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Genetic variability, character association and path analyses effects on fiber yield and yield attributing morpho-agronomic traits of tossa jute (*Corchorus olitorius* L.)

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Abstract

Jute (*Corchorus* spp.) is a natural fiber crop having a lower extent of genetic variability due to its self-pollinating nature. The success of any breeding program for variety development primarily depends on the presence of genetic variation in the parental genotypes. A field experiment was conducted in a randomized complete block design at ManikganjStation of Bangladesh Jute Research Institute (BJRI) during 2019-2020. The genetic divergence of 58 tossa jute (*C. olitorius*) genotypes including two pre-released standard varieties (O-9897, BJRI Tossa pat 4) and 56 accessions were studied to select genotypes having the most divergence in natural rainy condition. The jute genotypes were categorized into five clusters based on Mahalanobis D^2 analysis. Cluster I and IV showed maximum inter-cluster distance (181.44) while the maximum intra-cluster distance (16.15) was recorded in cluster I. Cluster V revealed the highest values for number of nodes, stem mid-diameter, core diameter, green weight with leaves, dry stick weight and dry fiber weight per plant while cluster IV showed higher means for plant height, green bark thickness and leaf area. The highest contribution (47.14%) was wielded by plant height of total deviations. The results recommended that hybridization between genotypes of cluster V, IV and III could provide a wide range of discrepancies in the segregating generation which could offer chance for isolation of good genotypes with high fibre yielding lines.

Keywords

Introduction

Jute is a biodegradable natural bast fiber which is known as golden fiber of Bangladesh (1, 2). It is one of the inexpensive and stoutest among natural fibers and well-thought-out as fiber for the future. After cotton, Jute is the second most significant vegetable fiber in terms of convention, global uses, manufacture and availability. Locally jute is known as Pat, kosta, Nalita, Bimli or Mesta (kenaf). Jute *(Corchorus spp.)* grows in tropical and subtropical areas all over the world in an inconceivable range of habitats from very dry and near deserts to swamps and flooded regions and on a wide range of soil types. According to Loumerem and Alercia (3), the

cultivated jute species (*Corchorus capsularis* L. & *C. olitorius* L. having 2n= 14) are tall, annual herbs grow up to 2-4m in height, are non-branched or with only a few side branches and mostly self-pollinating crop. Jute leaves are elliptic-lanceolate, simple, alternate, apically acute or acuminate, 5-15cm long, with an acuminate tip and a finely serrated lobed margin. Flowers are yellow colored, small in size (2-3cm diameter) and arranged in condensed cymes. Flowers are composed of 4-5 sepals & petals, 5 to numerous stamens and occur in the axel in leaves. Sepals are about 3mm long, apiculate and oblong. The ovary is locular and 2-6 in number. Seeds are numerous in number and smaller in size. Fibers are obtained from the secondary phloem fibers from the bark of the stem (4). More than 170 *Corchorus* species are mentioned in the index Kewensis but probably the total species is around 50 -60 (5). Only two species of jute namely *C. capsularis* L. (Deshi jute) and *C. olitorius* L. (Tossa jute) are white and golden colourfibre, respectively under the *Corchorus* genus.

According to the report of the Food and Agriculture Organization of the United Nations, Bangladesh is going to overcome India to become the largest producer of Jute throughout the world. Bangladesh accounts for 58% of the world's overall jute production. In India and Bangladesh, about 90% of the world's jute is grown in the Ganges-Brahmaputra delta (6). Kundu (4) has described the origin of jute, *C. capsularis* L. was originated from Indo-Burma (Indo -Myanmar) region and *C. olitorius* L. from Africa. According to Kundu (7) the secondary center may be Indo-Burma for *C. olitorius* L.

Apart from Bangladesh and India, the crop is now also cultivated in Myanmar, Nepal, China, Thailand, Cambodia, Vietnam, Taiwan, Tanzania, Brazil, Kenia and some other countries also. However, Bangladesh, India, China, Nepal, Myanmar and Thailand are the major growers having accountancy for over 98% of the global output (6).Agriculture is an important economic activity in Bangladesh. It currently employs about 50% of the country's labour force and donates about 20% of country's gross domestic product (GDP). It is progressively becoming established in the economic literature that the growth of a rising economy depends censoriously on the progress of the agricultural sector (8). In Bangladesh about 70% of poor people live in the village areas and these poor people are employed in the agricultural sector. Hence, mitigation of poverty requires reducing poverty among peasants in the village areas through agricultural improvement by means of jute and other crop cultivation.

At the farm level, about 4 million livings are directly or indirectly reliant on jute cultivation. The net area under jute production in Bangladesh has gone down from 772.47 thousand hectares in 1986-87 to 666 thousand hectares in 2013-14. At the same time, the total output of jute has augmented to 1323 thousand tons from 1125 thousand tons. However, the production per hectare improved from 1.58-11.15 tons/ha during 1972-73 to 2014-2015 (9). The reason for this increased output is attributed to the subsequent effect of research endeavors during this period.

Genetically diverse germplasm is significant for the development of new varieties with higher agronomic characteristics. BJRI has 6065 number of germplasms of jute, kenaf and Mesta of both indigenous and exotic sources (10). Among them, 1500 are *olitorius* species. These germplasms have a wider gene pool with various types of biotic and abiotic stress tolerance. The study of diversity of these materials is significant for searching variability and to isolate desired genotypes, which can be castoff for emerging a new variety of *olitorius* species. For this investigation, 58 germplasm were sourced from the Gene Bank of BJRI. The current study was undertaken to observe morphological genetic variability and estimate the diversity to select superior genotypes which would be used in future breeding programs for variety development of tossa jute.

Hence, this experiment was performed to evaluate the extent of genetic diversity and character relations among 58 genotypes of tossa jute and to select diverse genotypes as parents for further studies. The major aims of the study included (a) to assess genetic diversity among 58 tossa jute genotypes and (b) to identify promising germplasm having higher fibre yield and yield attributes to be used in breeding programs in future for varietal development.

Materials and methods

Study site and duration

The experiment was carried out at the Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI) in Manikganj District during 2019-2020. It was a part of higher study research work where firstly seeds were sourced from the Gene Bank of BJRI and grown in the field for genetic purity & seed multiplication in 2019. In 2020, the collected pure seeds were sown and plants were grown with proper care in field and data were collected for statistical analyses. The experimental site was at $23^0 53.95''$ N latitude and $90^0 04''$ E longitude with an elevation of 8.8m from the sea level. It goes to the Young Brahmaputra and Jamuna Flood Plain Agro-Ecological Zone (AEZ No. 8) of Bangladesh.

Plant materials

A total of 58 tossa jute genotypes including 56 accessions of different origins and two control varieties (O-9897 and BJRI Tossa pat 4) were utilized in this study (Table 1). The genetically pure and vigorous seeds of accessions and varieties were sourced from the Gene Bank and Breeding Division of BJRI, respectively.

Weather at study site

The geographical condition of the study site was under the tropical climate, characterized by heavy precipitation during May to September and scanty rainfall during the rest of the year. Meteorological data on temperature, rainfall and relative humidity for the rising season were attained from the Department of Meteorological Centre, Dhaka-1207, Bangladesh (Supplementary table 2).

Table 1. List of 58 tossa jute genotypes and their origin

Genotype SL.	Genotype/ Accession	Origin	Genotype SL.	Genotypes/ Accession	Origin
G_1	BJRI Tossa pat 4 (O-72)	Bangladesh	G_{30}	Acc.3705	Kenia
G_2	Acc.1282	Bangladesh	G_{31}	Acc.3708	Kenia
G_3	Acc.1283	Bangladesh	G_{32}	Acc.3988	Syria
G_4	Acc.1285	Bangladesh	G_{33}	Acc.3989	Syria
G_5	Acc.1331	Japan	G_{34}	Acc.3990	Syria
G_6	Acc.1335	Japan	G_{35}	Acc.4172	Tanzania
G_7	Acc.1337	Egypt	G_{36}	Acc.4177	Tanzania
G_8	Acc.1338	Philippine	G_{37}	Acc.4178	Tanzania
G_9	Acc.1341	India	G_{38}	Acc.4481	USA
G_{10}	Acc.1344	India	G_{39}	Acc.4483	USA
G_{11}	Acc.1345	India	G_{40}	Acc.4485	USA
G_{12}	Acc.1346	India	G_{41}	Acc.4546	Thailand
G_{13}	Acc.1349	Mozambique	G_{42}	Acc.4547	Thailand
G_{14}	Acc.1352	India	G_{43}	Acc.4548	Thailand
G_{15}	Acc.1354	India	G_{44}	Acc.4549	Thailand
G_{16}	Acc.1355	India	G_{45}	Acc.4550	Thailand
G_{17}	Acc.1357	Brazil	G_{46}	Acc.4563	Nepal
G_{18}	Acc.1360	Denmark	G_{47}	Acc.4564	Nepal
G_{19}	Acc.1480	Srilanka	G_{48}	Acc.4565	Nepal
G_{20}	Acc.1522	India	G_{49}	Acc.4566	Nepal
G_{21}	Acc.1523	Srilanka	G_{50}	Acc.4567	Nepal
G_{22}	Acc.1524	Srilanka	G_{51}	Acc.4569	Nepal
G_{23}	Acc.1525	Srilanka	G_{52}	Acc.4570	Nepal
G_{24}	Acc.1526	ICRISAT	G_{53}	Acc.4738	China
G_{25}	Acc.1773	Bangladesh	G_{54}	Acc.4739	China
G_{26}	Acc.1806	India	G_{55}	Acc.4740	China
G_{27}	Acc.1807	India	G_{56}	Acc.5001	China
G_{28}	Acc.1809	Australia	G_{57}	Acc.5008	China
G_{29}	Acc.3702	Kenia	G_{58}	O-9897	Bangladesh

Soil status

The research field was medium-high with unchanging topography and almost homogenous with respect to soil fertility. The land was infrequently flooded and drainage system was well. Depth of flood fluctuated from 0.60-1.25m. The soil was sandy and silty loam in consistency having pH around 6.0 to 6.65. The soil was deficient in all major nutrient elements (Nitrogen, Phosphorus, Potassium) and also in organic matter. Soil was supplemented with cow dung and N, P, K fertilizers were applied for the normal crop growth.

