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Biometric and Genetic Studies in Bamboo Genetic Resources

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Abstract: *Studies were carried out, to assess the growth performance, variability and association studies in biometric attribute and genetic divergence of seven bamboo species and also to screen thornless bamboo species for pulpwood during the year 2011-2012. The performance of selected trees was studied through evaluation trial established at the fields of Seshasayee Paper Board (SPB), Tirunelveli. The biometric observation indicated the wide range of variability for three biometric traits studied. Among seven species, two species viz., Bambusabalcooa and Bambusatuldaproved superior in terms of important biometric attributes investigated. The variability study indicated that number of culms registered highest phenotypic and genotypiccoefficient of variancefollowed by culm basal diameter and plant height. Plant height, culm basal diameter and number of culms registered high heritability values. The correlation studies revealed that culm basal diameter and plant height was highly and negatively associated with number of culms both at phenotypic and genotypic level. The Path analysis study indicated that plant height exercised negative direct effect on number of culms but culm basal diameter exercised positive direct effect on number of culms. Hence basal diameter could be effectively used as selection criteria to increase except number of culms in Bamboo species. But plant height could be effectively used as selection criteria to number of culms. The application of D^2 clustering technique in bamboo genetic resources resolved the six species into five clusters. The intra and inter cluster distance indicated the presence of wider genetic distance between bamboo genetic resources. Among the growth attributes number of culms contributed maximum to genetic divergence.*

1. INTRODUCTION

Bamboos form one of the very important natural resources playing a major role in the livelihood of the rural people and in the rural industry. They also act as a source of raw material for cottage industry in rural areas and in pulp and paper industry [17]. Among the Indian states, Manipur has richest Bamboo species diversity with 53 species, next is Arunachal Pradesh, with 50 species. So the North eastern States together support about 63 species [24]. The most widely distributed and economically very important species are *Bambusabambos* and *Dendrocalamusstrictus*. These species are tip of the Peninsular India and extending upto the lower found growing in the deciduous forests of the southern Himalayan regions. These species, are connected with the life of the villagers, tribals, and even middle class peasants, are widely cultivated for various purposes [20].

Although Bamboo is widely distributed with high species diversity in India, it is not fully exploited to meet industrial wood demand. Being a biological material, it is subjected to greater variability and complexity due to various growing conditions such as moisture, soil and competition [15]. For these circumstances, Genetic studies are necessary for scanning the available genetic variation, to utilize the best material for obtaining maximum productivity for further breeding work [25] and also help in analyzing and comparing superior and inferior characters which have great importance in breeding and tree improvement programmes besides preserving these variations intact for future research programme[9]. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures [29]. However such studies are very limited in many thornless bamboos.

2. MATERIALS AND METHODS

The experimental material for the present study consisted of seven bamboo species viz., Bambusa vulgaris var. striata, Bambusa vulgaris var. vulgaris, Bambusabalcooa, Bambusapolymorpha, Bambusatulda, Bambusabambos and Dendrocalamusstrictus. Among the various species, the culms of Bambusa vulgaris var. striata, Bambusa vulgaris var. vulgaris, Bambusabalcooa, Bambusabambos, Bambusapolymorpha and Dendrocalamusstrictus were collected from Tamil Nadu and Bambusatulda was collected from Kerala Forest Research Institute, Peechi, Kerala. From the selected clump of bamboo species, cuttings were collected

for multiplication. Necessary care was taken to raise a healthy planting stock for out planting.

The evaluation trial of different Bamboo species was laid out at the field of Seshasayee Paper Board (SPB), Tirunelvali, Tamil Nadu during September, 2011.

The healthy clones and seedlings were planted in a randomized block design with four replications. The spacing adopted was 5 m x 5 m with five ramets per replication per species. During the initial period, complete causality of *Bambusapolymorpha* was observed and hence the species was not included for the study and the analysis.

