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Genetic divergence analysis of *deshi* jute (*Corchorus capsularis*) based on fibre yield and its attributing traits

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Abstract

Commercially important natural fibres considered as fiber of the future are obtained from the bark of two jute species (*Corchorus capsularis* L. and *Corchorus olitorius* L.), and they are cultivated in different south-east Asian countries including India and Bangladesh. Unfortunately, they are characterized by narrow genetic variability for adaptability to not only various agronomic environments, but also fibre yield, quality and susceptibility to diseases and pests. Therefore, research on genetic divergence in this crop is very important in formulating a successful breeding program for evolving cultivars superior in both yield and quality to cater to the increasing demand of value added jute products in the domestic and international markets. In our study, which was conducted at the Central Jute Research Experiment Station of Bangladesh Jute Research Institute (BJRI), during Kharif seasons of 2015.44 accessions of deshi jute (*Corchorus capsularis* L.) originated from different countries and two varieties CVL-1 and CVE-3 (developed from Bangladesh Jute Research Institute) as check were investigated to study the genetic variability, genetic diversity and degree of association of different component characters related to fiber yield. The seeds of experimental plant materials were grown in Randomized Complete Block Design with three replications. Statistical analysis was run to find out the genotypic and phenotypic variances, correlations and cluster analysis for fibre yield related traits namely technical height (m), leaf angle (dg), leaf length (cm), leaf width (cm), petiole length (cm), node no., base diameter (mm), middle diameter (mm), top diameter (mm), core diameter (mm), dry fibre weight (g), dry stick weight (g). Highly significant differences were observed among the genotypes for all the characters. Substantial amounts of genotypic variance were also obtained for all characters. Fibre weight was significantly and positively correlated with node no., base diameter, middle diameter, top diameter and core diameter. The clustering pattern revealed considerable amount of genetic diversity observed among the genotypes studied here and the accessions were grouped into five clusters. From two years' evaluation it was revealed that the accessions 2512, 2445, 2749 and 2533performed better in most of the cases than the control varieties CVL-1 and CVE-3. These accessions may be used as parents for future variety development program.

Key words: Genetic divergence, correlation, cluster analysis, bast fibre, fibre yield, *deshi* jute

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Introduction

Jute fiber is 100% biodegradable, recyclable and therefore not harmful to the environment. They are perhaps the world's largest source of lingo-cellulosic bast fiber, which is extracted from plants through a natural microbial process called retting (Pan et al. 2000; Roy et al., 2002; Mohiuddin et al., 1987). Jute has the ability to blend with other fibers, both synthetic and natural, and accepts classes of cellulose dyes, such as natural, basic, vat, sulfur, reagent and pigment dyes. As the demand for natural comfortable fibers increases, the demand for jute and other natural fibers that can be blended with cotton increases (Sreenath et al., 1996; Basu et al., 2005).

Jute is a self-pollinating fibrous dicotyledonous plant of the genus *Corchorus* and family Tiliaceae. The genus *Corchorus* (Jute) consists of about 50-60 species distributed in tropical, subtropical and temperate regions of the world (Wild 1984; Edmonds 1990; Heywood 1993; Bayer and Kubitzki 2003). It is believed that jute cultivation began 200 years ago in the tropics (Basu *et al.,* 2004). Jute, the bastfibre are obtained from two commercially important species: *C. capsularis* L. (white jute) and *C. olitorius* L. (Tossa jute). The origin of the white jute is said to be in Indo-Burma, including southern China and Africa for soil and sand (Kundu, 1951). Bangladesh has the largest gene bank of jute and allied fibre (JAF) crops.

Bangladesh is the homeland of quality jute production. Once upon a time it was the principle exporting goods of Bangladesh. Most of foreign currency was earned from this sector before liberation and it was sold as raw and finished goods. Not only its golden color but also its currency earning gives it the name "Golden Fibre". Then, due to several factors including increased use of artificial fibres and low jute prices farmers found less incentive to grow jute. Many jute mills were forced to close, with jute production on the verge of extinction. Information on the genetic diversity within and among closely related crop varieties is essential for crop improvement and to meet the diverse goals like producing cultivars with increased yield (Joshi and Dhawan 1966), wider adaptability, desirable quality, pest and disease resistance, etc.

