Genetic variability in different accessions of *Dendrocalamus strictus* (Roxb.) Nees as assessed through culm characteristics

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Abstract

Dendrocalamus strictus (Roxb.) Nees is one of the commercially important species of India. The wide distribution and adaptability of *D. strictus* encompasses great diversity, which is expected to be reflected in its genetic constitution, hence identification and characterization of its genetic resources assumes great significance. Variability studies on the basis of culm characteristics in 20 accessions of *D. strictus* growing in a Germplasm revealed highly significant differences (0.1%) for most of the quantitative characteristics. Accession A35 hailing from Hoshiyarpur-I (Punjab) stood most conspicuous and tall among all the accessions. The accession A11 from Sahaspur recorded the maximum number of young shoots (3.67). The scored qualitative culm data was standardized to construct a dendrogram using Euclidean method. The whole dendrogram apportioned into three clusters, the first cluster was further segregated into two sub clusters, with sub cluster I comprising A1, A20 whereas sub cluster II contained the maximum proportion of the total accessions viz., A5, A10, A40, A38, A19, A8, A36, A7, A11, A88 and A13. The second cluster comprised of accessions A16, A23, A17, A18, A28 and A32. The third cluster embodied a single accession that is A35. Genotypic coefficient of variation in growth parameters was in vicinity of phenotypic coefficient of variation for culm length, internode length, leaf length and leaf width. Environmental coefficient was more than genotypic coefficient for internode diameter, number of culms and number of young shoots. Estimates of heritability (Broad sense) revealed heritability range spanning from 17.6% to 77.9%. Culm length and leaf length had maximum heritability 77.9% and 74.7 % respectively coupled with high genetic gain.

Key words : *Dendrocalamus strictus, Variability,* Culm Characters, clustering, qualitative, quantitative parameters, Heritability, genetic gain

Introduction :

Dendrocalamus strictus (Roxb.) Nees is one of the priority species distributed in different forest types of India. It occupies 53% of the total bamboo area in India, abundantly distributed in semi dry and dry zone along plains and hilly tracts usually up to an altitude of 1000 meters and is commonly cultivated throughout the plains and foothills. National Bamboo Mission (NBM) and International Network on Bamboo and Rattan (INBAR) also consider it a priority species from diversity, genetic improvement and conservation point of view.

With the gamut of uses spanning from industrial applications to construction, agricultural implements to musical instruments, furniture etc, the pressure on this resource has increased manifolds. Anthropogenic activities compounded with gregarious flowering in *D. strictus* have resulted in major depletion of its growing area and diversity, stressing an urgent need to increase its plantation with high productivity which can be achieved through ascertaining the potential genotype, analysis of genetic variability among traits and association of a particular character in relation to other traits contributing to yield (Mary and Goplan 2006).

Knowledge of genetic diversity and relationships among a set of germplasm plus the potential merit of the genetic diversity would be beneficial to all phases of improvement, optimizing hybridization and selection procedures, besides understanding the cohorts in the event of sporadic, erratic and disjunct flowering in this bamboo species. Germplasm characterization is an important link between conservation and utilization of plant genetic resources. The population level genetic diversity in *D. strictus* is still at its infancy. Efforts to quantitatively assess genetic diversity would assist in proper selection of desired genotypes for bamboo improvement programmes. The present work purports to assess diversity in 20 different accessions of *D. strictus* hailing from different geographical areas through morphological traits.

Table 1. Geographical information of the accessions

Material and Methods : 20 different accessions of *D. strictus* collected from different eco-geographical zones of India (Table 1) growing in Germplasm at Forest Research Institute (FRI) Dehradun ,were chosen for present study. The experimental site (Dendrosetum) situated at Latitude 30°20’10.31″N, Longitude 77°59’55.32″ and at altitude of 650 m comprised the germplasm of *D. strictus* raised through offsets. Offsets were planted in RBD with three replicates and each replicate carried three ramets. The material selected randomly from Dendrosetum (FRI) was eight months old at the time of study.

Morphological Characterization : For the study of morphological manifestations , 3 accessions of *D. strictus* were randomly selected. The culm characteristics were categorized as Quantitative or Qualitative.

