

## GENETIC DIVERGENCE IN *Corchorus capsularis* L.

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### ABSTRACT

Forty two white jute genotypes were analyzed through principal component analysis, principal coordinate analysis, canonical variate analysis and non-hierarchical clustering to identify suitable parents having distant relationship for hybridization programme. The genotypes were grouped into six different clusters. Cluster V had the maximum of eleven genotypes while cluster II had the minimum of three genotypes. The highest inter-genotypic distance was found between G36 and G39 and the lowest distance between G4 and G23. The highest inter-cluster distance was observed between clusters I and II, and the lowest inter-cluster distance was observed between clusters I and VI. The highest intra-cluster distance was found in cluster I and the lowest in cluster II. Cluster with large distances were considered more diverged than those with small distances. Genotypes of cluster II had the highest mean values for base diameter, middle diameter, top diameter, core diameter, dry fibre weight and dry stick weight and that of cluster V had the highest mean values for technical height, leaf angle, leaf length and petiole length. Yield and yield contributing characters such as technical height, base diameter, dry fibre weight and dry stick weight contributed more towards genetic divergence considering diversity pattern. Based on inter cluster distances and desirable characters the genotypes G36 and G33 from cluster I; G28 and G35 from cluster II; G7, G39 and G41 from cluster IV; G3 from cluster VI have been selected for hybridization programme.

**Key words:** *Corchorus capsularis* L., multivariate analysis, cluster analysis, genetic divergence

### INTRODUCTION

Bangladesh is a homeland of quality jute production and the second largest producer of jute around the world. Jute is the principal cash crop of Bangladesh. Genetic diversity is the fundamental law of plant breeding which is major tool and being used in parent selection for efficient hybridization programme. Modern breeding work needs diverse germplasm from which new genes can be introduced into the existing cultivars in order to improve their yield, stability and resistance to pests and adverse conditions. The importance of genetic diversity in the improvement of a crop has been stressed in both self and cross-pollinated crop (Griffin and Lindstone, 1954; Murty and Anand, 1966; Guar *et al.*, 1978). Therefore, the availability of transgressive segregant in any breeding programme depends upon the divergence of the involving parents. The quantification of genetic diversity through biometrical procedures (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization programme. Selection of parents based on geographic diversity alone is not always justified (Shreshtha, 1991). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). However, limited work has been done on the genetic divergence of jute. The present work was undertaken to understand the genetic divergence in white jute genotypes.

### MATERIALS AND METHODS

The experiment was conducted at the Jute Agriculture Experimental Station, Jagir, Manikganj during March to October, 2006. The materials consisted of 42 genotypes of white jute (*C. capsularis* L.) collected from the Gene Bank of Bangladesh Jute Research Institute (BJRI), Dhaka. These genotypes were collected from different regions of Bangladesh and from different countries.

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The experiment was laid out in Randomized Complete Block Design with three replications. Each plot had a single row of 3.0 m length. Space between rows was 0.3 m and block to block distance was 1 m. Plant to plant distance within a row was maintained at 6-7 cm. The genotypes were randomly distributed to each row within each block. The recommended doses of fertilizers were used. The whole amount of TSP, MP and half of the urea were applied during final land preparation. The remaining half of the urea was top dressed twice after first and final weeding. Thinning and weeding were done twice after 15 and 35 days of sowing to maintain uniform plant population. Insecticide was sprayed twice and hand picking was practiced to control the jute hairy caterpillars at larval. Diseased plants were wiped out from the field timely.

Data were recorded on the characters such as technical height (m), leaf angle (dg), leaf length (cm), leaf width (cm), petiole length (cm), node per plant, basal diameter (mm), middle diameter (mm), top diameter (mm), core diameter (mm), dry fibre weight (g), dry core weight (g). The data were analyzed by ANOVA, mean, range etc. were calculated by using MSTAT software. For both univariate and multivariate analysis, mean data for each character was used. In case of univariate analysis (UV), analysis of variance was done individually by F-test (Panse and Shukhatme, 1978). Multivariate analysis viz. principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CSA) and canonical vector analysis (CVA) were done by using GENSTAT 5.13 software (Copyright, 1987).