Preparation of Land

The study plot was ploughed with a manually operated power tiller in the last week of February 2019. After one week of sun drying, the land was prepared with good tilth by harrowing, ploughing and cross-ploughing several times followed by fertilizing and laddering. The soil was incorporated with recommended amount of organic fertilizer (cow dung: 5 t/ha) and inorganic fertilizers such as Urea (100kg/ha), TSP (25kg/ha) and MoP (45kg/ha). The half amount of urea and other fertilizers were applied during the preparation of land and the rest volume of urea was top dressed in two equal installments after first (20 days after sowing) and final weeding (45 days after sowing).

Experimental design and growing of plants

The experiment was laid out in a randomized complete block (RCB) design with three replications. Each genotype was grown in three rows of 2m length keeping row to row distance of about 30cm, plant to plant distance of about8-10cm, genotype to genotype distance of about 40cm and plant population of 35-40 plants m^{-2} or 3.5-4.0 L/ha. Proper intercultural practices were followed at proper time to ensure crop growth. Thinning and weeding were performed concurrently at the time of top dressing of urea fertilizer. Irrigation was provided as and when necessary, and crops also received rainwater and were saved from weeds, pests, and diseases. Soil moisture was maintained by proper irrigation throughout the cropping period along with the clear drainage system for fast release of excess rainwater from the research field.

Data Collection

Data for all morpho-agronomical characters were collected according to the jute descriptor issued by International Jute Organization (IJO) at vegetative, flowering, harvesting and post harvesting stage (Fig. 1 and Table 2). Plants were selected randomly from each row for data collection at harvesting time (120 days age).

Fig. 1. A. Field view of jute seedlings at growing stage, B. Jute plants at vegetative stage, C. Harvesting of plants at 120DAS, D. Collection of data

Data analysis

The collected raw data were compiled and replicated data were computed in MS Excel program 2021. The compiled data were subjected to analysis of variance (mean square) for RCB design (Appendix I) according to Panse and Sukhatme (11) and the genotype means were compared for the quantitative traits using the least significant difference (LSD) at P <0.05 level of significance (12). Genetic components, character associations and path analyses were carried out using 'R' statistical package (13). Analysis of Principal Component (PCA), Principal coordinate (PCoA) and Hierarchical clustering was carried out using 'Minitab19' statistical package (14).

Table 2. Traits recorded, their abbreviations and measurement details

SL. No.	Abbreviations	Traits & unit	Measurement method
1	PH	Plant height (m)	PHs were taken from three randomly selected plants for each of three replications using measuring tape from soil surface to the apex of main shoot at 120 days and the mean was computed.
2	NN	Number of nodes per plant	NN of three randomly selected plants for each of three replications were counted from the base to the apex of the shoot when the main stem started to divide.
3	BD	Base diameter (mm)	BD of three randomly selected plants for each of three replications were measured using slide calipers from close to soil surface at base of stem using slide calipers at 120 days after sowing.
4	SMD	Stem-mid diameter (mm)	SMD of three randomly selected plants for each of three replications were recorded at the midpoint between base and top of the stem using slide calipers during the harvest and average was computed.
5	CD	Core diameter (mm)	CD of three randomly selected plants for each of three replications were measured using slide calipers by pulling the basal bark of the stem after harvest and average was computed.
6	GBT	Green bark thickness (mm)	GBT of three randomly selected plants for each of three replications were measured using slide calipers from the green bark at base and average was computed.
7	LA	Leaf angle (Degree°)	Leaf angle was measured between the stem and the petioles of ten leaves in each plant in degree (°) before maturity. Three plants were considered for each of three replications.
8	LAr	Leaf area (cm²)	Leaf area was measured from leaf margins of ten leaves per plant using leaf area meter before maturity. Three plants were considered for each of three replications and average was computed.
9	GWL	Green weight with leaves per plant (g)	GWL of three randomly selected plants for each of three replications were measured in gram using electric balance just after harvest and average was computed.
10	GWL_0	Green weight without leaves per plant (g)	GWL_0 of three previously selected plants for each of three replications were measured using electric balance just after defoliation of leaves (7 days after harvest) and average was computed.
11	DSW	Dry stick weight per plant (g)	DSW of three randomly selected plants for each of three replications were measured using electric balance just after fibre extraction and sun-dry, and the mean was computed.
12	DFW	Dry fibre weight per plant (g)	DFW of three randomly selected plants for each of three replications were taken after proper retting, extraction, sun-drying and the mean weight was measured.
13	PTL	Petiole length (cm)	Petiole of five randomly selected leaves in each plant were measured between the stem to the leaf base before maturity. Three plants were considered for each of three replications.
14	SC	Stem color	Stem color, whether it is green, red or green pigmented was recorded by observing the stem during full vegetative stage.

Character associations at phenotypic and genotypic levels

The correlations at phenotypic and genotypic types among the studied morphological traits were estimated in 'R' statistical package.

Estimation of genetic components

The analysis of genetic divergence was done using Mahalonobis D^2 statistics. The variability was assessed using the variability package as per method for analysis of variance recommended by Panse and Sukhatme (11), variance components, environmental coefficient variation (ECV), phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) were estimated by the formula given by Burton (15), broad sense heritability (h^2_{bs}) by Burton and Devane (16) and genetic advance i.e., the expected genetic gain was calculated by using the technique given by Johnson et al. (17). The assessed values of PCV and GCV were classified as described by Khan et al. (18), 0-10% for low, 10-20% for intermediate, and ≥ 20% for high variance. Heritability was categorized as 0-30% for low, 30-60% for intermediate, and >60% as high (17). Genetic advance as percentage of the mean was categorized as follows: 0-10% as Low, 10–20% as Moderate, and 20% and above as high. The value of 'k' was considered as 2.06 assuming 5% selection intensity following the method of Khan et al. (18). Genotypic and phenotypic correlations and path analyses were performed using the corr. and path. function of the stats package in R, respectively. Both types of correlation coefficients were obtained using the formula used by Singh et al. (19). The phenotypic and genotypic correlations of all characters in the complete germplasm were assessed and numerous momentous correlations were found.

PCA, PCoA and Hierarchical clustering in 'Minitab' package

To study the inter-relationship among several traits principal component analysis PCA) is utilized to know the interrelations among several characteristics and can be performed from the sum of squares and products matrix for the traits. Therefore, principal components were calculated from the correlation matrix and genotype scores were found from the first component which has the property of accounting for maximum variance) and subsequent components with latent roots bigger than the unity (19). The latent roots are called "Eigen values". Most of the unique variability in a smaller number of magnitudes is displayed by PCA. From the latent vectors of the first two principal components influence of the different morphological traits towards deviation is discussed.

Analysis of Principal coordinate is equivalent to principal component analysis but to estimate inter-unit distances it is used. It gives the extreme distances between each pair of the N point using similarity matrix through the use of all dimensions of P. Principal coordinate (PCoA) was done to study the inter distance between genotypes.

Clustering was done using non-hierarchical categorization to split the genotypes of the experiment into some number of mutually special groups. The algorithm repetitively transfers genotypes from one group to another. This involves primary classification of the genotypes into obligatory groups. When no further allocation can be found to advance the criterion, the algorithm shifts to a second stage which examines the effect of swapping two genotypes of different classes and so on.

Average intra-cluster distances

The average intra-cluster distances for each cluster were estimated by taking probable D^2 values within the number of a cluster attained from the analysis of principal coordinate (PCoA) after the clusters were designed. The square root of the average D^2 values denotes the distances (D) inside cluster. The average intra cluster distances were estimated by the equation (Eqn. i) given by Singh and Chaudhary (20).

$$\text{Square of intra cluster distance} = \sum \frac{D_i^2}{n} \quad \text{………… (i)}$$

Where, $\sum D_i^2$ = sum of distance between all probable combinations, n= Number of all probable combinations between the population in a group.

Average inter-cluster distances

The average inter cluster distances were estimated using the formulae (Eqn. ii) defined by Singh and Chaudhary (20).

$$\text{Square of inter cluster distance} = \frac{D_i^2}{n_i n_j} \quad \text{………… (ii)}$$

Where, D_i^2 = sum of distances between all probable combinations ($n_i n_j$) of the entries comprised in the cluster study, n_i= Number of entries in cluster i, n_j= Number of entries in cluster j.

