GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF FIBRE YIELD AND ITS COMPONENT CHARACTERS OF TOSSA JUTE (*Corchorusolitorius*L.)

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CERTIFICATE

This is to certify that thesis entitled, ***"Genetic variability and character association of fiber yield and its component characters in tossa jute(Corchorusolitorius L.)"*** *submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by NazmonNahar, Registration No.: 11-04540 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has been duly been acknowledged by her.

Dated: June, 2017
Place: Dhaka, Bangladesh

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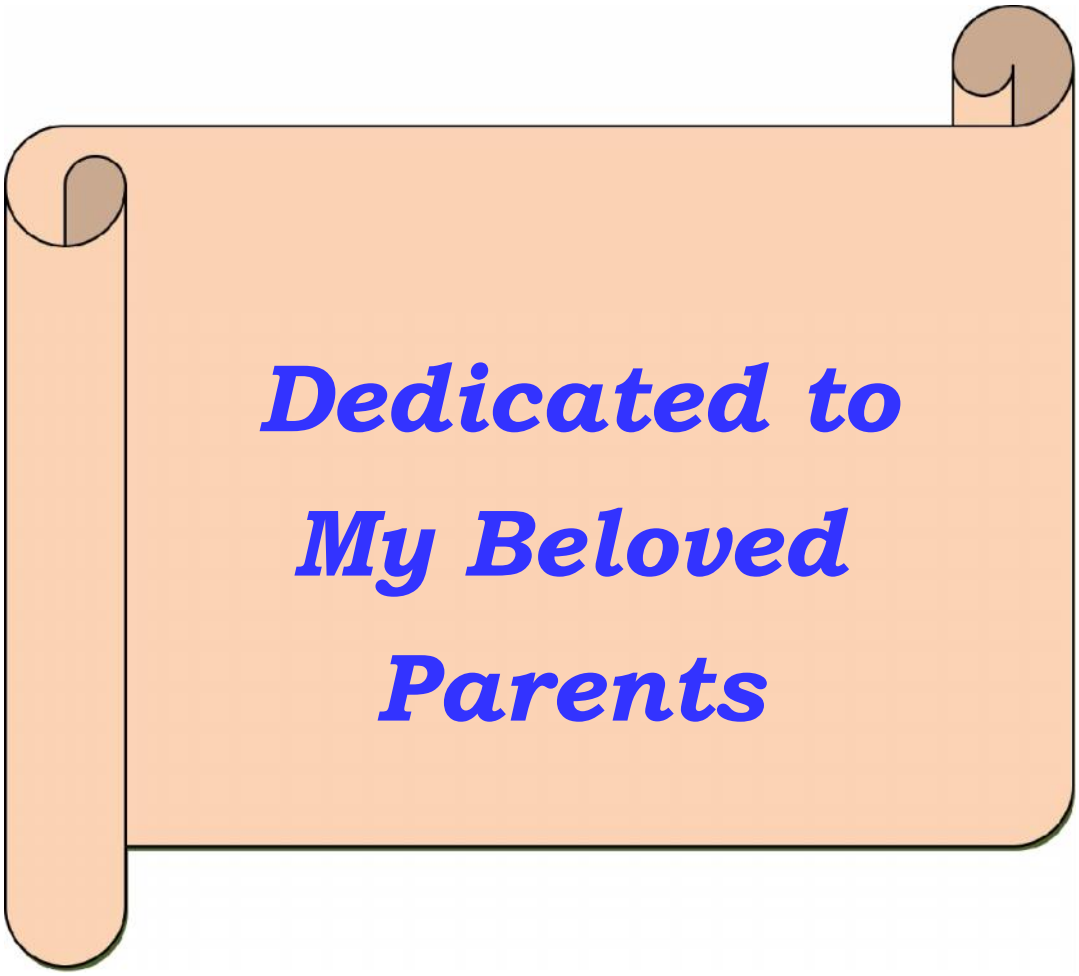
Supervisor


