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Estimation of Genetic Divergence in *Thamnocalamus falconeri* Hook f. ex Munro Accessions

Chandrakant Tiwari[1*], Dinesh Gupta[2], Ritik Roshan[1], Meena Bakshi[3], Balaji Vikram[4], Md. Nasir[5] and Sanjeev Kumar[2]

[1]Department College of Forestry, Forest Biology & Tree Improvement, Banda University of Agriculture & Technology (BUAT), Banda (Uttar Pradesh), India.
[2]Department of of Silviculture and Agroforestry, College of Forestry, Banda University of Agriculture & Technology (BUAT), Banda (Uttar Pradesh), India.
[3]Plant Physiology Discipline, Botany Division, Forest Research Institute, Dehradun (Uttarakhand), India.
[4]Department of Fruit Science, College of Horticulture, Banda University of Agriculture & Technology (BUAT), Banda (Uttar Pradesh), India.
[5]Department of Forest Product utilization, College of Forestry, Banda University of Agriculture & Technology (BUAT), Banda (Uttar Pradesh), India.

(Corresponding author: Chandrakant Tiwari)*
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ABSTRACT: An essential tool for researchers looking to further explore the variability present in a species' genetic resources is the examination of diversity in germplasm. In breeding programs, the calculation of genetic divergence aids in identifying the various genotypes that are susceptible to producing heterosis. Given that combining different groups will enhance the variability and range of frequency distribution, having a thorough grasp of the degree of divergence for economic features in the species will be advantageous. *T. falconeri* is found in the western Himalaya between Jammu and Nepal at elevations of 1700m - 2400 meters. It is extensively utilized in basketry, which greatly enhances the standard of living for impoverished rural residents and artisans. The present investigation was carried out on the basis of 51 vegetative traits to estimate Genetic divergence and various parameters of variability *viz.*, Analysis of variance (ANOVA), Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Environment coefficient of variation (ECV), Heritability, Genetic gain and Genetic advance. The genetic divergence revealed that maximum contribution was impacted by clump circumference followed by number of culms then no. of young shoots and minimum for culm sheath area. The manuscript concludes that the traits *viz*. clump circumference, number of culms, number of young shoots and culm height could be exploited as selection criteria for future bamboo breeding programs of the species.

Keywords: Analysis of variance (ANOVA), *Thamnocalamus falconeri,* Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Environment coefficient of variation (ECV).

INTRODUCTION

Variation in genes and genotypes within and between species is referred to as genetic diversity. It is the culmination of all the genetic variation seen in distinct plants, animals, and microbes. A species' diversity enables an organism to adjust to biotic and abiotic challenges as well as changes in the environment and climate. Sustainability is made possible by diversity (Sharma, 1980). The prosperity of social and economic structures that enable the poorest people to achieve their nutritional and dietary needs can only be sustained by diversity (Shiva, 1994).

Tree populations' potential for improvement has been exploited through the exploitation of genetic variability both within and between populations. The way a species reacts to its surroundings in terms of biotic, climatic, and edaphic characteristics is known as genetic variability.

Similar to other members of the Bambusoideae subfamily, *Thamnocalamus falconeri* gregariously flower during 1846 and 1847 in upper Pindari River, North – West Kumaon. Ed. Madden sent quantities of seed to England, which was the origin of the plant that flowered all over Europe and in Algeria during 1875 and 1876. In Sikkim also it flowered in 1876 and at Darjeeling in 1890. In 2002 *T. falconeri* gregariously flowered throughout Uttarakhand and after seeding whole of the plants died (Naithani *et al.,* 2003). Their vulnerability is therefore increased when a population blooms and then dies all at once. Maintaining bamboo variety requires scientific management of the forests that contain this plant as understorey. Owing to the pressing need for conservation, the current study was conducted to evaluate the variability of genotypes gathered from various geographical locations and cultivated at Germplasm at Khirsu (Garhwal, India).