Quantitative characters: The number of culms were counted and recorded for morphological and taxonomic studies.The height (m) of tallest culm was measured from base to the top of the bamboo clump

Serial No	Accession code	States	Provenances	Latitude (°N)	Longitude (°E)	Altitude (m)
1.	A-1	Uttarakhand	Biyasi	30°44′	78°27′	1352
2.	A-5		Devprayag	30°15′	78°6′	830
3.	A-7		Mansadevi	26°92′	78°15′	444
4.	A-8		Haridwar	26°96′	78°16′	315
5.	A-10		Shyampur	26°74′	78°11′	310
6.	A-11		Sahaspur	26°73′	78°05′	311
7.	A-13		Kalsi	30°32′	78°03′	510
8.	A-16	Haryana	Bhogpur	30°1′	77°28′	255
9.	A-17		Pinjore	30°79′	76°91′	550
10.	A-18		Thadugarh	30°73′	76°78′	225
11.	A-19		Seonthi	30°2′	74°23′	250
12.	A-20		Kurukshetra	29°6′	77°04′	222
13.	A-23		Hissar	29.15′	75.71′	210
14.	A-28	Punjab	Ropar	30°96′	76°53′	262
15.	A-32		Kahanpur	26°46′	80°33′	228
16.	A-35		Hoshiyarpur - I	31°53′	75°92′	296
17.	A-36		Hoshiyarpur - II	31°52′	75°90′	294
18.	A-38		Dasuya	31°82′	75°66′	240
19.	A-40		Jhelwa	31°5′	75°6′	250
20.	A-88	Andhra Pradesh	Dulapali, A P	17°36′	78°47′	536

by using scaled pole. The internodal diameter (cm) was recorded in the middle between 3rd and 4th node using an electronic Vernier Caliper (Mahr). Internode length (cm) was measured between 3rd and 4th node using a meter scale. For leaf measurements, 20 Leaves from different positions of an individual accession were taken and length and width measured using a plastic scale. The number of young shoots were counted for all the three ramets of each accession and averaged. The culm sheath of each accession was taken in a paper bag for comprehensive ocular inspection, tagged properly and the area was obtained by demarcating the boundary of culm sheath on the graph paper ($1cm^2$).

Statistical Analysis : The data recorded was subjected to statistical analysis as provided below to quantify the variation existing among accessions for various recorded parameters.

ANOVA (Analysis of variance) **:** The data was analysed using Genstat version 3.2 as per designed experiment i.e. randomized block design. The F values thus obtained were compared with the tabulated values at 0.1% level of significance and respective degrees of source and error. For better interpretation of significant results, critical difference (CD) or least significant difference (LSD) was calculated by Scheffe's method (1959)

CD=S.Em xt 0.005

CD=S.Emx0.001

Where S.Em is the standard error of difference calculated as

S.Em=$\sqrt{2Me/r}$

T 0.005 is the t value at 5% level of significance

T 0.001 is the t value at 1% level of significance.

The values of CD and LSD indicate the treatment (accession) to be statistically at par or not.

Computation of Diversity parameters

Genotypic, phenotypic, and environmental variances were calculated using the following equations:

Genotypic variance (Vg) = (Mt – Me)/r

Where Mt = Mean sum of square of treatment

Me = Mean sum of square of error, r = Block replicates,

Environmental variance (Ve) = M

Phenotypic variance (Vp) = Vg + Ve

Phenotypic coefficient of variation (PVC)

It is the measure of total variation existing in particular character and was calculated as suggested by Burton and Devane (1953)

$$PCV\ (\%) = \frac{\sqrt{Vp}}{x} * 100$$

Where, x = Total mean of the clones, Vp = Phenotypic variance

Genotypic coefficient of variation (GCV)

It is measure of total genetic variability existing in a particular character and was calculated by the formula as suggested by Burton and Devane (1953)

$$GCV\ (\%) = \frac{\sqrt{Vg}}{x} * 100$$

Where, x = Total mean of clones, Vg = Genotypic Variance

Environmental coefficient of variation (ECV)

It is the measure of total environment variability existing in a particular character and was calculated by using the formula as suggested by Burton and Devane (1953).

$$ECV\ (\%) = \frac{\sqrt{Ve}}{x} * 100$$

Where, x = Total mean of the clones, Ve = Environmental variance

Broad sense heritability (H^2)

Heritability is the ration of genetic variance to the total phenotypic variance and was calculated as suggested by Burton and Devane (1953) and Johnson *et al*., (1955)

$$H^2 = \frac{Vg}{Vp} * 100$$

Where, H^2 = Heritability in broad sense, Vg = Genotypic variance, Vp = Phenotypic variance.