2.1 Estimation of Biometric attributes

The observations were recorded at the time of planting, 3 Months After Planting (MAP) and 6 MAP on the various bamboo species planted in the field. The growth attributes were recorded as described below.

2.1.1 Plant height

The plant height was measured from basal portion to the tip of the culm and expressed in cm.

2.1.2 Basal diameter

It was measured at the base of the culm at the root collar region and expressed in cm.

2.1.3 Number of culms

All the live culms were counted and recorded.

Statistical analysis

The estimates of mean, variance and standard error were worked out using the method described by Panse and Sukhatme (1978). The significance test was carried out by referring to the standard 'F' table of Snedecor (1961).

2.2 Variability, heritability and association study

2.2.1 Variability studies

These parameters were estimated as per the method described by Johnson *et al.* (1955).

2.2.1.1 Genotypic variance (GV)

$$\sigma^2 g = (\sigma^2 g - \sigma^2 e)/\,\mathrm{r}$$

Where,

$\sigma^2 g$ = Genotypic mean square
$\sigma^2 e$ = Error variance
r = Number of replications

2.2.1.2 Phenotypic Variance (PV)

$$\sigma^2 p = (\sigma^2 g - \sigma^2 e)$$

Where,

$\sigma^2 g$ = Genotypic variance
$\sigma^2 e$ = Error variance

2.2.1.3 Phenotypic Co-efficient of Variability

Phenotypic Co-efficient of Variation (PCV) was arrived by using the formula as described by Burton (1952).

$$\mathrm{PCV}\ (\%) = \frac{(\text{Phenotypic Variance})^{1/2}}{\text{General Mean}} \times 100$$

2.2.1.4 Genotypic Co-efficient of Variability

Genotypic Co-efficient of Variation (GCV)was arrived by using the Burton's (1952) formula.

$$\mathrm{GCV}(\%) = \frac{(\text{Genotypic Variance})^{1/2}}{\text{General Mean}} \times 100$$

2.2.1.5. Heritability (h^2)

Broad sense heritability (h^2) was calculated according to Lush (1940)

$$h^2 = (\sigma^2 g/\,\sigma^2 p)$$

Heritability percentage= h^2 x 100

2.2.1.6 Genetic advance

Genetic advance was worked out after Johnson *et al.* (1955a).

$$\text{Genetic Advance (GA)} = [(\text{Genotypic Variance} / \text{Phenotypic Variance})^{1/2} \times \mathrm{K}$$

Where,
K = 2.06, a selection differential at 5 % selection intensity

2.2.1.7 Genetic advance as percentage of mean

$$\mathrm{GA}(\%) = \frac{\mathrm{GA}}{\text{Grand Mean}} \times 100$$

2.2.2Association studies

2.2.2.1. Correlation co-efficient studies

Genotypic and Phenotypic correlations coefficients were calculated according to the method suggested by Goulden (1952).

2.2.2.2 Genotypic correlation or Correlation co-efficient

Genotypic correlation was arrived by using the formula as given below

$$r_{g.}1.2 = \frac{\text{Genotypic Covariance between 1 \& 2}}{(\text{Genotypic variance of 1} \times \text{Genotypic variance of 2})^{1/2}}$$

2.2.2.3Phenotypic correlation

Phenotypic correlation was arrived by using the formula as given below

$$r_{p.}1.2 = \frac{\text{Phenotypic Covariance between1 \& 2}}{(\text{Phenotypic variance of 1} \times \text{Genotypic variance of 2})^{1/2}}$$

The genetic estimates for biometric attributes were classified as detailed below.

Genetic parameter	Low	Moderate	High
GCV and PCV	<20	20-30	>30
Heritability	<30	30-60	>60
GA as % of mean	<30	30-60	>60

2.2.2.4 Path coefficient studies

Path co-efficient analysis was carried out as suggested by Dewey and Lu (1959) to segregate the genotypic correlation coefficients in to direct and indirect effects.

2.2.3. Estimation of genetic diversity

The biometric data recorded at 6 MAP on various bamboo were used for diversity analysis.

