

GENETIC DIVERGENCE IN WHITE JUTE (*Corchorus capsularis* L.)

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ABSTRACT

Genetic divergence was estimated for identifying parental genotypes having distant relationship for hybridization program. Fifty one genotypes of white jute from different geographic origin were analyzed through principal component analysis, principal coordinate analysis, canonical variant analysis and cluster analysis by Mahalanobis D^2 statistics with 11 morphological characters. All the genotypes were grouped into six different clusters. The cluster V and VI had the maximum ten genotypes while cluster I had the minimum of seven genotypes. The highest inter-genotypic distance (1.844) was found between G_{15} and G_{50} and the lowest distance between G_{76} and G_{26} (0.233). The highest inter-cluster distance (14.367) was observed between cluster I and IV and the lowest distance (2.458) was found between cluster III and V. The highest intra-cluster distance was found in cluster I (0.835) and lowest in cluster V (0.604).

Key words: White jute, cluster and genetic divergence

INTRODUCTION

Jute is a biodegradable natural fibre and leading crop of Bangladesh. White jute (*Corchorus capsularis* L.) can grow both in low and high land and has better adaptability than the other cultivated species. Variable genotypes of white jute found in different areas of the world can play an important role in economy. Genetic divergence is one of the useful tools to select appropriate genetic resources for hybridization to develop high yield potential cultivars. The genetic diversity identified through biometrical procedures helps to choose genetically diverse parents or varieties (Anderson, 1957 and Rao, 1952). Multivariate analysis is an important tool for assessing the degree of divergence and the relative contribution of different characters to the total divergence (Golakia and Makne, 1992; Natarajan *et al.*, 1988; Das and Gupta, 1984; Sindhu *et al.*, 1989). Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Such study also permits to select the genetic divergent parents to obtain desirable recombinant in the segregating generations. Therefore, the present investigation was carried out to determine the genetic divergence among the genotypes.

MATERIALS AND METHODS

Fifty one different genotypes of white jute (Table 1), collected from Gene bank of BJRI, were grown at the Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikganj during the period from April to August, 2009.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each plot had a single row of 3.6 m length. Space between rows was 0.30 m and block to block distance was 1.0 m. The genotypes were randomly distributed to each row within each block. The recommended doses of fertilizers such as 166 kg/ha of Urea, 25 kg/ha of TSP and 30 kg/ha MP were applied. 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 after 45 days of sowing. Weeding and irrigation was done as and when was necessary. Data on plant height (m), leaf angle (dg), leaf length (cm), leaf width

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Table 1. Accession number and origin of the selected genotypes of white jute

Genotype No.	Accession number	Country of origin/Place of collection	Genotype No.	Accession number	Country of origin/Place of collection
1	890(CVL-1)	Bangladesh	27	944	Bangladesh
2	860	India	28	877	India
3	4616	Brazil	29	859	India
4	4591	Nepal	30	2020	India
5	4872	Thailand	31	2216	USA
6	4926	China	32	4472	Thailand
7	72	Bangladesh	33	78	Bangladesh
8	4617	Brazil	34	5060	Bangladesh
9	2212	USA	35	4463	Thailand
10	1513	India	36	4699	Thailand
11	4619	Brazil	37	4710	Nepal
12	4700	Brazil	38	2219	USA
13	4956	China	39	4879	Nepal
14	77	Bangladesh	40	2019	India
15	4706	Brazil	41	1515	Nepal
16	4961	China	42	4951	Nepal
17	5125(BJC-7370)	Bangladesh	43	70	Bangladesh
18	2214	USA	44	947	India
19	4474	Thailand	45	74	Bangladesh
20	1514	India	46	4871	Thailand
21	858	India	47	3693	China
22	2215	USA	48	865	India
23	891 (CVE-3)	Bangladesh	49	75	Bangladesh
24	80	Bangladesh	50	4615	Brazil
25	4468	Thailand	51	861	India
26	1832	Bangladesh			

(cm), petiole length (cm), base diameter (mm), nodes per plant, branches per plant, green weight (g), stick weight (g), fibre and yield per plant (g) was recorded. Data were analyzed based on Mahalanobis's D^2 and Canonical analysis using GENSTAT 5.13 software in IBM computer.

RESULTS AND DISCUSSION

Analysis of variance showed that the white jute genotypes varied significantly with each other for most of the characters studied. Inter genotypic distances obtained from principal component analysis revealed that the highest distance (1.844) was observed between the genotypes G50 and G15 and lowest distance (0.233) was observed between the genotypes G36 and G26 (Table 2).

Table 2. Ten higher and lower inter- genotypic distance (D^2) between pairs of white jute genotypes of different clusters

10 higher D^2 values	Genotypes combination	10 lower D^2 values	Genotypes Combination
1.8441	50 & 15	0.2328	36 & 26
1.8389	21 & 2	0.2527	42 & 26
1.8273	41 & 2	0.2712	39 & 29
1.8171	39 & 2	0.2729	34 & 25
1.7973	31 & 2	0.2766	32 & 29
1.7944	17 & 2	0.2776	10 & 3
1.7914	40 & 2	0.2800	23 & 3
1.7816	15 & 2	0.2830	44 & 25
1.7587	44 & 2	0.2869	37 & 8
1.7296	50 & 2	0.2880	28 & 26

Fifty one genotypes were grouped into six clusters on the basis of degree of divergence (Table 3). Distribution pattern indicated that maximum numbers of genotypes were included in cluster V (10) and VI (10) and minimum number in cluster I (7). Rest of the clusters namely cluster II, cluster III and