Genetic Advance (GA)

Genetic advance is the expected increase in the magnitude of a particular character when a selection pressure of chosen intensity (i) is applied. This was calculated as per Johnson *et al.,* (1955).

$$GA = \frac{Vg}{Vp} * K * \sqrt{Vp}$$

Where K = selection intensity

In this study, K was given the value of 2.06 which is its expectation in case of 5 % selection in large samples from normally distributed population (Allard, 1960)

Genetic gain

Genetic gain expected in percent of mean was calculated using the formula given by Johnson *et al*., (1955)

$$\text{Genetic gain} = \frac{GA}{X} * 100$$

Where, x = Total mean of the clones

Correlation matrix

The linear relationship between and within various morphological parameters were studied with the help of Minitab release 11.2 using Karl Pearson's simple correlation coefficients.

Qualitative characters: The culm descriptors used for study were ;

- Culm (shape, color and growth style)
- Presence or absence of swollen node
- Presence or absence of nodal sheath scar
- Presence or absence of curved lower nodal branches.

Culm sheath morphology was studied in detail taking into account the following qualitative characters:

- Texture (soft, hard, leathery, and glazed and others)
- Presence or absence of ciliate margin
- Surface (hairy, colour)
- Shape: A gamut of ligule shapes viz., straight, slanted, dome shaped and others of culm sheath were discernible with the help of magnifying lens. Ligule shape of all accession ramets of each replicate were measured qualitatively with the help scoring (0-4) given to ligule shape in different accessions viz. 4-straight, 3- slanted, 2- indented, 1-dome shaped and 0- wavy.

Estimation of genetic divergence

Genetic diversity was analyzed among the accessions through construction of different clusters based on taxonomic traits using Euclidean method, Linkage Ward cluster analysis by Minitab release 11.2. This is a "bottom up" approach, each observation starts in its own cluster, and pairs of clusters are merged as one moves up the hierarchy. Agglomerative hierarchical clustering and the average distance among the different groups were obtained by Euclidean distance procedure to draw dendrogram (Cluster Tree) The method of hierarchical grouping viz., unweighed pair grouping method (UPGMA) was carried out on morphological parameters of twenty accessions using SPSS (version 13.0) software. This hierarchical grouping is useful in developing a relationship between the genotypes that are maximally similar for specified characteristics.

Results :

Quantitative parameters:

The quantitative data on various culm and culm sheath characteristics pertaining to twenty accessions is cited in Table 2. The analysis of variance (ANOVA) revealed significant differences at 0.1% level among the accessions for all quantitative characters except for number of culms and young shoots.

As indicated in the Table 2, the maximum culm sheath area (210.2 cm^2), culm length (328.1 cm), internode length (16.37 cm) and maximum leaf length (13.13 cm) were observed in A35 hailing from Hoshiyarpur-I (Punjab). Interestingly, the same accession displayed highest culm length and culm sheath area. The accession exhibiting the maximum internode diameter (2.8 cm) was A16 from Bhogpur. The maximum leaf width (1.98 cm) and highest culm number (8.33) was displayed by A18 from Thadugarh (Haryana), followed by A88 (1.93cm) and A11 (1.92cm) which were at par statistically.

The young shoot is a new growth produced by the rhizome of a bamboo. Statistical analysis at 5.0 % level of significance showed significant variation among the twenty accessions with respect to average number of young shoots per accession as cited in Table 2. The accession A11 from Sahaspur recorded the maximum number (3.67) of young shoots.

Table 2. Morphological parameters of different accessions of *D. strictus*.

Accession number	Sheath area (cm²)	Culm length (cm)	Internode Diameter (cm)	Internodal Length (cm)	Leaf Length (cm)	Leaf Width (cm)	Number of Culms/clump	Number of young Shoots
A1	30.60	199.10	2.51	10.76	9.13	1.50	5.67	3.00
A5	27.43	137.30	2.10	11.50	9.41	1.52	5.67	1.67
A7	22.32	125.50	2.11	10.62	7.44	1.37	4.33	1.33
A8	15.27	112.80	2.03	10.96	7.56	1.58	6.67	1.67
A10	50.10	134.10	2.05	10.98	9.46	1.61	3.67	2.00
A11	97.16	141.70	2.36	11.90	11.16	1.92	5.33	3.67
A13	49.06	90.10	2.03	12.34	10.96	1.57	4.00	1.33
A16	104.10	324.90	2.80	11.54	7.06	1.27	7.33	3.00
A17	96.42	266.60	2.68	14.74	8.88	1.36	6.67	2.33
A18	94.80	234.40	2.39	14.22	10.30	1.98	8.33	1.67
A19	58.33	151.80	2.43	11.73	6.19	1.12	6.33	1.00
A20	43.28	192.40	2.04	13.90	10.94	1.63	7.67	3.00
A23	97.43	313.40	2.03	11.83	9.37	1.18	8.00	2.67
A28	102.60	211.90	2.29	10.99	11.00	1.33	4.33	1.67
A32	108.40	199.40	2.70	11.67	11.80	1.46	4.00	3.00