## RESULTS AND DISCUSSION

The analysis of variance showed significant variations among the genotypes for all characters studied. From principal component analysis the values were found as 74.75% in the first three components and it was 83.14% in the four components of the total variance. The two-dimensional scatter diagram was prepared by using score component 1 in X axis and 2 in Y axis, showing the groups into six clusters among the genotypes which are presented in Fig.1.

### Cluster analysis

On the basis of D<sup>2</sup> analysis, the 42 genotypes were grouped into six different clusters (Table 1). Cluster V contained the maximum number of eleven genotypes followed by cluster IV and I having nine and seven, respectively, and cluster III and VI having six genotypes in each and cluster II contained least number, three genotypes. In many cases, the same cluster included genotypes from different eco-geographic region indicating that the geographic distribution and genetic divergence did not follow the same trend. Similarly, Ziauddin *et al.* (1980), Ruat *et al.* (1985), and Dasgupta *et al.* (1982) reported the non-correspondence of genetic and geographic diversity.

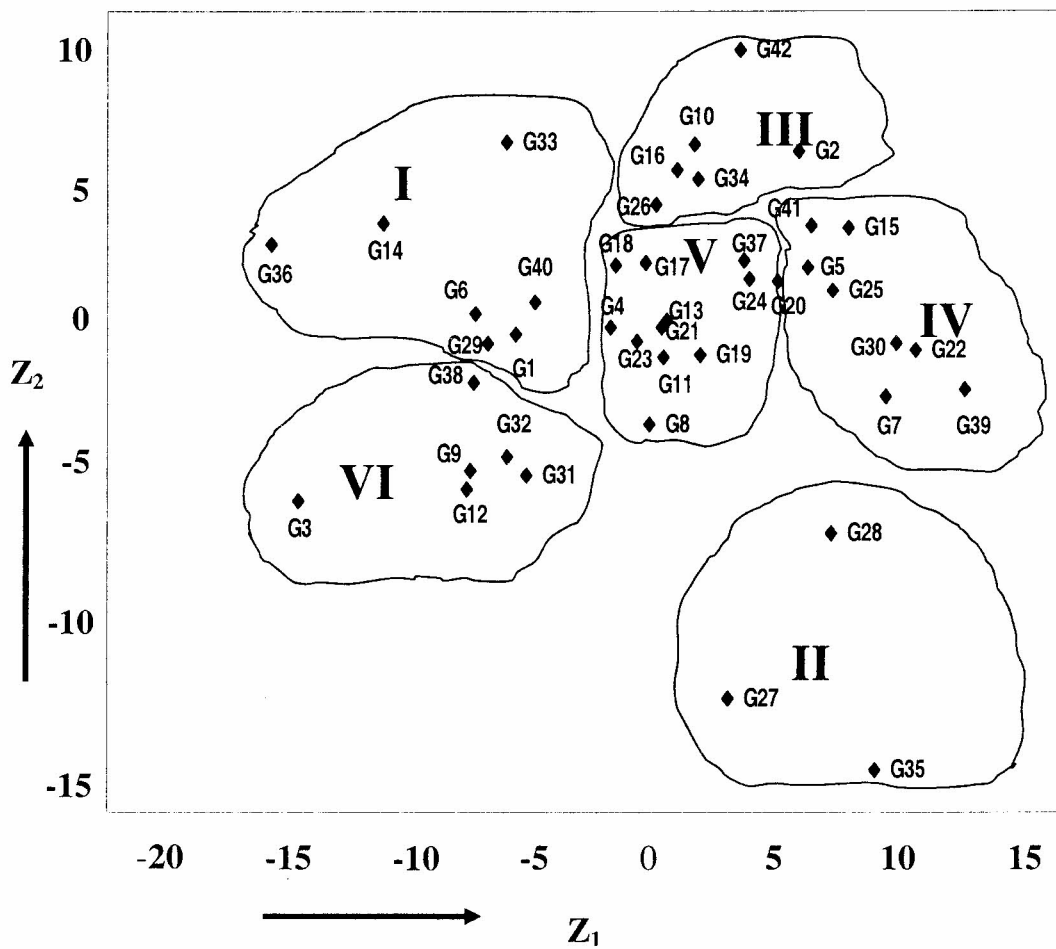


Fig. 1. Scatter distribution of 42 white jute (*C. capsularis* L.) genotypes based on their principal component scores superimposed with clustering