Influence of individual characters towards genetic divergence

The influence of individual character on genetic divergence was calculated using the method (Eqn. iii) opined by Singh and Chaudhary (20). In all associations, each character was graded on the basis of mean deviation values.

$$\text{Mean deviation} \quad D_i = Y_i^j - Y_i^k \quad \text{……….(iii)}$$

Where,

D_i = mean deviation

Y_i^j = mean value of the jth genotype for the ith character and

Y_i^k = mean value of the kth genotype for the ith character.

Rank 'I' is specified to the maximum mean difference and rank 'P' is given to the lowest mean difference

Where, P is the total number of traits.

Lastly, the number of times that each trait appeared in the first rank is calculated and percent influence of characters towards divergence was calculated.

Results

Trait analysis and genetic variability

Analysis of mean square values or ANOVA revealed that genotype was extremely significant for all the traits (p < 0.001) except number of nodes (NN) (not significant) and leaf area (LAr) (not significant) per plant (Supplementary Table1). The jute genotypes varied significantly in green weight with leaves (GWL), dry stick weight (DSW), dry fiber weight (DFW). Similarly, green bark thickness (GBT), core diameter (CD), stem mid diameter (SMD), leaf angle (LA) and plant height (PH) were also significant (p < 0.001). The occurrence of genetic variability in the base population of any plant is one of the important standards for the crop enhancement program (21). Proper knowledge concerning genetic variability is essential to obtain anticipated results in some important characters. The mean comparison from the LSD analysis for each genotype is shown in Table 3. The result offered that high level of variability and heterogeneity occurred among the accessions in response to the characters scored (Table 3).

The GWL per plant showed higher range (86.40-225.07g), medium ranges for NN (59.13-87.53), LA (80.89-117.74cm^2), DSW (9.13-47.13g), lower range for DFW (4.97-20.40g) and very low ranges for PH (2.51-3.62m) followed by GBT (0.82-2.92mm), SMD (7.71-12.13mm), LA (25.0-30.0degree) and CD (8.46-13.82mm) per plant (Table 3).

There was high difference among jute genotypes for yield and yield attributes, with higher (>20%) coefficient of variations (CV) observed in GWL (28.38%), DSW (28.17%), DFW (26.18%); medium CV (<20%) in GBT (19.35%), NN (13.86), LAr (12.83), CD (11.82), SMD (10.16); and lower CVs (<10%) were found in LA (5.67) and PH (7.19) (Table 3).

Analysis of Genetic Components

The genetic components analysis revealed that the phenotypic variance was more than the genotypic variance in all the characters. According to Khan et al. (18), lower PCV, GCV and ECV were found in plant height (8.99, 5.40, 7.19, resp.) and leaf angle (7.93, 5.11, 5.67, resp.); lower GCV recorded in NN, SMD, CD, LAr; intermediate ECV & PCV in NN, SMD, CD, LAr; intermediate GCV in GBT (12.79), GWL (16.78), DSW (16.97), DFW (16.39) (Table 4 and Fig. 2). Lower genotypic, environmental, and phenotypic variances were reported in GBT (0.04, 0.07, 0.10, resp.)
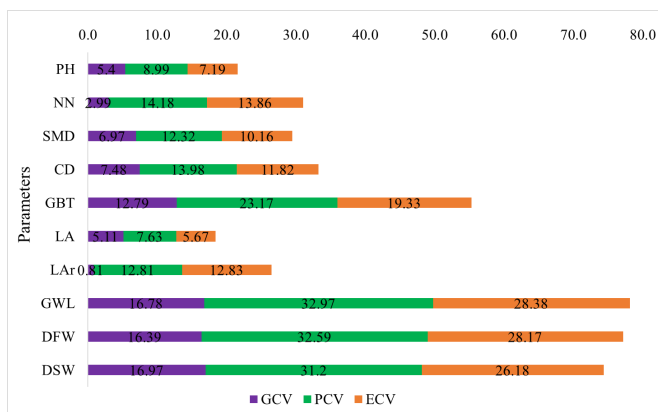
while higher variances for genotypic, environmental, and phenotypic effects were found in GWL (826.78, 2366.04, 3192.81, resp.). Lower ratios between GCV and PCV were found in the non-significant traits such as leaf area (0.06) and number of nodes (0.21) per plant while the highest ratio (0.67) was recorded in leaf angle (LA). There were no traits that showed GCV ≥ 20%, so improvement of jute crop can be based on traits with intermediate GCV (10-20%) recorded in DFW, DSW, GWL and GBT which specified high variability among these traits though they are inclined by additive genes. Due to the inferior GCV values (≤ 10%), LAr, NN, LA, PH, SMD and CD indicated the inadequate chance of assortment due to ecological effects on their phenotypic appearance (22).

The values of broad sense heritability were low for most of the characters (Table 4), which ranged from 0.4 (LAr) to 45.0 (LA). Very high heritability (≥60%) was not found in any of the traits. The heritability value 30-60% was marked for LA (45%), PH (36%), SMD (32%), GBT (30.01%) and DSW (30%) which indicated that the traits were moderately heritable whereas LAr (0.40%), NN (4.0%), DFW (25%), GWL (26%) and CD (29%) showed heritability below 30%, i.e., low heritability (17, 22) (Table 4 and Fig. 3).

The highest genetic advance (as percentage mean) value (≥ 20%) was not recorded for any traits in this study whereas the traits DSW (19.02%), GWL (17.59%), DFW (16.98%), GBT (14.54%), had moderate genetic advance (as percentage mean) value (10-20%) and the lowest was 1.3% for NN (Table 4 and Fig. 3). The trait Leaf Area (LAr) showed negative genetic advance (as percentage mean) value (-0.11%). Remarkably, the higher genetic gain was recorded for GWL (30.14%). The heritability and GA ratio were high for the PH (171.43) and GBT (150.05), and very low for GWL (0.86) while leaf area showed negative ratio due to the negative GA (%) (Table 4). Brunda et al. (23) reported that different crops have subsidized the overall parameters which contain the GCV and PCV traits.

Analysis of Correlations

Correlation analysis revealed significant correlations among the 10 quantitative characters at genotypic and phenotypic levels (Fig. 4). The significance level of the associations at p<0.05 is denoted by the asterisks. Either positive or negative associations, the asterisks indicate if it is statistically significant or not.

Fig. 2. Histogram depicting the genotypic, phenotypic and environmental coefficient of variation in 58 tossa jute genotypes for 10 parameters
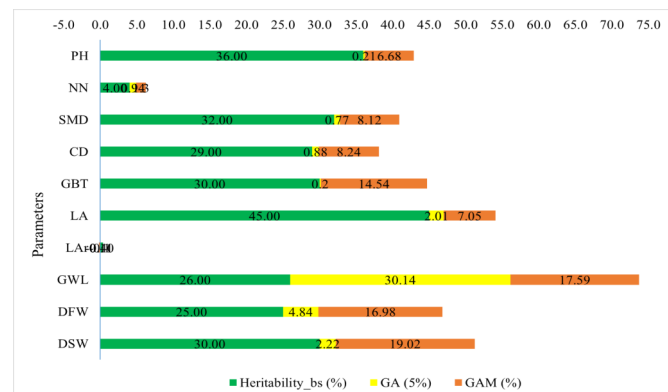

Fig. 3. Histogram depicting the heritability in broad sense (%), genetic advance (5%) and genetic advance in percentage of mean coefficient of variation in 58 tossa jute genotypes for 10 parameters

Table 3. Summary statistics for 10 quantitative characters of 58 tossa jute genotypes