Dedicated to
My Beloved
Parents

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ABSTRACT

The experiment was conducted with twenty one genotypes of tossa jute from different geographic origin at the Jute Agriculture Experimental Station, Jagir, Manikgonj, Bangladesh Jute Research Institute (BJRI), from April to August, 2016 to study their genetic divergence, variability, correlation, direct and indirect effect of 11 morphological characters. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed for base diameter per plant followed by fibre weight per plant. High heritability values with moderate genetic advance in percentage of mean were obtained for plant height, nodes number, core diameter, leaf length, fibre weight per plant. Correlation studies showed positive correlation between fibre yield and its most components. Path analysis showed the highest positive direct effect of stick weight on fibre weight followed by leaf area, base diameter, plant height, nodes per plant and core diameter. All the genotypes were grouped into five different clusters. Principal component analysis, principal coordinate analysis, canonical variate analysis and cluster analysis gave similar results. Cluster I had the maximum six genotypes while cluster V had the minimum of two genotypes. The highest inter-genotypic distance (124.10) was found between G_{14}, G_7 and the lowest distance (3.054) between G_{12} and G_6. The highest intra-cluster distance was found in cluster II (78.799) and the lowest in cluster III (42.119). Considering the cluster, inter-genotypic distance and other agronomic performance, the genotypes G9, G15, G21 from cluster I; G6, G12, G18, G20, from cluster III; G7, G11 from cluster V were considered to be better parents for future use in hybridization programme.

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SYMBOLS AND ABBREVIATIONS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
Acc	Accessions
BJRI	Bangladesh Jute Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
gm	Gram
h^2b	Heritability in broad sense
J.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MoP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

CHAPTER I

INTRODUCTION

Jute is the world's foremost bast fibre and second most important textile fibre after cotton. Jute *(Corchorus spp.)*grows in tropical and subtropical regions throughout the world. The number of *Corchorus* species is probably around 50-60 but over 170 *Corchorus* names are given in the Index Kewensis (Edmonds, 1990). In the genus *Corchorus* (Family: Tiliaceae) two species of jute, *Ccapsularis* L. (Deshi jute) and *C. olitorius* L. (Tossa jute) produce white and golden colour fibre respectively. About 90 percent of the world's jute is produced in the Ganges-Brammaputra delta in India and Bangladesh (Purseglove, 1979). Kundu (1951) has discussed the origin of jute, and viewed Indo-Burma (new connotation Indo-Myanmar) as the primary centre of origin of C. *capsularis* L. and Africa as the primary centre of C *olitorius* L. According to Kundu the secondary centre may be Indo-Burma for *C.olitorius* L.

Bangladesh is the second largest jute fibre producing country after India with its production of about 9.9 lakh tons of which 51%, 44% and 5% are used for mill consumption, raw jute export, and domestic use respectively. In pre-liberation era or just after liberation of the country one core bell of jute used to be produced, which has now come down to 40-50 lac bell a year (Anon., 2008).

Jute is a dicotyledonous plant of the genus *Corchorus* and family of the Tiliaceae. Jute is basically self pollinated and has fourteen diploid chromosomes (2n=14) which are distributed throughout the tropical regions of Africa, genotypes, *Corchorus capsularis* L and *Corchorus olitorius* L. are cultivated for fibres. Centre of origin of *Corchorus capsularis* L. in Bangladesh, India and Myanmar including South China (Singh, 1976).

Jute plays an important role in the national agro-economy of Bangladesh. At farm level about 4 million livelihoods is directly or indirectly dependent on jute

production. Yet area under jute cultivation in Bangladesh has gone down from 772.47 thousand hectares in 1986-87 to 666 thousand hectares in 2013-14.During the same corresponding period, total production of jute has increased to 1323 thousand tons from 1125thousand tons. However, the productivity per hectare increased from 1.46 tons to 1.98 tons during 1986-87 to 2013-2014 (BBS, 2013-2014). The reason for this increased productivity is attributed to resultant effect of research endeavors during this period. The use of jute dominates in various household and industrial goods like sacking, hessian, yarn, jute wool, bag, carpets, blankets, cloths, sofa cover, geo-jute, paper pulp and appears to have much potential.

Before 1970's, the ratio of cultivated area under tossa and deshi jute in Bangladesh was 30:70. However recently the area of tossajute cultivation increased and the ratio has been converted to 80:20 with the development of less photosensitive HYV tossa jute varieties such as 0-9897, 0-72 and O-795.

A major determination of fibre yield in jute is time of flowering, as the onset of flowering induces branching of the upper main stem and hence, cessation of main stems elongation. Jute is a photoperiod sensitive short-day plant (Ali, 1961). The critical photoperiod is 12.5 hrs for C. *olitorius* L. (Ali, 1961; Husain, 1977; Johansen *et al.*, 1985), and 12.0 hrs for C. *capsularis* L. plants (Kar, 1963), which indicate that C. *olitorius* L. is more sensitive to photo-period than to C. *capsularis* L. Thus, jute growth for fibre production is limited to that part of the year with day lengths exceeding the critical day-length; viz. mid March to May for C. *olitorius* L. in Bangladesh.

