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Assessment of Genetic Variation in Selected Germplasm of White Jute (*Corchorus capsularis* L.)

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ABSTRACT

Fifty-one genotypes of white jute from different geographic origins were evaluated to study their genetic variability with 11 morphological characters. Significant variation was observed among the genotypes for all the characters. Multivariate techniques were used to classify 51 genotypes. All the genotypes were grouped into six different clusters. Principal component analysis, principal coordinate analysis and canonical vector analysis gave similar results to that of cluster analysis. The highest inter-genotypic distance (1.84) was found between G15, G50 and the lowest distance between G38 and G26. The highest inter-cluster distance (14.37) was observed between cluster I, IV and the lowest distance (2.46) was between cluster III and V. The highest intra-cluster distance was found in cluster I and lowest in cluster V. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed in branches per plant. High heritability values with moderate genetic advance in percentage of mean were obtained for leaf width, petiole length, nodes per plant. Regarding the cluster distance, inter-genotypic distance and other agronomic performance, the genotypes G47, G33, G48 from cluster I; G27, G17, G23 from cluster III and G13, G40, G45 from cluster II were considered to be better parents for future use in hybridisation programmes.

Keywords: Principal component and coordinate analysis, canonical vector analysis, genotypic coefficient of variation, phenotypic coefficient of variation, white jute

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INTRODUCTION

The crop 'jute' belongs to the genus *Corchorus* and is the most important natural fibre crop next to cotton (Samanta *et al*., 2011). Jute is basically self-pollinated and has 14 diploid chromosomes (2n=14). The genus *Corchorus* contains about 50-60 genotypes, which are distributed throughout the tropical regions of Africa. Jute, the bast fibre, is obtained from the bark of two cultivated species of the genus, namely *Corchorus capsularis* L. and *Corchorus olitorius* L. of the family Tiliaceae. *Corchorus capsularis* L. originates from Bangladesh, India, Myanmar and South China (Singh, 1976).

Currently, the number of recommended jute varieties is limited in terms of meeting the requirements of wide agro-ecological conditions. Most of these varieties are quite old and have a narrow genetic base and are susceptible to various biotic and abiotic stressors such as insects, pests, diseases, drought, water logging and low temperature, among others. All these factors combined with the increasing demand of jute in the world market call for new types of jute to be developed to meet the requirement of various agro-industries. In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed. However, development of such parents is a long-term and tedious job. Islam and Ahmed (2003) studied variability in jute genotypes and revealed significant differences for all the characters with a wide range of variability. Considerable amount of genotypic variances was obtained for fibre weight per plant, stick weight per plant and plant height. Ahmed *et al*. (1993) reported the phenotypic coefficient of variation was relatively higher than the genotypic one for all characters. Plant height, basal diameter and dry fibre weight had high broad sense heritability estimate coupled with a moderate high genetic advance indicating the success of direct selection (Sardana *et al*., 1990). Node number was found to have low heritability and genetic advance. The quantification of genetic diversity and variability through biometrical procedures has made it possible to make selection based on geographic diversity alone but this is not always justified. Moreover, selection of parents' evaluation of genetic diversity is important to know the source of genes for a particular trait in the available germplasm (Tomooka, 1991). Mostafa *et al*. (2002) reported that high genotypic and phenotypic coefficients of variation were found in dry fibre yield, green weight and stick weight. Under the present context of global environment prospective, jute is getting highest priority as biodegradable agro-industrial crop. Therefore, the investigation was undertaken to assess the variability present in different genotypes and to select the desirable parents for hybridisation programmes.

MATERIALS AND METHODS

Site Description

The study was carried out at the Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Manikganj, Bangladesh from April to

August, 2010. The experimental site was situated in the tropical climate zone, at 23.85 ºN latitude and 90.01 ºE longitude and characterised by heavy rainfall during the months of May to September and scant rainfall during the rest of the year.