2.2.3.1 Determination of genetic divergence

The D^2 statistics was adopted for the estimation of genetic divergence (Mahalanobis, 1928). Using D^2 statistical results, the clustering of progenies was done.

2.2.3.2 D^2 statistics

The D^2 statistics was carried out using the traits *viz*., plant height, diameter at breast height and volume. The mean squares and the mean products were estimated between groups and within components by one-way analysis of variance, covariance and the significance were tested at progeny level. A variance–covariance was formed from the above and subjected to pivotal condensation to obtain the linear function for transformation of character mean values (x) to a set of independent variables (uncorrected mean) value (y).

The difference between any two mean values for each pair of progeny was squared and added to give the D^2 values. For each character Cumulative D^2 values in all the possible combination of progeny were estimated.

$$y_1 = x_1$$

$$y_2 = x_2 - a_2 x_1$$

$$y_3 = x_3 - a_{32} y_2 - a_{31} y_1$$

$$yp = yp - a_{pp-1} y_{p-1} \ldots\ldots ap_1 y_1$$

where,
x1 = normalized variables

$$a_{ij} = b_{ij}/v(y_j)\ S < -1$$

$$v(y_j) = \lambda \sum a_{(ij)}\, b_{ij} - b_{ij} = \lambda_{ij} - 1/atbt$$

$$\lambda_{ij} = \text{Covariance of i and } j^t = j^i$$

All possible $\frac{n(n-1)}{2}$ D^2 values were calculated by taking sum of difference between pair of corresponding 'y' values taking two progenies at a time.

2.2.3.3 Determination of clusters or grouping

The progenies were grouped into different clusters using 'GENERES' statistical package on the basis of D^2 values according to Tocher's method as suggested by Rao (1952).

2.2.3.4 Tocher's method

All the $\frac{n(n-1)}{2}$ D^2 values were clustered by using Tocher's method (Rao, 1952).

2.2.3.5 Average intra and inter cluster distances

On completion of clustering, the intra and inter cluster relationships were studied and the mutual relationship between clusters and their distances were represented. The average intra cluster distances was measured using the formula

$$D^2 = D^2/n$$

Where D^2 was the sum of distances between all possible combinations of the progeny included in a cluster whereas the average inter cluster divergences were arrived at by taking into consideration of all the component D^2 values possible among the numbers of the two clusters. Then the genetic distance 'D' between the clusters were obtained from square root of the average D^2 values.

3. RESULTS

3.1. Estimation of Biometric attributes.

3.1.1. Plant height

Among the six species evaluated, significant differences were observed for plant height. Plant height of six bamboo genetic resources at 1 MAP had ranged from 37.807 cm (*Bambusabalcooa*) to 22.533 cm (*Bambusabambos*). The species *Bambusa vulgaris var. striata* (33.643 cm) recorded higher plant height compared to general mean (29.233cm) (Table 1).

At 3 MAP, the plant height ranged from 119.447 cm (*Bambusabalcooa*) to 60.507 cm (*Bambusabambos*). The grand mean for this character was 90.757cm. At this stage, the following two species *viz*., *Bambusa vulgaris var. striata* (106.777 cm) and *Bambusa vulgaris var. vulgaris* (100.263 cm)

recorded higher plant height compared to grand mean (90.757cm). At 6 MAP, among the various bamboo species *Bambusabalcooa*(216.873 cm),*Bambusa vulgaris var. striata* (198.657 cm) and *Bambusa vulgaris var. vulgaris* (178.143 cm), were on proved superior compared to grand mean (163.713cm).