There are some biotic and abiotic constraints that affect the cultivation of jute. Biotic constraints are stem rot, anthracnose, nematode, yellow mite, apion, mosaic virus etc. Abiotic constraints are soil salinity, waterlogged condition, drought, short day, low temperature etc. Scarcity of seed is one of the main problems in jute sector especially in tossa jute.

In Bangladesh, the number of recommended jute varieties is limited in terms of meeting the requirements of wide agro-ecological conditions. Most of these varieties are quite old and have narrow genetic base and susceptible to various biotic and abiotic stresses such as insects, pests, diseases, drought, water logging, and low temperature and so on. About 49 jute varieties have been developed by Bangladesh Jute Research Institute till now All these factors combined with the increasing demand of jute in the world market, the new types of jute need to be developed to meet the due to fit in climate change situation various agro-industrial needs.

In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed. However, development of such parents is a long term and tedious job. Variability and genetic diversity are the fundamental laws of plant breeding which are major tools being used in parent selection for efficient hybridization programme. Modern breeding works needs variable and diverse germplasm from which new genes can be introduced into the existing cultivars in order to improve their yield, stability and resistance to pests and adverse conditions. The importance of genetic diversity and variability in the improvement of a crop has been stressed in both self and cross-pollinated crop (Griffin and Lindstone, 1954; Murty and Anand, 1966; Guar *et al.*,1978). The quantification of genetic diversity and variability through biometrical procedures (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse and variable parents for a successful hybridization programme. Selection of parents based on geographic diversity alone is not always justified (Shreshtha, 1991). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991).

Under the present context of global environment prospective, jute is getting the highest priority as biodegradable agro-industrial crop. To supplement

conventional breeding and to address the issues of modern biotechnological research, establishment of a modern biotechnological laboratory is under progress.

Therefore, the present investigation has been undertaken with the following objectives:

1. To study the genetic parameters among the different tossa jute genotypes,
2. To assess the variability present in different genotypes,
3. To assess the characters association and contribution of characters towards fibre yield in different genotypes, and
4. To generate information and genetic materials so as to use those in the future breeding programme.

CHAPTER II

REVIEW OF LITERATURE

Yield in tossa jute (*C. olitorius* L.) is a complex product. It is correlated with a number of characters such as plant height, base diameter, node number, green weight, leaf angle and stick weight etc. Selection for yield may be effective unless the associations between other yield components influencing it directly or indirectly are clearly known and taken into consideration. Selection should be based on yield components which are least affected by non genetic factors (Chaudhury *et al*. 1981).

Various researches is doing to improve the quality of this crop. Lot of divergence and genetic variability has already been reported but desired results so far as yield and quality aspects of this crop are eluding so far. Various literature related to the appropriate multivariate technique for genetic diversity, correlation, variability and path analysis in on *Corchorus olitorius* L. has been reviewed and here under being presented.

2.1 GENETIC VARIABILITY

In order to achieve improvement of crops, there must exist variability in materials. The extent of genetic variability existing of genotype of a crop plant is an index of its genetic dynamism. Plant breeding revolves around selection, which can be effectively practiced only in the presence of variability of desired traits. Hence the success of breeding depends entirely upon the variability. Information on the nature and magnitude of genetic variability for the desired characters in the base material and interrelationship among them is useful in breeding for high yield. Dudley and Moll (1969) reported that the improvement of a crop mainly depends upon the magnitude of genetic variability and the degree to which the yield and its components are heritable. More the variability better is the chance of selection.

The associations of various characters are also useful and provide criteria for selection of the component characters. Yield is character which is governed by several factors and is thus very complex.

Alam *et al*. (2016); studied on the assessment of genetic variation in fifty-one genotypes of white jute from different geographic origins with 11 morphological characters. Analysis of variance revealed the significant variation was observed among the genotypes for all the characters. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed in branches per plant. High heritability values with moderate genetic advance in percentage of mean were obtained for leaf width, petiole length, nodes per plant.

Arpita and Kumar (2016); studies on genetic variability and character association for yield and quality attributing characters in eighteen released varieties of tossa jute (*Corchorus olitorius* L.). Contributing characters viz., plant height, basal diameter, node no., fibre weight, stick weight, fibre strength, fibre fineness and fibre percentage based on yield and quality. High heritability with high genetic advance exhibited by plant height, fibre strength, fibre fineness, fibre weight and basal diameter indicated the influence of mainly additive gene action.

