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Genetic divergence analysis of Indian bamboo species based on morphological characters

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Abstract
Ten species of bamboo with twenty one morphological characters were analyzed for genetic divergence using Mahalanobis D^2 analysis led to their grouping into three clusters. The cluster I had maximum five species while cluster II comprised of three species. Minimum species were found in Cluster III with two species. Intra cluster average distances were maximum in cluster II followed by cluster III. The inter cluster average distance was maximum between cluster I and cluster III indicating that species falling in these clusters to be genetically diverse 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 diameter, culm to culm distance, internodal length, number of culms, number of leaves per node and culm sheath area. Culm sheath area, number of leaves per node, number of culms, leaf area and culm sheath length contributed maximum towards total divergence.

1. Introduction

Bamboos are a group of woody perennial, evergreen to deciduous plants belonging to the grass family Poaceae, sub-family Bambusoideae, tribe Bambuseae and unique in their distribution, growth, morphogenesis, taxonomy, reproduction, ecology as well as diversity. India has the second largest bamboo genetic resources in the world with over 136 species growing in the country [1] and occupies approximately 10.03 million hectares, which is about 12.8 per cent of the total forest area. The presence of genetic variation within and between populations is critical to exploit their improvement potential and contributes to adaptive capacities of population from environmental stress and mismanagement [2]. Bamboos as diverse taxa provide opportunity to evaluate and discuss the morphological and genetic concepts of species based on morphological, ecological and genetic parameters. Intra specific genetic diversity is pre requisite for evolution and speciation which is yet to be fully understood among bamboos. The knowledge of genetic diversity in crop plants as well as in tree species is of paramount importance for any breeding programme. Selection of diverse parents belonging to distant groups leads to wide spectrum of gene combinations for the quantitative and quality traits. Several measures of distance have been proposed in early studies to suit various objectives, of which Mahalanobis generalized distance has been considered as an important and unique approach in plant breeding [3, 4].

Statistical technique such as Mahalanobis D^2 and canonical variant analysis [4], which quantify the differences among quantitative traits are potent biometrical tool in quantifying the degree of divergence for economic characters in the germplasm collection of various plantation crops as a prerequisite before affecting successful crosses to increase variability range and create varieties with desired genetic architecture [5, 6, 7, 8]. The importance of genetic divergence in plant breeding has been emphasized by several workers [9, 10, 11]. Hence the investigation deals with estimation of genetic divergence among economically relevant bamboo species aimed at tree improvement.

2. Materials and Methods
2.1 Experimental Material

Experimental materials employed in the present study consisted of ten bamboo species *viz.*, *Bambusa balcooa, B. bambos, B. nutans, B. tulda, B. vulgaris, B. vulgaris striata, Dendrocalamus asper, D. gigenteus, D. hamiltonii* and *D. strictus*, planted under Bamboo Multilocation Trial at AFRC (Agroforestry Research Center), G.B.P.U.A. & T., Pantnagar. The experiment was planted in a Randomized Block Design with four replications in

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July-2005. Each species in a plot was planted in four rows and each row containing four clumps and consisted of total sixteen clumps in each treatment with row to row and clump to clump spacing of 5 m x 5 m. Four competitive culms were selected in each the four replication and were used for study of various morphological characters during 2014-16. Average data of these four culms was calculated. Observations were recorded twice a year (December and August) for three years and pooled data were analyzed statistically.

2.2 Characters Studied

Observations on twenty one morphological characters viz., bud length (cm), bud width (cm), culm to culm distance (cm), clump circumference (m), culm diameter (cm), culm height (m), internodal length (cm), leaf length (cm), leaf width (cm), leaf area (cm^2), number of culms, number of internodes per culm, number of leaves per node, number of nodes per branch, number of young shoots, blade length (cm), culm sheath length (cm), culm sheath breadth at base (cm), total culm sheath length/ breadth at base, total culm sheath length/ blade length and culm sheath area (cm^2) were recorded on four representative clumps in each treatment.

2.3 Statistical Analysis

The genetic divergence was estimated by Mahalanobis D^2 statistic as suggested by [4] Rao (1952). Average intra-cluster D$^2 = \sum D_i^2/n$ where, $\sum D_i^2$ = sum of all distances between all possible combinations (n) of the genotypes included in the cluster. Average inter-cluster distance D$^2 = \sum D_{ij}^2/n_i.....n_j$ where, $\sum D_{ij}^2$ = sum of all distances between all possible combinations ($n_i.n_j$) of the genotypes between the clusters (n_i = number of genotypes in ith cluster, n_j = number of genotypes in jth cluster). Using D^2 values, different genotypes were grouped into various clusters following Ward's minimum variance method [12]. The average D^2 value of all possible combination of genotypes/ varieties in one cluster with those in other was computed and its square root was used to represent the "Statistical distance" between two clusters.