Genot.	PH (m)	NN	SMD (mm)	CD (mm)	GBT (mm)	LA (^{0})	LAr (cm^2)	GWL (g)	DSW (g)	DFW (g)
G_1	3.00	71.37	9.03	10.59	1.59	30.00	84.34	131.17	21.53	9.27
G_2	3.04	68.73	8.43	9.95	1.46	29.17	91.71	121.50	21.33	8.20
G_3	3.06	68.50	9.54	10.89	1.47	30.00	95.92	176.00	28.93	10.50
G_4	3.09	68.93	9.35	10.17	1.65	30.00	96.01	144.27	27.57	10.60
G_5	3.06	81.30	9.16	10.89	1.24	30.00	99.17	167.97	27.50	10.80
G_6	3.25	70.00	9.08	10.90	1.25	29.00	88.33	180.90	29.40	11.47
G_7	3.30	66.33	10.04	12.36	1.55	30.00	91.18	220.23	36.03	13.57
G_8	3.16	68.00	9.00	10.03	1.04	29.17	96.46	153.47	27.77	9.80
G_9	3.11	66.50	9.00	10.57	1.22	29.17	94.41	177.57	28.47	11.77
G_{10}	3.10	72.10	9.04	10.94	0.85	26.67	101.85	160.87	25.80	10.60
G_{11}	3.53	79.90	10.01	12.24	1.37	25.83	93.76	170.00	29.53	14.50
G_{12}	2.92	65.13	8.92	9.72	1.51	30.00	95.85	131.13	19.33	8.27
G_{13}	2.99	59.37	8.70	9.42	1.42	30.00	86.62	125.20	20.23	8.37
G_{14}	3.26	67.60	9.90	11.21	1.84	30.00	95.63	169.03	27.13	11.73
G_{15}	3.13	68.83	11.39	12.84	1.50	26.67	85.21	174.83	29.40	12.53
G_{16}	3.00	68.83	9.45	10.49	1.78	29.17	92.43	147.13	22.10	9.57
G_{17}	2.97	72.53	8.35	9.88	1.30	30.00	100.82	164.80	25.63	9.73
G_{18}	3.06	67.60	10.03	9.61	2.03	30.00	97.91	214.10	34.37	14.37
G_{19}	2.93	62.70	9.38	8.60	2.05	30.00	108.70	167.30	32.83	12.97
G_{20}	2.51	76.90	8.97	10.20	1.24	30.00	102.52	151.63	23.10	10.23
G_{21}	3.08	75.83	8.72	9.99	1.27	30.00	104.56	170.00	21.87	10.17
G_{22}	3.06	75.27	8.56	10.03	1.36	29.17	91.23	172.13	24.63	10.00
G_{23}	3.09	71.77	9.39	10.31	1.54	30.00	90.23	131.50	27.77	11.70
G_{24}	3.44	70.50	9.04	10.18	1.40	30.00	84.50	224.10	34.50	13.83
G_{25}	3.16	63.13	9.23	9.92	1.38	30.00	94.66	154.60	28.30	9.60
G_{26}	3.06	68.20	9.12	9.81	1.39	30.00	108.83	172.47	29.40	14.67
G_{27}	3.29	80.27	10.32	11.82	1.24	28.33	92.59	311.47	47.13	20.40
G_{28}	3.62	87.53	11.25	12.51	1.31	25.00	105.03	227.73	34.67	13.53
G_{29}	3.43	81.47	10.08	11.76	1.39	25.00	87.86	219.67	36.67	15.07
G_{30}	3.41	77.60	9.73	10.76	1.42	25.00	96.58	196.67	31.40	13.00
G_{31}	3.18	71.20	9.61	11.10	1.42	25.00	92.83	197.13	33.60	12.80
G_{32}	3.19	64.20	9.56	10.67	1.29	26.67	105.18	172.07	28.33	12.07
G_{33}	3.42	78.00	9.98	11.98	1.52	28.33	109.92	228.33	37.33	14.93
G_{34}	3.08	68.73	9.46	10.85	1.68	26.67	84.02	181.87	32.27	10.93
G_{35}	3.25	69.93	9.70	10.95	1.42	26.67	95.22	193.60	31.27	14.33
G_{36}	3.43	77.07	10.25	12.15	1.44	26.67	98.51	227.87	41.20	17.67
G_{37}	3.36	76.47	9.05	11.11	1.21	26.67	117.74	229.33	31.80	13.40
G_{38}	3.26	77.27	9.63	10.84	0.82	30.00	95.84	174.97	22.20	9.30
G_{39}	3.43	79.00	10.05	11.99	1.35	30.00	102.90	193.73	30.57	12.13
G_{40}	3.37	78.83	9.99	11.59	1.26	26.67	80.89	86.40	9.13	4.97
G_{41}	3.18	67.43	9.27	10.72	1.37	26.67	101.85	171.23	25.43	10.97
G_{42}	3.07	69.67	9.75	10.80	1.46	30.00	96.93	168.27	26.60	9.30
G_{43}	3.21	73.57	10.48	11.66	1.40	28.33	96.63	217.00	30.13	12.17
G_{44}	3.14	67.93	9.31	11.11	1.10	27.50	103.82	148.87	28.00	12.13
G_{45}	3.02	66.07	9.61	10.66	1.27	30.00	98.97	174.13	33.53	13.70
G_{46}	3.02	64.63	8.79	9.53	1.46	30.00	103.00	125.40	23.33	9.40
G_{47}	3.05	79.80	8.79	10.70	1.37	30.00	100.44	136.87	27.00	11.37
G_{48}	3.12	77.37	9.25	10.20	1.33	29.17	94.02	134.27	23.93	10.70
G_{49}	3.14	74.50	9.00	10.67	1.51	25.00	108.08	114.27	22.97	9.20
G_{50}	2.90	71.50	8.61	9.57	1.14	26.67	95.31	129.33	22.37	9.73
G_{51}	2.82	61.67	7.71	8.76	1.14	26.67	94.70	107.53	19.37	8.27
G_{52}	3.45	80.73	10.56	12.35	1.14	28.33	97.98	195.33	37.43	15.23
G_{53}	2.62	59.13	7.85	8.46	1.39	26.67	93.01	126.67	21.63	9.43
G_{54}	2.87	67.03	8.21	9.68	1.08	30.00	95.22	137.83	22.97	9.77
G_{55}	3.36	77.47	11.99	9.01	1.52	28.33	97.34	182.10	30.37	13.00
G_{56}	3.00	77.03	9.22	9.54	1.19	28.33	104.11	138.90	29.10	11.20
G_{57}	3.33	75.63	9.45	11.51	1.19	27.50	94.96	162.23	30.83	11.53
G_{58}	3.55	73.87	12.13	13.82	1.84	30.00	94.71	255.40	46.73	17.63
GM	3.15	71.87	9.47	10.70	1.39	28.45	96.71	171.39	28.51	11.69
S.E.m	0.13	5.75	0.56	0.73	0.15	0.93	7.17	28.08	4.64	1.77
Range	1.11	28.40	4.42	5.36	2.10	5.00	36.85	225.07	38.00	15.43
CV (%)	7.19	13.86	10.16	11.82	19.35	5.67	12.83	28.38	28.17	26.18
S.D.	0.21	6.14	0.86	1.08	0.37	1.73	7.12	40.19	6.58	2.66
Lsd(0.05)	***	ns	***	***	***	***	ns	***	***	***

Note: GM- Grand Mean, CV (%)-Co-efficient of variation in percentage, SEm-Standard Error of a mean, Range-Maximum value minus Minimum value, SD-Standard Deviation, Lsd (0.05)-Least Significant Difference at 5% probability level, 'ns'-non-significant, '***' means significant at 0.0001 probability level

Table 4. Estimation of genetic parameters for yield and yield attributes of tossa jute

Components	PH	NN	SMD	CD	GBT	LA	LAr	GWL	DSW	DFW
σ^2_e	0.05	99.18	0.93	1.60	0.07	2.60	153.05	2366.04	9.37	64.53
σ^2_g	0.03	4.63	0.44	0.64	0.04	2.11	-0.61	826.78	3.94	21.84
σ^2_p	0.08	103.81	1.36	2.24	0.10	4.71	153.44	3192.81	13.31	86.37
GCV: PCV	0.60	0.21	0.57	0.54	0.55	0.67	0.06	0.51	0.54	0.50
H_{bs}: GA	171.43	4.26	41.56	32.95	150.05	22.39	-4.00	0.86	13.51	5.17
F ratio	**	ns	**	**	**	**	ns	**	**	**

Note: PH= Plant height (m), NN= Nodes number, SMD= Stem mid diameter (mm), CD= Core diameter (mm), GBT= Green bark thickness (mm), LA= leaf angle⁰, LAr= Leaf area (cm²), GW= Green weight with leaves (g), DFW= Dry fibre wt. (g), DSW= Dry stick wt.(g), r_g= Genotypic correlation, r_p= Phenotypic correlation, ** = Significant at 1% level. * = Significant at 5% level.

Phenotypic correlation

At phenotypic level of association (Fig. 4) among the 10 morphological traits of jute genotypes the highly strong positive correlations (p<0.01) were observed between DFW & DSW (0.91**), DSW & GWL (0.84**), DFW & GWL (0.80**); strong correlations between PH & CD (0.63**) and PH & SMD (0.61**); the PH showed moderate relations with DFW (0.48**), DSW (0.44**), GWL (0.52**) and NN (0.52**); moderate associations were observed in NN with CD (0.43**); in SMD with DFW (0.41**), DSW (0.42**), GWL (0.47**), CD (0.58**); in CD with DFW (0.48**), DSW (0.49**), GWL (0.51**); weak relations were recorded in NN with DFW (0.36**), DSW (0.29**), GWL (0.33**), SMD (0.37**), between DFW & LAr (0.25**), SMD & GBT (0.30**), GWL & LAr (0.20**). Leaf area showed non-significant relations with PH, NN, SMD, CD; leaf angle showed weak or non-significant negative relations with DFW, DSW, GWL, PH, NN, SMD, CD (Fig. 4). Similar reports were explained by Ghosh (24) in the field experiment of jute.

Genotypic correlation

Highly strong positive genotypic relations (p<0.01) were observed in PH related to NN (0.95**), CD (0.86**); in GWL with DFW (0.99**) & DSW (0.99**), DSW with DFW (0.99**); NN showed highly strong correlations with CD (0.94**) and SMD (0.91**); SMD with DSW (0.92**), DFW (0.88**), CD (0.86**), GWL (0.81**); strong relations in PH with SMD (0.79**), GWL (0.73**), DSW (0.75**), DFW (0.65**); in NN with GWL (0.71**); in CD with GWL (0.69*) & DSW (0.64**); leaf area showed weak relation with GBT (0.35**) but negative non-significant or weak relations with other traits

and the results were supported by Khatun *et al.* (25). NN gave highly strong negative correlations with GBT (-0.95**) & LA (-0.92**); GBT showed non-significant relations with PH, CD, GWL; weak relation with SMD (0.30**), DSW (0.36**), DFW (0.27*) (Fig. 4).

Path coefficient analysis

The correlations at phenotypic and genotypic levels revealed the extent and direction of connotation between different traits. The direct and indirect effects of different yield components on fiber yield (Table 5 and 6, respectively) derived from the association study have an agreement with the results attained by Sawarkar *et al.* (26) in tossa jute and suggest that assortment for these traits indirectly advances fiber yield.