Table 1: Bamboospecies variation for plant height at three growth periods

S. No	Name of the species	Plant Height (cm)		
		1MAP	3MAP	6MAP
1	Bambusa vulgaris var. vulgaris	28.977	100.263*	178.143*
2	Bambusa vulgaris var. striata	33.643*	106.777*	198.657*
3	Bambusabalcooa	37.807*	119.447*	216.873*
4	Bambusatulda	25.163	72.767	132.387
5	Bambusabambos	22.533	60.507	103.627
6	Dendrocalmusstrictus	27.280	84.787	152.590
	Mean	29.233	90.757	163.712
	SEd	1.794	2.588	5.851
	CD (p=0.05)	3.998	5.767	13.037

* Significant at 5% level

The plant height recorded the minimum value of 103.627 cm (*Bambusatulda*) and maximum value of 216.873 cm (*Bambusabalcooa*) at 6 MAP. Considering all the growth periods into account three species *viz., Bambusabalcooa, Bambusa vulgaris var. striata*and *Bambusa vulgaris var. vulgaris* proved superior consistently.

3.1.2. Culm basal Diameter

Culm basal diameter differed significantly among the evaluated species at three growth periods. At 1 MAP, the culm basal diameter ranged between 1.701 cm (*Bambusabalcooa*) and 0.535 cm (*Bambusabambos*). Compared to grand mean (1.192cm), four species *viz., Bambusabalcooa*(1.701), *Bambusa vulgaris var. striata* (1.519 cm),*Bambusa vulgaris var. vulgaris* (1.444 cm) and *Bambusatulda*(1.373 cm) recorded significantly higher values (Table 2). At 3 MAP, the culm basal diameter ranged between 2.571 cm (*Bambusabalcooa*) and 0.916 cm (*Bambusabambos*). Compared to the mean basal diameter (1.811cm), three species *viz., Bambusabalcooa*(2.571 cm), *Bambusa vulgaris var. striata* (2.309 cm) and *Bambusa vulgaris var. vulgaris* (2.108 cm) registered significantly higher culm basal diameter. Significantly higher value for culm basal diameter was recorded by three species *viz.,Bambusabalcooa* (3.565 cm), *Bambusa vulgaris var. striata*(3.227 cm) and *Bambusa vulgaris var. vulgaris* (2.885 cm) at 6 MAP compared to grand mean (2.549cm). Considering all the three growth periods into account only two species *viz., Bambusabalcooa*and *Bambusa vulgaris var. striata* consistently proved superior.

Table 2: Bamboospecies variation for culm basal diameter at three growth periods

S. No	Name of the species	Culm Basal Diameter (cm)		
		1MAP	3MAP	6MAP
1	Bambusa vulgaris var. vulgaris	1.444*	2.108*	2.885*
2	Bambusa vulgaris var. striata	1.519*	2.309*	3.227*
3	Bambusabalcooa	1.701*	2.571*	3.565*
4	Bambusatulda	1.373*	1.838	2.461
5	Bambusabambos	0.535	0.916	1.356
6	Dendrocalmusstrictus	0.583	1.129	1.806
	Mean	1.192	1.811	2.549
	SEd	0.018	0.032	0.073
	CD (p=0.05)	0.040	0.072	0.163

* Significant at 5% level

3.1.3. Number of culms

Various bamboo species differed significantly due to number of culms over three growth periods. At 1 MAP, two species *viz., Bambusatulda* (2.465) and*Dendrocalamusstrictus*(2.190) registered higher number of culms compared to the grand mean (1.952).At 3 MAP, the species *Bambusatulda* recorded highest (2.984) number of culms followed by *Dendrocalamusstrictus* (2.846). At 6 MAP, two species *Bambusatulda* (4.230) and *Bambusabambos*(4.010) proved superior compared to grand mean (3.245) (Table 3).

Table 3: Bamboospecies variation for number of culms at three growth periods

S. No	Name of the species	Number of Culms		
		1MAP	3MAP	6MAP
1	Bambusa vulgaris var. vulgaris	1.343	2.016	2.175
2	Bambusa vulgaris var. striata	1.968	2.190	2.417
3	Bambusabalcooa	1.730	2.016	2.486
4	Bambusatulda	2.465*	2.984*	4.230*
5	Bambusabambos	2.016	2.190	4.010*
6	Dendrocalmusstrictus	2.190*	2.846	3.551
	Mean	1.952	2.574	3.245
	SEd	0.075	0.194	0.335
	CD (p=0.05)	0.169	0.432	0.747

* Significant at 5% level

3.2 Variability, heritability and association study

The variability estimates *viz.*, PCV, GCV, heritability and genetic advance as per cent of mean are furnished in Table 5.