The contribution of individual character to the total divergence and cluster means of bamboo genotypes falling under different clusters were also calculated. Percentage contribution of each character was calculated as under:

$$\text{Percentage contribution of X character} = \frac{N(X) \times 100}{n(n-1)/2}$$

Where, N (X) = number of genotypic combinations which were ranked for character X out of the total genotypic combinations of n (n-1)/2; n(n-1)/2 = total possible genotypic combinations among 'n' number of genotypes.

3. Results and Discussion

The Analysis of Variance (ANOVA) exhibited significant differences among the bamboo genotypes for all the characters studied. Based on D^2 values, the constellation of genotypes into clusters was done. D^2 analysis grouped ten bamboo species into three clusters. The cluster pattern of these genotypes is shown in Table 1. The cluster I comprised

of five species while cluster II comprised of three species. Cluster III had two species.

Table 1: Clustering pattern of ten bamboo species on the basis of genetic divergence

	Cluster		
	I	**II**	**III**
Species	*Dendrocalamus hamiltonii*	*Bambusa nutans*	*Bambusa bambos*
	Bambusa vulgaris striata	*Dendrocalamus asper*	*Dendrocalamus gigenteus*
	Bambusa balcooa	*Bambusa tulda*	
	Dendrocalamus strictus		
	Bambusa vulgaris		

3.1 Intra and Inter cluster distance

Average intra and inter cluster distances are represented in Table 2. Intra cluster average distances ranged from 4.95 to 6.21. It was maximum in cluster II (6.33) with three species followed by cluster III (6.21) with two species and minimum in cluster I (4.95) represented by five species. The inter cluster average distance was maximum (9.1) between cluster I and cluster III indicating that species falling in these clusters to be genetically diverse. Many species involving one or both similar genera were scattered into different clusters. Such genetic diversity among the species of common origin could be due to several factors like heterogeneity, genetic architecture of populations, past history of selection, developmental traits and degree of general combining ability [13]. The results indicated that species in cluster III (*Bambusa bambos*) and cluster I (*Bambusa vulgaris striata, Bambusa balcooa, Bambusa vulgaris*) were more divergent. Similarly, *Dendrocalamus gigenteus* of cluster III was found to be more diverse two *Dendrocalamus* species of cluster I. Minimum average inter cluster distance was observed between cluster I and cluster II (7.61). It indicated that the species of these two clusters were similar to each other for the studied characters.

Table 2: Intra cluster and inter cluster distances of 21 characters made from ten species of bamboo

Clusters	I	II	III
I	(4.95)		
II	7.61	(6.33)	
III	9.1	7.71	(6.21)

(Values in parenthesis are intra-cluster distance)

The comparatively less values (inter-cluster D^2 value) observed between any cluster pair indicate close relationship of species of different clusters for various characters. Based on the genetic divergence analysis, it would be possible to figure out some potential species, subject to the condition that environments maintain the relative expression of characters with regard to the species.

3.2 Cluster mean

Cluster mean values for twenty one characters are given in Table 3. A perusal of these cluster means for different characters indicated considerable difference between the clusters for certain characters.

Table 3: Mean values of different characters in three clusters made from ten bamboo species

S. No	Characters studied	Cluster I	Cluster II	Cluster III
1	Bud length (cm)	1.89	1.54	1.97
2	Bud width (cm)	2.56	2.32	2.38
3	Clum to clum distance (cm)	11.83	12.43	10.21
4	Clump circumference (m)	6.97	8.32	6.93

5	Culm diameter (cm)	5.96	4.77	8.69
6	Culm height (m)	11.07	10.91	11.22
7	Inter-nodal length (cm)	22.80	31.67	23.73
8	Leaf length (cm)	26.03	24.83	27.39
9	Leaf width (cm)	2.83	3.52	3.24
10	Leaf area (cm^2)	53.13	63.88	69.43
11	Number of culms	59.03	52.38	49.25
12	Number of internodes per culm	39.02	37.47	36.82
13	Number of leaves per node	152.36	156.05	169.34
14	Number of nodes per branch	15.78	14.22	16.75
15	Number of young shoots	8.33	14.17	9.44
16	Blade length (cm)	15.70	14.17	16.42
17	Culm sheath length (cm)	42.18	39.04	48.26
18	Culm sheath breadth at base (cm)	23.71	20.93	31.21
19	Total Culm sheath length/ breadth at base	1.85	1.91	1.62
20	Total Culm sheath length/ blade length	2.74	2.96	3.09
21	Culm sheath area (cm^2)	502.84	415.75	732.59