Table 3. Distribution of 51 genotypes of white jute germplasm in six clusters

Cluster	Number of genotypes	Genotype number	Accession number
I	7	8, 12, 14, 15, 33, 47, 48	4617, 4700, 77, 4706, 78, BJC83, 865
II	8	7, 13, 16, 22, 37, 40, 43, 45	72, 4956, 4961, 2215, 4710, 2019, 70, 74
III	8	3, 6, 10, 17, 18, 23, 27, 46	4616, 4926, 1513, BJC7370, 2214, CVE-3, 944, 4871
IV	8	11, 24, 28, 32, 35, 36, 49, 50	4619, 80, 877, 4472, 4463, 4699, 75, 4615
V	10	1, 2, 5, 20, 21, 29, 30, 31, 34, 51	CVL-1, 860, 4872, 1514, 858, 859, 2020, 2216, 5060, CVE3
VI	10	4, 9, 19, 25, 26, 38, 39, 41, 42, 44	4591, 2212, 4474, 4468, 1832, 2219, 4879, 1515, 4951, 947

cluster IV contains 8 genotypes in each . Statistical distances represent the index of genetic diversity among the clusters. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. The results revealed that genotypes collected from the same places did not form a single cluster. Thus genetic diversity and geographic distribution were not directly related. This is in conformity with the findings of Manjunatha and Sheriff (1991) in kenaf. Similar results also found by Shrestha (1991) in jute. It may be due to frequent movement of plant material through introduction. It was also reported by Murty and Arunachalam (1996). Considering this, parents should be selected on the basis of genetic diversity rather than geographic diversity. The minimum inter cluster distance was observed between cluster III and cluster V (2.458) and maximum between the cluster I and cluster IV (14.367). The intra cluster divergence varied from 0.609 to 0.835, maximum was recorded in cluster I and minimum in cluster V (Table 4). The genotypes belonging to the distant clusters could be used as parents in hybridization programme for obtaining a wide spectrum of variation among the segregant. Singh and Gupta (1968) reported it in upland cotton. Islam and Mostofa (2003) in *Hibiscus cannabinus* and Sasmal (1978) in jute.

Table 4. Average intra (Diagonal) and inter cluster distances (D^2) for 51 white jute genotypes

Cluster	Cluster					
	I	II	III	IV	V	VI
I	0.835					
II	5.557	0.781				
III	10.920	5.587	0.737			
IV	14.367	8.838	3.775	0.635		
V	12.032	6.475	2.458	2.504	0.609	
VI	8.638	3.285	4.208	6.335	3.831	0.715

Bold figures denote intra-cluster distances

Mean performances of different genotypes included in different clusters are shown in table 5. Difference in cluster mean existed for almost all the characters. Cluster I had genotypes with highest plant height, base diameter, nodes per plant, green weight, stick weight and fibre yield. None of the eleven characters had the highest mean value under cluster II. Cluster III was constituted with the genotypes that had highest leaf length. Cluster IV included the genotypes that had highest leaf width and petiole length. Cluster V included the genotypes that had highest branches per plant and cluster VI included the genotypes that had highest leaf angle. Yield and yield contributing characters such as plant height, base diameter, nodes per plant, green weight, stick weight and fibre yield contributed more towards genetic divergence considering diversity pattern. Similar phenomenon also observed by

Table 5. Cluster means for eleven characters in white jute

Parameters	Cluster					
	I	II	III	IV	V	VI
Plant height (m)	2.66	2.51	2.60	2.54	2.48	2.57
Leaf angle(dg)	77.94	78.77	75.96	76.37	75.10	78.83
leaf length (cm)	13.34	13.76	14.12	13.53	13.56	13.67
Leaf width (cm)	5.14	5.20	5.27	5.30	4.80	4.92
Petiole length (cm)	4.93	5.04	5.04	5.10	4.55	4.74
Base diameter (mm)	19.35	16.96	17.68	17.04	16.44	17.06
Nodes /plant	54.11	50.02	52.29	49.47	47.58	51.69
Branches/plant	2.21	2.40	2.19	1.88	2.78	2.03
Green weight (g)	219.71	180.37	137.88	114.32	133.31	160.31
Stick weight (g)	48.17	38.04	40.71	26.18	29.74	27.40
Fibre yield (g)	17.35	11.99	13.97	8.71	10.13	9.69

Yahiya (2007) in white jute. Contribution of the characters towards divergence is presented in Table 6. The canonical analysis revealed that values in both the vectors (vector 1 and 2) for plant height, base diameter, nodes per plant, green weight, sticks weight and fibre yield were found positive. Such result indicated that these

Table 6. Latent vector for eleven morphological characters in white jute genotypes

Parameters	Vectors 1	Vectors 2
Plant height (m)	0.6805	0.2313
Leaf angle (dg)	-0.0229	-0.1594
leaf length (cm)	-0.0352	-0.0133
Leaf width (cm)	-0.2678	-0.3850
Petiole length (cm)	-0.3410	-0.0463
Base diameter (mm)	0.0146	0.1779
Nodes /plant	0.0189	0.0341
Branches /plant	-0.0549	-0.0760
Green weight (g)	0.1280	0.0223
Stick weight (g)	0.0199	0.1711
Fibre yield (g).	0.0391	0.0952

characters contributed maximum towards divergence of the genotypes. Maximum heterosis will be expected using parents belonging to the divergent clusters. Mian and Bhal (1989) reported that the parents separated by D^2 value of medium magnitude generally showed higher heterosis in chick pea. It is clear from Table 5 that the highest intra cluster means for yield and five other most important yield contributing characters are obtained from cluster 1. Therefore more emphasis should be given on this cluster for selecting genotypes as a variety and they might be used as parents for future breeding programme in white jute.

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