Plant Materials

The experimental material comprised 51 genotypes of white jute (*C. capsularis*) including three improved varieties, CVL-1, BJC-7370 and CVE-3. The genetically pure and physically healthy seeds of these genotypes were collected from the gene bank of the Bangladesh Jute Research Institute (BJRI), Dhaka. Accession number and origin of the genotypes are presented in Table 1.

TABLE 1
Accession number and origin of the selected genotypes of white jute (*C. capsularis* L.)

Serial No.	Genotype No.	Accession number	Country of origin/Place of collection
1	G1	890(CVL-1)	Bangladesh
2	G2	860	India
3	G3	4616	Brazil
4	G4	4591	Nepal
5	G5	4872	Thailand
6	G6	4926	China
7	G7	72	Bangladesh
8	G8	4617	Brazil
9	G9	2212	USA
10	G10	1513	India
11	G11	4619	Brazil
12	G12	4700	Brazil
13	G13	4956	China
14	G14	77	Bangladesh
15	G15	4706	Brazil
16	G16	4961	China
17	G17	5125(BJC-7370)	Bangladesh
18	G18	2214	USA
19	G19	4474	Thailand
20	G20	1514	India
21	G21	858	India
22	G22	2215	USA
23	G23	891 (CVE-3)	Bangladesh
24	G24	80	Bangladesh
25	G25	4468	Thailand
26	G26	1832	Bangladesh
27	G27	944	-
28	G28	877	India
29	G29	859	India
30	G30	2020	India
31	G31	2216	USA
32	G32	4472	Thailand
33	G33	78	Bangladesh
34	G34	5060	-
35	G35	4463	Thailand
36	G36	4699	-
37	G37	4710	Nepal
38	G38	2219	USA
39	G39	4879	Nepal
40	G40	2019	India
41	G41	1515	Nepal
42	G42	4951	Nepal
43	G43	70	Bangladesh
44	G44	947	India
45	G45	74	Bangladesh
46	G46	4871	Thailand
47	G47	3693	China
48	G48	865	India
49	G49	75	Bangladesh

cont'd Table 1

50	G50	4615	Brazil
51	G51	861	India

Note: G = Genotype

Seed Sowing, Intercultural Operation and Data Collection

The experiment was laid out in Randomised Complete Block Design (RCBD) with three replications. Each plot had a single row of 3.6 m length. The 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. Seeds were sown on 2 April, 2010. Thinning and weeding were done twice after 15 and 45 days of sowing to maintain uniform plant population. Insecticide was not applied. Hand-picking was practised to control the hairy caterpillar at larval and pupal stage. The data were recorded on five randomly taken plants from each row of each genotype. Mean values for each characters in each plot were used for statistical analysis.

Statistical Analysis and Genetic Parameters

The analysis of variance was done following the ANOVA test and the mean values were adjusted by DMRT (P=0.05) method (Steel & Torrie, 1981). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were evaluated according to the methods of Johnson *et al*. (1955). Genetic advance (GA) expected and GA as percent of the mean assuming selection of the superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson *et al*. (1955) and Robinson *et al*. (1949).

Cluster Analysis

Using Mahalanobis D^2-statistics and its auxiliary analysis assessed genetic divergence among the genotypes studied. Both techniques estimate divergences among a set of genotypes on multivariate scale. The Mahalanobis distance $(D)^2$ values were calculated from transformed uncorrelated means of characters (Bansal *et al*., 1999). The D^2 values of genotypes were arranged in order of relative distance from each other and a method suggested by Bansal *et al*. (1999) was used for cluster formation.

RESULTS AND DISCUSSION

The principal component analysis gave Eigen values for each principal component axes of coordination of genotypes with the first axes accounting totally for the variation among the genotypes, whereas four of these Eigen values above unity accounted for 90.81% (Table 2).