Cluster I had highest cluster mean value for bud width, number of culms and number of internodes per culm. Cluster II had shown highest cluster mean value for culm to culm distance, clump circumference, inter-node length, leaf width, number of young shoots, total culm sheath length/ breadth at base and total culm sheath length/ blade length. Cluster III showed highest cluster mean for maximum number of traits including bud length, culm diameter, culm height, leaf length, leaf area, number of leaves per node, number of nodes per branch, blade length, culm sheath length, culm sheath breadth at base and culm sheath area.

The importance of different characters in the inter-cluster divergence can be studied further by comparing cluster means for different characters. The donors for different characters may be selected from clusters on the basis of their cluster mean values. The genotypes/species belonging to distant clusters with high cluster mean may be identified to be utilized in the selection and hybridization programme with high breeding value can be selected on the basis of performance of a genotype. *Bambusa bambos* and *Dendrocalamus giganteus* in cluster III which showed highest cluster mean for maximum number of traits can be used in hybridization with bamboo species belonging to cluster I and II. This information will also facilitate the selection of species with desirable attributes.

3.3 Character Contribution towards Genetic Divergence
The relative contribution of different characters towards the expression of genetic divergence was calculated following standard method as suggested by [14] Singh and Chaudary (1985) and is given in Table 4. The maximum contribution towards divergence was given by inter-node length followed by culm sheath breadth at base and culm sheath area. These characters may be considered important from the point of view of genetic diversity in general and in experimental material in specific. The character showing substantial contribution towards divergence may be emphasized while practicing stringent selection programme. Similar results were reported by [15] Generoso *et al.* (2016). Other characters were found to made lowest contribution towards total genetic divergence. Despite the low contribution of plant height to divergence, this descriptor cannot be ignored, as it is decisive when utilising the species. As pointed out by [16] Wahab *et al.* (2010), plant height, number of internodes per culm, internode length and culm diameter are important factors in determining the most appropriate use for each species of bamboo.

Table 4: Contribution of different characters toward genetic divergence in 10 bamboo species

S. No	Characters studied	Per cent contribution to genetic divergence
1	Inter-nodal length	20.00
2	Culm sheath breadth at base	16.00
3	Culm sheath area	13.20
4	Leaf width	11.20
5	Culm sheath length	10.90
6	Leaf area	8.68
7	Culm diameter	6.88
8	Leaf length	3.69
9	Blade length	2.07
10	Culm height	1.19
11	Number of leaves per node	1.06
12	Total Culm sheath length/ breadth at base	1.02
13	Bud width	0.93
14	Number of internodes per culm	0.74
15	Clum to clum distance	0.59
16	Number of young shoots	0.47
17	Total Culm sheath length/ blade length	0.34
18	Number of culms	0.33
19	Clump circumference	0.29
20	Bud length	0.28
21	Number of nodes per branch	0.02

[14] Singh and Chaudhary (1985) suggested three important points to be considered while selecting genotypes for breeding programme i.e (i) choice of particular cluster from which genotypes is to be selected as parent, (ii) selection of particular genotype from a particular cluster and (iii) relative contribution of character to total divergence. In this regard, the concept of genetic distance has been of vital utility in differentiating well defined populations [17]. There is less work carried out in bamboo regarding genetic divergence. [18] Singh (1993) assessed nineteen representative genotypes of *Bambusa tulda* Roxb. from North-East India was using Mahalanobis D^2 statistics [19]. Lewis *et al.* (2010) applied D^2 analysis for diversity study in fifteen species of bamboo. In other genera of Poaceae family similar results have been reported by [20] Vijaykumar *et al.* (1988) in rice and [21] Tareen *et al.* (1994) in barley. The estimation of genetic divergence has wide scope in the breeding as it helps in identifying the diverse genotypes for developing heterosis in crossing programme [5, 8, 23].

4. Conclusion

The selection of suitable diverse parents is of paramount importance in hybridization programme of any crop breeding strategy for getting desirable recombinants. A clear understanding of the degree of divergence for economic characters in these species will be an added advantage as inter mating of divergent groups would increase the range and variability in traits of commercial importance. The species selected from these clusters in hybridization programme might yield desired heterosis and release variability in subsequent generations.

5. Acknowledgement

6. References

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