



Research article

Morpho-anatomical variability, principal component analysis and Euclidean clustering of tossa jute (*Corchorus olitorius* L.)Md. Mia Mukul^{*}, Nargis Akter

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ABSTRACT

Jute, the second most important natural fibre crop after cotton in the world. Bangladesh occupied the first position for jute fibre production and exportation after India among south-east Asian countries. Tossa jute is cultivated more (80–85%) here among the commercial cultivation of jute and allied fibre crops. It produces quality fibre but yield is low due to stress susceptibility compared to *capsularis* jute. The self-pollination nature and sexual incompatibility between two jute species (*C. capsularis* and *C. olitorius*) cause narrower genetic base and restrict genetic exchange. So, intra specific hybridization using diversified jute germplasms or genetic change will be the best option to the jute breeders for genetic improvement of existing cultivars. Hence, 20 tossa jute genotypes were investigated through field based morphological study (RCBD) and laboratory oriented anatomical study (CRD) for yield and yield attributing morpho-anatomical variability at BJRI during March, 2019 to July, 2020. Among 20 tossa jute genotypes, Acc. 1318, O-043-7-9(G), Acc. 4311, Acc. 1306, O-0411-10-4, O-049-1-3, O-0512-6-2, Acc. 4160 showed good results for yield and yield related morphological traits at 120 days after sowing and stem anatomical traits at 100 days after sowing. Higher significant genotypic correlation coefficient values were recorded than phenotypic associations among all the morphological traits. Plant height, fresh weight, fibre yield content gave high heritability (>80%) in broad sense along with possibility of more genetic advance in percentage. The average inter-cluster distances were higher than the average intra-cluster distances, which shows the presence of wide genetic diversity among the genotypes of different clusters than those of the same cluster. The first three principal components, whose Eigen values are greater than one, accounted for 99.96% of the total variation among the studied characters. The information obtained from this investigation is useful in planning further breeding programme for tossa jute improvement.

1. Introduction

Tossa jute (*Corchorus olitorius* L.) is an important lingo-cellulosic natural, annual, herbaceous bast (phloem) fibre crop in the world provides biodegradable, eco-friendly long and shiny fibres next to cotton (*Gossypium* spp. L.) that attracts diversified product manufacturing companies, including textile and paper (Mir et al., 2008a; Samira et al., 2010; Majumdar et al., 2020; Mukul et al., 2020b). It is a traditional cash crop in Bangladesh (Islam and Ali, 2017; Mukul et al., 2020a). It is a principal coarse fibre crop grown for commercial purposes in many south Asian countries (Alam and Rahman, 2000; Rahman et al., 2021), predominately in India and Bangladesh (Ghosh et al., 2015). Jute is a 'Golden Fibre' (Kundu, 1951; Ghosh et al., 2015) contributing about 4% GDP to the national economy and earns about 5% of the foreign exchange as well in Bangladesh (Islam and Ali, 2017). During the period of 1980,

80% white jute, 10% tossa jute and 10% of both *Hibiscus cannabinus* (Kenaf) and *H. sabdariffa* (Mesta) were cultivated among the total cultivable jute crops in Bangladesh (Hossain, 2014). In 1987, a mega variety of tossa jute developed by BJRI named O-9897 (O-9897) called Falguni Tossa was cultivated in a large scale for its good fibre yield and quality. From that period, tossa jute occupied 80%, white jute 10% and both Kenaf and Mesta 10% of total jute cultivation. According to Saha et al. (2001), the desirable traits of white jute are its wider adaptability to diverse environments, early sowing without the risk of premature flowering, which affects fibre yield by terminating vegetative growth, and tolerance to waterlog condition in the late stage in lowland areas, on the other hand, tossa jute can't tolerate this abiotic stress. Tossa jute is high yielding than white jute, except under inundated conditions. Tossa jute is characterized by its delayed periderm formation, resulting in lesser periderm compared with white jute, which is a desirable trait that

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improves the retting quality of fibres. In earlier research report, jute improvement attempts were restricted to selection from natural populations with quantitative traits like plant height and quality of fibre as the target characters. Hence, genetic diversity in the cultigens of the two species has been narrowed down through such pure-line selections. Average genetic diversity in the cultivars of *C. olitorius* and *C. capsularis* was 7.2% (range 2.8–12.3%) and 7.6% (range 2.2–13.1%), respectively (Rana et al., 2013). Moreover, a strong sexual incompatibility barrier exists between the two cultivated species preventing any genetic introgression through cross-breeding (Kundu et al., 1959; Patel and Datta, 1960). The genetic diversity for improvement in jute crop is very narrow, and it is the major hurdle, which is a demand at priority for any crop improvement programme (Ghosh et al., 2015). Now, tossa jute is highly demand crop in Bangladesh (Hossain, 2014). So, the genetic improvement as well as high yielding new variety development is a crying need for this species in Bangladesh (Mukul et al., 2020c).

Hossain (2014) reported that, Sir William Roxburgh, Curator of the Kalata Botanical Garden, introduced jute to the world market in 1795 as the only cultivable plant for fibre extraction. The East India Company immediately took the initiative to use Bengali jute fibre in the Dundee factory, excluding linen. Thomas Neigh was the first to invent jute yarn by spinning jute fibre in Dundee's linen fibre machine (Lenman et al., 1969). In 1938, the Indian Central Jute Committee (ICJC) was formed which later set up a Jute Agricultural Research Laboratory (JARL) in Dhaka and a Jute Technological Research Laboratory (JTRL) in Taliganj, Calcutta for research on jute. From 1936 to 1947, large scale research on jute was carried out, but due to the partition of India in 1947, research activities came to a standstill. Then the Pakistan Government formed the Pakistan Central Jute Committee (PCJC). In 1951–52, Jute Research Institute (JRI) which is known as Bangladesh Jute Research Institute (BJRI) was established in Dhaka under this committee (Hossain, 2014). This institute works on both agricultural and industrial aspects on jute and allied fibre crops from seeding in field to ultimate fibre and jute products for its various uses at the end users level (Islam and Ali, 2017).

According to Bhandari et al. (2017), the evolution of crop plants is directed by the nature or human activities. The intra- and inter-specific differences existing at the base of all crop improvement programmes. The degree of differentiation between or within plant species known as genetic diversity in zoological world. There is no crop improvement opportunity for various desirable traits if all the individuals within the species would have been similar genotypic and phenotypic basis. Since the beginning of systematic plant breeding, natural variability and divergence between crops have been extensively identified and used in improvement of crop species (Mostofa et al., 2020). A reduction in genetic diversity in cultivated tossa jute is associated with domestication bottlenecks (Kundu et al., 2013) that are known to cause selective sweeps in genomic areas containing genes of agronomic importance (Doebley et al., 2006). Information generated on the genetic diversity within and among closely related crop species is essential for crop improvement and to meet the diverse goals like producing cultivars with increased yield, wider adaptability, desirable quality, pest and disease resistance. For most of the *C. olitorius* landraces are yet to be extensively characterized, a lack of knowledge about their biological history and value restricts them to be utilized in breeding programs (Sarkar et al., 2019).

Jute is a fibrous plant bearing chromosome number $2n = 2x = 14$ belonging to the *Tiliaceae* or *Malvaceae* family and *Grewioideae* subfamily (Basu et al., 2016) under the *Corchorus* genus (Bhaduri and Bairagi, 1968; Sarkar et al., 2011; Zhang et al., 2019) and a few tetraploids ($2n = 28$) are also known (Bhaduri and Bairagi, 1968). Initially jute was classified in the family Tiliaceae (Steward, 1969). Recently the genus has been reclassified within the family Sparrmanniaceae (Heywood et al., 2007). The jute scientists identified approximately 100 jute species of this genus (Choudhary et al., 2017). The genus consists of annual or short-lived perennials (Benor et al., 2010), 40–100 species of flowering plants in the family *Tiliaceae* distributed in tropical, sub-tropical and warm temperate regions of the world, majority of the species being confined to

Africa (Kundu 1951; Edmonds, 1990; Olawuyi et al., 2014; Mukul et al., 2020a). The genus *Corchorus*, is endowed with about 215 species, subspecies, varieties and land races; however, there are probably 50–60 species are important surviving at present and still continues to be extremely variable (Edmonds, 1990; Mahapatra et al., 1998, 2009; Saunders, 2006; Benor et al., 2010; Hossain, 2014). Among these, only two species namely *Corchorus capsularis* L. (White or Bitter or Deshi jute) and *Corchorus olitorius* L. (Dark or Tossa or Bogi jute) which evolved through conventional breeding and pure line selection based on their yield and agronomic performances (Ghosh, 1983) are cultivated commercially (Maity et al., 2012). The white jute was originated in South East Asia or Indo Burma Sub Continent and the Tossa jute was originated in Tropical Africa (Kundu, 1951; Palit, 1999; Kundu et al., 2013). These species contain ~70% of the neutral genetic diversity present in their wild species. *C. aestuans* was identified as the common ancestor to both the cultivated species through the phylogenetic analyses of 38 highly polymorphic nuclear microsatellites. The nuclear progenitor of *C. olitorius* was found the *C. urticifolius* but no close nuclear progenitor was identified for *C. capsularis* (Kundu et al., 2013). Both the cultivated jute species are mostly self-fertilized (Basu et al., 2016), however, as high as 15 % natural outcrossing occurs in *C. olitorius* (Mir et al., 2008a) and 5% in *C. capsularis* (Basak and Chaudhuri, 1966). Seeds of white jute are coppery in colour and weigh 500–600 seeds g^{-1} , whereas those of dark jute are greyish in colour with 1000 seeds g^{-1} (Benor, 2011); they have no dormancy, however (Palit and Meshram, 2008). A single jute fibre (i.e. ultimate fibre cell) which is 0.75–5.0 mm in length with an average of 2.3 mm and 15–25 μm in width (Rowell and Stout, 2007) is extracted from the bark of the jute stem by stepping and retting in water, usually 120 days after sowing, followed by stripping, washing, squeezing and drying and bailing (Palit, 1999; Palit et al., 2006).

Jute is a self-pollinated crop bearing very limited genetic variation (La Farge et al., 1997). Reduced genetic variability and diversity among jute species has raised serious concern among the jute breeders in Bangladesh. Due to the reduction in genetic diversity, further improvement in jute varieties will be a strenuous task. The breeders will be unable to meet the requirements arising out of ever-increasing demand on account of over population and jute yield barriers will be very difficult to overcome. Considering the climatic change and related unforeseen events as it may serve as the reservoir of many novel traits conferring tolerance to different biotic and abiotic stresses becomes more essential. Genetic diversity is an important underlying fact to search for heterosis and transgressive segregation in jute crops (Bhandari et al., 2017). The jute genotypes having more genetic diversity are needed for defect correction of commercial varieties and development of novel varieties (Mukul et al., 2020a). Hence, identification of diverse lines (if available), creation of diversity (if not available or limited) and its subsequent utilization are the major goals of any crop improvement programmes (Bhandari et al., 2017). In this regard, knowledge on diversity of jute crops, factors affecting genetic diversity, method of diversity analyses using different important software programs should be explored and utilized properly. Through identification of jute germplasm with broaden genetic diversity, the traditional jute breeding through hybridization or molecular breeding using markers assisted selection would be helpful for the jute breeders (Roy et al., 2006). High yielding new jute variety would be developed to benefit the farmers. The farmers will be able to get more currency from jute cultivation and will contribute to the national economy of Bangladesh.