MATERIAL AND METHODS

To score the accessions, a number of taxonomic descriptors were selected as morphological characteristics (Table 1). For each of the quantitative morphological descriptors, the mean values from three separate replications served as representative data, and each accession was considered an independent operational taxonomic unit (OTU). As morphological descriptors, a total of twenty quantitative and thirty-one qualitative features were prioritized for each OTU.

Estimation of variation. The data recorded were subjected to statistical analysis as provided below to quantify the variation existing among accessions for various recorded parameters.

ANOVA (Analysis of variance). The data were analyzed using **Genstat version 3.2** for one way Anova. The source of variation was accession. The F value thus obtained was 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) were calculated by Scheffe's method (1959).

$CD = S.E._m \times t_{0.05}$ $CD = S.E._m \times t_{0.01}$

Where $S.E._m$ is the standard error of difference calculated as $S.E._m = \sqrt{2Me/r}$

$t_{0.05}$ is the t value at 5% level of significance, $t_{0.01}$ is the t value at 1% level of significance.

The values of CD/ LSD indicate that 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 (V_g) = (M_t – M_e)/r

Where; M_t = Mean sum of square of treatment, M_e = Mean sum of square of error r = Block replicates, Environmental variance (V_e) = Me

Phenotypic variance (V_p) = V_g + V_e

Phenotypic coefficient of variation (PVC), Genotypic coefficient of variation (GCV) and Environmental coefficient of variation (ECV) by Burton and De Vane (1953) method:

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

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

Where, x = Total mean of the clones, V_p = Phenotypic variance, V_g = Genotypic Variance, V_e = Environmental variance

Broad sense heritability (H^2), Genetic Advance (GA) and Genetic gain by Burton and De Vane (1953); Johnson *et al.* (1955) method:

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

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

$GA = \frac{Vg}{Vp} * K * \sqrt{Vp}$; 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, 1999).

Genetic gain = $\frac{GA}{x} * 100$; Where, x = Total mean of the clones

Contribution of different characters towards divergence: The percentage contribution of distinct morphological characters to divergence was assessed using Principal Component Analysis (PCA) with the correlation matrix method in SPSS (version 16.0) software.

RESULTS AND DISCUSSION

The growth of any plant species results from the accumulation of photosynthates, which is a valuable and effective tool for forecasting the growth performance of plants. Numerous traits differ among the species, but only a small number are helpful for intraspecific classification (Kupicha, 1976). The current investigation analyzed twenty quantitative traits, including clump circumference, culm count, young shoot count, culm height, culm diameter, internodal length, number of internodes in each culm, leaf length, leaf width, node count per branch, leaf count per node, bud length, bud width, culm sheath length, culm sheath width, blade length, base ratio of total length to breadth, ratio of total length to blade length, and area of the culm sheath. The results showed notable interspecific and intraspecific differences concerning morphological characteristics.

Variability is fundamental to every tree enhancement program. Variation is typically utilized as an estimate of overall genetic variation and to assess the extent of genetic influence on a specific trait. Morphological differences offer insights into genetic variations; nevertheless, the two do not always align. A significant portion of the differences present among individuals in a population may be selectively neutral. The differences in phenotypic traits, particularly quantitative ones, vary significantly between populations rather than within a single

population (Cornelissen *et al*., 2003; Schemske *et al*., 1994).

Different genetic metrics exist to evaluate the underlying genetic variability. Among different genetic factors, the coefficient of variation and range of means provide insight into the relative variability within a population.

A. Variance and coefficient of variability

A broad spectrum of means along with an adequate coefficient of variation for the majority of the traits indicates the existence of intrinsic genetic diversity in the Germplasm. The majority of the traits such as clump circumference, number of culms, number of young shoots, internodal length, number of internodes per culm, number of leaves per branch, number of leaves per node, bud length, bud width, culm sheath length, culm sheath breadth, ratio of total length to blade length, and culm sheath area demonstrated a greater degree of variance and coefficient of variability at the genotypic level compared to the environmental level. The estimation of genetic variation for these traits via the additive component might hold greater significance.