A35	210.20	328.10	2.60	16.37	13.13	1.36	4.33	0.67
A36	7.05	163.80	1.78	12.54	10.16	1.51	4.00	1.00
A38	41.10	103.30	1.72	8.78	8.36	1.40	2.00	1.67
A40	46.00	121.10	2.24	10.66	9.36	1.41	3.67	1.33
A88	114.90	150.20	2.36	12.76	12.14	1.93	6.33	3.00
Mean	73.38	185.1	2.28	12.03	9.69	1.51	5.42	2.03
Significance	***	***	***	***	***	***	NS	*
C.D	6.77	68.9	0.464	2.19	1.61	0.24	-	1.73

*** Significant at the 0.1% level , * Significant at 5.0 % level, NS- Nonsignificant.

Qualitative Characters: Comprehensive morphological study was conducted on score accessions based on various taxonomic descriptors. Each accession was considered as separate independent operational taxonomic unit (OTU). Twenty-three morphological descriptors were assessed for each of the twenty OTU's (three replication per OTU) studied in the field. The scored qualitative data as cited in Tables 3 and 4 was standardized to construct a dendrogram using Euclidean method. A comparison of key culm descriptors used to evaluate phylogenetic relationship among twenty bamboo species (OTU's) were:

- Bending of culm (absent = 0, present =1)
- Color of the culm (0 = brown green, 1 = pale green, 2 = bright green, 3 = glossy green and 4 = dark green)
- Swollen node (Absent = 0, present = 1)
- Nodal sheath scar (absent = 0, present = 1)
- Piercing culm sheath (absent = 0, present = 1)
- Curved lower nodal branches (absent = 0, present = 1)
- Different culm leaf and branch leaf size (absent = 0, present = 1), nodal ring (absent = 0, present = 1).

Further, a comparative account of key culm sheath descriptors were used to evaluate phylogenetic relationships among 20 accessions (OTU's) which are as follows:

- Ratio of total length/breadth at base
- Ciliate margin (absent = 0, present = 1)
- Pubescent adaxial hair (absent = 0, present = 1)
- Pubescent abaxial hair (absent = 0, present = 1)
- Hair color (none = 0, golden brown = 1, brown = 2, dark brown = 3)
- Density of hair (absent = 0, scanty = 1, profuse = 2)
- Ratio of total length versus blade length
- Shape of blade (triangular = 0, acuminate = 1)
- Blade reflexed (absent = 0, present = 1)
- Hairy margin on the blade (absent = 0, present = 1)
- Ligule shape (0 = wavy, 1 = dome shaped, 2 = indented, 3 = slanted or oblique, 4 = straight or entire)
- Ligule shape : A gamut of ligule shapes viz., straight, slanted, dome shaped and others of culm sheath were discernible with the help of magnifying lens
- Hairs on ligule (absent = 0, present = 1)
- Auricles (0 = absent, 1 = present)
- Variable sheath sizes at different culm heights (0 = absent, 1 = present).

Euclidean method linkage ward cluster was performed for the mentioned taxonomic descriptors. The whole dendrogram apportioned into three clusters with the distances among the clusters, indicated in xaxis showing how entities are fused together (agglomerated) in large and larger classes. As observed in Fig 1., the first cluster was further segregated into two sub clusters, with sub cluster I comprising A1, A20 whereas sub cluster II contained the maximum proportion of the total accessions viz., A5, A10, A40, A38, A19, A8, A36, A7, A11, A88 and A13. Taxonomically these accessions seem to be closely related, as they were contiguous in the taxonomic dendrogram. The second cluster comprised of accessions A16, A23, A17, A18, A28 and A32, again reflecting phylogenetic proximity owing to their sorting in similar cluster. The third cluster embodied a single accession that is A35, which ramified separately in the dendrogram inferring the apparent remoteness from the rest of the accessions.