3.2.1. Plant height

The plant height exercised phenotypic and genotypic coefficient of variations of 26.118 and 25.749 per cent respectively. Plant height recorded higher heritability of 0.972 and the genetic advance as per cent of mean was 52.293 (Table 4).

Table 4: Genetic estimates for growth attribute–6 MAP

Traits	PCV	GCV	Heritability	GA (%) of Mean
Plant height	26.119	25.749	0.972	52.293
Culm basal diameter	33.344	33.158	0.988	67.924
Number of culms	38.595	36.460	0.892	70.953

3.2.2. Culm basal Diameter

The PCV and GCV for culm basal diameter were 33.344 and 33.158 per cent respectively. The culm basal diameter recorded higher heritability of 0.988 and the genetic advance as percentage of mean was 67.924 (Table 4).

3.2.3. Number of culms

Number of culms recorded maximum PCV (38.595) and GCV (36.460) compared to the PCV and GCV estimates of other parameters. It recorded higher heritability value of 0.892. The genetic advance as per cent of mean recorded by this trait was 70.953 which was highest among all the traits (Table 4).

3.3. Association studies

3.3.1. Correlation studies

3.3.1.1 Plant height

Plant height exhibited negative and significant phenotypic (-0.733) and significant genotypic (-0.709) correlations with number of culms. The phenotypic and genotypic inter correlations were positive and significant at one percent level, for plant height (0.928 and 0.908).

Table5: Phenotypic correlation coefficient of morphometric attributes–6MAP

Characters	Culm basal diameter	Plant height	No. of Culms
Plant height	1.000 **	0.928**	-0.733**
Culm basal Diameter		1.000**	-0.581
No. of Culms			1.000**

** Significant at 1% level

3.3.1.2 Culm Basal Diameter

Culm basal diameter showed negative correlation with number of culms at phenotypic (-0.581) and genotypic (-0.550) levels.

Table 6: Genotypic correlation coefficient of morphometric attributes–6 MAP

Characters	Culm basal diameter	Plant height	No. of Culms
Plant height	1.000 **	0.908**	-0.709**
Culm basal diameter		1.000**	-0.550
No. of Culms			1.000**

** Significant at 1% level

3.3.2. Path coefficient analysis

The estimates of direct and indirect effects of morphometric traits on number of culms under field condition after 6 MAP are presented in Table 7. The residual effect was 0.62692.

Table7: Path coefficient analysis of morphometric traits on Number of Culms

Traits	Plant height	Culm basal Diameter
Plant height	-1.39176	0.65912
Culm basal diameter	-1.29132	0.71039

Residual effect =0.62692

3.3.2.1. Direct effect

Among the traits studied, plant height exercised negative direct effect on number of culms but culm basal diameter showed positive direct effect on number of culms (Table 7).

3.3.2.2. Indirect effect

The plant height exerted positive indirect effect via culm basal diameter (0.65912) and culm basal diameter recorded minimum indirect effect via plant height (-1.29132) on number of culms (Table 7).

3.4. Determination of genetic diversity

3.4.1. Genetic divergence

The mean values were transformed into standardized uncorrelated mean values. The D^2 values were computed for all positive pairs. Mahalanobis D^2 clustering techniques resolved the six species into five clusters.

3.4.2. Cluster components

The clustering pattern revealed that the six species were resolved into five different clusters. The cluster I constituted two species *viz., Bambusabalcooa,Bambusa vulgaris var. striata*; whereas cluster II, III, IV and V consisted of one species *viz., Dendroclamusstrictus, Bambusatulda, Bambusabambos*and *Bambusa vulgaris var. vulgaris*respectively.