Bangladesh Jute Research Institute (BJRI) has established a gene bank in 1982 now having world's largest collection of about 6060 accession of jute and allied fiber (JAF) germplasm from home and abroad (Akter and Bhuiyan, 2016). As jute is largely a self-fertilized crop, its natural genetic variability is very narrow making it difficult for the plant breeders to develop new varieties of this crop through conventional breeding. In Bangladesh, the number of recommended jute varieties is limited in meeting the requirements of wide agro-ecological conditions. Most of these varieties are quite old and have narrow genetic base and susceptible to various biotic and abiotic stresses such as insects, pests, diseases, drought, water logging, and low temperature and so on. All of these factors, together with the growing demand for jute in the world market, require the development of new types of jute to meet various agro-industrial needs.

For the above considerations, jute breeders have become more aware of maintaining the genetic diversity among varieties and improving the management of genetic resources through the conservation of traditional land races and germplasm. In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed no find out. However, development of such parents is a long term and tiring job. Variability and genetic diversity are the fundamental laws of plant breeding which are major tools being used in parent selection for efficient hybridization program. Modern breeding works needs variable and 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 and variation in plant breeding was emphasized on both self and cross-pollinated crop (Griffin and

Lindstone, 1954: Murty and Anand, 1966: Guar et al., l978). Quantification of genetic diversity and variability with biometric methods (Anderson, 1957) enabled the selection of genetically diverse and variable parents for a successful hybridization program. The choice of parents based on geographical diversity is not always justified (Shreshtha, 1991). In addition, it is important to assess genetic diversity in order to know the genetic source of a particular trait with the available bacterial plasma (Tomooka, 1991). In the current situation in the global environment, jute will be one of the most important priorities as a biodegradable agro-industrial culture.

Materials and Methods

The experiment was carried out at the Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikgonj during the period from April to August 2015.

***Experimental site*:** The experimental site was situated at 230 53.95" N latitude and 90004" E longitude with an elevation of 8.8 m from the sea level.

***Climate and soil*:** The experimental site was situated in the tropical climate zone, characterized by heavy rainfall during the month from May to September and scantly rainfall during rest of the year. The soil of the experimental field was sandy loam in texture having pH around 6.5 to 7.5. The land was medium high with uniform topography and almost homogenous with respect to soil fertilizer.

***Experimental material*:** The material comprised of 46 accessions of white jute (*C. cupsularis*). Two varieties CVL-1 and CVE-3 (developed from Bangladesh Jute Research Institute) were taken to this study as control. The genetically pure and physically healthy seeds of these accessions and varieties were collected from the gene bank of Bangladesh Jute Research Institute (BJRI), Dhaka. Accession numbers of all selected Jute landraces are shown in Table 1.

Table 1. Accession number of white jute (*C. capsularis* L.).

Genotype No.	Accession number	Genotype No.	Accession number
01	1780	24	2823
02	1784	25	2860
03	2253	26	2891
04	2415	27	2971
05	2440	28	3047
06	2445	29	3069
07	2448	30	3126
08	2497	31	3134
09	2512	32	3176
10	2528	33	3251
11	2533	34	3255
12	2535	35	3272
13	2549	36	3276
14	2552	37	3281
15	2556	38	3309
16	2571	39	3410
17	2582	40	3914
18	2607	41	3917
19	2628	42	4351
20	2696	43	4616
21	2705	44	4618
22	2749	45	4683
23	*CVL-1	46	*CVE-3

* = Check variety

***Design and layout*:** The experiment was laid out in RCBD design with three replications. Each accession was sown in 5 rows of 3 m length, spacing was 30 cm between rows, 5-6 cm between plants and 1 m between plots. Standard cultural and inter-cultural practices were followed.