Zheng *et al*.(2015);studied on the genetic variability and DNA fingerprinting in jute (*Corchorus spp*.) to assesses the genetic diversity of 58 jute accessions indicating that high genetic variation was present in white and dark jutes. Their genetic similarity coefficients ranged from 0.520 to 0.910 with average of 0.749, indicating relatively great genetic diversity among them. The 58 jute accessions were divided into four groups with the coefficient 0.710 used as a value for classification, consistent with their species and pedigrees. All these results may be useful both for protection of intellectual property rights of jute accession and for jute improvement. To broaden the genetic variation in jute, the parental lines in

cross-breeding programs should be selected from different geographical or collection regions. Moreover, other biotechnologies, such as somatic hybridization and genetic transformation, could be used to overcome the sexual incompatibility between dark and white jute.

Ghosh *et al*. (2013); a wide range of study has been conducted based on 25 traits among 63 jute genotypes of *C. capsularis* and *C. olitorius*, were evaluated to assess the extent and patterns of variability and their relationships. Seed traits exhibited a wider range of variation than fibre traits and the genotypes in *C. olitorius* varied the most than those in *C. capsularis* . The accession BRA/4792 and BRA/4794 and variety O-9897 of *C. olitorius* were identified as the most promising genotypes, based on their phenotypic variability and high yield performance, for use as genetic material for future jute breeding programs and for germplasm conservation.

Pervin and Haque, (2012); studied on 11 genotypes of jute based on the genotypic and phenotypic variances, correlation and path coefficient for plant height, base diameter, green weight, stick weight, number of pod per plant, number of seed per pod, 1000 seed weight, seed yield per plant and fibre yield per plant. Highly significant differences were observed among the genotypes for all the characters. Substantial amounts of genotypic variance were also obtained for all characters.

Al-mamun *et al*. (2010); studied on 18 genotypes of white jute from different geographic origin with a view to find out the genetic variability and association for fibre yield and its component characters. All the characters tasted showed significant variation among the different genotypes. The highest genetic variability was obtained in green weight. High heritability together with high genetic advance in percentage of mean was observed in green weight, stick weight and fibre weight.

Alam (2009), reported that the phenotypic coefficient of variation was higher for all the characters than their corresponding genotypic coefficient of variation. Among the characters the highest genotypic coefficient of variation was recorded for branches per plant followed by stick weight, fiber weight, green weight, leaf width, nodes per plant, base diameter, petiole length, Plant height, leaf angle and leaf length in order of merit. All the genotypes varied significantly with each other for all the characters studied. Among the characters studied comparatively high genotypic coefficient of variation, high heritability value and high genetic advance were recorded for the character branch per plant, stick weight, fibre weight, and green weight which suggest that these characters are under control of additive gene effects. High heritability value with moderate genetic advance were found for the characters leaf width, petiole length, nodes per plant indicated that this characters might be under the control of non-additive gene effect.

Islam and Ahmed (2003), studied variability in jute genotypes and revealed significant differences for all the characters with wide range of variability. Considerable amount of genotypic variances were obtained for fibre weight per plant, stick weight per plant and plant height.

Cheng *et al*.(2002), found that the characters, such as middle stem diameter, whole stalk weight, and days to 50% flowering vary significantly among kenaf varieties. Morphological differences in characters such as seed character, leaf shape, stem colour, flower colour, and plant maturity were small. Most of the kenaf accessions tested had red or green stems, yellow flowers and large seeds, entire- or palmate- leaves and four maturity types were observed.

Heliyanto *et al*.(1998); studied genetic variability of kenaf germplasm and found appreciable genetic variability exists within the germplasm for the characters plant height, base diameter, node number, fibre percentage, stick weight, days to flowering and fibre yield.

Siepe *et al*.(1997);evaluated genetic variability in a collection of *Hibiscus cannabinus* L. and other *Hibiscus* spp. Characters that have been evaluated for morphological and agronomical characteristics include: Days to flowering, distribution of flower pattern, leaf form, average basal stem diameter, plant height, fresh biomass yield, and total dry matter. A wide variability was observed among the genotypes for all the characters that have been tested.

Ahmed *et al*. (1993); reported the phenotypic coefficient of variation was relatively higher than the genotypic one for all characters. Both genotypic and phenotypic coefficients of variation were the highest for fibre yield followed by green weight and the lowest for base diameter.