More than 99% of total global jute production is from Asian countries, where India contributed the highest (56.85%) followed by Bangladesh (40.67%) and China (1.03%) (Majumder et al., 2020). Jute is an important cash crop in Bangladesh and India, which together accounts for about 84% of world production of jute fibre (JDPC, 2006). Jute fibre is used to prepare the biodegradable products like 'Sonali Bag' which is used alternative to 'Polythene Bag' in Bangladesh; other products like geo-textile, cloths, pulp & paper, sacs, carpets, fabrics, textiles, gunny bags and packaging materials for agricultural and industrial products

(JDPC, 2006; Maity et al., 2012). Jute sticks are used as fuel, to prepare fence, fuel (charcoal), carbon or inks of printer-photocopier, elements of cosmetics, toothpaste, desk board of car etc. in various countries of the world. According to MoF-BD (2017), the Government of Bangladesh implemented the Mandatory Jute Packaging Act 2010, which was enforced in January 2014, to promote the country's jute sector to preserve various agricultural products for a long time and to prevent environmental pollution. Jute is an eco-friendly biodegradable fibre crop having great contribution to our environment (Abdullah, 2013; Jahan, 2019). Jute plants consume 15 t of CO₂ and releases 11 t of O₂ ha⁻¹ which helps to protect the environment from the greenhouse effects and preserves the ozone (O₃) layer (Palit and Meshram, 2008). Jute leaves have been used as a vegetable (jute mallow) and medicine since ancient times. Jute mallow rich in proteins, vitamins and essential amino acids is an important leafy vegetable in Africa (Nyadanu et al., 2016). The contribution of jute in increasing soil fertility is immense. From jute seed sowing to jute harvesting, jute leaves rotten in one hectare of land add about 4.0 tons of organic manure (OM) to the soil which plays a helpful role in fertilizer management in subsequent crop cultivation (Hossain, 2014). No harmful gases evolved from jute products or jute crop (Maity et al., 2012; Hossain, 2014). In the face of global environmental change, the notion of climate smart agriculture (CSA) has emerged as an approach which can contribute to increased agricultural production and income of poor households (Sarkar et al., 2019).

Jute grows in tropical lowland areas with 60–90 % relative humidity and 24–37 °C temperature (Rowell and Stout, 2007). Jute is photosensitive long day (>12.5 h) plant. Generally it is cultivated for fibre. Some varieties or species are cultivated for vegetable purposes. At seedling stage (7–30 days), jute leaves can be used as vegetable. For fibre purpose, jute seeds should be sown after 15 March in Bangladesh climate when day length is > 12.5 h. Long day fosters its vegetative growth that supports bast (secondary phloem) fibre production, whereas short day induces its reproductive growth (flowering) that requires a critical day-length of 12.5 h (Palit and Meshram, 2008). In Bangladesh, Jute seeds can be sown from mid-march to April month for fibre production. For seed production purpose, these plants can be used for top cutting followed by placing in field, and late seeding can be done when day length is < 12.5 h in the context of Bangladesh. Tossa jute is susceptible to most of the biotic and abiotic stresses (Maity et al., 2012). Biotic stresses, particularly insect attacks, adversely affect the yield potential and the fibre quality of jute and allied fibre crops. Insect and mite pests attack these plants at seedling, growth and fibre development stages (Selvaraj et al., 2016). Moreover, fibre crops have witnessed the effect of the gradual shift in the climatic pattern in terms of increased diversity and intensity of biotic stresses. The BJRI developed a salt (8.0 dS/m) tolerant white jute variety named BJRI Deshi pat 8 during 2013, another one salt (1.2 ds/m) tolerant variety named BJRI Deshi pat-10 is in pipeline to release on 2021, but no stress tolerant tossa jute variety has been developed yet (BJRI, 2021). Now it is very crying need to develop stress tolerant photo & thermo insensitive high yielding and climate smart tossa jute variety having quality fibre producing capacity through hybridization or molecular breeding approaches to cultivate throughout the year.

The exploitation of existing diversity of each individual accession by using phenotypic traits is an initial step towards crop improvement (Nwangburuka and Denton, 2012). The cultivated jute species are globally important for fibre yield and the wild species are potential source for abiotic and biotic stress tolerant genes and proved to be important genetic resources (Maity et al., 2012). Interspecific hybridization between wild and cultivated species may lead to conserve the wild germplasms and to create genetic diversity in jute plants (Roy et al., 2006; Maity et al., 2012). Stable and authentic hybrid line in jute is rather lacking (Mandal et al., 2013). To improve fibre yield of Jute, the knowledge required on genetic diversity and variability as well as genetic architecture of germplasm for fibre yield and its components (Ngomuo et al., 2017).

In jute crop, plant height, girth of stem, fresh weight are important morphological traits significantly contribute to the ultimate fibre and stick yield performances (Maity et al., 2012). Destructive sampling is required to be done prior to seed production for anatomical study of jute stem (Kumar et al., 2014). The plant used for anatomical study as well as to know morphology can't be used as seed yielder. The anatomical features like bark diameter, bark thickness, cell wedge or fibre bundle area, trapezoid area, fibre bundle layer in the transverse section of jute stem are helpful to predict the fibre and stick yield capacities. The correlations among jute fibre yield and other attributing anatomical characters are helpful to improve desired characters as well as to select good germplasm for breeding purposes (Karmakar et al., 2007). The estimation of genetic parameters like variance, covariance components at genotypic and phenotypic levels, heritability in broad sense, genetic gain is important to predict the desirable traits to be improved in the respective plant materials (Alam, 2009). The Euclidean clustering and analysis of principal components (PCA) are the effective ways to know the similarities and dissimilarities among the experimental plant genotypes based on their desirable traits (Suryanarayana et al., 2017). It is important to develop new high yielding and good quality varieties of jute to meet the expanding demand of jute fibre. Therefore, 20 Tossa jute genotypes including accession, varieties, segregate, breeding lines were investigated for variabilities and genetic relationships among them in respect of morpho-anatomical traits contributing to fibre yield components.

2. Materials and methods

2.1. Location and timing of the experiment

In 2019, experimental plants were grown and morphological investigations were conducted at Jute Agriculture Experimental Station (JAES) of BJRI, Manikganj District [23°52'56.1"N 90°01'53.0"E] of Bangladesh having loamy soil, 0.76% organic carbon, 6.85 soil pH, 12.7°C–36 °C annual average temperatures, 2376 mm annual rainfall with 49.21ft elevation level above from sea level. Anatomical works were done in the molecular laboratory of Breeding Division, BJRI Head Office, Dhaka [23°45'26"N, 90°22'47"E]; the whole works were completed from March, 2019 to July, 2020.

2.2. Plant/Seed materials

There are twenty Tossa jute genotypes including accessions, advanced lines, segregating line, pre-released varieties were used in this study to observe their genetic variability for phenological and anatomical traits contributing to fibre production followed by identifying superior genotype(s) for further high yielding tossa jute variety development (Table 1, Figure 5). In this investigation, 7 pre-released tossa jute varieties cultivating in farmers' fields were used as controls to compare the genetic diversity with other germplasms including accessions or lines or segregants based on their morphological and anatomical features.

2.3. Experimental design, seeding and plants growing

The morphological experiment was laid out in a Randomized Complete Block Design (RCBD) and anatomical observation was done in laboratory followed by completely randomized design (CRD) keeping three replications (Gomez and Gomez, 1983; Lawal, 2014). The jute seeds were treated with fungicide (Bavistin@0.25% of seed weight) to remove seed borne pathogens, and sun dried to break the dormancy (Ahad et al., 2019; Talukder et al., 2021). The critical day length for *Oritorius* jute seed germination is more than 10.5–12.5 h. Seeds were sown on 15 March, 2019. Plants were grown followed by agronomic practices. The plot size was 3.0m² (3 m × 1 m) for each replicate having plot to plot 80cm; line to line 30cm; plant to plant 10–12cm distances and 3m line length.

Table 1. List of plant materials, type of plants, sources of collection and country of origin.

Genotype No.	Genotype, Variety with Release year	Ancestors or method of development	Plant type	Source of collection	Country of origin		
G ₁	Acc. 1306	Pure line selection (PLS)	Accession	Gene Bank of BJRI	Bangladesh		
G ₂	Acc. 1318	PLS			Bangladesh		
G ₃	Acc. 1749	PLS			Bangladesh		
G ₄	Acc. 4160	PLS			Kenya		
G ₅	Acc. 4311	PLS			Tanzania		
G ₆	O-0512-6-2	O-795 × O-4	True breeding lines	Breeding Division, BJRI	Bangladesh		
G ₇	O-0412-9-4	JRO-524 × A-4582					
G ₈	O-0411-10-4	JRO-524 × A. 4311					
G ₉	O-043-7-9G (Green)	SLDT ₁ × A-1749					
G ₁₀	O-043-7-9R (Red)	SLDT ₁ × A-1749					
G ₁₁	O-049-1-3	O-72 × SLDT ₂					
G ₁₂	O-0419-3-1	JRO-524 × A-1749					
G ₁₃	JRO-524 (R) (S ₁ -Segregant)	PLS from JRO-524			Red stem, Segregating line	India	
G ₁₄	BJRI Tossa pat-2 (O-9897); 1987	O-5 × BZ-5			Pre-released variety		Bangladesh
G ₁₅	BJRI Tossa pat-3 (OM-1); 1995	PLS					
G ₁₆	BJRI Tossa pat-5 (O-795); 2008	Uganda red × O-4					
G ₁₇	BJRI Tossa pat-6 (O-3820); 2013	PLS by anatomy					
G ₁₈	BJRI Tossa pat-7 (MG-1); 2017	PLS from OM-1					
G ₁₉	BJRI Tossa pat-8 (Robi-1); 2018	PLS of mutants					
G ₂₀	JRO-524 (Navin); 1977	African (cv. Sudan Green) × indigenous (cv. JRO-632)	India				

2.4. Specimen collection, preservation and anatomy of jute stem

At 110–120 days age, the experimental jute plants attained physiological maturity for fibre production as well as anatomical study (Mahapatra et al., 2009). Three plants (110 days old) were selected randomly from the middle row of each genotype and harvested at base with the help of a jute harvesting sharpen knife without causing any injury for anatomical studies. According to Kumar et al. (2014) and Atkinson (1965), a rapid and easy method was used for jute anatomy, 3–4cm long jute stems including fibre (Phloem) and stick (Xylem) were excised out with the help of sharp knife from 4–5cm above the base of each plant. Specimens were properly labelled and preserved in Formaldehyde Acetic Acid (FAA) solution [formalin: acetic acid: alcohol = 5:15:80] for further anatomical studies (Verma, 2008). Hands-free T.S.-transverse sections (0.3–0.5mm thin) of 110 old plants were made using base sledge Microtome machine (WSL Lab Microtome-modified Reichert-type) and the additional mucilage was removed by rinsing with clean water, and then T.S. were stained with 1% safranin (aqueous) solution followed by mounting with a drop of glycerine-water on clear

glass slide with a cover slip (Tolivia and Tolivia, 1987; Sadhukhan, 2019). The prepared slide was observed under electrical modern trinocular microscope with digital USB camera setup and anatomical data i.e. bark diameter, bark thickness, area of fibre cell containing trapezoid, average number of trapezoid per T. section, fibre bundle layer per trapezoid etc. were observed and recorded carefully as reported in earlier by Kumar et al. (2014) (Figure 1 a–c).