***Harvesting*:** The experiment was conducted by sowing seeds on 5 April, 2015. Pigmentation data on stem color, leaf color, vein color, petiole color, stipule color, bud color, and fruit color were collected at 60 days after sowing and pre-bud stage. Plants were harvested at 120 days after sowing. Harvesting was done during the cooler time of day, such as early morning or late afternoon, and kept in cool and shaded place. Post-harvest data were collected as per *Corchorus* Descriptor. Data was analyzed following standard statistical procedures.

Results and Discussion

Observations were recorded from ten plants selected randomly from each replication for the 12 fibre yield related traits namely technical height (m), leaf angle (dg), leaf length (cm), leaf width (cm), petiole length (cm), node no., base diameter (mm), middle diameter (mm), top diameter (mm), core diameter (mm), dry fibre weight (g), dry stick weight (g). Combined analysis of variance was performed for all characters according to Yassin (1973). Simple correlation coefficients were obtained between all possible combinations of characters related to fibre yield. Fibre yield was considered as the resultant (dependent) variable.

A total of 46 jute accessions and varieties were collected from Bangladesh Jute Research Institute (BJRI), were phenotypically evaluated for fibre yield and other Attributing Traits. The analysis of variance (ANOVA) showed that the accessions had significant or very significant differences for all the studied characteristics (Table 2). Accessions ranged from 2.76 to 3.86 m for Technical height (Table 3).

Table 2. Analysis of variance (mean square).

Source of variation	df	Technical height (m)	Leaf angle (dg)	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Node no.	Base diameter (mm)	Middle diameter (mm)	Top diameter (mm)	Core diameter (mm)	Dry fibre weight (g)	Dry stick weight (g)
Replication	2	0.006	0.543	0.037	0.039	0.070	7.457	0.047	0.005	0.062	0.662	0.020	0.016
Accessions	45	0.178**	5.449*	7.017**	1.277**	2.000**	204.19**	14.670**	5.347**	1.642**	19.087**	8.635**	50.191**
Error	90	0.018	3.410	0.253	0.046	0.035	6.057	0.376	0.245	0.053	0.270	0.080	0.569

** = Significant at 1% level of probability, * = Significant at 5% level of probability

Table 3. Mean performance for different characters of 46 jute accessions and varieties.

Accessions	Technical height (m)	Leaf angle (dg)	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Node no.	Base diameter (mm)	Middle diameter (mm)	Top diameter (mm)	Core Diameter (mm)	Dry fibre weight (g)	Dry stick weight (g)
1780	3.67	40.00	15.49	5.42l	5.88	74.00	24.16	11.48	4.63	19.55	9.83	24.15
1784	3.73	40.00	14.06	5.48	5.08	77.00	24.68	12.81	4.94	20.85	10.57	27.52
2253	3.16	40.00	14.15	5.86	5.22	66.00	20.96	11.09	5.13	16.88	7.69	23.79
2415	3.29	40.00	15.68	5.96	5.84	71.00	21.64	12.09	5.05	18.28	8.57	22.32
2440	3.57	38.00	17.02	5.25	6.74	71.00	23.12	12.61	5.32	18.68	10.64	27.35
2445	3.74	40.00	16.02	5.52	6.58	84.00	22.96	12.63	4.45	18.72	12.15	29.19
2448	3.53	42.00	15.72	5.14	5.42	75.00	22.22	12.34	5.36	18.05	9.62	25.27
2497	3.71	40.00	14.12	4.48	4.96	67.00	23.27	13.12	5.64	20.17	10.58	26.61
2512	3.53	40.00	14.38	5.56	5.88	81.00	22.67	12.23	4.75	19.41	16.68	42.97
2528	3.54	38.00	17.45	6.02	5.71	65.00	21.35	12.23	4.23	17.35	8.713	22.62
2533	3.52	40.00	16.84	8.04	8.38	75.00	24.34	15.69	7.81	24.55	13.53	29.84
2535	3.59	40.00	17.84	7.04	7.24	75.00	23.95	13.69	5.81	20.55	10.53	26.84