Fifty-one genotypes of white jute were grouped into six different clusters with the application of Mahalanobis's D^2 statistics (Table 3). Ghosh *et al*. (2013) reported five clusters in *C. capsularis* and four clusters in *C. olitorius* while Golakia and Makne (1992) found five and seven clusters, respectively, in groundnuts. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. The results presented

in Table 3 represent the composition of different clusters with their corresponding genotypes and origin included in each cluster. A maximum of 10 genotypes were in cluster V and VI, followed by eight in cluster II, III and IV. There were seven genotypes in cluster I. The genotypes of cluster I produced the highest cluster mean for plant height (2.66), base diameter (19.35), node per plant (54.11), green weight per plant (219.71), stick weight per plant (48.17) and fibre yield per plant (17.35) (Table 4). Cluster II represented eight genotypes of this group that produced the cluster mean for plant height (2.51), base diameter (16.96), green weight per plant (180.37), stick weight per plant (38.04) and fibre yield per plant (11.99). This group contained the second highest cluster mean in branches per plant (2.40) (Table 4).

Inter-genotypic distances obtained from principal component analysis showed that the greatest distance (1.84) was observed between the genotypes G50 and G15 followed by G21 and G2 (1.84), G41 and G2 (1.83), G39 and G2 (1.82), G31 and G2 (1.80), and shortest distance (0.23) was found between the genotypes G36 and G26 followed by G42 and G26 (0.25), G39 and G29 (0.27), G34 and G25 (0.27), G32 and G29 (0.28) (Table 5). Inter cluster distances were calculated from inter-genotypic distances (Table 6). The greatest intra-cluster distance was observed in cluster I (0.83), which was composed of seven genotypes followed by cluster II (0.78) (composed of eight genotypes). Both cluster III (0.74) and IV (0.63) were composed of eight genotypes.

Cluster V showed the shortest intra-cluster distance (0.61), which contained 10 genotypes followed by cluster IV (0.64) (composed of eight genotypes). Cluster VI (0.72) had 10 genotypes. These results revealed that the genotypes in cluster I were distantly related. On the other hand, the genotypes in cluster V were closely related. Cluster III was composed of eight genotypes (Table 3). Genotypes of this group produced the highest cluster mean for leaf length (14.12). This group contained the second highest cluster mean value for plant height (2.60), leaf width (5.27), petiole length (5.04), base diameter (17.68), nodes per plant (52.29), stick weight per plant (40.71) and fibre yield per plant (13.97), respectively. Cluster IV also contained eight genotypes. This cluster had the highest cluster mean for leaf width (5.30) and petiole length (5.10). This group contained a cluster mean value for plant height (2.54), base diameter (17.04) and fibre yield (8.71). Cluster V was composed of the highest 10 genotypes. The highest cluster mean was observed in branches per plant (2.78). This group contained the lowest nodes per plant (47.58). This cluster showed medium mean values for other characters. Cluster VI also contained 10 genotypes. The highest cluster mean was found in leaf angle (78.83). This group contained second lowest cluster mean value for leaf width (4.92), branches per plant (2.03), stick weight (27.40) and fibre yield per plant (9.69) (Table 4).

TABLE 2
Eigen values and percentage of variation in respect of eleven characters in white jute (*C. capsularis* L.) germplasm

Parameters	Eigen values	Percentage of total variation accounted for individual characters	Percentage of cumulative variation
Plant height (m)	7.96	46.10	46.10
Leaf angle (degree)	4.92	28.46	74.56
Leaf length (cm)	1.43	8.30	82.86
Leaf width (cm)	1.37	7.95	90.81
Petiole length (cm)	0.61	3.52	94.33
Base diameter (mm)	0.36	2.12	96.45
Nodes / plant	0.23	1.34	97.79
Branch / plant	0.15	0.87	98.66
Green weight (gm)	0.11	0.66	99.32
Stick weight (gm)	0.09	0.50	99.82
Fibre yield / plant	0.03	0.18	100.00

TABLE 3
Distribution of 51 genotypes of white jute (*C. capsularis* L.) 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, CVE3, 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

TABLE 4
Cluster means for eleven characters in white jute (*C. capsularis* L.)