Phenotypic path correlation

The phenotypic path analyses results (Table 5) revealed a highly positive direct effect (0.81) of dry stick weight and higher negative direct effect (-0.04) of leaf area (Table 5 and Fig. 5). DSW showed higher positive indirect effect (0.67) with GWL contributing to jute fiber yield and both these traits showed highly strong correlations with dry fiber weight (r = 0.91**, r = 0.80**) (Table 5). DSW also showed higher negative indirect effect (-0.10) with leaf angle contributing to jute fiber yield. Stem mid diameter (SMD) and core diameter (CD) showed negative indirect effects with PH, NN, SMD, CD, GBT, LAr, GWL, DSW. The phenotypic path correlation analysis showed the residual effect of 0.1448 with an average direct effect of 0.1244 and an average indirect effect of 0.0363 for nine morphological traits contributing to fiber yield (Table 5, Fig. 5).

**Fig. 4.** Phenotypic and genotypic correlation coefficients among ten yield and yield contributing characters of 58 tossa jute genotypes ['ns' means non-significant; the asterisks '**' & '*' denote relations significant at 0.01 & 0.05 level of probability, respectively; more intensity of colour indicates more significance of the correlation in the variable; The brown colors showed negative correlations while the green colors showed positive correlations. The deeper the colors, the stronger the correlations; Correlations: 0-0.30 negligible, 0.30-0.50 low, 0.5-0.7 moderate, 0.7-0.9 high or strong, 0.10-0.90 very strong (Mukaka, 2012)]

Table 5. Phenotypic path correlation analysis showing direct (Diagonal bold) and indirect effects of different characters on fiber yield of tossa jute genotypes

Traits	PH	NN	SMD	CD	GBT	LA	LAr	GWL	DSW	DFW (r$_g$)
PH	**0.04**	0.04	-0.01	-0.01	0.001	0.01	0.01	0.03	0.36	0.48**
NN	0.02	**0.08**	-0.01	-0.01	-0.00	0.01	0.01	0.02	0.23	0.36**
SMD	0.03	0.03	**-0.02**	-0.01	0.004	0.004	0.01	0.03	0.34	0.41**
CD	0.03	0.03	-0.01	**-0.01**	0.00	0.01	0.01	0.03	0.40	0.48**
GBT	0.01	-0.01	-0.01	-0.00	**0.01**	-0.004	-0.01	0.01	0.13	0.14ns
LA	-0.01	-0.01	0.001	0.003	0.001	**-0.04**	-0.00	-0.004	-0.10	-0.16*
LAr	0.01	0.01	-0.001	-0.00	-0.001	0.00	**0.11**	0.01	0.12	0.25**
GWL	0.02	0.03	-0.01	-0.01	0.002	0.003	0.02	**0.06**	0.67	0.80**
DSW	0.02	0.02	-0.01	-0.01	0.002	0.01	0.02	0.05	**0.81**	0.91**

Note: * and ** indicate phenotypic correlations (r$_g$) significant at 0.005 and 0.001 level of probability, respectively. Residual effect= 0.1448
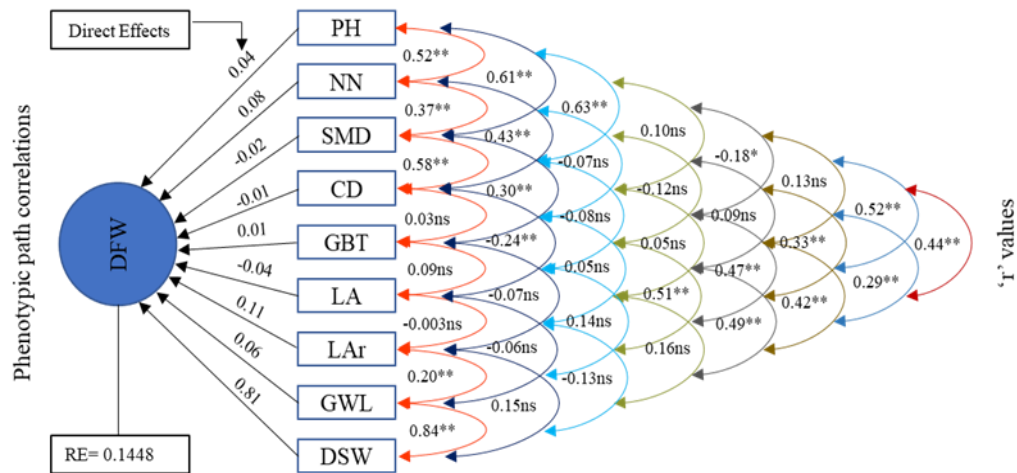
Fig. 5. Phenotypic path diagram for fiber yield of 10 yield components in 58 tossa jute genotypes

Genotypic path relations

Genotypic path relations exposed a highly positive straight effect of core diameter (1.37) and a highly negative direct effect of stem mid diameter (-1.33) (Table 5 and Fig. 6). Leaf area (LAr) showed a highly positive indirect genotypic path coefficient analysis effect (2.08) with stem mid diameter and a highly negative indirect genotypic path coefficient analysis effect (-3.26) with core diameter. Highly significant and positive correlation coefficient analyses were observed in DFW with GWL (0.99**), DSW (0.99**) and SMD (0.88**). DFW showed significant increase and positive correlation coefficient analyses with PH (0.65**) and CD (0.59**). The genotypic path correlation analysis showed a residual effect (RE) of 0.0886 with an average direct effect of 0.1244 and an average indirect effect of 0.0449 for nine morphological traits contributing to fiber yield (Table 6, Fig. 6).

Principal Component Analysis

The principal component of the variances occupied by each accession and the overall component response of the accessions on the characters were denoted in biplot (Fig. 7; Table 7). The scree plot (Supplementary figure 1) is used to determine the number of factors to retain in an exploratory factor analysis (FA) or principal components to keep in a principal component analysis (PCA). PC1 (Dim-1) and PC2 (Dim-2) accounted for 62.37% of the total variances detected. PC1 described for 47.14% of the total variations while PC2 reported for 15.23%. PCA Biplot loading both variables and accessions presented how strongly each trait impacts a PC and how they are associated with each other. The lesser angle between two vectors (Fig. 8) indicated a higher and positive correlation (e.g., I=GWL & K=DFW; K=DFW & J=DSW; I=GWL & D=SMD). Though, when the angle between two vectors forms 90°, it indicated no relationship

Table 6. Genotypic path correlation analysis showing direct (Diagonal bold) and indirect effects of different characters on fiber yield of tossa jute genotypes

Characters	PH	NN	SMD	CD	GBT	LA	LAr	GWL	DSW	DFW (r$_g$)
PH	**-0.42**	0.03	-1.06	1.18	-0.05	0.16	-0.22	0.07	1.00	0.65**
NN	-0.40	**0.03**	-1.21	1.57	-0.66	0.30	0.21	0.07	0.49	0.40**
SMD	-0.34	0.02	**-1.33**	1.18	0.15	0.08	-0.17	0.08	1.19	0.88**
CD	-0.37	0.03	-1.15	**1.37**	-0.03	0.10	-0.26	0.07	0.83	0.59**
GBT	0.04	-0.04	-0.40	-0.08	**0.51**	-0.11	-0.13	0.01	0.46	0.27*
LA	0.21	-0.03	0.35	-0.42	0.18	**-0.32**	-0.04	-0.02	-0.06	-0.14ns
LAr	0.84	0.05	2.08	-3.26	-0.60	0.12	**-0.11**	-0.07	0.68	NaN
GWL	-0.31	0.02	-1.08	0.94	0.06	0.05	-0.08	**0.10**	1.28	0.99**
DSW	-0.32	0.01	-1.23	0.88	0.18	0.02	0.06	0.10	**1.29**	0.99**

Note: * and ** indicate genotypic correlations (r$_g$) significant at 0.005 and 0.001 level of probability, respectively. Residual effect= 0.0886; NaN-Not a number which is basically numeric calculations with an undefined result
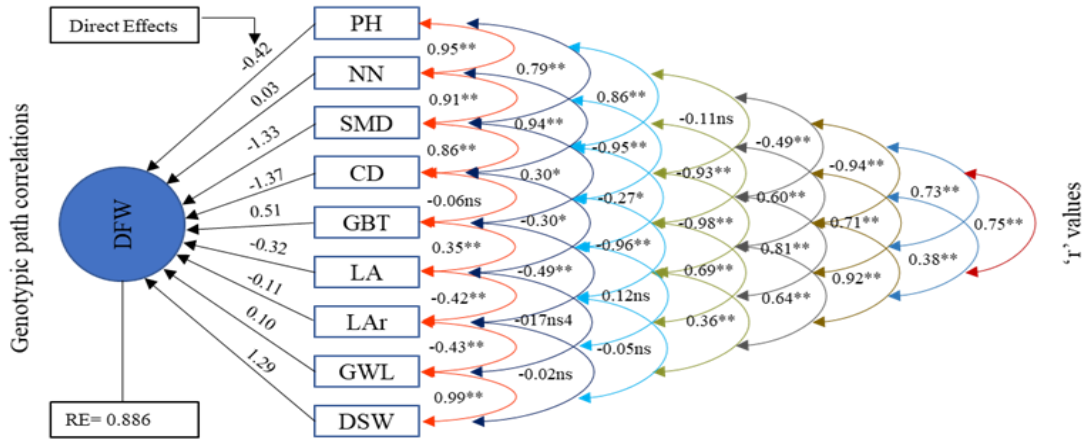
Fig. 6. Genotypic path diagram for fiber yield of 10 yield components in 58 tossa jute genotypes

(e.g., E=CD & F=GBT) and when it is between 90°-180°, it specified negative correlation between the traits (e.g., F=GBT&C=NN, H; G=LA&B=PH, C=NN, D=SMD, E=CD, H=LAr, I=GWL, J=DSW, K=DFW) (Fig. 8). Among the variables, green weight with leaves (0.40%), dry stick weight (0.40%), dry fiber weight (0.40%), plant height (0.38%), stem mid-diameter (0.38%), core diameter (0.36%) and number of nodes per plant (0.30%) were the major contributing traits in PC1 while green bark thickness (0.61%) and leaf angle (0.51%) had the highest contributions to PC2 (Table 7). The individual PCA plot (Fig. 8) exhibited that most of the accessions were disseminated at low distances while few were distributed at high distances as reflected by eigenvector (Table 7). From the biplot, we can sum up that the accessions loading on PC1 were high yielding with maximum plant height, stem mid-diameter, core diameter, fresh bark thickness, fresh weight with leaves while at the

same time having high dry stick weight. Accessions loading on PC2 had higher leaf area (Fig. 8).