Figure 1. Clustering analysis based on Taxonomic descriptors in *D. strictus*

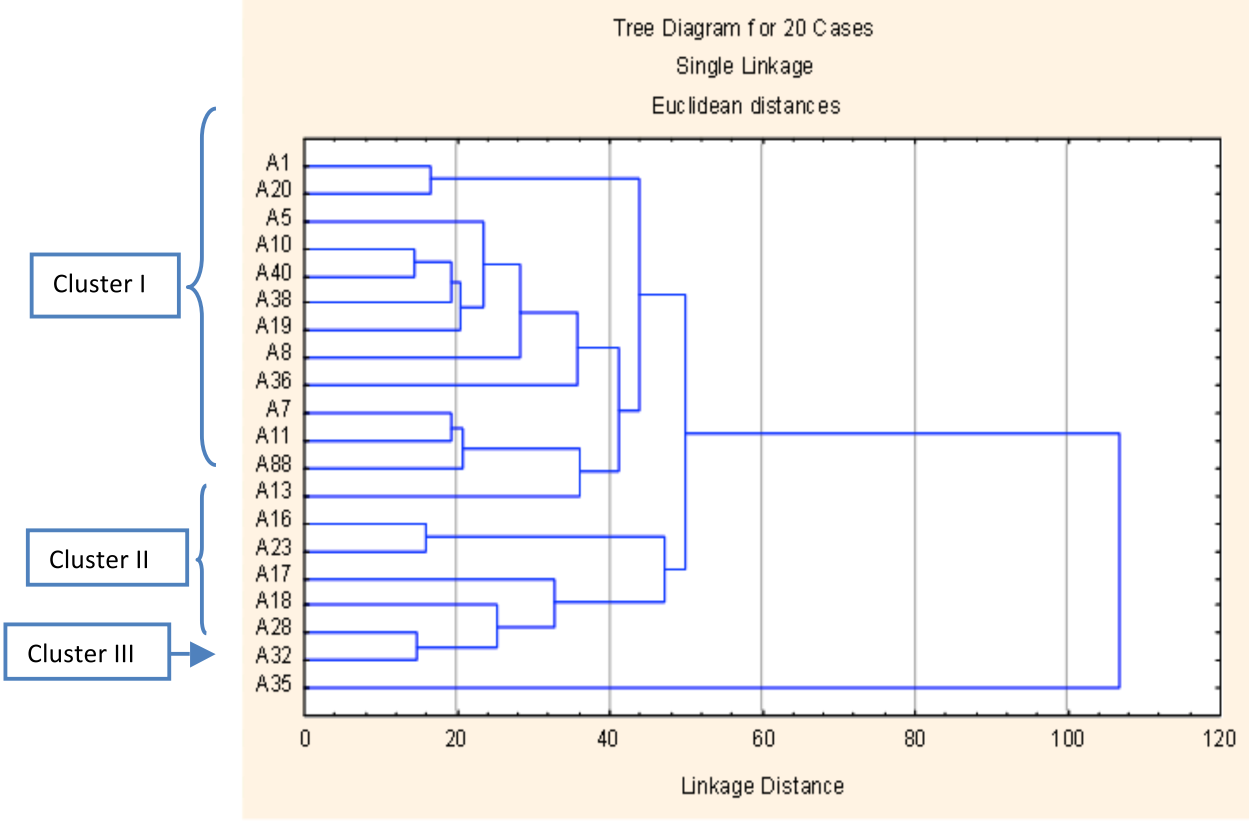


Table 3. Taxonomic clustering

Clusters	Accessions
Cluster I	A1, A20, A5, A10, A40, A38, A19, A8, A36, A7, A11, A88, A13
Cluster II	A16, A23, A17, A18, A28, A32
Cluster III	A35

The linear relationship between and within various morphological parameters was studied using Karl Pearson's simple correlation coefficients (Table 4.0). Culm sheath area showed a significant positive correlation at 5% level of significance with culm length (r = 0.566), internode length (r = 0.534), internode diameter (r = 0.512) and leaf length (0.520). Culm length showed significant positive correlation at 5% level of significance with internode length (r = 0.567).

Table 4. Correlation between various quantitative parameters

Parameters	Culm length	Internode length	Internode diameter	Leaf length	Leaf Width	Culm Sheath area
Culm length	1.000					
Internode length	0.567*	1.000				
Internodal diameter	0.346	0.162	1.000			
Leaf length	0.596*	0.177	-0.022	1.000		
Leaf width	0.485	0.056	-0.102	0.310	1.000	
Culm sheath area	0.566*	0.534*	0.512*	0.520*	0.011	1.000

* Significance at 5.0 % level.