The analysis of variance (genotypic, phenotypic and environmental) for various morphological parameters (Table 2) indicated that the highest variance occurred at the phenotypic level, followed by the genotypic and environmental levels across all accessions' morphological parameters. Variance components in different morphological parameters are illustrated in the Table 3. Partition of the variance into genotypic, phenotypic and environmental variances revealed the maximum variance recorded at phenotypic level followed by genotypic and environmental levels for morphological parameters of all accessions.

Genotypic coefficient of variation in growth parameters was in vicinity of phenotypic coefficient of variation for clump circumference, no. of culms, culm height, no. of internodes per culm, bud length, bud width, culm sheath length and total sheath length to breadth at base ratio. Environmental coefficient was more than genotypic coefficient for culm diameter, leaf length, leaf width and no. of nodes per branch. Phenotypic coefficient of variability (PCV) and Genotypic coefficient of variation (GCV) were maximum (76%) and (56%) for blade length followed by total sheath length /blade length (59%) and 50% respectively while Environmental coefficient of variation (ECV) was maximum (52%) for leaf width and blade length (Table 2).

B. Estimates of genetic components for morphological traits

Heritability estimates, along with variation, are utilized to forecast genetic gain based on specific selection intensity. Heritability estimates and anticipated genetic progress provide insights into the overall variation within the population and the impact of the environment on a specific trait. The extent of heritability reflects how consistently genotypes can be identified through their phenotypic traits (Chandrababu and Sharma 1999). Genetic parameters worked out were heritability (Broad sense), genetic gain and genetic advance (Table 3).

Estimates of heritability (Broad sense) and genetic gain for different parameters revealed heritability ranged between 98.25% (bud width) to 3.03% (leaf width). Bud length (98.16), clump circumference (96.64), no. of culms (94.14) and no. of internodes per culm (92.28) recorded high heritability whereas total sheath length to blade length ratio (87.64), culm sheath breadth (84.94) and no. of young shoots showed high genetic gain (82.64) with high heritability.

Johnson *et al.* (1955) stated that heritability values combined with estimates of genetic gain were more effective than heritability alone in forecasting the impact of selection. A significant heritability along with a degree of genetic improvement was observed for clump circumference, culm count, young shoot quantity, and node count per branch. This indicates that these parameters are highly influenced by genetics and possess significant heritable additive genetic traits, showing effective responsiveness to phenotypic selection. Rasool (2011) noted considerable heritability and significant genetic improvement for culm length, leaf length, and leaf width in *Dendrocalamus strictus*. Similarly, Dhillon *et al*. (1995) found considerable heritability and notable genetic advancement for different growth traits in *Dalbergia sissoo*, Devar (2003) in *D. strictus*, and Rawat and Nautiyal (2007) in Shisham. Singh and Beniwal (1993) employed culm and its traits to evaluate variability and heritability in *Bambusa balcoa*. Singh *et al.* (2004) found substantial heritability and notable genetic improvement for culm diameter, height, and internode number, suggesting that these traits are greatly affected by genetic factors and will show favorable responses to phenotypic selection. The outcomes obtained correspond with earlier findings (Singh, 2000). The most significant variations were observed at the phenotypic level, succeeded by environmental and genotypic levels, suggesting a complex impact of the environment on phenotypic expression. The coefficients of genotypic and phenotypic variation were comparable for characteristics like clump circumference and the number of culms, indicating that these characteristics are less influenced by environmental factors and hence offer greater potential for improvement. Similar results were also noted by Dhillon *et al*. (2003) in *Azadirachta indica*. Heritability combined with minimal genetic improvement indicates the significant influence of non-additive genes.

C. Contribution of different morphological characters towards divergence

The estimation of genetic divergence has wide scope in the breeding as it helps in identifying the diverse genotypes for developing heterosis in breeding programme (Fischer, 1936). The

percentage contribution of different characters was calculated by Principal component analysis with standard correlation matrix method in SPSS version. 16 software. The results obtained are given in the Table 4. The percent contribution among various morphological characters towards genetic divergence was maximum by clump circumference (23.27%) followed by no. of culms (14.58%) then no. of young shoots (13.40%) then by culm height (11.07%) and minimum for culm sheath area (0.04%) (Table 4). Importance of relative contribution of character to total divergence has been suggested while selecting genotypes for breeding programme by Singh and Chaudhary (1985). The traits *viz.* clump circumference, number of young shoots and culm height could be key selection criteria for choosing better genotype under bamboo breeding programme. A clear understanding of the degree of divergence for economic characters in the species will be an added advantage as intermating of divergent groups would increase the variability and range of frequency distribution (Alicchio and Palenzona 1974).