2.5. Morphological data collection

The matured jute plants were harvested after 120 days of sowing and the morphological data like plant height (m), basal diameter (mm), green weight with leaves (g plant⁻¹), green weight without leaves (g plant⁻¹), dry fibre yield (g plant⁻¹, t ha⁻¹), stick yield (g plant⁻¹, t ha⁻¹), ratio between stick and fibre yield were recorded from randomly selected 20 plants for each genotype (Zhang et al., 2019). Area wise yield also calculated for field performances. The harvested plants were dumped or submerged in clean water and retted properly after 20–25 days of inundation (Maity et al., 2012). Then the fibres were collected, washed

Anatomical transverse sectioning (T.S.) of jute stem

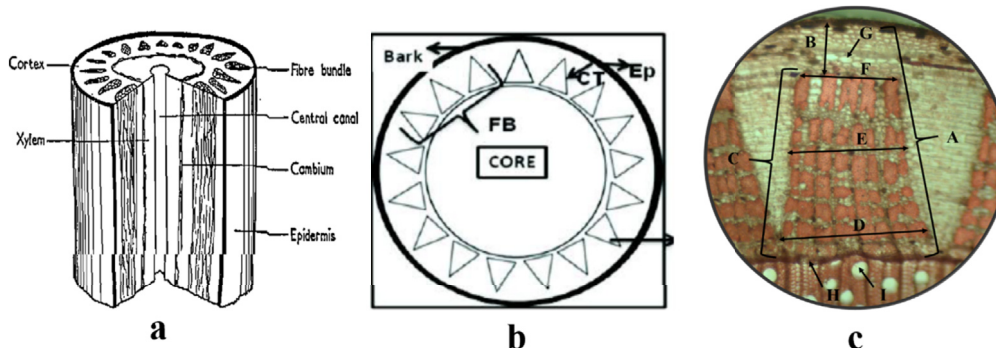


Figure 1. a. Sample view of jute stem anatomy with different elements (Atkinson, 1965); b. View of bark, cortex, epidermis, fibre cell/bundle arrangement on the cambium layer (Kumar et al., 2014); c. Transverse section of jute stem showing fibre cell structure measurements; Note: FB-Fibre bundle or trapezoids, Ep-Epidermis, CT-Cortex, A-Total bark thickness, B-Difference between fibre wedge tip and epidermis, C-Average length/height of trapezoid, D-Average width of trapezoid at base, E-Average width of trapezoid at middle, F-Average width of trapezoid at top, G-Schlerenchyma cell, H-Cambium layer, I-Vacuole.

clearly, sun dried by hanging from bamboo stick manually (Shambhu et al., 2018). Then dry fibre and stick yields were recorded carefully.

2.6. Method of data collection

Jute plant height (m) and base diameter (mm) were measured using meter scale and Vernier calliper, respectively, and averaged from randomly selected 20 plants. Green weight (g plant⁻¹) with leaves and without leaves of these 20 plants were taken using weighing balance. After collecting and drying, the weight (g plant⁻¹ from 20 plants; t ha⁻¹ from the conversion of yield plot⁻¹) of jute fibre and stick were recorded using weighing balance (Islam et al., 2001). The stained specimens (T.S.) of jute genotypes were observed and anatomical data were taken using modern microscope with digital camera setup adjusted with laptop and photomicrographs of the stained specimens were taken. In the digital camera scale, 1.0 unit was equal to 15.38µm.

2.7. Morphological and anatomical data analyses

The morphological and anatomical data were collected, compiled carefully using Microsoft Excel program (Windows 10 Pro, MS Office 2016). The analysis of variance, descriptive analyses, correlation coefficients, least significance differences (LSD), Duncan multiple range tests (DMRT) were estimated using statistix10 (Statistix10.0.0.9); and genetic analyses, hierarchical clustering, principal component analysis were done using Minitab19 [Minitab 19.1.1.0] and OriginPro (OriginPro 9.1) statistical analysis software.

2.8. Estimation of statistical parameters and genetic components

Mean, range, LSD, standard error (S. E.), standard deviation (σx) and coefficient of variation (CV) for each variable were estimated. The genotype mean square (MS_G) and error (MS_E) were estimated according to Johnson et al. (1955). The MS_E was considered as an error variance (σ_E²) component. LSD tests were described based on the 'P' at both P < 0.05 and P < 0.01 levels of significance. The associations among all variables were estimated in both genotypic and phenotypic levels according to Cohen (1988).

The mean square values from ANOVA table were used to estimate the genetic parameters like genotypic and phenotypic variances of the trait(s) by using Eqs. (1) and (2); and the genotypic, phenotypic and environmental co-variance components between traits were computed using the formulae (Eqs. (3), (4), and (5)) suggested by Burton (1952).

$$\sigma_G^2 = \frac{MS_G - MS_E}{r} \quad (1)$$

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2 \quad (2)$$

$$GCV (\%) = \frac{\sqrt{\sigma_G^2}}{\bar{X}} \times 100 \quad (3)$$

$$PCV (\%) = \frac{\sqrt{\sigma_P^2}}{\bar{X}} \times 100 \quad (4)$$

$$ECV (\%) = \frac{\sqrt{\sigma_E^2}}{\bar{X}} \times 100 \quad (5)$$

Here,

MS_G = Genotypic mean square value

MS_E = Error mean square value

r = Number of replication

σ_G² = Genotypic variance (GV)

σ_P² = Phenotypic variance (PV)

σ_E² = Error variance = $\frac{MS_E}{r}$

here,

GCV = Genotypic coefficient of variation (%)

PCV = Phenotypic coefficient of variation (%)

ECV = Environmental coefficient of variation (%)

\bar{X} or \bar{Y} = Mean value of the variable X or Y being evaluated

The heritability in broad sense was estimated using the formula (Eqn. 6) suggested by Johnson et al. (1955) and Burton and Devane (1953).

$$h_{bs}^2 (\%) = \frac{\sqrt{\sigma_G^2}}{\sqrt{\sigma_P^2}} \times 100 \quad (6)$$

The expected genetic advance for different characters under selection was estimated using the formula (Eqn. 7) suggested by Lush (1949) and Johnson et al. (1955). Genetic advance in percentage of mean was calculated from the formula (Eqn. 8) given by Comstock and Robinson (1952).

$$GA = \frac{\sqrt{\sigma_G^2}}{\sqrt{\sigma_P^2}} \times K \times \sigma_P \quad (7)$$

$$GAM (\%) = \frac{GA}{\bar{X}} \times 100 \quad (8)$$

Here,

K = 2.06 (Standardized selection intensity at 0.05 level)

σ_P = Phenotypic standard deviation

GA = Genetic advance is taken as percent of the mean assuming selection of the superior 5% of the breeding lines

GAM (%) = Genetic advance in percentage of mean

The covariance components among the traits were computed using the formula (Eqn. 9). The genotypic and phenotypic correlations (r_{G_{XY}} and r_{P_{XY}}) for all possible combinations were estimated using these covariance components and the formula (Eqs. (9), (10), (11), and (12)) suggested by Karim et al. (2014) and Johnson et al. (1955).

$$Cov_{XY} = \frac{\sum_{i=1,2,\dots,n} [(X_i - \bar{X}) \cdot (Y_i - \bar{Y})]}{N - 1} \quad (9)$$

$$r_{XY} = \frac{Cov_{XY}}{\sqrt{\sigma^2 X \times \sigma^2 Y}} \quad (10)$$

$$r_{G_{XY}} = \frac{Cov_{G_{XY}}}{\sqrt{\sigma_G^2 X \times \sigma_G^2 Y}} \quad (11)$$

$$r_{P_{XY}} = \frac{Cov_{P_{XY}}}{\sqrt{\sigma_P^2 X \times \sigma_P^2 Y}} \quad (12)$$

here,

Cov_{XY} = Covariance between character X and Y

N = Number of observation in the variable X or Y

σ² X or σ² Y = Variance of variable X or Y

σ_G² X or σ_G² Y = Genotypic variance of variable X or Y

r_{XY} = Correlation between variable X and Y

r_{G_{XY}} = Genotypic correlation between variable X and Y

$r_{P_{xy}}$ = Phenotypic correlation between variable X and Y

2.9. Euclidean clustering and principle component analysis (PCA)

It is very difficult to interpret the experimental large datasets. PCA is an effective way to solve this problem through reducing the dimensionalities of huge datasets, increasing interpretability as well as minimizing the information loss (Jolliffe and Cadima, 2016). It does so by creating new uncorrelated variables that successively maximize variances. Finding new variables with the maximum variance, the principal components, reduces to solve an eigenvalue/eigenvector problem, and the new variables are defined by the dataset at hand; hence making PCA an adaptive data analysis technique (Jolliffe and Cadima, 2016). Mahalanobis D^2 statistics was analysed for genetic diversity among all genotypes. The Euclidean squared distances grouped the genotypes according to Ward's method (Sawarkar et al., 2015a,b). D^2 statistics, cluster mean analysis and Two-dimensional principal component analysis were carried out by using statistical software package Minitab19 and OriginPro 9.1.

3. Results

3.1. Morphological study

3.1.1. Morphological variability

The statistical analyses revealed that, genotype mean square values for plant height, fresh weight of plant, fibre yield content recorded highly significant variations ($p < 0.01$), and girth of plant, dry stick yield showed significant variations ($p < 0.05$) and no significant variation was found for the ratio between fibre and stick yield (Table 2). Such variabilities can be further considered for varietal development of tossa jute species.