2549	3.39	40.00	12.58	5.77	6.36	79.00	22.47	13.49	4.39	18.77	8.890	22.73
2552	3.36	42.00	8.92	6.34	6.78	72.00	23.05	12.48	5.48	18.86	9.760	25.88
2556	3.63	44.00	14.36	6.18	6.54	87.00	21.37	12.51	4.66	17.04	10.74	27.86
2571	3.47	40.00	16.62	6.52	6.68	63.00	23.06	12.27	5.36	19.36	11.18	29.53
2582	3.24	40.00	14.48	5.86	6.19	65.00	21.56	9.880	5.32	17.81	7.250	25.71
2607	2.96	42.00	13.76	4.92	4.38	59.00	19.56	10.53	4.94	16.86	9.27	19.69
2628	3.60	40.00	13.76	5.38	5.82	79.00	22.84	12.27	4.28	18.47	9.54	23.85
2696	3.59	40.00	14.18	5.58	6.34	80.00	22.75	12.07	3.81	19.37	9.18	24.28
2705	3.47	44.00	15.58	6.64	5.54	67.00	24.82	14.34	5.38	20.85	9.79	25.82
2749	3.86	40.00	15.15	5.46	6.12	87.00	19.63	12.87	3.94	19.75	12.25	34.14
*CVL-1	3.54	40.00	13.44	5.23	4.66	67.00	23.86	13.42	4.72	19.53	10.83	26.84
2823	3.55	40.00	13.46	5.16	5.92	89.00	22.06	11.82	5.28	18.43	8.50	21.72
2860	3.49	42.00	16.71	5.53	5.96	85.00	22.96	12.14	4.92	19.55	9.74	22.92
2891	3.55	42.00	15.56	6.32	6.76	83.00	21.52	11.78	5.69	18.07	9.19	23.17
2971	3.29	40.00	14.98	6.08	6.72	70.00	18.77	11.53	4.31	15.75	9.15	25.92
3047	3.15	42.00	15.56	6.98	6.44	67.00	22.92	12.85	4.65	18.99	8.92	22.75
3069	3.05l	40.00	14.06	5.84	6.17	67.00	20.02	11.61	4.88	16.65	8.78	23.12
3126	3.58	42.00	14.72	5.44	5.64	71.00	22.18	12.69	4.59	18.88	10.43	26.89
3134	3.69	40.00	18.46	6.72	7.19	83.00	23.92	13.33	5.67	19.92	10.21	29.36
3176	3.57	42.00	16.22	6.35	7.36	80.00	21.46	11.57	4.25	17.98	10.19	28.74
3251	3.28	40.00	14.84	5.73	7.18	79.00	20.18	11.78	6.37	19.95	11.85	27.82
3255	3.46	40.00	15.54	5.96	7.36	76.00	22.15	12.21	5.68	18.87	10.45	25.93
3272	3.47	42.00	13.73	5.58	5.66	75.00	19.94	11.12	3.85	16.47	10.24	25.38
3276	3.43	42.00	15.02	5.82	6.16	60.00	19.09	10.83	4.96	15.86	9.26	25.13
3281	3.35	40.00	14.19	5.73	5.53	60.00	17.02	9.890	4.15	13.95	8.52	21.26
3309	3.31	40.00	14.22	6.64	5.65	68.00	17.83	9.830	4.47	15.01	9.48	25.58
3410	3.36	42.00	14.16	5.68	5.48	73.00	19.14	12.42	4.59	15.44	8.94	24.85
3914	3.16	40.00	15.28	6.66	5.84	66.00	20.01	11.67	4.33	15.49	7.52	22.92
3917	3.14	40.00	14.25	5.84	4.56	75.00	19.87	10.84	4.28	15.01	9.87	26.38
4351	2.76	44.00	14.48	6.52	5.68	69.00	18.34	10.33	4.16	14.01	8.79	24.39
4616	2.82	40.00	15.78	6.82	5.28	74.00	18.89	10.57	4.39	14.59	8.94	23.85
4618	3.37	42.00	14.62	5.16	4.92	68.00	18.64	9.990	4.09	10.57	9.82	27.94
4683	3.28	40.00	14.42	6.18	5.85	88.00	18.21	11.03	4.12	13.53	8.25	25.59
*CVE-3	3.85	40.00	14.85	5.72	6.14	91.00	27.45	15.98	4.86	22.45	13.62	37.74
CV (%)	3.91	4.54	3.37	3.63	3.10	3.33	2.84	4.10	4.73	2.90	2.84	2.88