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 (gm)	219.71	180.37	137.88	114.32	133.31	160.31
Stick weight (gm)	48.17	38.04	40.71	26.18	29.74	27.40
Fibre yield/plant (gm)	17.35	11.99	13.97	8.71	10.13	9.69

TABLE 5
Ten higher and lower inter-genotypic distance (D^2) between pairs of white jute (*C. capsularis* L.) genotypes of different clusters

10 higher D^2 values	Genotypes Combination (GC)	10 lower D^2 values	Genotypes Combination (GC)
1.8441	G50 & G15	0.2328	G36 & G26
1.8389	G21 & G2	0.2527	G42 & G26
1.8273	G41 & G2	0.2712	G39 & G29
1.8171	G39 & G2	0.2729	G34 & G25
1.7973	G31 & G2	0.2766	G32 & G29
1.7944	G17 & G2	0.2776	G10 & G3
1.7914	G40 & G2	0.2800	G23 & G3
1.7816	G15 & G2	0.2830	G44 & G25
1.7587	G44 & G2	0.2869	G37 & G8
1.7296	G50 & G2	0.2880	G28 & G26

Note: G = Genotype

The two important economic characteristics of jute plant are the fibre and stick yield per plant. In the case of fibre yield, cluster I possessed the highest mean values followed by cluster III, cluster II, cluster V, cluster VI and cluster IV (Table 4). The clustering pattern of genotypes did not follow geographical distribution. The genotypes evolved at one centre even exhibited considerable amount of diversity and was grouped into different clusters, including geographical diversity that may not necessarily be related to genetic diversity. This result is in conformity with the findings of Sinha *et al*. (1991). The probable cause of this situation might be due to frequent movement of plant material through introduction. Varieties developed at the same place have different genetic makeup. Certain entries also possessed similar characters even though they had their origin in different places. One of the reasons could be that the farmers from one place might have used different cultivars from various sources. That is why enormous variability in the materials even in a single location might arise.

To compute the inter-cluster Mahalonobis' (D^2) values, canonical variate analysis was used. The intra and inter-clusters for distance (D^2) values are presented in Table 6. The greatest inter-cluster distance (14.37) was between cluster I and IV, indicating wider genetic diversity between these two clusters followed by cluster I and V, I and III, II and IV, I and VI, II and V. The lowest inter-cluster distance (2.46) was found between the cluster III and V, suggesting a closer relationship among the genotypes followed by IV and V, II and VI, III and IV, V and VI, III and VI and so on included in these clusters. Similar distance was found between cluster III and V, IV and V, II and VI and III and IV, reflecting a close relationship among these clusters (Table 6). However, the maximum inter-cluster distance was recorded between cluster I and IV (14.64). Genotypes from cluster I and IV having the greatest distance if involved in hybridisation might produce a wide spectrum of segregating population. It is the theoretical concept that the maximum amount of heterosis would be obtained in hybrids involving the genotypes belonging to the more divergent origins. However, for a plant breeder the objective is not only to get high heterosis but also to achieve a high level of production by improving and utilising other yield contributing traits so that it could be adjusted in various types of cropping systems rather than getting only high heterosis. The intra-cluster distance varied from 0.61 to 0.84, having the highest in cluster I, which was composed of seven genotypes of diverse origin, while the minimum distance was found in cluster V, which comprised 10 genotypes (Table 6).