Plant height: Stem height in jute plant play important role to increase fibre yield content. Among all genotypes, the accession Acc. 1318 showed higher stem height (3.22m) followed by O-0512-6-2 (3.18m), BJRI Tossa Pat 7, BJRI Tossa Pat 5, Acc. 1306 etc (Table 3).

Base diameter: The fibre is mainly produced from basal and middle portions of jute plant. In this investigation, Acc. 4160 gave maximum base diameter (16.85mm) with higher fibre content followed by JRO-524, O-0512-6-2, BJRI Tossa Pat 7, O-049-1-3, Acc. 1318 and so on (Table 3). The fibrous plant material with high stem base diameter contribute to the fibre yield and could be used as breeding materials for hybridization (Zhang et al., 2019).

Fresh weight of plant: Green weight or fresh weight of Jute means the plant weight including green leaves. According to Maity et al. (2012), the jute fibre yield is related with green weight of jute plant. Fresh weight of jute plants directly associated to yield performances. In this study, the Acc. 4311 showed higher fresh weight (263.89g) with leaves followed by Acc. 4160, line O-0512-6-2, variety JRO-524 and so on (Table 3). Almost similar results were found for fresh weight

without leaves except the Acc. 4160. The jute genotypes having higher biomass content could play important role to increase fibre yield content as well as contribute to enhance soil fertility by dropping green leaves.

Dry fibre and stick yield: The main desirable trait of jute plant is fibre yield (Kumar et al., 2016). Among 20 genotypes, Acc. 1318 showed higher fibre yield (15.26g plant⁻¹; 3.97t ha⁻¹) followed by O-043-7-9 (G), Acc. 4311, Acc. 1306, O-0411-10-4, O-049-1-3, O-0512-6-2 etc (Table 3). The genotypes having good fibre yield content could be improved through breeding techniques and would be further cultivated for the next generation to develop high yielding new tossa jute varieties, and similar reports were opined by Constable et al. (2015) in cotton breeding for fibre quality improvement.

3.1.2. Correlation analysis among the morphological traits

Yield (fibre and stick) content is the dependent variable which is attributed by the jute plant height, stem diameter and green weight (Maity et al., 2012). The correlation study (Table 4) revealed that, the positive highly significant genotypic associations ($r = \geq 7.0$) were found in plant height with stem base diameter, green weight, stick yield; and significant relation ($r = 0.3$ to < 7.0) with fibre yield content. Base diameter showed highly significant relation ($r = \geq 7.0$) with all characters. Green weight of jute plants showed highly significant relation ($r = \geq 7.0$) with stick yield and significant correlation ($r = 0.3$ to < 7.0) with fibre yield. Fibre and stick yield recorded highly significant relation ($r = \geq 7.0$) with each other. In case of phenotypic association, all the characters showed significant positive relation ($r = 0.3$ to < 7.0) with one another where fibre and stick yield recorded highly strong association ($r = \geq 7.0$) each with other. Ghosh et al. (2013) observed plant height to be highly associated with basal diameter, green weight and fibre yield. The estimated correlations among the studied characters would be useful to breeders for parental selection (Aditya et al., 2011). The values of genotypic correlations were higher than phenotypic correlation for all traits (Table 4).

3.1.3. Genetic components for morphological study

The values for genetic analyses (Table 5) of eight morphological traits regarding the genotypic and phenotypic variances (σ^2_G, σ^2_P) were ranged from 0.05 to 1162.47 and 0.06 to 1272.21 for plant height and green weight without leaves per plant, respectively. The values for genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were ranged from 4.51% to 19.61% and 6.85% to 20.52% for plant base diameter and green weight without leaves per plant, respectively (Table 5). The highest PCV (>20%) was found for green weight plant⁻¹ without jute leaves; medium PCVs (10–20%) for green weight, dry stick yield and the ratio between fibre & stick yield; and lower PCVs (<10%) for plant height, base diameter and dry fibre yield content. There was no high GCV value but medium and lower GCVs grading were found similar to PCVs (Table 5).

Table 2. Analysis of variance (MS) for yield and contributing morphological characters of 20 tossa jute genotypes.

Sources of variation→	Replication	Genotype	Error	P value
d.f. (Total d.f. = 59)	2	19	38	
Plant height- PH (m)	0.001	0.17**	0.029	<0.001
Base diameter-BD (mm)	0.84	3.30*	1.87	<0.005
Green wt. with leaves-GWL (g plant ⁻¹)	662.66	3328.93**	1068.67	<0.001
Green wt. without leaves-GWL1 (g plant ⁻¹)	485.32	3816.62**	329.21	<0.001
Dry fibre yield-FY (g plant ⁻¹)	2.93	4.64**	1.40	<0.001
Dry fibre yield-FY1 (t ha ⁻¹)	0.30	0.36**	0.05	<0.001
Dry stick yield-SY(g plant ⁻¹)	11.29	49.20*	27.52	<0.005
Dry stick yield-SY1 (t ha ⁻¹)	0.88	3.34*	1.82	<0.005
Ratio between stick yield & fibre yield-SFR	0.18	0.09 ^{NS}	0.17	>0.005

Note: df-Degree of freedom; * and ** indicate significant at 0.05 and 0.01 probability level, respectively; NS means non-significant.

Table 3. Mean performance of 20 genotypes for yield and yield attributing morphological characters.

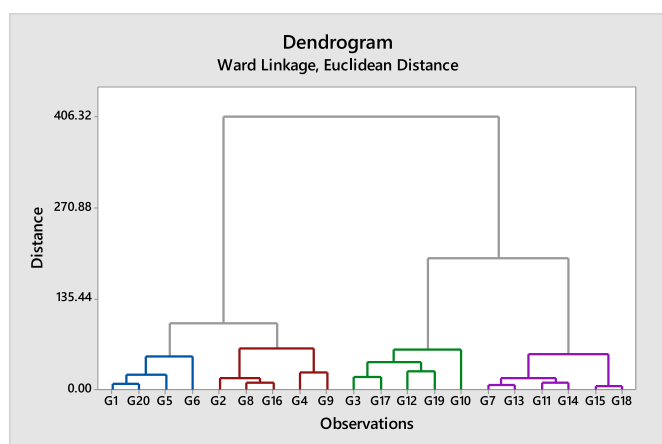
Genotypes (varieties, lines)	Plant height (m)	Base diameter (mm)	Green weight with leaves (g plant ⁻¹)	Green weight without leaves (g plant ⁻¹)	Dry fibre yield (g plant ⁻¹)	Dry fibre yield (t ha ⁻¹)	Dry Stick yield (g plant ⁻¹)	Dry Stick yield (t ha ⁻¹)	Stick yield: Fibre yield
G ₁	3.12 ^{a-d}	15.37 ^{a-c}	242.42 ^{a-d}	211.31 ^{bc}	14.74 ^a	3.38 ^{c-e}	35.33 ^{bc}	9.19	2.73
G ₂	3.22 ^a	16.21 ^{ab}	229.98 ^{a-e}	198.33 ^{b-d}	15.26 ^a	3.97 ^a	44.57 ^a	11.59	2.93
G ₃	2.42 ^{hi}	14.51 ^{b-d}	187.22 ^{e-h}	126.22 ^{hi}	13.69 ^{a-c}	2.98 ^{fg}	33.29 ^{cd}	8.66	2.90
G ₄	3.08 ^{a-e}	16.85 ^a	261.11 ^{ab}	170.22 ^{d-g}	14.03 ^{ab}	3.65 ^{a-d}	36.10 ^{a-c}	9.39	2.57
G ₅	2.87 ^{c-g}	15.48 ^{a-c}	263.89 ^a	209.33 ^{bc}	14.76 ^a	3.84 ^{ab}	36.33 ^{a-c}	9.67	2.53
G ₆	3.18 ^{ab}	16.27 ^{ab}	258.39 ^{a-c}	248.09 ^a	14.23 ^{ab}	3.70 ^{a-c}	42.13 ^{ab}	10.95	2.97
G ₇	2.77 ^{fg}	14.57 ^{b-d}	208.62 ^{b-g}	183.33 ^{c-e}	11.93 ^{c-e}	3.10 ^{e-g}	31.67 ^{cd}	8.23	2.68
G ₈	3.01 ^{a-f}	15.91 ^{ab}	222.18 ^{a-f}	196.67 ^{b-e}	14.37 ^{ab}	3.74 ^{a-c}	37.67 ^{a-c}	9.79	2.63
G ₉	2.93 ^{b-g}	16.13 ^{ab}	240.00 ^{a-e}	183.00 ^{c-e}	14.92 ^a	3.88 ^{ab}	39.27 ^{a-c}	10.21	2.64
G ₁₀	2.39 ⁱ	14.23 ^{b-d}	137.67 ^h	113.67 ⁱ	11.52 ^{d-e}	2.95 ^{fg}	26.33 ^d	6.85	2.32
G ₁₁	3.12 ^{a-d}	16.24 ^{ab}	206.93 ^{c-g}	171.96 ^{d-f}	14.33 ^{ab}	3.73 ^{a-c}	38.13 ^{a-c}	9.91	2.67
G ₁₂	2.84 ^{d-g}	13.29 ^{cd}	188.62 ^{d-h}	152.00 ^{f-h}	10.21 ^e	2.80 ^g	31.33 ^{cd}	8.15	2.92
G ₁₃	2.97 ^{a-g}	14.53 ^{b-d}	207.36 ^{b-g}	176.36 ^{d-f}	12.41 ^{b-d}	2.97 ^{fg}	33.07 ^{cd}	8.60	2.89
G ₁₄	3.08 ^{a-e}	15.48 ^{a-c}	215.22 ^{a-g}	167.56 ^{e-g}	13.70 ^{a-c}	3.56 ^{b-d}	37.15 ^{a-c}	9.66	2.70
G ₁₅	2.69 ^{gh}	15.44 ^{a-c}	211.67 ^{a-g}	152.00 ^{f-h}	13.99 ^{ab}	3.64 ^{a-d}	38.67 ^{a-c}	10.05	2.79
G ₁₆	3.13 ^{a-c}	15.14 ^{a-d}	214.07 ^{a-g}	198.93 ^{b-d}	14.00 ^{ab}	3.31 ^{d-f}	33.67 ^{b-d}	8.75	2.65
G ₁₇	2.98 ^{a-f}	14.67 ^{a-d}	174.33 ^{f-h}	112.67 ⁱ	13.62 ^{a-c}	3.54 ^{b-d}	32.67 ^{cd}	8.49	2.40
G ₁₈	3.17 ^{ab}	16.25 ^{ab}	215.67 ^{a-g}	148.33 ^{f-h}	14.07 ^{ab}	3.66 ^{a-d}	38.33 ^{a-c}	9.97	2.72
G ₁₉	2.83 ^{e-g}	13.00 ^d	164.11 ^{gh}	141.56 ^{ghi}	13.83 ^{a-c}	3.60 ^{a-d}	34.67 ^{b-d}	9.01	2.52
G ₂₀	3.08 ^{a-e}	16.37 ^{ab}	249.11 ^{a-c}	215.44 ^b	13.81 ^{a-c}	3.32 ^{d-f}	35.07 ^{bc}	9.12	2.76
Maximum	3.22	16.85	263.89	248.09	15.26	3.97	44.57	11.59	2.97
Range	0.84	3.85	126.22	135.42	5.05	1.16	18.23	4.74	0.64
±SE	2.94 ± 0.14	15.30 ± 1.12	214.93 ± 26.69	173.85 ± 14.82	13.67 ± 0.97	3.47 ± 0.19	35.77 ± 4.28	9.31 ± 1.10	2.70 ± 0.33
CV (%)	5.83	8.95	15.21	10.44	8.66	6.61	14.66	14.49	15.21
LSD _(0.05)	0.28**	2.26*	54.03**	29.99**	1.96**	0.38**	8.67*	2.23*	0.68 ^{NS}

Note: CV (Coefficient of variation) = $(\sqrt{\text{EMS}/\text{Mean}}) \times 100$; LSD (0.05)-Least significant difference at 5% probability level; List of genotypes: G₁...G₂₀ (Table 1); * & ** means statistically significant at 0.05 and 0.01 probability levels, respectively. Values with different letters are statistically significant for the same variable.