Cluster Analysis

The tossa jute genotypes were assembled into 4 clusters based on ten agro-morphological traits (Fig. 8), with cluster (I) in blue and red colour (II) having the same and higher number of accessions (21 Acc.) followed by cluster (III) in green colour (10 Acc.), cluster (V) in ash colour had 5 and the violet cluster (IV) with one accession (Table 8 and Fig.8). The accessions (G_{30}, G_{31}, G_{35}, G_{39}, G_{52}) in the ash cluster (V) were characterized by high mean values for NN, SMD, CD, GWL, DSW, and DFW while the accession (G_{27}) in the violet cluster (IV) was characterized by high mean values for PH, GBT, LAr. The accessions (G_1, G_2, G_4, G_8, G_{12}, G_{13}, G_{16}, G_{20}, G_{23}, G_{25}, G_{40}, G_{44}, G_{46}, G_{48}, G_{50}, G_{49}, G_{51}, G_{47}, G_{53}, G_{54}, G_{56}) in the blue cluster (I) were characterized by high
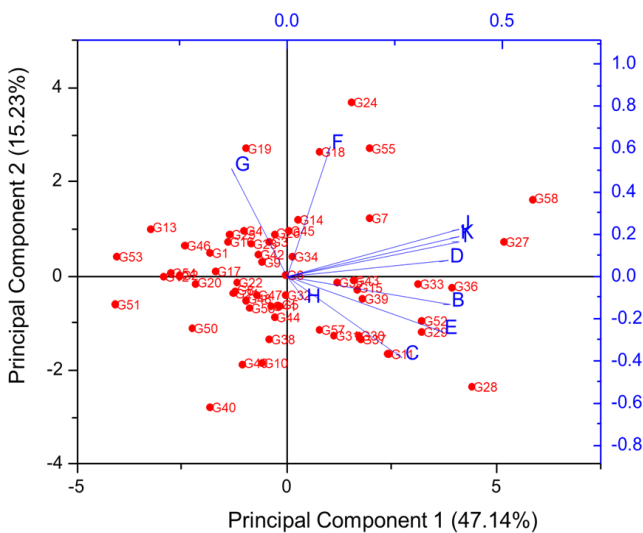

Fig. 7. PC1 and PC2 biplot using quantitative trait scores of the 58 tossa jute genotypes in PCA; B=PH, C=NN, D=SMD, E=CD, F=GBT, G=LA, H=LAr, I=GWL, J=DSW, K=DFW
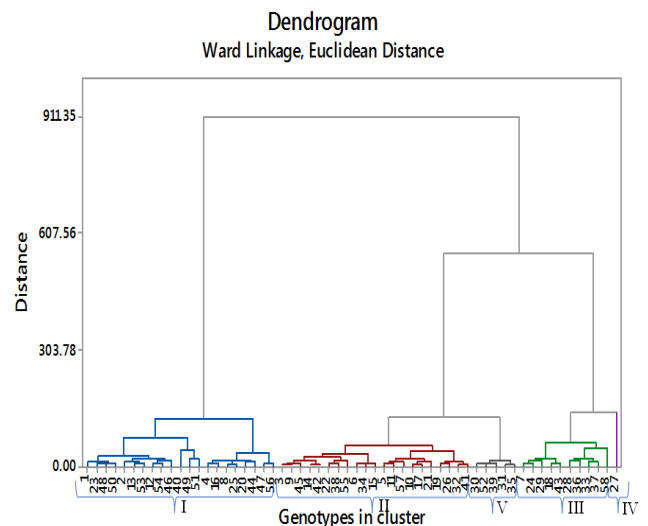

Fig. 8. Hierarchical clustering dendrogram analysis; Euclidean distance was used and the associations between groups were done by the Ward method for yield and yield associated traits in 58 jute genotypes

Table 7. Latent roots (Eigen values) and variability of principal component and extracted eigenvectors for ten quantitative traits of 58 tossa jute genotypes

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigenvalue	4.71	1.52	1.22	0.75	0.74	0.43	0.28	0.14	0.13	0.05
% of total variation	47.14	15.23	12.29	7.54	7.40	4.31	2.86	1.36	1.32	0.55
Cumulative precent	47.14	62.37	74.66	82.19	89.59	93.90	96.76	98.13	99.45	100.0
Trait contributions (Extracted Eigenvectors) to PC1 & PC2										
PCs	PH	NN	SMD	CD	GBT	LA	LAr	GWL	DSW	DFW
PC1	0.38	0.30	0.38	0.36	0.10	-0.13	0.04	0.40	0.40	0.40
PC2	-0.14	-0.38	0.07	-0.26	0.61	0.51	-0.12	0.17	0.23	0.18

Table 8. Distribution of 58 genotypes of tossa jute genotypes in five different clusters

Cluster number	Total no. of genotypes	Genotypes included	Origin	Most representative genotype	Least representative genotype
I	21	G_1, G_2, G_4, G_{25}	Bangladesh	G_2 (Acc.1282)	G_{25} (Acc.1773)
		G_8	Philippine		
		G_{13}	Mozambique		
		G_{12}, G_{16}, G_{20}	India		
		G_{23}	Srilanka		
		G_{40}	USA		
		$G_{44},$	Thailand		
		$G_{46}, G_{47}, G_{48}, G_{49}, G_{50}, G_{51}$	Nepal		
		G_{53}, G_{54}, G_{56}	China		
II	21	G_3	Bangladesh	G_3 (Acc.1283)	G_{19} (Acc.1480)
		G_5, G_6	Japan		
		$G_9, G_{10}, G_{11}, G_{14}, G_{15}, G_{26}$	India		
		G_{17}	Brazil		
		G_{19}, G_{21}, G_{22}	Srilanka		
		G_{32}, G_{34}	Syria		
		G_{38}	USA		
		G_{41}, G_{42}, G_{45}	Thailand		
		G_{55}, G_{57}	China		
III	10	G_{58}	Bangladesh	G_{36} (Acc.4177)	G_{18} (Acc.1360)
		G_7	Egypt		
		G_{24}	ICRISAT		
		G_{29}	Kenya		
		G_{18}	Denmark		
		G_{43}	Thailand		
		G_{28}	Australia		
		G_{36}, G_{37}	Tanzania		
		G_{33}	Syria		
IV	1	G_{27}	India	G_{27} (Acc.1807)	G_{27} (Acc.1807)
V	5	G_{30}, G_{31}	Kenya	G_{30} (Acc.3705)	G_{31} (Acc.3708)
		G_{52}	Nepal		
		G_{39}	USA		
		G_{35}	Tanzania		

mean value for leaf angle but lower mean values for PH, NN, SMD, CD, LAr, GWL, DSW, and DFW (Table 9). On the other hand, the lowest mean values for leaf angle and green bark thickness were observed in the accessions of clusters III and V, respectively (Table 9). Interestingly, the blue and red clusters are dominated by accessions whose origins are Asian regions (Bangladesh, Philippines, India, Srilanka, Thailand, Nepal, China, Japan, and Syria) except the genotypes G13 and G40 of cluster I originated from Mozambique and USA, respectively; and the genotype G17 originated from Brazil. Remarkably, the green cluster consisted of accessions from Asia (Bangladesh, India, Thailand, Syria), Africa (Egypt), East Africa (Kenya, Tanzania), Europe (Denmark), and Oceania (Australia). The ash cluster consists of the accessions from East Africa (Kenya, Tanzania), Asia (Nepal) and America and the accession (Acc. 1807) of the violet cluster originated from India (Table 8). The genotypes G2 (Acc. 1282), G_3 (Acc.1283), G_{36} (Acc.4177), G_{27} (Acc.1807) and G_{30} (Acc.3705) are the most representative accessions of cluster I, II, III, IV and IV, respectively (Table 8). Hence, accessions from cluster III are more required for selection for upgraded breeding programs while those in cluster V, IV and II subjugated by accessions from Asia, East Africa and USA, can also be well-thought-out.