Table 1: Geographical Details of genotypes of *T. falconeri* in Hill bamboo Germplasm at Khirsu, Garhwal, Uttarakhand (India).

T. falconeri		
Accession. No.	**ID. No.**	**Place of Collection**
B1.	13	FRH, Mandal I, Chamoli
B2.	73	Van I, Bedni bugyal, Chamoli
B3.	15	FRH II, Mandal, Chamoli
B4.	77	Van II, Bedni bugyal, Chamoli
B5.	103	Munsyari I, Pithoragarh
B6.	16	Musk deer farm I Chopta, Chamoli
B7.	80	Van III, Bedni bugyal, Chamoli
B8.	17	Musk deer farm II Chopta, Chamoli
B9.	12	Musk deer farm III Chopta, Chamoli
B10.	100	Munsyari II, Pithoragarh

Table 2: Variance and coefficient of variability for morphological parameters of *T. falconeri.*

Characters	**Vg**	**Vp**	**Ve**	**PCV%**	**GCV%**	**ECV%**
Clump Circumference	1415.07	1464.33	49.27	28.88	28.39	5.30
Number of Culms	95.90	101.87	5.97	37.80	36.68	9.15
Number of Young Shoots	5.33	6.36	1.03	47.90	43.83	19.30
Culm Height	219.47	381.17	161.70	**12.27**	9.31	7.99
Culm Diameter	0.00	0.02	0.02	36.24	15.54	32.74
Culm to Culm Distance	1.51	2.30	0.78	46.88	38.04	27.40
Internodal Length	3.72	5.63	1.91	17.64	14.33	10.28
Number of internodes per Culm	45.44	49.24	3.80	33.36	32.05	9.27
Leaf Length	0.15	0.45	0.31	25.01	14.26	20.54
Leaf Width	0.00	0.02	0.02	52.63	**9.16**	**51.83**
Number of nodes per branch	3.21	10.98	7.77	24.12	13.04	20.29
Number of leaves per node	42.53	61.43	18.90	46.93	39.05	26.03
Bud Length	0.01	0.01	0.00	30.76	30.48	4.17
Bud Width	0.01	0.01	0.00	16.25	16.11	**2.15**
Culm Sheath Length	4.17	6.18	2.01	20.00	16.43	11.40
Culm Sheath Breadth	0.30	0.41	0.12	29.21	24.73	15.55
Blade Length	0.16	0.30	0.14	**76.35**	**56.11**	51.78
Total sheath length to Base Breadth ratio	4.45	5.21	0.76	37.11	34.31	14.14
Total sheath length to Blade Length ratio	153.16	210.93	57.77	58.59	49.93	30.66
Culm Sheath Area	39.92	56.93	17.01	38.52	32.25	21.05

Table 3: Estimates of heritability, genetic advance and genetic gain for morphological parameters of *T. falconeri.*

Characters	H^2 (Heritability)	Genetic Advance	Genetic Gain
Clump Circumference	96.64	**76.18**	57.49
Number of Culms	94.14	19.57	73.31
Number of Young Shoots	83.76	4.35	82.64
Culm Height	57.58	23.16	14.55
Culm Diameter	18.38	0.06	13.72
Culm to Culm Distance	65.85	2.06	63.59
Internodal Length	66.00	3.23	23.98
Number of internodes per Culm	92.28	13.34	63.42
Leaf Length	32.52	0.45	16.76
Leaf Width	**3.03**	**0.01**	**3.28**
Number of nodes per branch	29.24	2.00	14.53
Number of leaves per node	69.23	11.18	66.93
Bud Length	**98.16**	0.21	62.20
Bud Width	**98.25**	0.17	32.89
Culm Sheath Length	67.50	3.46	27.81
Culm Sheath Breadth	71.66	0.95	43.12
Blade Length	54.01	0.61	84.94
Total sheath length to Base Breadth ratio	85.48	4.02	65.35
Total sheath length to Blade Length ratio	72.61	21.72	**87.64**
Culm Sheath Area	70.12	10.90	55.63

Table 4: Percent contribution of different parameters of *T. falconeri* towards divergence.