*= Check variety

Accession 2749 showed highest values while accession4351 showed lowest means for Technical height. In case of leaf angle mean values ranged from 38.00 dg for accession 2440 and 2528 to 44.00 dg for 2556 and 2705, respectively. Accession 3134 showed the highest and accession 2552 showed the lowest leaf length. Accession 2533 showed the highest mean values for leaf width and petiole length. While accession 2497 showed lowest mean values for leaf width and accession 2607 showed lowest mean values for petiole length. Highest number of node was produced by the genotype CVE-3 which was closely followed by 2823. Lowest number of node was produced by the accession 3276 and 3281. Maximum base diameter was obtained from the CVE-3 and minimum in 3281. The accession 2533 showed highest value of middle diameter, top diameter and core diameter. In case of dry fibre weight accession 2512 gave the maximum weight of 16.68g and 2582 produced the lowest value of 7.250g. The accession 2512 showed highest and 2607 represented lowest value of dry stick weight.

The ratios of Variability, heritability (h2b), genetic advance (GA) and GA in percent of mean for twelve parameters are shown in Table 4. The large ratios of genotypic to phenotypic variances among the accessions for all characters indicate that these characters were highly inherited and the differences among the accessions are real. Simple correlation coefficients between different pairs of characters are presented in Table 5. Dry fibre weight was positively and significantly correlated with node no, base diameter, middle diameter, top diameter and core diameter. Cluster analysis was performed using ward's method. The euclidean distance was calculated based on morphological data and a UPGMA dendogram was produced using the dissimilarity matrix for 46 jute accessions and varieties (Figure 1).

Table 4. Variability, heritability (h2b), genetic advance (GA) and GA in percent of mean for twelve related characters of deshi jute.

Characters	Minimum	Maximum	Mean	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	GCV (%)	PCV (%)	Heritability (h^2b)	GA	GA(%)
Technical height (m)	2.76	3.86	3.43	0.053	0.071	6.74	7.79	74.77	0.41	12.00
Leaf angle (dg)	38.00	44.00	40.70	0.680	4.09	2.03	4.97	16.62	0.69	1.70
Leaf length (cm)	8.92	18.46	14.93	2.255	2.508	10.06	10.61	89.91	2.93	19.65
Leaf width (cm)	4.48	8.04	5.92	0.410	0.456	10.83	11.42	89.92	1.25	21.15
Petiole length (cm)	4.38	8.38	6.04	0.655	0.690	13.40	13.75	94.93	1.62	26.90
Node no.	59.00	91.00	73.98	66.044	72.101	10.99	11.48	91.60	16.02	21.66
Base diameter (mm)	17.03	27.45	21.59	4.765	5.141	10.11	10.50	92.69	4.33	20.05
Middle diameter (mm)	9.83	15.98	12.09	1.701	1.946	10.79	11.54	87.41	2.51	20.78
Top diameter (mm)	3.81	7.81	4.87	0.530	0.583	14.95	15.68	90.90	1.43	29.37
Core diameter (mm)	10.57	24.55	17.94	6.272	6.542	13.96	14.26	95.87	5.05	28.16
Dry fibre weight (g)	7.25	16.68	9.97	2.852	2.932	16.94	17.17	97.27	3.43	34.41
Dry stick weight (g)	19.69	42.97	26.18	16.541	17.110	15.54	15.80	96.67	8.24	31.47

Cluster analysis based on morphological traits provides five clusters (Table 6). Clustering pattern showed that cluster II is composed of the highest number of accessions (18) followed by cluster I consisting of 9 accessions, cluster v consisting of 8 accessions, cluster III consisting of 7 accessions and cluster IV consisting of 4 accessions. Cluster IV represented highest values of technical height, node no., middle diameter, dry fibre weight, dry stick weight. Cluster III has highest values of leaf width, petiole length, top diameter, core diameter while cluster v has the highest leaf angle and leaf length (Table 7).