Table 9. Cluster mean value for yield and yield contributing characters of tossa jute

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Grand centroid
PH (m)	3.00	3.15	3.34	3.38	3.29	3.15
NN	69.60	71.23	75.69	75.24	80.27	71.87
SMD (mm)	8.91	9.52	9.93	10.23	10.32	9.47
CD (mm)	10.03	10.66	11.43	11.72	11.82	10.70
GBT (mm)	2.68	2.87	2.56	3.32	2.48	2.85
LA (°)	28.77	28.68	27.00	28.00	28.33	28.45
LAr (cm^2)	95.40	97.31	97.10	98.40	92.59	96.71
GWL (g)	132.28	171.94	195.29	226.38	311.47	171.39
DSW (g)	23.28	28.10	32.85	36.34	47.13	28.51
DFW (g)	9.61	11.54	13.50	14.62	20.40	11.69

Principal Coordinate Analysis (PCoA)

Inter genotypic distance attained from principal coordinate analysis presented (Table 10) that the maximum distance (93.0968) was noticed between the genotypes G_{24} and G_{23} followed by the genotypes G_{52} and G_{51} (92.09872), G_{27} and G_{26} (81.08111) and the lowest distance was obtained from the genotypic combination G_{42} and G_{41} (7.319906) which was followed by G_{31} and G_{30} (7.800397), G_{48} and G_{47} (8.056084) and G_{13} and G_{12} (12.4431). The occurrence of the genetic diversity among the 58 tossa jute genotypes was designated by the difference between the uppermost and lowest inter genotypic distance. From distance matrix by exploiting the distances, the intra cluster distances were estimated which was recommended by Singh and Chaudhary (27), the degree of the intra cluster distance was not always comparative to the number of genotypes in the cluster.

Canonical variate Analysis (CVA)

The intra and inter cluster values worked out from canonical variate analysis within and among the cluster are displayed in Fig. 9. The degree of genetic diversity among genotypes within the same cluster is designated by the magnitude of intra cluster distances (28). The inter group distances in all cases seemed much greater than intra groups which specified that a greater diversity occurred among the lines of different clusters than those from same cluster. This cooperated with the results of Ivy
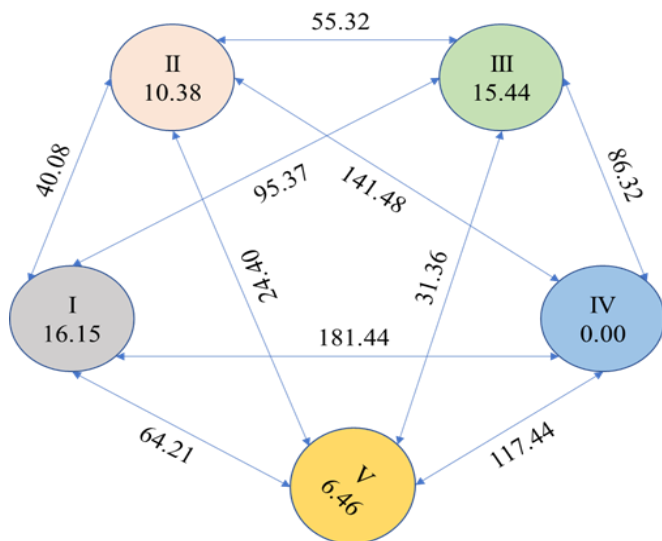
et al. (29), Azam et al. (30) and Alam et al. (31). The inter cluster D^2 values vary from 181.44 to 24.40. The uppermost inter-cluster distance was detected between clusters I and IV (181.44), followed by the distance between cluster II and IV (141.48), IV and V (117.44), I and III (95.37) (Fig.9) signifying wide diversity between them and for getting transgressive segregates the genotypes in these cluster could be utilized as parents in breeding program. Clusters with reasonably less degree of discrepancy showed variability due to low divergence, while widely divergent clusters endured distinctly in different environments (32). The lowest inter-cluster distance existed between clusters II and V (24.40), followed by III and V (31.36) which directed a close relationship between the same groups. The highest contribution towards the yield component was found in plant height (47.14%) in D^2 statistics (Fig. 10).

Discussion

The short-term strategy for identifying jute genotypes with good morphological traits to meet up the breeders' need for breeding of new high yielding cultivars is needed to analyze, detect and explore the existing genetic diversity (33). The success of any breeding program primarily depends on the presence of genetic variation in the genotypes (34). The important differences for the unlike traits scored on the accessions designate the incidence of inconsistency in the particular population that can be utilized for an upgraded breeding program. Trait changeability facilitates trait-assisted choice of best lines
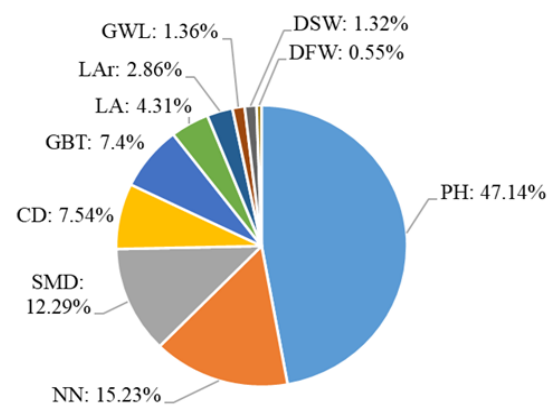

Fig. 9. Diagram showing average inter cluster distance (D^2) and intra cluster distance for 58 tossa jute genotypes obtained by canonical variate analysis

Fig. 10. Percent contribution of characters towards divergence D^2 statistics

Table 10. Ten of each higher and lower inter-genotypic distance (D^2) between pair of tossa jute genotypes

	Higher-inter genotypic distances			Lower-inter genotypic distances	
Sl. No.	Genotypic combination	Distance (D^2) Value	Sl. No.	Genotypic combination	Distance (D^2) Value
1	G_{24} × G_{23}	93.0968	1	G_{42} × G_{41}	7.319906
2	G_{52} × G_{51}	92.09872	2	G_{31} × G_{30}	7.800397
3	G_{27} × G_{26}	81.08111	3	G_{48} × G_{47}	8.056084
4	G_{53} × G_{52}	74.26733	4	G_{13} × G_{12}	12.4431
5	G_{25} × G_{24}	71.09063	5	G_2 × G_1	12.5431
6	G_{44} × G_{43}	68.79574	6	G_{15} × G_{14}	12.88597
7	G_8 × G_7	67.6695	7	G_{22} × G_{21}	13.82372
8	G_{38} × G_{37}	59.64026	8	G_{54} × G_{53}	14.38772
9	G_{33} × G_{32}	58.93224	9	G_{11} × G_{10}	15.60395
10	G_3 × G_2	55.26243	10	G_{35} × G_{34}	16.65871

Table 11. Finally selected genotypes for important traits

SL. No.	Selection traits	Genotypes	Cluster form	Selected genotypes mean	Grand mean
1.	Plant height (m)	G_{28}, G_{58}, G_{24}, G_{29}, G_{36}	III	3.49	3.15
2.	Stem mid-diameter (mm)	G_{15}, G_{55}; G_{58}, G_{28}	II; III	11.69	9.47
3.	GBT (mm)	G_{14}, G_{19}; G_{18}, G_{58}	II; III	1.94	1.39
4.	GWL (g)	G_{58}, G_{37}, G_{33}, G_{36}, G_{28}, G_{24}; G_{27}	III; IV	243.46	171.39
5.	DSW(g)	G_{58}, G_{36}; G_{27}	III; IV	45.02	28.51
6.	DFW(g)	G_{58}, G_{36}; G_{27}	III; IV	18.57	11.69

for crop advancement (35). Plant germplasm has a high degree of variability in its morphology. This high range of variability is harnessed to develop enhanced varieties in major crops (22). Lesser known or underutilized crops need to benefit from this progress too, as they also have a high level of multiplicity between (inter-variation) and within (intra-variation) their accessions. The morphological description in various locations supports breeders in selecting superior lines for further enhancement (36). The genetic diversity between the genotypes is significant as the genetically diverse parents are able to produce heterotic effects. The achievement of any crop improvement program with outlined objectives depends on the quantity of diversity obtainable in the crop, assigning inbreeds to heterotic groups and scheduling an appropriate mating design. The analysis of variance exposed significant differences among accessions for all agronomic characters studied. The results are steady with the report of Ghosh (24), who described significant inconsistency in a different gene pool of *C. olitorius* accessions from East Africa and Asian countries. Similar reports have been described in *Corchorus* germplasm for variability in quantitative traits (37). The presence of variation among accessions proposes that they will respond to enhancement through assortment in future breeding programs. The jute genotypes showed significant variations in green weight with leaves, dry stick weight, dry fiber weight, green bark thickness, core diameter, stem mid diameter, leaf angle and plant height. The jute genotypes having higher genetic variability and diversity with higher results for plant height (G_{28}, G_{58}, G_{24}, G_{29}, G_{36}), Stem mid-diameter (G_{15}, G_{55}; G_{58}, G_{28}), green bark thickness (G_{14}, G_{19}; G_{18}, G_{58}), green weight with leaves (G_{58}, G_{37}, G_{33}, G_{36}, G_{28}, G_{24}; G_{27}), dry stick weight (G_{58}, G_{36}; G_{27}) and dry fiber weight (G_{58}, G_{36}; G_{27}) would be used in breeding programs to develop high yielding new varieties through different breeding techniques (26, 38, 33, 34). The information gained from PCV and GCV provides insight into the response of the accessions to their environment. The large inconsistency between PCV and GCV indicates a robust environmental effect for these traits. The genotypic variance was lower than the phenotypic variance in all the traits of studied jute genotypes which was supported by Al -Mamun et al., (39). High PCV and GCV estimates for green weight with leaves, dry stick weight and dry fiber weight in each plant are further indications that there is difference among accessions for these traits. On the other hand, plant height, number of nodes, stem mid diameter, core diameter, leaf angle and leaf area had low GCV and plant

