A Comprehensive Analysis of Genetic Divergence in Indian Bamboo

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Abstract: Fifteen species of bamboo with ten component characters were analyzed for genetic divergence using Mahalanobis D^2 analysis led to their grouping into four clusters. One species fall under cluster I, three in cluster II, nine in cluster III and two in cluster IV. The maximum inter cluster value was obtained between cluster I and IV, indicating that the species in cluster I (***Dendrocalamus asper***) and cluster IV (***Dendrocalamus strictus*** and ***Dendrocalamus membraneceous***) were more divergent and can be used for multicultural plantation or as parents in hybridization programme to get heterotic response. Significant differences between cluster means in these two clusters were observed for culm height, diameter, internode length, number of culm, clump girth, leaf length, culm wall thickness and biomass. [New York Science Journal 2010;3(2):90-93]. (ISSN: 1554-0200).

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1. Introduction

Bamboo is fast growing species and it occupies a special place in the lives of the people especially in Asia. India has the second largest bamboo genetic resources in the world with over 136 species growing in the country (Gielis, 1998). The importance of genetic diversity in any breeding programme is well known, as it is the pre-requisite for any breeding programme. Variation in the tree species for growth parameters attributable to its market price necessitates exploitation and improvement of the traits for higher productivity. Beside it, many of the commercially important traits in the forest trees are under polygenic control (Wright, 1976) and bamboo is no exception.

Multivariate analysis (using Mahalanobis D^2 and canonical variety analysis of Rao, 1952) has been found to be potent biometrical tool in quantifying the degree of divergence among all possible pairs of population at genotypic level before affecting actual crosses in modeling the varieties in a desired genetic architecture. A clear understanding of the degree of divergence for economic characters in the species will be an added advantage in this regard, as inter-mating of divergent groups would increase variability and range of frequency distribution (Alicchio and Palenzona, 1974). The estimation of genetic divergence has wide scope in tree breeding as it helps in identifying the diverse genotypes for a crossing programme (Fisher 1936; Pandey *et al.*, 1995 and Tewari *et al.*, 1989).

2. Material and Methods

Fifteen different bamboo species collected from different parts of the India (Table 1) were selected for study. In September 2005, these species were planted in randomized block design with three replications and sixteen plants were maintained in each block. Three plants from each block were randomly selected for recording observations. Observations were recorded twice a year (December and August) for three years and pooled data were analyzed statistically.

Observations on ten characters were recorded on three representative trees in each treatment. Culm height (m) was measured of tallest culm from base to the topmost tip of the bamboo plant by using scaled pole; Diameter of the plant (cm) was taken in the middle between at 3rd and 4th node using tree caliper**;** Internode length (cm) of each plant was taken by measuring the distance from the base between 3rd and 4th node; Culm wall thickness (cm) was taken of a representative culm , sample of which was cut between 3rd and 4th node from base and thickness was taken using vernier caliper; Number of new sprouts in each plant was counted in every season; Leaf length (cm) of the basal leaf near to DBH was measured with the help of scale from the joining point of leaf blade upto leaf tip; Leaf breadth of the same basal leaf was measured at the broadest point from one end to the other of which leaf length was recorded; Clump girth (cm) of the whole clump was measured at the height of 30cm from the ground; Total number of culms new and old

Table 1: List of Bamboo species and their selectionsite:

S. No.	Species	Place of Collection
1	*Bambusa vulgaris*	Collection Block, Pantnagar, Uttarakhand
2	*Bambusa vulgaris* var.*striata*	Collection Block, Pantnagar, Uttarakhand
3	*Bambusa multiplex*	Forest Research Institute (FRI) Dehradun, Uttarakhand
4	*Bambusa tulda*	Forest Research Institute(FRI) Dehradun, Uttarakhand
5	*Bambusa bambos*	Collection Block, Pantnagar, Uttarakhand
6	*Bambusa nutans*	Forest Research Institute(FRI) Dehradun, Uttarakhand
7	*Dendrocalamus giganteus*	Forest Research Institute(FRI) Dehradun, Uttarakhand
8	*Dendrocalamus strictus*	Collection Block, Pantnagar, Uttarakhand
9	*Bambusa vulgaris* var. *wamin*	Forest Research Institute (FRI) Dehradun, Uttarakhand
10	*Dendrocalamus asper*	Marino Pvt. Ltd., Hapur, Uttar Pradesh
11	*Dendrocalamus membraneceous*	Forest Research Institute (FRI) Dehradun
12	*Dendrocalamus hamiltonii*	Forest Research Institute(FRI) Dehradun, Uttarakhand
13	*Mellocana baccifera*	Collection Block, Pantnagar, Uttarakhand
14	*Arundinaria falcata*	Pratap Nursery, Dehradun
15	*Arundinaria falconerii*	Ranichauri, Tehri, Uttarakhand