Sardana *et al*. (1990); observed higher phenotypic coefficient of variation than the corresponding genetic coefficient of variance value for plant height, basal diameter, number of node and fibre weight.

Sinha *et al*.(1986); found that the character plant height was significantly correlated with most of the characters viz., basal diameter, internodal length, green weight and fibre yield except node number and stick weight.

Zheng *et al*. (1985); observed that plant height, thickness of stem and fresh weight of the stem were positively correlated with dry fibre weight of jute. In mesta, Sinha*et al*,.(1986) found that the character plant height was significantly correlated with most of the characters viz., basal diameter, internodal length, green weight and fibre yield except node number and stick weight.

Chaudhury (1984),conducted path coefficient analysis in jute and concluded plant height contributed the maximum direct effect (0.481) on fibre yield followed middle diameter (0.234), top diameter (0.164), node number (0.108), basal di

(0.076) and inter nodal length (0.036). Further, plant height also influences fibre through the indirect paths of inter nodal length, middle diameter and basal. at the phenotypic level, and through inter nodal length, middle diameter, diameter and basal diameter at the genotypic level.

Sinhamahapatra and Rakshit (1977), have reported that fibre yield for plant was genotypically and phenotypically correlated with plant height, basal diameter, node number and internodal length in tossa jute.

Sasmal and Chakraborty (1978), reported that the magnitude of genotypic correlation was much higher than the phenotypic correlation in mesta, showing the influence of environment in reducing the actual inherent association between various characters. They further observed that the number of nodes has high degree of relationship with fibre weight.

Maiti and Chakravarty (1977), reported that the analysis of variance for different yield contributing components obtained the differences among means for the characters of plant height, basal diameter, fibre yield as highly significant.

Sasmal and Chakraborty (1977), stated that stripped green weight, wood weight and fibre weight had genotypic and phenotypic coefficients of variability of about 30%, while for days to flowering, plant height and basal diameter these were about 10%.

Maiti *et at.*(1975); observed that stem diameter is significantly correlated with number of nodes both *capsularis* and *olitorius* of *Corchorus.*Joseph (1976), found higher genetic variability in case of fibre percentage, green weight and fibre weight than plant height, basal diameter and number of nodes in *Corchorus capsularis.*

Joseph (1974), studied genetic parameters in segregating population of *C. capsularis*and noted that green weight and fibre weight had higher genetic variability than plant height, basal diameter and node number.

Arunachalam and Lyer (1974), considered plant height as the highest contributor to fibre yield then the basal diameter and middle diameter. Singh (1970), observed plant height and base diameter were found to have less genetic variability than stick weight and fibre weight respectively.

Shukla *et al*.(1967); reported high positive correlation of stick weight with fibre weight and basal diameter. They also reported significant positive correlation of plant height and basal diameter with each other in jute.

Eunus (1968), reported that fibre yield has much more direct correlation with basal diameter in jute and further suggested that plant height is not a dependable indicator in performance of fibre yield.

Dutta and Abbas (1969), considered that plant height and basal diameter are not only highly significantly and positively correlated with the fibre yield of Kenaf but alsowith each other.

Roy (1965), found negative association between plant height and fibre; wood ratio and fibre yield in jute. Roy (1966), reported in *C. olitorius* that highly significant negative correlation exists between two characters (taller the plants, earlier the flowering) and that the negative correlation is beneficial from the agronomic point of view since taller plants will not only give higher yield but also earlier harvest by virtue of earlier flowering and maturity.

Robinson *et al*. (1951); stressed the need to estimate genotypic and phenotypic variances for various characters for choosing individuals based on phenotypic expression with an aim to identify superior genotypes.

Ghosh and Patel (1945), observed in a population of *capsularis* jute that plant height and basal diameter are strongly but positively correlated. Kar and Desar Ker (1952), suggested that the yield of fibre in jute is proportional in the height of the plant and its diameter.

Sanayal and Dutta (1961), observed high values of total correlation coefficients between fibre yield and green weight in *H. sabdarifa.*

2.2 CORRELATION BETWEEN YIELD AND YIELD CONTRIBUTING CHARACTERS

Association of commercially important quantitative characters that are statistically determined by correlation coefficient has been quite helpful as a basis of selection. Selection pressure can be more easily exerted on any of the characters which reflect close association with yield. In the investigation a number of morphological characters of the plant in different genotypes of *C. olitorius* were studied with a view to find out suitable basis for selection that are likely to be correlated with the yield of fibre.