Table 5. Correlation coefficients among twelve characters in *deshi* jute.

Characters	Leaf angl (dg)	Leaf lnth (cm)	Leaf width (cm)	Petiol lnth (cm)	Node no.	Base dia (mm)	Middle dia (mm)	Top dia (mm)	Core dia (mm)	Dry fibre wt. (g)	Dry stick wt. (g)
Technical height (m)	-0.186	0.201	-0.258	0.268	0.497**	0.606**	0.580**	0.140	0.587**	0.506**	0.477**
Leaf Angle (dg)		-0.211	0.102	-0.105	-0.023	-0.117	-0.076	-0.074	-0.178	-0.098	-0.113
Leaf Length (cm)			0.332*	0.353*	0.063	0.184	0.210	0.237	0.213	0.144	0.124
Leaf Width (cm)				0.567**	-0.032	0.020	0.198	0.326*	0.120	-0.017	0.019
Petiole Length (cm)					0.326*	0.275	0.386**	0.507**	0.454**	0.278	0.233
Node No.						0.311*	0.374**	0.011	0.309*	0.388**	0.412**
Base Diameter (mm)							0.809**	0.447**	0.860**	0.442**	0.353*
Middle Diameter (mm)								0.483**	0.825**	0.533**	0.421**
Top Diameter (mm)									0.616**	0.336*	0.148
Core Diameter(mm)										0.539**	0.370*
Dry Fibre wt. (g)											0.874**

Table 6. Number, percent and name of accessions in different cluster.

Cluster number	Number of varieties	Percent (%)	Name of Accessions
I	9	19.57	Ac 01, Ac 02, Ac 08, Ac 13, Ac 14, Ac 19, Ac 20, Ac 23 and Ac 24
II	18	39.13	Ac 03, Ac 04, Ac 10, Ac 17, Ac 18, Ac 27, Ac 29, Ac 35, Ac 36, Ac 37, Ac 38, Ac 39, Ac 40, Ac 41, Ac 42, Ac 43, Ac 44 and Ac 45
III	7	15.22	Ac 05, Ac 11, Ac 12, Ac 16, Ac 31, Ac 33 and Ac 34
IV	4	8.70	Ac 06, Ac 09, Ac 22 and Ac 46
V	8	17.39	Ac 07, Ac 15, Ac 21, Ac 25, Ac 26, Ac 28, Ac 30 and Ac 32

A comparison between cluster means for different traits and relative contribution of the different traits to the total divergence revealed that the accessions with the desirable traits (highest mean values) where distributed mainly into different clusters. Thus from the cluster analysis the accessions 2512, 2445, 2749 and 2533were found to be distinct with the desirable characteristics and may be incorporated in breeding programs to improve fibre yield and quality of jute.

Table 7. Cluster mean for twelve yield and yield characters of 46 accessions and varieties.

Characters	I	II	III	IV	V
Technical height (m)	3.57	3.22	3.51	3.75	3.50
Leaf Angle (dg)	40.22	40.67	39.71	40.00	42.50
Leaf Length (cm)	13.33	14.71	16.74	15.10	15.55
Leaf Width (cm)	5.43	5.95	6.47	5.57	6.07
Petiole Length (cm)	5.76	5.60	7.25	6.18	6.21
Node No.	76.00	68.83	74.57	85.75	76.88
Base Diameter (mm)	23.24	19.50	22.96	23.18	22.43
Middle Diameter (mm)	12.55	10.97	13.08	13.43	12.53
Top Diameter (mm)	4.80	4.50	6.00	4.57	4.94
Core Diameter (mm)	19.33	15.53	20.27	20.08	18.68
Dry Fibre weight (g)	9.74	8.84	11.23	13.68	9.83
Dry Stick weight (g)	24.84	24.25	28.10	36.01	25.43