Table 2. Clustering pattern of 15 species of bamboo on the basis of genetic divergence

Cluster	I	II	III	IV
Species	*Dendrocalamus asper*	*Bambusa nutans*	*B. vulgaris var. wamin*	*D. strictus*
		Dendrocalamus giganteus	*B.vulgaris*	*D. membraneceous*
		Dendrocalmaus hamiltonii	*M. baccifera*	
			A. falcatta	
			A. falconerii	
			B.vulgaris var. striata	
			B. multiplex	
			B. tulda	
			B. bamboos	

Table 3. Average intra and inter-cluster distance between cluster centroids

Cluster	I	II	II	IV
I	(0.00)			
II	5.95	(2.06)		
III	4.95	4.03	(2.16)	
IV	6.80	3.29	3.29	(1.72)

(Values in parenthesis are intra-cluster distance).

Table 4. Cluster means for ten characters among 15 species of Bamboo

Cluster	Culm height (m)	Diameter (cm.)	Internode length (cm.)	No. of new sprouts	No. of culms.	clump girth (cm.)	leaf length (cm.)	leaf breadth (cm.)	Culm wall thickness (cm.)	Biomass (Kg.)
I	10.33	2.00	32.33	0.00	4.00	271.67	22.73	3.57	0.51	0.733
II	9.29	4.96	28.22	2.00	15.00	433.33	21.61	3.93	1.71	6.716
III	6.37	3.82	19.48	0.85	10.56	304.07	13.93	2.42	1.48	4.749
IV	8.93	5.62	19.83	1.00	15.00	432.00	14.87	2.52	1.78	12.128

were counted manually and for Biomass, fresh weight of the representative culm was taken after harvesting the culm 5cm above the ground. Mahalanobis D^2 statistic (generalized distance) was used to analyze the genetic divergence as suggested by **Rao, 1952**.

Result and Discussion

The Analysis of Variance (ANOVA) exhibited significant differences among the bamboo genotypes for all the characters studied. Based on D^2 values fifteen experimental bamboo species were grouped into four clusters according to the method described by **Rao (1952)**. The criterion used for clustering is that any two genotypes belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to different clusters. Average intra and inter-cluster distance between cluster centroids obtained for fifteen experimental bamboo species are presented in Table 2.

Cluster I contains one species, cluster II three species, Cluster III was largest and had nine species while cluster IV consisted of two species. Cluster means for ten characters studied for fifteen bamboo species are presented in Table 4. Cluster I exhibited maximum mean value for culm height (10.33 m), internode length (32.33 cm) while cluster II recorded maximum mean value for number of new sprouts (2.0), no. of culms (15.00), Clump girth (433.33 cm), and leaf breadth (3.93 cm). Mean value for diameter (5.61 cm), number of culms (15.0), culm wall thickness (1.78 cm) and biomass (12.128Kg) was found maximum in cluster IV.

The maximum inter-cluster value was obtained between cluster I and IV (6.80) indicating that the species in cluster I (***Dendrocalamus asper***) and cluster IV (***Dendrocalamus strictus*** and ***Dendrocalamus membraneceous***) were more divergent. Significant differences between cluster means in these two clusters were observed for culm height, diameter, internode length, number of culm, clump girth, leaf length, culm wall thickness and biomass (Table 4). It indicated that these characters contributed maximum towards the genetic distance between cluster I and IV. To have a broad genetic base for insurance against disease/insect or environmental vagaries multi-culture plantation involving selection of species from different and diverse clusters is recommended. The species selected from these clusters in hybridization programme might yield desired heterosis and release variability in subsequent generations. However, crossing of very diverse genotypes may not yield proportionate heterotic response because a cross between extremely divergent parents might create situation wherein harmonious functioning of alleles is somewhat disturbed and consequently the physiological functions are not so efficient as in a situation where the alleles were exposed to similar selection pressure (**Prasad and Singh,1986; Tewari *et al.*, 2002**).This suggests that the selection of parents should also be based upon their *per se* performance.

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