Philippine, Australia	Dudhia White	13
Total			98

Table 3. Average intercluster and intracluster (Bold) distances of 98 genotypes in mulberry

Cluster	I	II	III	IV	V	VI	VII
I	**64.85**	82.99	122.14	113.31	128.66	151.98	116.34
II		**39.14**	83.63	50.05	66.77	86.63	69.00
III			**73.05**	91.39	111.65	119.50	126.24
IV				**27.02**	34.17	49.93	51.40
V					**16.58**	32.72	38.26
VI						**24.44**	59.81
VII							**26.66**

Table 4. Clusterwise mean values of 11 characters in mulberry

Characters	Clusters							Contribution towards divergence %
	I	II	III	IV	V	VI	VII	
MC (%)	76.44	72.20	71.56	71.31	72.72	70.35	72.90	0.08
MRC (%)	95.89	93.94	91.82	93.33	93.72	90.77	93.37	0.04
LI (%)	86.10	84.91	83.29	85.88	81.61	81.33	83.77	0.44
NC (cm)	3.30	3.47	3.93	3.38	3.45	3.95	3.74	0.00
100 LDW (gm)	134.66	75.12	30.87	51.02	51.19	28.26	82.27	41.41
LT (sq. cm)	7.62	6.54	6.04	6.32	6.04	5.24	6.85	0.00
NBD (no.)	102.22	79.40	114.65	57.99	39.03	33.50	36.90	41.43
DSP	9.56	10.02	8.54	9.81	9.67	8.48	10.57	0.17
BIO (wt.)	17.00	14.54	16.86	9.45	9.62	5.73	7.37	1.58
GR (cm)	0.78	1.02	1.27	0.91	1.11	1.07	0.66	0.00
TWG (no.)	102.33	76.33	99.39	56.98	39.22	30.46	33.87	14.83

MC = Moisture content, MRC = Moisture retention capacity, LI = Laminar index, ND = Nodal distance, 100 LDW = 100 leaves dry wt., LT = Lenticel/sq. cm, NBS = No. of buds sprouted, DS = Days to sprout, BIO = Biomass wt., GR = Growth rate at 90 days, TWG = Twig no./ plant.

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