Table 4. Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients among morphological traits.

r_{p}^2	PH	BD	GWL	GWL ₁	FY	FY ₁	SY	SY ₁
PH	1.00	0.99**	0.82**	0.72**	0.66*	0.64*	0.76**	0.74**
BD	0.59*	1.00	0.84**	0.85**	0.73**	0.77**	0.87**	0.89**
GWL	0.62*	0.76**	1.00	0.87**	0.84**	0.68*	0.75**	0.79**
GWL ₁	0.62*	0.53*	0.83**	1.00	0.54*	0.40*	0.86**	0.87**
FY	0.50*	0.67*	0.58*	0.43*	1.00	0.91**	0.84**	0.88**
FY ₁	0.54*	0.64*	0.52*	0.36*	0.84**	1.00	0.93**	0.94**
SY	0.64*	0.67*	0.64*	0.55*	0.76**	0.82**	1.00	0.99**
SY ₁	0.64*	0.67*	0.65*	0.56*	0.76**	0.83**	0.99**	1.00

Note: PH-Plant height (m), BD- Base diameter (mm), GWL-Green weight (g) with leaves plant⁻¹, GWL₁-Green weight without leaves plant⁻¹, FY-Dry fibre yield (g) plant⁻¹, FY₁- Dry fibre yield (t ha⁻¹), SY-Dry stick yield (g) plant⁻¹, SY₁-Dry stick yield (t ha⁻¹), SFR-Ratio between fibre and stick yield. ** means very strong or strong, and * means moderately strong association.

**Figure 2.** Dendrogram showing the genetic diversity of 20 jute genotypes for studied morphological characters.

Estimates of heritability in broad sense ranged from 56.57% for fibre and stick yield ratio to 95.59% for green weight (g) without leaves per plant (Table 5). According to Sawarkar et al. (2014), jute plant height, green weight and fibre yield showed high heritability; plant base diameter and jute stick yield gave moderate heritability, and the ratio between stick and fibre showed lower heritability in broad sense (Table 5). The breeders should have well knowledge on heritability of desired traits in jute crops to manage breeding objectives through hybridization (Mukul et al., 2020a).

From the analysis for the possibility of genetic advance, there was very low opportunity to improve the desired traits of jute characters like plant height, base diameter, fibre yield and ratio with stick yield (Table 5). More opportunity were found for green weight, stick yield

followed by fibre yield of jute plants. The main target of jute crop is to increase the fibre yield content. Here, 2.14 GA was found for fibre yield per plant, 0.44 for plant height, 1.42 for base diameter, 56–70 for fresh weight of jute plants (Table 5).

The genetic advance in percent of mean (GAM %) was ranged from 7.54% to 40.40% for fibre yield-stick yield ratio and green weight without leaves per plant of jute crops, respectively (Table 5). According to Johnson et al. (1955), high GAM% was found for green weight; moderate GAM% for plant height, fibre and stick yield, and low GAM% for base diameter and fibre yield-stick yield ratio in jute plants (Table 5).

3.1.4. Euclidean cluster analysis

The Euclidean cluster analysis grouped the experimental 20 tossa jute genotypes into four major clusters at 63.49 genetic dissimilarity distance (Figure 2) using all morphological traits depicting the existing genetic divergence among all tossa jute genotypes. The jute genotypes having similar morphological traits were placed in the same cluster of Euclidean Dendrogram. The genotypes of different cluster showed genetic divergence. In Euclidean Dendrogram, the cluster IV was larger consisting of 30% jute genotypes including two breeding lines (O-0412-9-4, O-049-1-3), one segregating line (JRO-524 (R)) and three pre-released varieties (O-9897, BJRI Tossa Pat 3, BJRI Tossa Pat 7) (Table 6). The second cluster contains 5 genotypes (25%) including two accessions (Acc. 1318, Acc. 4160), two breeding lines (O-0411-10-4, O-043-7-9Gr) and a variety (BJRI Tossa Pat 5) having good performance for all traits (Table 6). The third cluster also contains 5 genotypes (25%) including Acc. 1749, O-043-7-9 (R), O-0419-3-1, BJRI Tossa Pat 6 and BJRI Tossa Pat 8. The first cluster occupied four genotypes (25%) including Acc. 1306, Acc. 4311, O-0512-6-2, JRO-524 having good performance after the genotypes of cluster II.

Average values of different morphological traits of 20 Tossa jute genotypes in four different clusters were estimated (Table 7). The cluster II recorded higher mean values for plant height, base diameter, fibre yield

Table 5. Genetic analyses for studied morphological traits.

Characters	GV (σ^2_G)	PV (σ^2_P)	GCV (%)	PCV (%)	ECV (%)	h^2_{bs} (%)	GA	GAM (%)
PH	0.05	0.06	7.27	8.00	5.79	90.85	0.44	14.98
BD	0.48	1.10	4.51	6.85	8.94	65.76	1.42	9.29
GWL	753.42	1109.64	12.77	15.50	15.21	82.40	56.54	26.31
GWL ₁	1162.47	1272.21	19.61	20.52	10.44	95.59	70.24	40.40
FY	1.08	1.55	7.60	9.10	8.66	83.56	2.14	15.67
FY ₁	0.10	0.12	9.26	9.98	6.44	92.80	0.66	18.97
SY	7.23	16.40	7.52	11.32	14.67	66.38	5.54	15.48
SY ₁	0.51	1.11	7.65	11.33	14.49	67.46	1.47	15.76
SFR	0.03	0.08	6.05	10.69	15.27	56.57	0.20	7.54

Note: GV (σ^2_G)-Genotypic variance, PV (σ^2_P)-Phenotypic variance, GCV-Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation, ECV-Environmental covariance, h^2_{bs} -Heritability in broad sense, GA-Genetic advance, GAM (%) -Genetic advance in percent of mean; PH ~ SFR: See in Table 2.

Table 6. Cluster groups of jute genotypes with their percentages.

Cluster	No. of genotypes	Percentage	Genotypes
I	4	20.0	G ₁ , G ₂₀ , G ₅ , G ₆
II	5	25.0	G ₂ , G ₈ , G ₁₆ , G ₄ , G ₉
III	5	25.0	G ₃ , G ₁₇ , G ₁₂ , G ₁₉ , G ₁₀
IV	6	30.0	G ₇ , G ₁₃ , G ₁₁ , G ₁₄ , G ₁₅ , G ₁₈

Table 7. Average values of different clusters for morphological characters.

Variables	Cluster I	Cluster II	Cluster III	Cluster IV	Grand centroid
PH (m)	3.06	3.07	2.69	2.96	2.94
BD (mm)	15.87	16.05	13.94	15.42	15.30
GWL (g plant ⁻¹)	253.45	233.47	170.39	210.91	214.93
GWL1 (g plant ⁻¹)	221.04	189.43	129.22	166.59	173.85
FY (g plant ⁻¹)	14.39	14.52	12.58	13.41	13.67
FY1 (t ha ⁻¹)	3.56	3.71	3.18	3.44	3.47
SY (g plant ⁻¹)	37.22	38.25	31.66	36.17	35.77
SY1 (t ha ⁻¹)	9.73	9.95	8.23	9.40	9.31
SFR	2.75	2.68	2.61	2.74	2.70

Table 8. Distance between cluster centroids.

Cluster No.	No. of observation	I	II	III	IV	Distance from cluster centroids	
						Average	Maximum
I	4	0.00				16.50	27.96
II	5	37.42	0.00			18.03	33.75
III	5	123.98	87.51	0.00		22.91	36.67
IV	6	69.12	32.20	55.34	0.00	12.35	19.03

and stick yield; while green weight of jute plants and fibre-stick yield ratio showed higher mean values in the genotypes of cluster I. The jute genotypes of these two cluster gave best results for desirable traits. The cluster III revealed the lowest means for all the traits. The genotypes of clusters (II, I, IV) having higher means than their respective grand centroids would be considered as good genotypes compared to the genotypes of cluster (III) having lower means (Table 7). The average inter and intra cluster distances among all jute genotypes were assessed (Table 8). The higher inter cluster distance (123.98) was recorded between the cluster I and III; while minimum distance (32.20) was found between the cluster II and IV; and medium distance (87.51) between cluster II and III. The average and maximum intra cluster distances among the genotypes were assessed where more variations were found in cluster III (Table 8).

3.1.5. Analyses of principal components (PCA) for morphological data

Principal components were analysed for genetic diversity among all jute genotypes for the studied morphological traits. The Euclidean

clustering was confirmed by the PCA. From the scree plot in principal component analyses, the eigenvalues, variances and cumulative variances among the components were estimated (Table 9). The variances and chi-squares were increased with increasing the eigenvalues but vice-versa to the cumulative variances (Table 9). In the scree plot analysis of PCA (Figure 3), the first three principal components having Eigen values > 1.0, accounting for 99.96% cumulative variations. Among the total variances in PCA, 90.89% were recorded in 1st component, 8.62% in 2nd, 0.45% in 3rd, 0.03% in 4th and 0.01% in 5th component (Table 9). There are 20 Tossa jute genotypes were categorized into six groups in the score plot of PCA (Figure 4). The genotypes were grouped based on their similarities with one another and their positions in different quadrants distant from the central point.

The genotypes Acc. 4160, O-0411-10-4, O-043-7-9G, Acc. 4311, O-049-1-3, O-9897, BJRI Tossa Pat 3 and BJRI Tossa Pat 7 located distantly from the central point in score plot of PCA and grouped as I. The line O-0512-6-2 of cluster I and Acc. 1318 of cluster II showing

Table 9. Eigenvalues of the covariance matrix.