**Table 1. Distribution of 42 genotypes of white jute (*C. capsularis* L.) germplasm in six clusters**

Cluster	Number of genotypes	Name of genotypes	BJRI Accession No.
I	7	G1, G6, G14, G29, G33, G36, G40	862, 924, 1489, 2581, 3332, 4456, 4940
II	3	G27, G28, G35	2390, 2408, 3564
III	6	G2, G10, G16, G26, G34, G42	863, 945, 1491, 2389, 3484, 5125
IV	9	G5, G7, G15, G20, G22, G25, G30, G39, G41	890, 927, 1490, 1939, 1958, 2344, 2593, 4619, 5066
V	11	G4, G8, G11, G13, G17, G18, G19, G21, G23, G24, G37	880, 928, 957, 1483, 1520, 1800, 1920, 1947, 1973, 2040, 4484
VI	6	G3, G9, G12, G31, G32, G38	864, 941, 1482, 2699, 3311, 4618

**Canonical Variate Analysis**

Canonical variate analysis was done to compute the intra and inter cluster distances ( $D^2$ ) values. The inter cluster distances were larger than intra cluster distances which indicated that wider genetic diversity among the genotypes of different groups. Golakin *et al.* (1992) also reported about the cluster by using  $D^2$  statistics found five clusters in groundnut. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

Inter genotypic distances ( $D^2$ ) among the 42 white jute genotypes were computed and ranged from 0.109 (between G4 and G23) to 1.449 (between G36 and G39). The maximum inter cluster distance was observed between cluster I and II (10.060) followed by IV and VI (9.825), II and III (9.030); the minimum inter cluster distance was observed between the cluster I and VI (3.987) followed by III and V and I and V (Table 2).

**Table 2. Average intra (Diagonal) and inter cluster distances ( $D^2$ ) for 42 white jute (*C. capsularis* L.) genotypes**

Cluster	I	II	III	IV	V	VI
<b>I</b>	<b>1.3414</b>					
<b>II</b>	10.060	<b>0.3487</b>				
<b>III</b>	6.033	9.030	<b>0.5506</b>			
<b>IV</b>	8.785	6.950	4.660	<b>0.9391</b>		
<b>V</b>	4.599	7.476	4.198	4.673	<b>1.3052</b>	
<b>VI</b>	3.987	8.677	8.223	9.825	5.963	<b>0.8045</b>

Bold figures denote intra-cluster distances

The maximum intra cluster distance was noticed for the cluster I (1.3414) followed by cluster V (1.3052) and cluster IV (0.9391). The minimum intra cluster was found in cluster II (0.3487) followed by cluster III (0.5506) and cluster VI (0.8045).

These results confined the clustering pattern of the genotypes according to principal component analysis (PCA). Simultaneously, a two dimensional chart ( $Z_1$ - $Z_2$ ) of the genotypes is presented (Fig.-1). The clustering pattern confirmed the results obtained by divergence analysis.

The results revealed that the crosses between the genotypes of cluster I and II, IV and VI would exhibit high heterosis and produce new recombinant with desirable traits. The cluster stability depended on magnitude of divergence. The genotypes of distant cluster could be used for future hybridization.

### Cluster means for the characters

The mean performances of twelve characters in six clusters are shown in Table 3. Most of the characters showed distinct differences among the clusters. In cluster I, it contained lowest mean values for technical height, leaf length, leaf width, base diameter, middle diameter, core diameter, dry fibre weight and dry stick weight. The cluster II produced the six highest mean values for base diameter, middle diameter, top diameter, core diameter, dry fibre weight and dry stick weight and the lowest values for leaf angle.