The extent of variation among the genotypes in respect of 11 characters was studied and the means value, range and coefficient of variation are presented in Table 7. Variance of the genotypes, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), heritability and genetic advance are

shown in Table 8. Significant differences were observed among the genotypes for plant height. Plant height ranged from 2.04 to 3.02 m and mean height was 2.56 m (Table 7). The moderate heritability (37.40) together with considerable genetic advance (8.77%) indicated the effectiveness for selection of this character (Table 8). Similar results were also reported by Chaudhury *et al*. (1981) in jute. Significant differences among the genotypes were recorded in leaf angles per plant. The maximum leaf angle was 84.08 dg and the minimum and mean values were 66.30 and 7713 dg, respectively (Table 7). The phenotypic coefficient of variation (8.01) and genotypic

TABLE 6
Average intra (diagonal) and inter-cluster distances (D^2) for 51 white jute (*C.capsularis* L.) 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**

TABLE 7
Estimation of statistical parameters of 10 different characters of fifty-one different genotypes of white jute (*C. capsularis*)

Characters	Range	Mean	CV%
Plant height (m)	2.04-3.02	2.56	9.03
Leaf angle (dg)	66.30-84.08	77.13	5.50
Leaf length (cm)	11.04-15.26	13.67	8.89
Leaf width (cm)	3.90-6.45	5.09	8.52
Petiole length (cm)	3.82-6.15	4.88	13.17
Base diameter (mm)	14.50-23.58	17.33	11.47
Nodes/plant	37.33-68.87	50.70	11.02
Branches/plant	1.00-10.67	2.26	27.89
Green weight (gm)	97.50-238.1	155.6	12.05
Stick weight (gm)	17.46-63.05	34.27	7.97
Fibre yield/plant (gm).	6.98-28.12	11.70	10.46

(5.82) coefficient of variation were close to each other, indicating less environmental influence in case of leaf angle (Table 8).

The mean value of leaf length showed significant differences among the genotypes. The minimum and maximum leaf length was 11.04 and 15.26 cm, respectively (Table 7). The phenotypic variance (2.08) is higher than the genotypic variance (0.60). Heritability was low (28.96) and genetic advance as percentage of mean was low (6.29) (Table 8). With such low heritability and low genetic advance, selection on leaf length would not be judicious. Leaf area was significantly variable among the genotypes. The mean value for leaf width was 5.09 cm (Table 7). The phenotypic variance (0.51) and genotypic variance (0.33) were close to each other, indicating negligible environment influence on leaf width. Moderate high heritability (63.42) with considerable genetic advance (18.41%) for this trait might be taken into consideration (Table 8) while selecting a suitable line as suggested by Sardana *et al.* (1990). Similar results were found by Ghosdastidar and Bhaduri (1983). The petiole length showed significant differences among the genotypes. It ranged from 3.82 to 6.15 cm with a mean value of 4.88 cm (Table

TABLE 8
Estimation of genetic parameters of 10 different characters of fifty-one different genotypes (*C. capsularis*)

Characters	σ^2g	σ^2p	σ^2e	GCV	PCV	ECV	h^2b	GA (5%)	GA in % of Mean (5%)
PH (m)	0.03	0.08	0.05	6.96	11.38	9.01	37.40	0.22	8.77
LA (dg)	20.15	38.14	17.99	5.82	8.01	5.50	52.83	6.72	8.71
LL (cm)	0.60	2.08	1.48	5.67	10.54	8.89	28.96	0.86	6.29
LW (cm)	0.33	0.51	0.19	11.22	14.09	8.52	63.42	0.94	18.41
PL (cm)	0.20	0.62	0.41	9.27	16.11	13.17	33.10	0.54	10.98
BD (mm)	1.70	5.65	3.95	7.53	13.72	11.47	30.10	1.47	8.50
NP	20.34	51.54	31.20	8.89	14.16	11.02	39.46	5.84	11.51
BP	2.11	2.51	0.40	64.26	70.05	27.90	84.13	2.75	121.41
GW (gm)	1153.67	1507.85	354.18	21.75	24.86	12.05	76.51	61.20	39.19
StW (gm)	15.04	15.91	0.87	33.13	34.08	7.97	94.53	7.77	66.35
Fibre yield (gm)	92.81	105.66	12.85	28.11	29.99	10.46	87.84	18.60	54.27