Components	Eigenvalue	Variance (%)	Cumulative Variance (%)	Chisq.
PC1	2183.32	90.89	90.89	898.90
PC2	207.02	8.62	99.51	654.41
PC3	10.82	0.45	99.96	389.83
PC4	0.66	0.03	99.98	210.81
PC5	0.32	0.01	100.00	169.35
PC6	0.04	0.00	100.00	92.95
PC7	0.02	0.00	100.00	78.29
PC8	0.001	0.00	100.00	14.82
PC9	1.28E-4	0.00	100.00	0.00

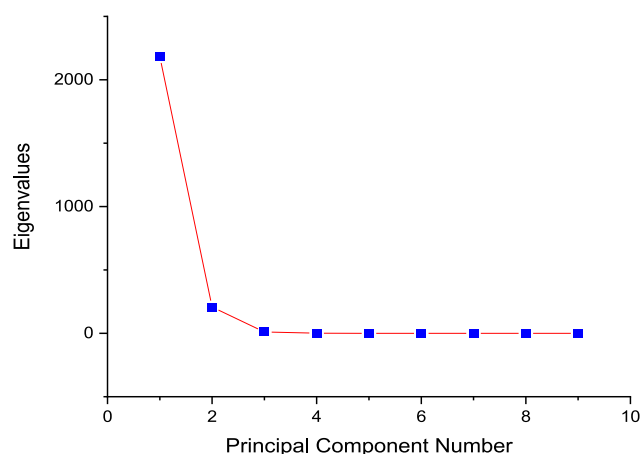


Figure 3. Scree plot in PCA analysis.

good results were found in group II. The genotypes (Acc. 1306, JRO-524, BJRI Tossa Pat 5) of group III were found in cluster I and II. The genotypes (BJRI Tossa Pat 8, BJRI Tossa Pat 6) of group IV were found in cluster III. The group V was consisted of Acc. 1749, O-0412-9-4, JRO-524 (R) and O-0419-3-1 which were found in cluster III and IV. The last genotype O-043-7-9 of cluster III was found in group VI. In PCA and Euclidean clustering, the best genotypes of Tossa jute were

found in group I followed by group II, III and IV which were distributed in cluster I, II and IV. The other genotypes showing less or no good performances for the studied morphological traits were found in group V, VI and cluster III and IV (Figures 2 and 4). So, the experimental results were justified in both Euclidean cluster and Principal component analyses. In this study, the first three PCs showing Eigenvalues >1.0 contributed mainly in the total variances among the genotypes for the studied characters (Table 9). Total nine principal components were estimated for the studied morphological variables where all the variables gave positive values in 1st principal component (PC). The green weight of jute plants without leaves plant⁻¹ and fibre-stick yield ratio showed positive values in 2nd PC, and the green weight of jute plants with & without leaves plant⁻¹ recorded positive values in 3rd PC (Table 10).

3.2. Anatomical study

3.2.1. Anatomical variability

The analyses of variances for anatomical study of 20 Tossa jute genotypes revealed presence of variability among the genotypes (Table 11). Highly significant (p < 0.01) variations were found for anatomical traits i.e. stem diameter, bark thickness, height & width of trapezoid, area of trapezoid, number of trapezoid T.section⁻¹, total fibre bundle area trapezoid⁻¹ and number of bundle layer trapezoid⁻¹ (Table 11). The jute anatomical structure for fibre cell development and statistical parameters of 20 jute genotypes were estimated (Table 12; Figures 1 A–C And 5. A–T).

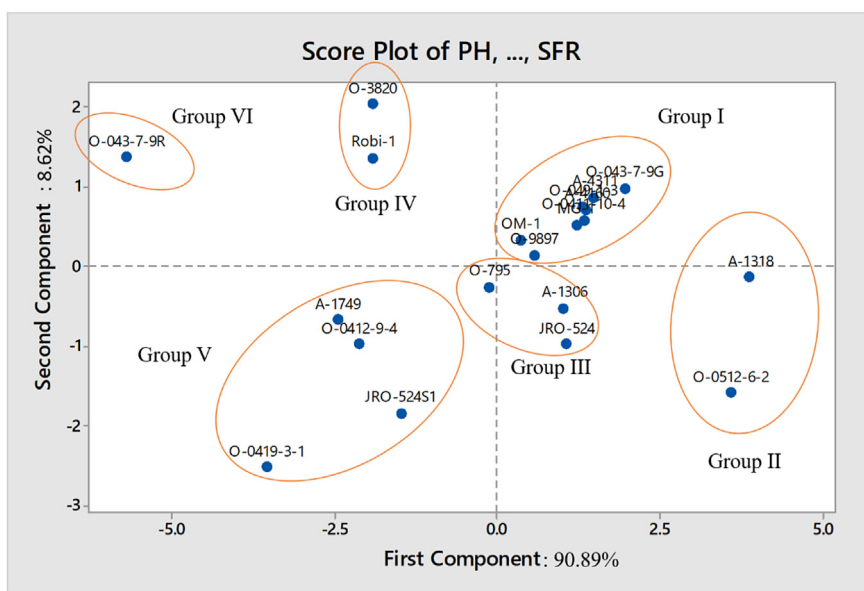


Figure 4. Score plot in PCA showing relationships among 20 Tossa jute genotypes for six anatomical characters.

Table 10. Vector components among the morphological traits studied.

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
PH	0.003	-0.000	-0.022	0.007	-0.059	0.403	-0.909	0.091	-0.005
BD	0.015	-0.029	-0.083	0.342	-0.931	-0.064	0.039	0.035	0.018
GWL	0.676	-0.731	0.082	-0.018	0.019	0.001	-0.001	-0.002	-0.001
GWL1	0.734	0.679	0.004	0.010	-0.006	0.000	0.003	0.000	0.000
FY	0.014	-0.023	-0.203	0.893	0.355	-0.164	-0.084	0.003	-0.001
FY1	0.003	-0.007	-0.069	0.132	0.033	0.710	0.317	0.046	0.608
SY	0.054	-0.050	-0.939	-0.220	-0.003	-0.027	-0.015	-0.252	-0.000
SY1	0.014	-0.014	-0.241	-0.050	0.035	0.060	0.124	0.932	-0.225
SFR	0.002	0.001	-0.015	-0.127	0.007	-0.546	-0.223	0.238	0.761

Table 11. Analysis of variances (Mean square values) for anatomical characters.

Sources	df	BDM	BT	HT	AWT	AT	Av.NT	TABS	BLT
Variety	19	14.393**	1.114**	0.025**	0.006**	0.014**	47.580**	73.460**	1.834**
Error	40	0.094	0.060	0.006	0.001	0.003	10.292	12.096	0.145
	T.df = 59	P < 0.001	P < 0.001	P < 0.001	P < 0.001	P < 0.001	P < 0.001	P < 0.001	P < 0.001

Note: T.df-Total degree of freedom, BDM- Bark diameter (mm), BT- Bark thickness (mm), HT- Height of trapezoid (mm), WT- Av. width of trapezoid (mm), AT- Area of trapezoid (sqmm), Av.NT- Average number of trapezoid T.section⁻¹, TABS- Total bundle area section⁻¹(sqmm), BLT- No. of Bundle layer trapezoid⁻¹, ** means statistically significant at 0.05 and 0.01 probability level, respectively.

3.2.2. Bark diameter, bark thickness, fibre bundle number & bundle area in transverse section (T.S.) of jute stem

The jute genotypes showed highly statistical significant variations for fibre yield attributing anatomical traits. Among the studied anatomical characters of jute plant, higher results for bark diameter (16.17 mm), bark thickness (3.95 mm), area of trapezoid (3.54 sqmm), average number of trapezoid per T.S. (69.50) and total fibre bundle area (37.48 sqmm) were found in Acc. 1318 (Figure 5.B), the highest number of bundle layer per T.S. (10.67) in BJRI Tossa pat-5 (Table 12; Figure 5.P). In respect of these anatomical traits, the other genotypes i.e. Acc. 1306 (Figure 5.A), BJRI Tossa Pat 5 (Figure 5.P), segregating line JRO-524R (Figure 5.M), advanced lines O-0412-9-4 (Figure 5.G), O-0512-6-2 (Figure 5.F), O-0411-10-4 (Figure 5.H) showed good results. The area of a trapezoid depends on its height and width. Jute genotypes having more stem height and base diameter gave maximum number of trapezoid per transverse section (Miah et al., 2020). Similar findings were reported in jute crops by Oram et al. (1983) in earlier.

Highly significant variations ($p < 0.01$) were found among the genotypes for the fibre bundle area per transverse section (TS). Inter-varietal differences were reported earlier by Majumdar (2002) in respect of fibre bundle character in jute crops. The genotypes having good records for bark diameter (≥ 12 mm), bark thickness (≥ 3.20 mm), area of a trapezoid (≥ 0.40 sqmm), average number of trapezoid (≥ 60.0) per T.S., number of fibre bundle layer (≥ 9.50) per T.S. and total fibre bundle area (25.0 sqmm) per T.S. would be considered as good and these will be selected for crop improvement purpose of hybridization approaches.

3.2.3. Correlation co-efficient among the anatomical characters of jute

The strongly significant associations were recorded between base diameter and bark thickness; in trapezoidal area with its height and width and; in total fibre bundle area per T.S. with the trapezoid height, width and area (Table 13). The other associations among all the traits were found positively significant but non-significant relations were recorded in average number of trapezoid per T.S. with bark thickness,

Table 12. Mean performance for anatomical features of the studied jute genotypes.