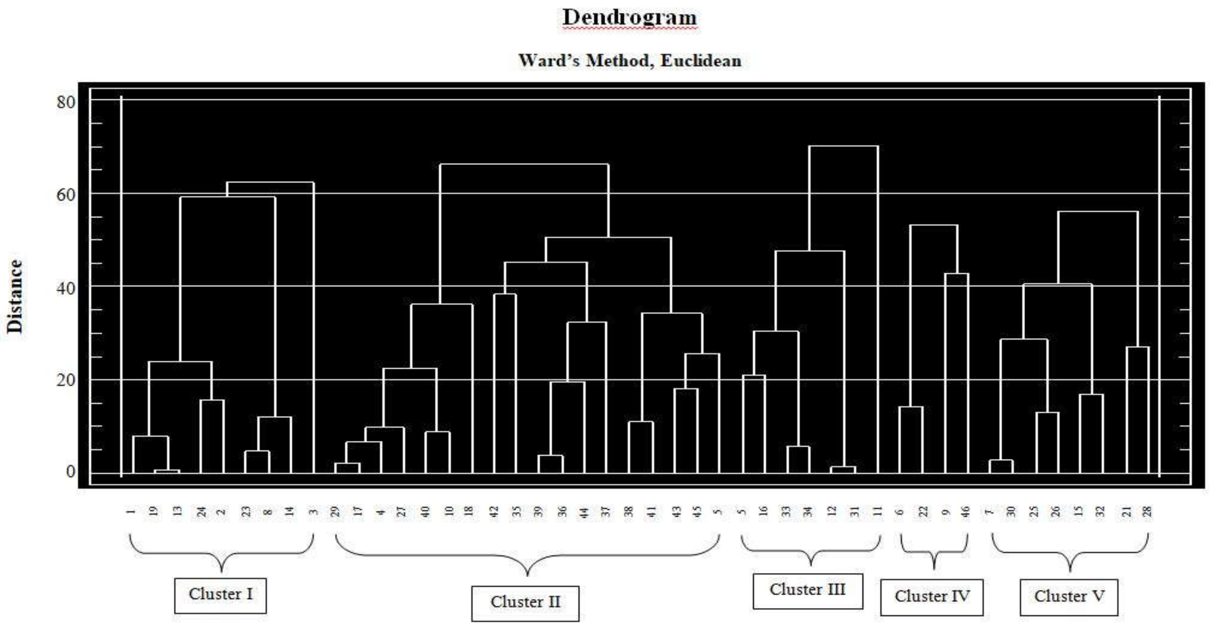

Figure 1. Dendrogram based on summarized data on differentiation among 46 accessions and varieties according to Ward's method.

Conclusion

Varietal improvement in jute, a predominantly self-pollinated crop, has been impaired due to lack of adequate genetic diversity within the available genetic stock. Information on the nature and magnitude of genetic variability for the desired characters in the base material and interrelationship among them is useful in breeding for high yield. The genetically diverse parents are likely to produce high heterotic effects and desirable segregates. Yield by itself may not be the best criterion for selection. It is quantitatively inherited and influenced by genetic factors as well as environments. In order to have a good choice of character for selection of desirable genotypes under planned breeding program, the knowledge of nature and magnitude of variation existing in available breeding materials, the association of component characters with fibre yield and their exact contribution through direct and indirect effects are very important.

The present study was visualized to divulge the nature and magnitude of genetic variability, the pattern of character association among the characters, the direct and indirect effects of component characters towards fiber yield and the degree of genetic divergence in germplasm accessions of deshi jute. The material for the present study comprised of forty-six accessions and varieties of jute (*Corchorus capsularis* L.) collected from BJRI, were evaluated using RCBD design for 12 quantitative characters. The analysis of variance showed significant differences among the genotypes for almost all the characters and from our study, we can insist that the accessions 2512, 2445, 2749 and 2533 were found to be distinct with the desirable characteristics and may be incorporated in breeding programs to improve fibre yield and quality of jute.

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