3.4.3. Intra and inter cluster average distance

The cluster II, III, IV and V showed no intra cluster generalized distance since it contained only one species. The maximum intra cluster distance was shown by the cluster I (5.331). The maximum inter cluster distance was observed between cluster IV and V (434.799). The minimum inter cluster distance was recorded between cluster III and V (93.284).

3.4.4. Clustermean performance

The maximum cluster mean of 3.396 cm was observed for culm basal diameter in cluster I whereas the least cluster mean for culm basal diameter (1.356 cm) was exhibited by the cluster IV. The members in cluster I showed highest performance of accounting 207.765 cm for plant height followed by cluster V (178.143 cm) and II (152.590 cm) while, the minimum was observed for the cluster IV (103.627 cm). In case of number of culms, the cluster mean was highest for cluster III (5.052) and the lowest was exhibited by the cluster V (1.670).

4. DISCUSSIONS

4.1. Estimation of Biometric attribute

4.1.1. Mean performance of *bamboo* species

Among the seven species evaluated, the superiority of two species *viz.*, *Bambusabalcooa* and*Bambusatulda* was evidenced consistently in all the three growth periods investigated (Table 1, 2 and 3). Variation in growth attribute due to species and the associated provenances, progenies and clones are very well documented among 15 species bamboo evaluated indicated significant difference among the species for all the growth characters investigated [2]. The results of current study also indicated significant variability among different bamboo species and expressed superiority of *Bambusabalcooa* at 6 Months of evaluation.Genetic selection of rapid juvenile growth rate was also advocated as a means of improving competitive ability of forest trees [12, 28] which thereby extent the scope of exploiting the early superiority of *Bambusabalcooa*for immediate incorporation in the bamboo plantation programmes.

4.2. Variability, heritability and association study

The genetic variation which is heritable can be exploited for further improvement programme. In the present study, number of culms scored highest PCV and GCV. The Culm basal diameter recorded moderate PCV and GCV followed by plant height. Higher GCV for number of branches and low GCV for height in *E. tereticornis*[19] and low GCV for height in the same species was also established [7]. Low GCV and PCV for height and collar diameter were also reported in *Bambusapallida*[26]. Existence of high variability for number of culms, culm diameter, wall thickness, internodal length and culm height of clonal population of *Bambusabambos*[3] and *Dendrocalamusstrictus* [23] also lend support to the current study.

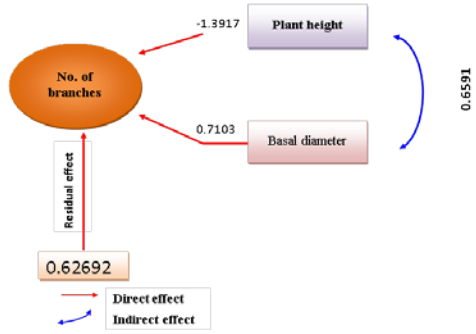
In the present study, the highest heritability and genetic advance was recorded by culm basal diameter followed by plant height and number of culms. In fifteen species of bamboo, estimates of heritability in broad sense were observed generally high for leaf breadth, biomass, leaf length, culm height and internode length [2] which support the present findings.Bagchi and Singh (1994) had indicated that high heritability in combination with high GCV as advantageous for selection programmes. In the present experiment, plant height which expressed highest GCV and higher heritability could be used as tool for selection programmes in *Bamboo* improvement programme.

4.2.3. Association studies

Inheritance of most of the economic traits is complex in nature and is affected by a wide range of associated characters. Presence of significant correlation among the characters of higher heritability and are less affected by environmental variable, permits better use of indirect selection. On the contrary, negative associations between desired attributes under selection may result in genetic slippage [11] and limit expected genetic gain. Hence association studies have been conducted and the study in the present investigation indicated that plant height shows negative correlation with number of culms at phenotypic (-0.733) and genotypic level (-0.709).