Genotypes	BDM	BT	HT	AWT	AT	Av.NT	BLT	TABS
G ₁	13.19 ^{bc}	3.69 ^a	1.10 ^{ab}	0.51 ^{ab}	0.54 ^a	60.67 ^{a-d}	9.89 ^{abc}	34.00 ^{ab}
G ₂	16.17 ^a	3.95 ^a	1.17 ^a	0.49 ^{abc}	0.54 ^a	69.50 ^a	10.56 ^{ab}	37.48 ^a
G ₃	8.30 ^{ij}	2.36 ^{ef}	0.96 ^{abc}	0.37 ^d	0.36 ^b	60.33 ^{a-d}	8.48 ^f	21.79 ^d
G ₄	9.55 ^{gh}	2.32 ^{ef}	0.88 ^{bc}	0.43 ^{a-d}	0.36 ^b	66.33 ^{abc}	8.92 ^{c-f}	24.35 ^{bcd}
G ₅	8.37 ^{ij}	2.29 ^{ef}	0.92 ^{bc}	0.38 ^{cd}	0.34 ^b	65.00 ^{a-d}	8.34 ^f	22.65 ^{cd}
G ₆	12.22 ^{de}	3.22 ^{abc}	0.90 ^{bc}	0.37 ^{cd}	0.32 ^b	65.33 ^{a-d}	8.33 ^f	21.43 ^d
G ₇	12.27 ^{cd}	3.25 ^{abc}	0.90 ^{bc}	0.37 ^{cd}	0.33 ^b	64.50 ^{a-d}	8.51 ^{e-f}	21.43 ^d
G ₈	11.72 ^{de}	3.12 ^{bcd}	0.92 ^{bc}	0.51 ^a	0.44 ^{ab}	59.33 ^{bcd}	9.67 ^{a-e}	26.31 ^{bcd}
G ₉	11.31 ^{ef}	3.01 ^{b-e}	0.88 ^{bc}	0.42 ^{a-d}	0.36 ^b	58.67 ^{bcd}	8.78 ^{c-f}	21.12 ^d
G ₁₀	9.06 ^{hi}	1.90 ^f	0.91 ^{bc}	0.38 ^{cd}	0.33 ^b	64.67 ^{a-d}	8.73 ^{c-f}	21.74 ^d
G ₁₁	11.78 ^{de}	3.19 ^{bc}	0.91 ^{bc}	0.39 ^{bcd}	0.35 ^b	64.00 ^{a-d}	9.78 ^{a-d}	22.94 ^{cd}
G ₁₂	10.31 ^g	2.90 ^{cde}	0.84 ^c	0.47 ^{a-d}	0.38 ^b	59.83 ^{a-d}	8.67 ^{d-f}	22.72 ^{cd}
G ₁₃	13.50 ^b	3.75 ^{ab}	1.10 ^{ab}	0.40 ^{a-d}	0.43 ^{ab}	56.83 ^{cd}	10.61 ^a	25.39 ^{bcd}
G ₁₄	9.07 ^{hi}	2.04 ^f	0.98 ^{abc}	0.40 ^{a-d}	0.38 ^b	63.50 ^{a-d}	8.33 ^f	24.36 ^{bcd}
G ₁₅	7.89 ^j	2.30 ^{ef}	0.99 ^{abc}	0.45 ^{a-d}	0.42 ^{ab}	56.83 ^{cd}	9.43 ^{b-f}	24.26 ^{bcd}
G ₁₆	13.50 ^b	3.66 ^{ab}	1.09 ^{ab}	0.43 ^{a-d}	0.47 ^{ab}	67.83 ^{ab}	10.67 ^a	33.00 ^{abc}
G ₁₇	8.66 ^{hij}	2.37 ^{def}	0.91 ^{bc}	0.37 ^d	0.34 ^b	57.50 ^{cd}	8.84 ^{c-f}	19.43 ^d
G ₁₈	9.48 ^{gh}	2.58 ^{c-f}	0.90 ^{bc}	0.40 ^{bcd}	0.35 ^b	59.83 ^{a-d}	9.83 ^{a-d}	21.01 ^d
G ₁₉	10.42 ^{fg}	3.27 ^{abc}	0.91 ^{bc}	0.42 ^{a-d}	0.38 ^b	55.50 ^d	9.50 ^{a-f}	21.32 ^d
G ₂₀	11.92 ^{de}	3.03 ^{b-e}	0.87 ^{bc}	0.38 ^{cd}	0.32 ^b	59.67 ^{a-d}	9.39 ^{b-f}	19.13 ^d
Maximum	16.17	3.95	1.17	0.51	0.54	69.50	10.67	37.48
Range	8.27	2.05	0.33	0.15	0.23	14.00	2.34	18.35
Mean	10.93	2.91	0.95	0.42	0.39	61.78	9.26	24.29
S.E.	0.25	0.2	0.06	0.03	0.04	2.62	0.31	2.84
CV (%)	2.8	8.42	8.13	9.53	12.99	5.19	4.12	14.32
LSD _(0.05)	0.95	0.76	0.24	0.12	0.16	9.91	1.19	10.75

Note: d.f.-degree of freedom, BDM- Bark diameter (mm), BT- Bark thickness (mm), HT- Height of trapezoid (mm), WT- Av. width of trapezoid (mm), AT- Area of trapezoid (sqmm), Av.NT- Average number of trapezoid T.section⁻¹, TABS- Total bundle area section⁻¹(sqmm), BLT- No. of Bundle layer trapezoid⁻¹.

Morpho-anatomical observation 20 tossa jute stem T.S.



Figure 5. Morphological observation and anatomical transverse section for fibre cell distribution of 110 days old jute plants.

trapezoid height, trapezoid width, trapezoid area, and bundle layer per trapezoid in T.S. of jute stem (Table 13).

4. Discussion

4.1. Morphological studies

Analyses of variances for morphological data revealed that, significant variations were found among all jute genotypes used in this experiment for the studied morphological characters indicating the extent of genetic variability present among them. Irrespective of origins all the traits showed more than 60–80% diversity in both species. Trait means of diversity were significant but not the origin means (Palit et al., 1996). The

morphological traits like plant height, fresh weight and fibre yield content showing highly significant variations should be more emphasized than other characters showing significant variations like base diameter, stick yield content, and non-significant variations like the ratio between fibre & stick yield for crop improvement purposes (Kar et al., 2009). In earlier, significant variations were described for various morphological traits in jute plants (Ngomuo et al., 2017; Jatothu et al., 2018). It can be concluded from the variances analysis, fibre yield was the main target in jute crop, and the Acc. 1318, O-043-7-9G, Acc. 4311, Acc. 1306, O-0411-10-4, O-049-1-3, O-0512-6-2 were good performer among 20 genotypes. High yielding genotypes having greater variability for desired traits would be selected as best plant for tossa jute varietal development and it was supported by Jatothu et al. (2018). The desirable traits should be managed in

Table 13. Test of associations among the anatomical traits of jute stem.

	BDM	BT	HT	AWT	AT	Av.NT	TABS	BLT
BDM	1.00							
BT	0.87**	1.00						
HT	0.47*	0.41*	1.00					
AWT	0.35*	0.34*	0.23*	1.00				
AT	0.51*	0.49*	0.76**	0.77**	1.00			
Av.NT	0.29*	0.07	0.14	0.01	0.07	1.00		
TABS	0.57*	0.47*	0.74**	0.70**	0.93**	0.42*	1.00	
BLT	0.60*	0.60*	0.56*	0.42*	0.60*	0.05	0.59*	1.00

Note: ** means very strong or strong, and * means moderately strong association.

the selected parents based on their nature of adaptability in nature (Kar et al., 2009). Jute is a natural fibre producing plant having phloem or bast fibre producing habit (Maity et al., 2012). Its fibre elongation is essential to obtain good fibre yield which directly dependent on the height of stem (Das et al., 2014). In this study, the Acc. 1318, O-0512-6-2 (3.18m), BJRI Tossa Pat 7, BJRI Tossa Pat 5, Acc. 1306 showing best plant height would be used as breeding materials to develop new variety. Similar results were opined by Mukul et al. (2020a) in Tossa jute.

The jute plant height and girth of its stem are significantly correlated contributing to fibre yield (Sawarkar et al., 2014). The jute plant with higher base diameter is important for fibre yield (Miah et al., 2020). The Acc. 4160, JRO-524, O-0512-6-2, BJRI Tossa Pat 7, O-049-1-3, Acc. 1318 showed good base diameter would be used for varietal development through hybridization. The green weight of jute plants contribute to fibre yield; specially the jute green stem without leaves having higher bark thickness play significant role in fibre yield capacity (Mandal and Datta, 2014). The Acc. 4311, Acc. 4160, line O-0512-6-2, variety JRO-524 showed good results for fresh weight of green fibre and would be used for varietal development. The fibre yield is the main objective in jute crops (Islam and Ali, 2017). Among 20 tossa jute genotypes, the genotypes i.e. Acc. 1318, O-043-7-9G, Acc. 4311, Acc. 1306, O-0411-10-4, O-049-1-3, O-0512-6-2 performed well for fibre yield content, and these materials could be used for developing high yielding tossa jute variety in Bangladesh (Kar et al., 2009; Zhang et al., 2019; Priyadarshan, 2019). Jute sticks had also important use as fuel, to produce inks, elements of cosmetics etc. So, jute can be cultivated both for fibre and stick regarding its utilization in households and industries (Islam, 2020). Jute sticks are useful materials which are now using in various aspects to produce charcoal, desk board of valuable cars, ink (BCSIR, 2018).

The associations in all combinations among the morphological traits were estimated and partitioned into genotypic and phenotypic levels where genotypic relations were higher than phenotypic relations, and it was reported earlier in jute by Ghosh et al. (2013). The plant breeders should have good knowledge on the correlations among all studied morphological traits of Jute crop for the selection of parents properly (Aditya et al., 2011). The characters showing highly significant relations would be considered for parental selection by the breeders to design hybridization program. Similar records were reported by Xing et al. (2014) in Rapeseed (*Brassica napus* L.). In this study, all the characters except jute fibre and stick yield ratio showed significant relations. Moreover, plant height, base diameter, bark thickness are the main traits contributing to fibre yield in jute plants (Islam et al., 2001).

Analyses of genetic parameters like variance and co-variances at genotypic and phenotypic levels, environmental covariance, heritability in broad sense, genetic advance in percentage & in percentage of mean are very important for the breeders to target the desirable traits in jute crop improvement systems; it was reported by Denton and Nwangburuka (2011) in *Solanum anguivi*. According to Deshmukh et al. (1986), PCV and GCV values were classified as high (>20%), medium (10–20%) and low (<10%). In 20 jute genotypes, the PCVs were found relatively higher than the GCVs for all traits indicating high contribution of genotypic effects for phenotypic expression of such characters. Similar results were reported in hot pepper by Palit et al. (1996) and Yadeta et al. (2011). Moderate and high values for these respective parameters indicated the existence of substantial variabilities and selection may be effective based on these characters. Similar finding was reported earlier for plant height, stem base diameter, dry fibre yield per plant, dry fibre yield per hectare of land, dry stick yield per plant, for green weight per plant in jute crop (Yadeta et al., 2011). The estimation of heritability along with GCV, PCV would give the best figure of the amount of advance to be expected from the selection (Burton and Devane, 1953). Knowledge on heritability coupled with genetic advance is more useful for genetic improvement through selection (Johnson et al., 1955) and to predict the expected