Partition of the variance into genotypic (Vg), phenotypic (Vp) and environmental variances (Ve) revealed the maximum variance recorded at phenotypic level followed by genotypic and environmental levels for morphological parameters of all accessions (Table 5).

Genotypic coefficient of variation (GCV) in growth parameters was in vicinity of phenotypic coefficient of variation (PCV) for culm length, internode length, leaf length and leaf width. Environmental coefficient of variation (ECV) was more than genotypic coeffient of variation (GCV) for internode diameter, number of culms and number of young shoots (Table 5).

Table 5. Variance and coefficient of variability for morphological parameters

Character	Vg	Vp	Ve	PCV	GCV	ECV
Culm length	1.9	2.5	0.51	85.1	75.2	40.0
Internode length	6.9	12.5	5.50	29.34	21.9	19.5
Internode diameter	0.18	0.4	0.25	28.9	18.73	22.1
Leaf length	8.7	11.75	2.90	35.37	30.57	5.14
Leaf width	0.14	0.21	0.06	30.46	25.19	17.13
Culm number	1.15	6.6	5.40	47.24	19.85	42.87
Young shoot	0.37	1.5	1.10	59.70	29.92	51.66

Estimate of genetic component for morphological traits: Genetic parameters worked out were heritability (Broad sense), genetic gain and genetic advance. Estimates of heritability (Broad sense) and genetic gain for different parameters revealed heritability range spanning from 17.6% to 77.9%. Culm length and leaf length had maximum heritability 77.9% and 74.7 % respectively coupled with high genetic gain. Similarly, leaf width registered high heritability value of 68.4 percent with genetic gain of 42.9 percent. Internode length depicted high heritability 55.5 percent (above 50%) but less genetic gain 33.52 (Table 6).

Table 6. Estimates of heritability, genetic advance and genetic gain for morphological parameters

Character	H^2 (Heritability)	Genetic Advance	Genetic gain
Culm length	77.90	2.53	136.7

Internode length	55.50	4.04	33.55
Internode diameter	41.87	0.56	24.95
Leaf length	74.65	5.27	54.40
Leaf width	68.40	0.64	42.9
Number of Culms	17.60	0.93	17.18
Number of young shoot	25.20	0.63	30.89

Discussion :

To assess the genotypic variability in various accessions of *D. strictus* in morphometric characteristics in the field conditions., the present work was carried out in uniform environmental conditions in a Dendrosetum raised at FRI, Dehradun in the year 2008 under National Bamboo Mission Project. The present work has shown significant intraspecific variations (0.1%) with respect to morphological traits. Many characters vary within the species but few prove useful for infraspecific grouping (Kupicha 1976). Based on culm height, genotypes 35, 16, 23, 17, 18 and 28 were identified as superior performing accessions. The culm straightness, an important diagonostic feature spanned from either strictly erect, erect with pendulous tips, ascending, arched or clambering identified accessions 16, 17, 28 and 35 as erect and 18, 23 as pendulous. Similar structural anomalies in culm length were also observed by Wong (1986) in Malayan bamboos and Bhattacharya et al. (2006) in *Bambusa tulda*. Accessions 16, 32, 17, 35, 1 and 19 were found best for internode diameter. Internodal length, an important character for handicrafts and paper pulp industries where long internodes are desirable were discernible in genotypes 35, 17, 18, 20, 88, 36 and 13 (Table 2). Short internodal length (having more internodes) which provide strength to clumps and preferred for construction purposes was discernible in genotypes 38 and 7. Similar internodal variability at population level was observed by Bhattacharya et al. (2009) in *Thamnocalamus spathiflorus* subsps. *spathiflorus*. Two functionally divergent forms of leaves were studied in bamboo. Culm sheath plays a protective role for younger shoots, while the green foliage leaves are basically required for photosynthetic purposes. Green foliage leaves are the quintessential organs in the plant kingdom and an important feature in assessing variability. Variability in terms of leaf length and leaf width was seen with best genotypes in terms of leaf length 35, 88, 32, 11 and in leaf width in genotypes 18, 88 and 11 (Table 2). The key leaf characters exhibited variations for size, texture and colour; however, the leaf characters are often not enough to determine the species as indicated by Clark (1989). These variations in the morphological characteristics may be attributed to the inherent genetic factors as well as the prevailing environmental conditions, which may vary from provenance to provenance. Pathak and Nema (1985) have also reported that the genetic and the environmental factors influenced the growth and other morphological characteristics in many monocots such as landraces of wheat varieties. Accession 35 (Hoshiyarpur-I) was the best genotype in context to the parameters like culm height, internode length, internode diameter and leaf length. The better growth in this genotype is attributable to larger leaves converting more solar energy and fixing more carbondioxide, therby producing higher amounts of photosynthates proceeding to growth. Overall, the accessions of Punjab performed better in growth attributes than other accessions which could be due to edapho-climatic conditions of this site supporting the congenial environment for growth of these accessions. Similar variations in various morphological characteristics were also observed by many researchers (Singh and Bhangarwa 1995; Singh and Ceccarelli 1995; Rawat and Nautiyal 2007; Husen 2009; Batola et al. 2010). Dormling (1979); Sorensen (1979) and Rehfeldt and Wycoff (1981) reported that plants from different provenances often display different pattern of growth. New shoots of bamboo has immense nutritional value used in cuisines and decoction used for various remedial purposes viz., Asthama. Hence, young shoots have immense potential in food industry. Accessions 11, 20, 16, 32 and 88 displayed the maximum average number of young shoots (Table 2). Variability in young shoot growth was also reported by Kleinhenz and Midmore (2000) in various bamboos and in *Phyllostachys pubescens* by Lu et al. (2009).