Note: PH = Plant height (m), LA = leaf angle (dg), LL = leaf length (cm), LW = Leaf width (cm), PL = Petiole length (cm), BD = Base diameter (mm), BP = branches per plant, NP = Nodes/plant, GW = Green weight (gm), StW = Stick weight (gm) and FW = fibre weight per plant (gm), σ^2g = genotypic variance, σ^2p = phenotypic variance, σ^2e = error variance, GCV = genotypic coefficient of variance, PCV = phenotypic coefficient variance, ECV = error coefficient variance, GA = genetic advance

7). The phenotypic variance (0.62) was much higher than the genotypic variance (0.20). The heritability (33.10) was low with low genetic advance (10.98%) (Table 8). With such low heritability and low genetic advance, selection on petiole length was not judicious. The base diameter also showed significant differences among the genotypes. It varied from 14.50 to 23.58 mm and the mean value was 17.33 mm (Table 7). This trait showed higher differences of phenotypic coefficient of variation than the corresponding genotypic coefficient of variation (Table 8). The higher differences of PCV and GCV suggest that the expression of character was mostly under the control of environment. Low heritability (30.10) and low genetic advance (8.50) indicated that the selection for this character would not be effective. The results of this experiment support the findings of Islam *et al*. (2002), who found higher PCV than the corresponding GCV value and heritability coupled with low genetic advance for basal diameter. The node number was significantly varied among the genotypes. The maximum and minimum node numbers were 68.87 and 37.33, respectively (Table 7). The phenotypic coefficient of variation (14.16) and genotypic coefficient of variation (8.89) closely related to each other. It showed moderate high heritability (39.46%) with considerable genetic advance (11.51) (Table 8). Similarly, the greatest genetic advance (35.5%) and highest heritability (52.9%) were found in fibre yield (Ahmed *et al*., 1993). The mean value for number of branches per plant showed significant differences among the genotypes. The highest and lowest branches per plant were 10.67 and 1.00, respectively. The high heritability (84.13%) with high genetic advance (Table 8) indicated that this trait could be taken into consideration while selecting suitable genotypes for a breeding programme. Significant differences were observed among the genotypes in respect of green weight. Green weight ranged from 97.50 to 238.1 gm (Table 7). The estimates of phenotypic variance were very high (1507.85). Heritability (76.51%) and genetic advance (39.19) were also very high (Table 8). Differences between phenotypic and genotypic coefficient of variation were small.

Stick weight ranged from 17.46 to 63.05 gm and mean weight was 34.27 gm (Table 7). The phenotypic (15.91) and genotypic (15.04) variance were close to each other. A minimum difference between phenotypic coefficient of variation (34.08) and genotypic coefficient of variation (33.13) indicate less influence of environmental factors on expression of this character (Table 8). Therefore, selection based on phenotypic expression of this character would be effective for the improvement of this crop. Dry fibre weight showed significant differences among the genotypes and ranged from 6.98 to 28.12 gm (Table 7). The genotypic coefficient of variation (28.11) and phenotypic coefficient of variation (29.99) were close to each other. The heritability (87.84%) and genetic advance (54.27%) were higher (Table 8). The higher heritability with high genetic advance

provided opportunity for selecting high valued genotypes for breeding programmes.

CONCLUSION

Results of the present studies indicated significant variation among the genotypes for all the characters. High heritability coupled with genetic advance was observed in green weight, stick weight, fibre weight, branches per plant and nodes per plant. These characters were under control of additive gene effect and selection for genetic improvement for these might be effective. However, the investigation revealed that no single quantitative trait had major contribution to the fibre yield. An integrated approach of improving quantitative traits would consequently help to increase the yield potential of jute. Considering the cluster, inter-genotypic distance and other agronomic performance, the genotypes G47, G33, G48 from cluster I, G27, G17, G23 from cluster III and G13, G40, G45 from cluster II were considered to be better parents for future use in hybridisation.

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