4.2.3.1. Path analysis

The path analysis permits the separation of direct effects from indirect effects through other related traits by partitioning the genotypic correlation coefficients [10]. Moderate estimates of residual effects reflect the just fulfillment of required characters chosen for path analysis.



In various *bamboo* species, plant height exercised negative and lowest direct effect on number of culms. Culm basal diameter showed positive and highest direct effect on number of culms. The present results are in conformity with the results of Sasikumar (2003) in *Acacia* hybridsclones.

4.2.4. Determination of genetic diversity

4.2.4.1. Cluster composition

The application of D^2 clustering technique in *Bamboo* resolved the six genotypes into five clusters. Among the five clusters, the cluster I was the biggest with two species. In *Acacia nilotica*also by D^2 clustering technique, 27 seed sources were grouped into five clusters (A, B, C, D and E)

which showed that group A was the largest in size and possessed 21 seed sources. Group B and C included two seed sources each and Group D and E included only one seed source each [4]. Similarly, 80 batches of teak had been grouped into eight clusters, of which group A formed the largest cluster containing 46 batches [5]. In the current study all the species of bamboo grouped into a separate cluster barring *Bambusabalcooa*and*Bambusa vulgaris var. striata* which indicated the wider divergence among various bamboo species.

The *intra* and *inter* cluster analysis indicated that the cluster II, III, IV and V showed that there is no intra cluster generalized distance since it contained only one progeny. The maximum intra cluster distance was shown by the cluster I. From the *inter* cluster distance, it is inferred that clusters III and V were the closest while the maximum *inter* cluster distance was recorded between cluster IV and V which indicated the presence of wider genetic distance between *Bambusabambos* and *Bambusa vulgaris var. vulgaris*. Such *inter* and *intra* cluster distance among *Pinusgerardiana* genotypes was also evidenced which support the current conclusion [1].

4.2.4.2. Contribution of traits towards genetic divergence

Number of culms contributed maximum towards genetic divergence followed by basal diameter and the least by plant height. The findings of the present study are also in line with the results of Burley and Burrows (1972), who employed multivariate analysis in *Pinuskesiya* and suggested that, the technique helps in separating a large number of plus tree progenies into many clusters and accordingly the use of superior clusters in its afforestation and reforestation programmes. Hopefully such knowledge will aid propagators, geneticists, breeder and tree improvement specialists in enhancing the quality and productivity of the forest ecosystems to meet their market demand.

5. CONCLUSION

Among the seven species evaluated in the field condition, only two species *viz*., *Bambusabalcooa* and *Bambusatulda* consistently expressed superiority for all three biometric traits *viz*., plant height, Culm basal diameter and number of culms at three growth periods and these two species could be exploited for future tree improvement programme.The number of culms registered maximum PCV and GCV followed by culm basal diameter and plant height. Culm basal diameter, Plant height and number of culms registered high heritability. With regard to GA as per cent of mean, the number of culms was high followed by culm basal diameter and plant height which recorded moderate value.Number of culms exhibited negative correlation with culm basal diameter and plant height both at phenotypic and genotypic levels.

Plant height exercised negative direct effect on number of culms and culm basal diameter exercised positive direct effect on number of culms. Plant height exerted positive indirect effect via culm basal diameter. Hence from the current study, plant height and basal diameter could be used as valuable, reliable and relevant measure for Bambootree improvement programme.The application of D^2 clustering technique in *Bamboo* genetic resources revealed that the six species were resolved into five clusters. Among the five clusters, the clusters I were the biggest with two members *viz*., *Bambusabalcooa,Bambusa vulgaris var. striata.* The maximum intra cluster distance was shown by the cluster I. The maximum *inter* cluster distance was observed between cluster IV and V which indicated the presence of wider genetic distance between *Bambusabambos and Bambusa vulgaris var. vulgaris*. Among the growth attributes, number of culms contributed maximum percentage towards genetic divergence followed by culm basal diameter while the plant height recorded minimum percentage contribution.

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