**Table 3. Cluster means for twelve characters in white jute (*C. capsularis* L.)**

Parameters/characters	Clusters					
	I	II	III	IV	V	VI
1. Technical height (m)	2.27	2.50	2.58	2.73	2.60	2.32
2. Leaf angle (dg)	83.62	80.89	82.27	83.81	84.33	82.28
3. Leaf length (cm)	14.51	14.80	14.59	14.87	15.15	14.83
4. Leaf width (cm)	5.74	6.05	6.10	6.19	6.02	6.05
5. Petiole length (cm)	5.84	5.97	5.78	5.92	6.00	5.64
6. Node per plant	48.05	50.56	57.78	58.74	53.06	44.41
7. Base diameter (mm)	16.37	20.07	17.37	19.05	18.03	17.38
8. Middle diameter (mm)	8.80	11.12	9.50	10.23	9.73	9.48
9. Top diameter (mm)	4.08	4.80	4.04	4.33	4.36	4.54
10. Core diameter (mm)	12.64	15.97	13.51	15.27	14.46	14.29
11. Dry fibre weight (g)	6.28	10.91	7.61	9.92	8.41	7.25
12. Dry stick weight (g)	15.59	31.71	17.83	24.42	20.78	19.66

Cluster III had the lowest mean value for top diameter the second highest mean value for node number. The cluster IV comprising the highest mean values for leaf width and node number. Cluster V produced the highest mean values for technical height, leaf angle, leaf length, and petiole length. Finally, the cluster VI showed the second highest mean value for top diameter and the lowest mean value for petiole length. About similar results have been reported by Shreshtha (1991) in deshi jute, Mian *et al.* (1991) in field pea, Saha (1993), Murty and Anand (1966) in linseed flax, Shewe *et al.* (1972) in groundnut, Anand and Rawat (1984) in brown mustard and Das and Gupta (1984) in black gram.

### Contribution of characters towards divergence of the genotypes

The characters contributed towards divergence by using canonical variate analysis revealed that in both vector I ( $Z_1$ ) and vector II ( $Z_2$ ), the most important characters responsible for genetic divergence in the major two axes of differentiation were technical height (0.284-0.2913), node number (0.218-0.183), base diameter (0.399-0.057), dry fibre weight (0.376-0.157) and dry stick weight (0.365-0.168) which are presented in Table 4. On the other hand, the highest positive value for base diameter (0.399) was observed in vector I and the highest positive value for technical height (0.291) was observed in vector II. Such a result indicates that these four characters contributed maximum towards divergence. In this case vector I played a vital role than vector II for differentiation. Jatasra (1980) found the plant height as most contributing character towards the genetic divergence.

**Table 4. Latent vectors for twelve morphological characters in white jute (*C. capsularis* L.) genotypes**

Characters	Vector-I	Vector-II
1. Technical height (m)	0.284	0.291
2. Leaf angle (dg)	-0.003	-0.114
3. Leaf length (cm)	-0.156	-0.592
4. Leaf width (cm)	-0.173	-0.493
5. Petiole length (cm)	-0.139	-0.436
6. Node per plant	0.218	0.183
7. Base diameter (mm)	0.399	0.057
8. Middle diameter (mm)	-0.397	0.051
9. Top diameter (mm)	-0.218	-0.160
10. Core diameter (mm)	-0.399	-0.033
11. Dry fibre weight (g)	0.376	0.157
12. Dry stick weight (g)	0.365	0.168

### Selection of genotypes

It is generally assumed that maximum amount of heterosis would be manifested in cross combinations involving the genotypes belonging to most divergent clusters. Genotypes in cluster I if crossed with cluster II and cluster IV might exhibit high heterosis as well as wide spectrum of genetic variation in F<sub>2</sub> generation. Based on the inter cluster distance and consideration of desirable characters for high yield potential, the genotypes G36 and G33 from cluster I; G28 and G35 from cluster II; G7, G39 and G41 from cluster IV and G3 from cluster VI are considered better parents for future breeding program.

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