Sr. No.	Characters	Percent contribution (%)
1.	Clump Circumference	**23.27**
2.	Number of Culms	14.58
3.	Number of Young Shoots	13.40
4.	Culm Height	11.07
5.	Culm Diameter	7.86
6.	Culm to Culm Distance	6.88
7.	Internodal Length	5.85
8.	Number of internodes per Culm	4.97
9.	Leaf Length	3.65
10.	Leaf Width	2.67
11.	Number of nodes per branch	1.94
12.	Number of leaves per node	0.89
13.	Bud Length	0.76
14.	Bud Width	0.68
15.	Culm Sheath Length	0.55
16.	Culm Sheath Breadth	0.34
17.	Blade Length	0.31
18.	Total sheath length to Base Breadth ratio	0.17

19.	Total sheath length to Blade Length ratio	0.13
20.	Culm Sheath Area	**0.04**

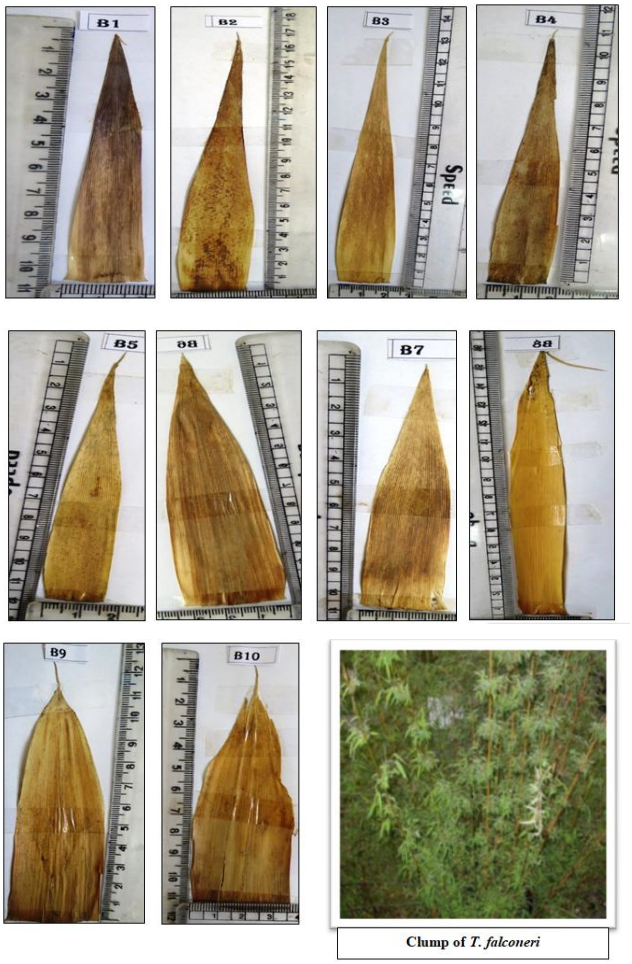

Fig. 1. Culm sheath variation among accessions of *T. falconeri.*

CONCLUSIONS

Present investigation concludes that the morphological variations within a species specially in *T. falconeri* is minimal and impart modest difference in evaluated genotypes, the characterization and distinction of the accessions must be based on the qualitative selection of few vegetative traits. Towards genetic divergence maximum contribution was made by clump circumference (23.27%) followed by no. of culms (14.58%) then no. of young shoots (13.40%) then by culm height (11.07%) and minimum for culm sheath area (0.04%) in *T. falconeri*. Therefore, the variability prevailing in the traits *viz*. clump circumference, number of culms, number of young shoots and culm height must be exploited in future bamboo breeding programs.

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