genetic gain from one selection cycle (Bicer and Sakar, 2004). Thus, the heritable portion of the variation in respective desired traits could be more useful for the plant breeders. According to Singh (2001), more than 80% heritability was categorized as very high, 60–79% were moderately high, 40–59% were medium and less than 40% were low. The characters having very high heritability indicated relative small contribution of the environment factors to the phenotype and selection for such characters could be fairly easy due to high additive effects (Rosmaina et al., 2016). High and medium estimates of broad sense heritability (50–60% h^2_{bs}) have been also reported by previous researchers for plant height, stem base diameter; for fresh weight with and without leaves; dry fibre yield and stick yield per plant in jute crops (Palit et al., 1996; Sawarkar et al., 2014). Estimates of genetic advance for dry fibre yield per plant was 2.14g and per hectare of land was 0.66 ton, indicating that whenever we select the best, 5% high yielding genotypes as parents, mean dry fibre yield of the offspring could be improved, i.e., mean genotypic value of the new population for dry fibre yield $g\ plant^{-1}$ and $ton\ ha^{-1}$ will be improved from 13.47 to 15.61 $g\ plant^{-1}$, and 3.67 to 4.33 $t\ ha^{-1}$. In the same way, plant height will be improved from 2.94m to 3.38m; plant base diameter: 15.30–16.72mm; and 35.77g–41.17g for dry stick yield per plant. According to Johnson et al. (1955), the genetic advance in percent of mean (GAM) is categorized as low (<10%), moderate (10–20%) and high (>20%). High heritability estimates along with the GAM is usually more helpful in predicting genetic gain under selection than heritability alone. In the present study, high heritabilities were found for green weight without leaves (95.59%), fibre yield ha^{-1} (92.80%), plant height (90.85%), fibre yield per plant (83.56%), green weight with leaves (82.40%). The fresh weight of jute genotypes without leaves and fresh weight with leaves showed high heritability and GAM; while the other characters exhibited moderate heritability with low GAM reflecting the absence of additive gene action for the expression of these desirable traits which are fixable for the next generations, and selection in next population based on these characters. Similar results were also reported by Adhikari et al. (2018) in rice crop. All the traits can be simultaneously utilized for genetic gain (Palit et al., 1996).

Hierarchical cluster analysis grouped all jute genotypes into four distinct clusters and significant differences observed among them indicating the existence of considerable genetic divergence for their morphological traits in Euclidean clustering system (Kar et al., 2009). The jute genotypes showing more or less similar desirable traits were grouped in the same cluster; on the other hand, the genotypes showing more dissimilarities for their traits were grouped in different clusters (Kar et al., 2009). In jute crop, higher values for plant height, stem diameter, fibre thickness, and fibre yield are main target (Zhang et al., 2019). The genotypes having good performance for these traits are grouped in a cluster with more similarities among them, and these genotypes to be selected for breeding purposes or varietal development. Similar results were reported for potato crop in Bangladesh by Haydar et al. (2007). Crop improvement is made through generating variability in desired traits followed by selection (Roy et al., 2013). Continued success in crop improvement can only be realized when new substantial variability is found and used in a population. Divergence between any two parents expresses the allelic differences between them (Dias et al., 2003). The genotypes grouped into the same cluster presumably diverge very little from one another. Crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants (Ayenew et al., 2020). The genotypes of respective cluster showing higher cluster mean values would be selected as superior for parental selection (Sawarkar et al., 2015a,b).

The principal component analysis (PCA) method has been widely used on jute crop for various objectives. In the PCA, a scatter plot of the quantitative traits revealed that the first three principal components (PC) with eigenvalues greater than 1.0 had large contribution to the variances

(Tetteh et al., 2019). In this study, the first two PCs accounted for 99.51% of the total variance, with PC1 90.89% and PC2 8.62%. The cumulative variance of 100.0% by the first 5 axes (Table 9), indicates the identified traits within the axes exhibited great influence on the phenotype of the jute genotypes, and could effectively be used for selection. According to Ghosh et al. (2013), the first 3 components (PC1, PC2 and PC3) and associated traits are the most reliable to explain variation patterns among different jute genotypes. The genotypes of group I, II, III and IV were found best for their position in principal coordinate analyses. In conclusion, the distribution of populations of the first two component scores was in agreement with cluster analysis (Jolliffe, 2002). In our experiment, the PC analysis ultimately showed the amount of variability for the traits among the genotypes that could be used for the improvement of jute.

4.2. Anatomical studies

Prediction of fibre yield and quality are essential in jute breeding program within a short period of time (Zhang et al., 2019). Jute plant morphological data are moderately reliable indicators of fibre yield, but not useful to judge fibre quality owing to the large variability among the genotypes for fibre content and fibre bundle structure, which is again dependent on retting condition in jute crop. The anatomical study is an easy, effective and rapid method to judge the fibre quality and yield capacity of Tossa jute plant, but are rarely used in breeding programs (Maity et al., 2012; Kumar, 2020). A rapid method for selection of good Tossa jute (*Corchorus olitorius* L.) genotype was described and the usefulness of fibre anatomical traits for predicting fibre yield was studied comparing with morphological characters. The results indicated that fibre anatomical characters are highly suitable for predicting fibre yield and quality. Significant variations among the jute genotypes were recorded for the studied anatomical traits.

Diameter of jute plant play important role in fibre and stick yield content (Maity et al., 2012). Jute fibre consists of several sclerenchymatous cells. These cells are formed out of cellulose-based helical crystalline microfibrils and cambium cells beneath the cambium layer, with helical angles ranging from 20–30°, which are connected to a complete layer by amorphous lignin and hemicellulose (Lord, 2003). Lignin is a complex phenolic polymer, and jute fibre contains 12%–14% of it (Majumdar et al., 2020). Unlike cotton, jute is a multicellular and multi-constituent fibre. Apart from a cellulose (=60%) the other two major constituents are hemicellulose (=23%) and lignin (=14%). Due to its bio-degradability and annual renewability, jute fibre has diversified commercial and household applications (Palit, 1999). In this study, Acc. 1318, Acc. 1306, BJRI Tossa Pat 5, segregating line JRO-524 (R), advanced lines O-0412-9-4, O-0512-6-2, O-0411-10-4 etc. having good records for bark diameter (≥ 12 mm) would be used as breeding parents for yield improvement in tossa jute. Similar results were opined by Kar et al. (2009) in *Corchorus olitorius*. The space between the upper surfaces of cambium cell to the epidermis of phloem tissue is known as the bark thickness of jute plant (Sengupta and Palit, 2004). Development of bast fibre in jute (*Corchorus* spp.) is a complex process involving differentiation of secondary phloem fibres from the cambium accompanied by lignification of the fibre cell wall (Kundu et al., 2012). Phloem fibre or bast fibre is consisting of sclerenchymatous cells which are generally absent in primary phloem but are found in the secondary phloem (Snegireva et al., 2015). The formation of secondary phloem fibres starts long after the initiation of secondary xylem (Snegireva et al., 2015). Genotypes with thinner cell wall, thicker bark tissues and lesser lignin may be utilized in breeding for improving the fibre fineness of jute (Meshram and Palit, 2013). Among 20 jute genotypes, the genotypes having more bark thickness (≥ 3.20 mm) like Acc. 1318, Acc. 1306, BJRI Tossa Pat 5, segregating line JRO-524 (R), advanced lines O-0412-9-4, O-0512-6-2, O-0411-10-4 etc. would be used as parental materials to improve the fibre thickness around the stem of the existing jute cultivars through breeding systems. The prediction of fibre quality from anatomical study of plant stem, therefore, offers a probable alternative. Majumdar (2002)

and Sommerville (2005) reported firstly in earlier such a possibility and observed that the fineness of fibre is directly correlated with fibre bundle area per T.S. and number of fibre cells per bundle. He classified a number of jute varieties as fine, medium fine and coarse depending on the area of fibre bundles. The genotypes i.e. Acc. 1318, Acc. 1306, BJRI Tossa Pat 5, segregating line JRO-524 (R), advanced lines O-0412-9-4, O-0512-6-2, O-0411-10-4 with higher fibre bundle area were categorized as fine and would be used as breeding materials to develop new variety for good fibre production. The number of pyramid shaped trapezoid in a T.S. of jute stem directly affects the area of fibre cell as well as fibre yield performances (Majumdar, 2002). The more number of trapezoid per T.S. increases the area of fibre cell proportionately (Mir et al., 2008b). The Acc. 1318, Acc. 1306, BJRI Tossa Pat 5, segregating line JRO-524 (R), advanced lines O-0412-9-4, O-0512-6-2, O-0411-10-4 etc. showed good results for average number of trapezoid (≥ 60.0) per T.S. in jute crop, these will be used to improve the fibre anatomy of existing varieties or to develop new high yielding variety. According to (Majumdar, 2002; Jatothu et al., 2018), the jute fibre yield as well as total fibre bundle area depend on the number of trapezoid, number of fibre bundle layer per trapezoid and area of trapezoid per T.S. directly. In this investigation, Acc. 1318, Acc. 1306, BJRI Tossa Pat 5, segregating line JRO-524 (R), advanced lines O-0412-9-4, O-0512-6-2, O-0411-10-4 etc. showed good results for these traits. Highly significant variabilities were reported among the white jute genotypes in earlier (Islam et al., 2001). The genotypes with higher records for bark diameter, bark thickness, area of a trapezoid, average number of trapezoid per T.S., number of fibre bundle layer per T.S. and total fibre bundle area per T.S. would be considered as good and these will be selected for crop improvement purpose of hybridization approaches.

Maity et al. (2012) reported in earlier, the character associations at genotypic and phenotypic levels were found significant for the anatomical study in jute crops. In the stem anatomy of jute, the variable jute fibre yield resulting from fibre bundle area depends on the other independent variable i.e. bark diameter, bark thickness, trapezoid area, number of trapezoid, bundle layer per trapezoid etc. Genotypic relations were found highly significant than the phenotypic associations which indicates the greater possibility of improvement at genotypic level (Oladosu et al., 2018).

5. Conclusion

Among 20 tossa jute genotypes investigated in this study, the Accession (Acc. 1318, Acc. 4160, Acc. 1306, Acc. 4311), advanced breeding lines (O-0512-6-2, O-043-7-9G, O-0411-10-4, O-049-1-3) and pre-released varieties (BJRI Tossa Pat 5, JRO-524) showed good performances for morphological traits i.e. plant height, stem base diameter, fresh weight of plants, fibre yield content, and anatomical traits i.e. bark diameter, bark thickness, trapezoid area, fibre bundle area and fibre bundle layer per trapezoid. The existing variabilities among these tossa jute genotypes due to genetic factors contributing to quantitative and qualitative traits indicate the high potentialities for jute crop improvement, and would be served as potential parents for development of improved Tossa jute cultivars through hybridization or molecular breeding approaches. These advanced breeding lines would be developed directly as good varieties through further pure line selection in field experiments. The anatomical study would be considered as an easy and effective method for screening of jute genotypes for specific goal without destructive sampling within a short period of time. This study will be useful in future jute breeding programs.

Declarations

Author contribution statement

Md. Mia Mukul: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Wrote the paper.

Nargis Akter: Conceived and designed the experiments; Wrote the paper.

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Data will be made available on request.

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The authors declare no conflict of interest.

Additional information

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