Theme: Biology, Morphology and Taxonomy

Taxonomic characterization

The culm sheath is the most important diagonistic feature for taxonomic characterization. The culm sheath was found to vary immensely among the accessions. Vegetative characters mainly describing culm and culm sheath are widely used for bamboo species determination (Ohrenberger and Goerrings 1986). Exclusively depending on culm and culm sheath variations, three subspecies and two varieties had been described within *T. spathiflorus* (Stapleton 1994). In the absence of flower or fruit characters, the culm sheath (Raizada and Chatterji 1963) and culm characters were treated as two major taxonomic keys for the identification of bamboos (Das et al. 2007); however, Wu (1962) expressed concern on the reliability of vegetative characters due to potential influence of environment. The genotypes displaying maximum culm sheath area were 35, 88, 32 and 16. The variation in shape, color, size of some accessions is depicted in Plate 1. Based on non-parametric traits, the accessions were sundered into three clusters with majority of accessions (A1, A20, A5, A10, A40, A38, A19, A8, A36, A7, A11, A88 and A13) falling into first cluster and (A16, A23, A17, 18, A28, A32) into second cluster respectively. The third cluster harboring a single accession A35 distanced separately from the rest (Figure 1 & Table 4). Similar grouping of a non-parametric trait (stem straightness) was performed in *D.sissoo* clones by Bakshi and Arvind (2013). The taxonomic research of bamboos has been extensively taken by various Researchers (Lin 1978; Kiang 1974; Chou and Hwang 1985; Das et al. 2007).

Plate-2. Variation in Various Qualitative Characters

Variation in Culm Color Variation in culm growth style

Presence of hair

Variation in Internode characters Absence of hair

Variation in hair density

Expression of a character is the sum total of contributions of so many other characters and therefore selection should be made on the basis of components contributing towards that character; the biometrical tool for helping this is correlation. Estimates of correlation coefficients measures the degree of relationship between pair of characters and are useful to a breeder in improving the efficiency of selection therefore, it is important to have the knowledge of genetic association between various characters (Ehdaie and Waines 1989). If the correlation is strong, then probably the linkage is more conspicuous but if the correlation is low, it may be due to interdependent inheritance or non-linkage of two traits or they could be under the control of different set of genes (Jain 1982).

A simple correlation matrix (Table 5) revealed that morphological traits had significant correlations of varying magnitude among themselves. In the present investigation, culm sheath area showed positive correlation with the culm length, internode length, internode diameter and leaf length. Similar significant correlations among morphological parameters were reported by many researchers. (Janssen 1981; Liese 1987, Kitamura et al 1975; Latif et al. 1990). Positive correlations of tree height and diameter at breast height have been reported by Foster (1986); Tiwari et al (1994); Singh (2000) and Sharma (2010). Variation is commonly used as an estimate of total genetic variation and to calculate the degree of genetic control for a particular trait. Among various genetic parameters, co-efficient of variation and range of means give an idea of relative variability in a population.Wide range of means coupled with sufficient coefficient of variation for most of the characters in our study suggested presence of inherent genetic variability in germplasm. Most of the characters studied viz., culm length, internode length, leaf length and leaf width showed high variance and coefficient of variability at genotypic level than environmental level which is also supported by good heritability and genetic gain clearly indicating the expression of these characters under genetic control. Maximum variance was observed at phenotypic level, followed by genotypic level and environmental level in the various morphological characteristics of these accessions. The difference between GCV and PCV for leaf length and internode length was little showing the minimum effect of environment on their expression. Similar type of findings was also reported by Dhillon et al. (2003) in *Azardirachita Indica* and Sharma (2010) in *D. sissoo*.