height and leaf angle showed low PCV values, representing a narrow genetic base. The estimation of heritability is decisive in breeding as they contract with the consistency of phenotypic presentation of a genotype. The high heritability of *Corchorus* accessions for some agronomic characters like plant height (171.43%), green bark thickness (150.05%) and intermediate for stem mid diameter (41.56%) and core diameter (32.95%) suggests that they are heritable in highly and medium extent, respectively, less prejudiced by the environment and that selection for enhancement of these traits is effective. On the contrary, number of nodes, leaf angle, leaf area, fresh weight with leaves, dry stick weight and dry fiber weight in each plant imitate a robust influence of the environment on their expressions. The highest genetic advance was obtained in green weight with leaves (30.14) followed by dry fiber weight (4.84), and dry stick weight (2.22) indicating the possibility of increasing these traits from 171.39 to 201.53g green weight with leaves, 11.69 to 16.53g dry fiber weight and 28.51 to 30.73g dry stick weight per plant contributing to fiber yield improvement in jute. Moderate genetic advances in percentage of means were obtained for dry stick weight, green weight with leaves, dry fiber weight, green bark thickness indicating the greater possibility of improvement for these traits contributing to higher fiber yield (17). The character(s) with high heritability and GAM are usually more supportive in forecasting genetic gain under choice than heritability alone. In a breeding activity, the correlation coefficient regulates the strength of the association between the traits. A strong positive association between plant height and stem width means that the taller the plant grows, the thicker the stem, which is a signal of the plant's vigour (40). The accessions that were taller formed more green fiber and had lengthier leaves, which means more foliage and high fiber yielding; a trait that is extremely required in *Corchorus*. Accessions with copious stems had longer petioles and were taller. The association of plant stature with most of the measured traits designates its importance for agronomic enhancement in *Corchorus*. The associations among the studied traits of jute genotypes were partitioned at genotypic and phenotypic levels. In contrast to the reports by Ghosh (24) and Nyadanu et al. (41), our phenotypic correlation results revealed highly strong positive correlations between dry fiber weight & dry stick weight, dry stick weight & green weight with leaves, dry fiber weight & green weight with leaves; strong correlations between plant height & core diameter, plant height & stem mid diameter; the PH showed moderate

correlations with dry fiber weight, dry stick weight, green weight with leaves and number of nodes; moderate associations in number of nodes with core diameter; stem mid diameter with dry fiber weight, dry stick weight, green weight with leaves, core diameter; core diameter with dry fiber weight, dry stick weight, green weight with leaves per plant. The results were reported in jute crop by Sawarkar *et al*. (26). A robust and positive association between these measured characters means that an enhancement in the principal traits is likely to have a consequence on the secondary traits with which it is connected through incidental selection (42). It can also be decided that they are most probably controlled by a similar gene. This may be a consequence of connection or pleiotropy, signifying that these pairs of characters may be concurrently improved.

The genotypic correlation results revealed highly strong positive relations in plant height with number of nodes, core diameter; green weight with leaves with dry fiber weight, dry stick weight, dry stick weight with dry fiber weight; number of nodes with core diameter, stem mid diameter; stem mid diameter with dry stick weight, dry fiber weight, core diameter, green weight with leaves which was supported by Mukul (43). Strong relations in plant height with stem mid diameter, green weight with leaves, dry stick weight, dry fiber weight; number of nodes with green weight with leaves; in core diameter with green weight with leaves & dry stick weight. Number of nodes showed strong negative correlations with green bark thickness & leaf angle; green bark thickness showed non-significant relations with plant height, core diameter, green weight with leaves; weak relations with stem mid diameter, dry stick weight, dry fiber weight. The results were supported by Sawarkar *et al*. (26).

The correlations for phenotypic and genotypic paths revealed the extent and direction of association between different characters and the results were supported by Sawarkar *et al*. (26) in tossa jute and propose that assortment for these traits ramblingly improves fiber yield. The phenotypic path analysis results revealed a highly positive direct effect (0.81) of dry stick weight and higher negative direct effect of leaf area. Dry stick weight showed higher positive indirect effect with green weight with leaves contributing to jute fiber yield and both these traits showed highly strong correlations with dry fiber weight. A residual effect of 0.1448 with an average direct effect of 0.1244 and an average indirect effect of 0.0363 was obtained for nine morphological traits contributing to fiber yield of jute crops. More or less similar results were reported in tossa jute by Islam *et al*. (44).

The genotypic path analysis showed a highly positive direct effect of core diameter and a highly negative direct effect of stem mid diameter. Leaf area showed a highly positive indirect genotypic path coefficient analysis effect with stem mid diameter and a highly negative indirect genotypic path coefficient analysis effect with core diameter. Highly significant and positive correlation coefficient analyses were observed in dry fiber weight with green weight with leaves, dry stick weight and

stem mid diameter. Dry fiber weight showed significant increase and positive correlation coefficient analyses with plant height and core diameter. The genotypic path correlation analysis showed the residual effect of 0.0886 with an average direct effect of 0.1244 and an average indirect effect of 0.0449 for nine morphological traits contributing to fiber yield in jute crops. According to Islam *et al*. (44), tossa jute showed more or less similar results for different agronomic traits. The breeders need to emphasize on the traits having strong relations at genotypic and phenotypic levels for breeding of jute with higher yield and yield attributes (45).

The residual effects of phenotypic (0.1448) and genotypic (0.0886) analyses indicated that the characters under study contributed 85.52% and 91.14% to the yield at phenotypic and genotypic levels, respectively (44). It is recommended that more importance should be given to the characters considered for selecting tossa jute genotypes with higher fibre yield. The other characters which subsidized to the yield might be comprised for further study (45, 46).

Principal component analysis considers the involvement of each trait to the total variance and each trait is considered a significant supplier to the experiential variation if its factor loading has an overall value ≥ 0.30 (47).

In this study, the first two PCs reported for 62.37% of the total phenotypic difference between accessions. This variation was higher than that described by Ngomuo *et al*. (37). Some agronomic traits report the total inconsistency observed among accessions. The traits grouped in each PC are connected and controlled by same gene action. Accordingly, traits with high loading value within the first four PCs such as plant height, stem mid diameter, green bark thickness and dry fiber weight per plant are of great importance and should be measured for selection in the *Corchorus* enhancement program (42).

The clustering of the 58 *Corchorus* accessions into five unlike cluster makes the variances between the accessions even clearer. The reasonable clarification for the lack of association between cluster pattern and assortment area could be the effect of natural or artificial selection and exchange of wanted seeds by farmers across the country. The close grouping of the accessions could be due to the low degree of intra-specific changeability in *C. olitorius* (48), as they are naturally self-pollinated. However, accessions in each group are similar to each other and dissimilar from those in other groups. Considering the grouping, the presentation of an accession for a trait with maximum influence to divergence should be duly measured in the selection of the progeny. The accession (Acc.1807) was recognized as singletons because it was secluded from the other accessions. It was higher in two or more needed traits and offered a great chance for their use as a source of changeability, as recommended by Choudhary *et al*. (49). Genetic diversity in *Corchorus* germplasm has been described using cluster analysis (50). *Corchorus* accessions assembled within the same cluster are projected to be comparable, while those between clusters may show high heterogeneity (50). Subsequently, crosses between

accessions from unlike clusters are likely to produce useful recombinants in the segregating populations. Furthermore, hybridization between accessions with large distance between clusters may assist heterosis as a result of genetic divergence between parental lines (26). Jute leaves contain vitamins, minerals, macromolecules, phytochemicals, micronutrients, amino acids, anti-oxidants essential to promote human health. The young twigs and leaves of *olitroius* jute are used as delicious vegetable beside the use as fiber source (51). The diversity experiential among *Corchorus* accessions in this study can support the advancement of new varieties, which is a significant objective in crop enhancement programs. Consequently, this study is crucial for the effective preservation of *Corchorus* accessions and their upcoming use in breeding programs.

Conclusion

The study was successfully completed and the results specified the incidence of significant genetic variability among the studied jute genotypes. Some good genotypes or accessions of tossa jute (Acc.1809, O-9897, Acc.1526, Acc.1354, Acc.4740, Acc.1352, Acc.1480, Acc.1360, Acc.4177, Acc.1807) were selected on the basis of diversity analysis. The selected genotypes would be considered for breeding programs by the breeders.

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Authors' contributions

MJA designed the experiment and carried out the trials and collected the data; MSRB & MFM supervised and investigated the whole work; ASMY helped in data collection; MMM compiled the data, performed the statistical analyses, wrote the manuscript, submitted to the journal and communicated for publication. All authors contributed to the article and approved the submitted version for publication.

Recommendation

The selected genotypes can be upgraded through progressive research systems. Based on diversity analysis of parents from distant clusters with high mean values for fiber yield and yield attributing traits can be used as parents in crossing program to advance economically useful recombinants and high yielding new jute varieties in future.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None.

Use generative AI to write this manuscript: No AI tool was used to write this manuscript.

Data Availability Statement

The data will be available to the respective person on urgent request to the corresponding author.

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