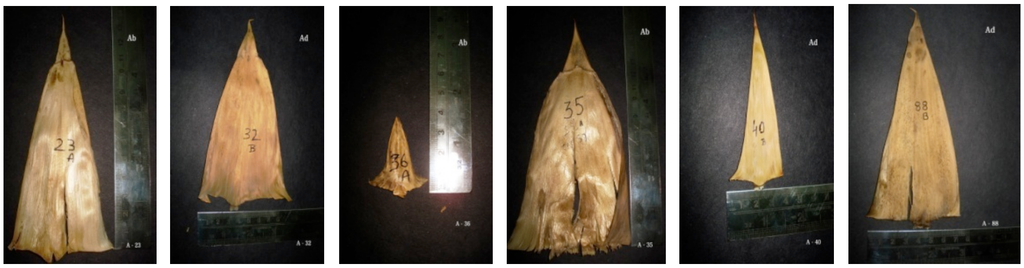
Heritability in broad sense was more than 70% in culm length and leaf length. Johnson et al. (1955) indicated that heritability values along with estimates of genetic gain were more useful than heritability alone in predicting the effect of selection. High heritability coupled with high genetic gain was observed for culm length, leaf length and leaf width which indicated that these characters are controlled by additive gene action (Johnson et al. 1955) and will respond effectively on phenotypic selection. The results were in agreement to earlier findings of Randall (1987); Foster (1986); Tiwari et al. (1992); Singh (2002) and Lewis et al. (2010). High heritability accompanied with high genetic advance for several growth parameters have also been reported by Devar (2003) in *D. strictus*. Singh and Beniwal (1993) used culm and culm characteristics for variability and heritability studies in *B. balcooa.* Heritability accompanied with low genetic gain suggests the predominant effects of non-additive genes in this population.

Many of the commercially important traits in the forest trees are under polygenic control (Wright 1976) and bamboo is no exception. UPGMA has been found to be a potent biometrical tool in quantifying the degree of divergence among the possible pairs of populations at genotypic level before affecting actual crosses in modeling the varieties in a desired genetic architechture. A clear understanding of the degree of divergence for economic characters in the species will be an added advantage in this regard as intermating of divergent groups would increase the variability and range of frequency distribution. (Alicchio and Palenzona 1974). 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 (Fisher 1936; Pandey et al. 1995 and Tiwari et al. 1989). The results with UPGMA (unweighed pair grouping method) shows four distinct clusters based on morphometric traits (Table 6). The whole dendrogram segregated into four clusters (Figure 1). The genotypes 5, 8, 7, 38, 40, 10, 13, 19, 36, 11, 88, 20 and 1 form cluster I and is the largest while cluster IV (monogenic cluster) consists of only one accession A35 and is the smallest. The maximum intercluster distance from cluster centroids is 220.35 units, specifying that the accessions in cluster I and cluster IV were more divergent; hence, genotypes selected from these clusters might yield desired heterosis. The significant difference between the cluster means for cluster I and cluster IV were observed for culm length, internode length, internode diameter, leaf width, culm sheath area, It indicated that these factors specifically contributed maximum towards genetic distance between Cluster I and

Cluster IV. To have a broad genetic base for insurance against diseases or environmental vagaries; hybridization programme involving genotypes of cluster I and cluster IV as parents, might yield desired heterosis and release wide spectrum of 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 as efficient as in a situation where the alleles were exposed to similar selection pressure (Prasad and Singh 1986; Tewari et al. 2002).
Cluster IV comprises a single accession A35 having highest value for many promising traits in the field conditions (Growth parameters) and hence should be recommended for crossing programmes as one could anticipate good heterotic response.

Plate-2. Variability in Ligule shape

A1 – Biyasi A5 - Devprayag A7 – Mansadevi A8 – Haridwar A11 – Sahaspur A-20 – Kurukshetra



A23 – Hissar A32 – Kahanpur A36 – Hoshiarpur II A35 – Hoshiyarpur I A40 – Jhelwa A88 – Dulapali (AP)

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