In an investigation regarding genotypic and phenotypic correlation of 18 released varieties of tossa jute (*C. olitorius*) several contributing characteristics such as plant height, node number, basal diameter, stick weight, fibre fineness and fibre percentages had significant and positive correlation with fibre weight. Only character fibre strength exhibit negative correlation had been studied by Arpita and Kumar (2016).

Denton and Nwangburuka (2011), reported significant genetic variation**s** in six yield related characters in eighteen accessions in *Solanumanguivi*. shows the mean, standard error, phenotypic, genotypic and environmental variances, Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of

Variability (GCV), heritability in the broad-sense and genetic advance observed in the characters studied in the fifteen accessions of *Corchoru solitorius*. Generally, the value of PCV was slightly higher than the GCV value in all the traits except for stem weight per plant. This may suggest slight environmental effect on the phenotype of all the other characters except stem weight per plant.

Islam and Ahmed (2003), reported fibre weight showed significant positive association with all the characters at both phenotypic and genotypic levels. Genotypic correlations were higher than their corresponding phenotypic correlation coefficients in all the characters.

Biswanath *et al.* (2002); reported that spacing at 20 cm and broadcast at 1.2 kg/ha resulted in high dry matter accumulation, crop growth rate and relative growth rate. Spacing at 20 cm, broadcast at 1.2 kg/ha and harvesting at 120 DAS resulted in higher fibre yield compared to the other treatments. Breadth of leaf or multiple of length and breadth can be successfully used to estimate the leaf area in situ in tossa jute irrespective of cultivars.

Gayen and Roy (2001), in an experiment with six cultivars of white jute (c. *capsularis* L.) observed that correlation coefficients of leaf area with length, breadth, multiple of length and breadth and dry weight of leaves were highly significant and positive in each cultivar and over all cultivars.

Guha and Das (1997), reported that seed yield was affected and decreased by delay in planting, but not affected by plant spacing.Manjunatha and Sheriff (1991) observed high genotypic and phenotypic coefficients of variation were observed for dry fibre yield, green weight and stick weight.Sardana*et al.* (1990); observed that plant height, basal diameter and node number had highly significant and positive correlation with dry fibre yield per plant.

Banerjee *et al*. (1988); selfed seed of 20 genotypes of *Hibiscus sabdarifa* and assessed for 10 characters related to fibre yield. Fibre yield was significantly and positively correlated with plant height, green weight, base diameter and stick weight.

Ghosdastidar and Bhaduri (1983), observed strong positive genetic association of plant height and basal diameter with fibre yield, but poor correlation was observed between the node number and other components in *capsularis* jute.

Srivastava *et al*. (1979); found in *capsularis* jute that the correlation coefficient was non significant and negative between yield and plant height but positive between yield and node number. It was close to unity between yield and basal diameter.

Gupta and Das (1977); measured five characters associated with yield in nine varieties of *C. capsularis*. He reported that fibre yield was significantly correlated with plant height in all varieties and with basal diameters in most varieties.

Maiti and Chakravarti (1977), studied yield components of common Indian bastfibres. Analysis on correlation coefficients revealed that fibre yield was highly positive correlated with plant height and basal diameter.

Das (1968), found positive correlation coefficients and indicated that fibre yield in jute was directly correlated with basal diameter while plant height was not a dependable indicator of fibre yield performance.

Roy (1965), found high positive correlation between basal diameter and fibre yield (0.929) and followed by plant height and fibre yield (0.889). Hence taller and thicker the plant the higher is its yield.

Arangzeb and Biswas (1964), studied the UFC (ultimate fibre cell) length in different varieties of *C. capsularis* L. They reported that the length of UFC was higher towards the top position of the Plant.

2.3 PATH COEFFICIENT ANALYSIS

Path analysis is used to describe the directed dependencies among a set of variables. To find out the direct and indirect causes of association Path analysis helps. Path coefficient analysis is a standardized partial regression coefficient analysis and as such measures the direct influence of one variable upon other and allows the partitioning of correlation coefficient into direct and indirect effects of component characters. So it is used to analysis the real contribution of individual complex characters in yield.

Path coefficient analysis has widely been used by the animal breeders to understand the cause and effect relationship of important characters. However, it has been used in crop plant to analyze the real contribution of individual complex characters in yield.

Satyanarayana *et al.* (2017); an experiment was conducted to study the correlation coefficient and path coefficient based on quantitative traits among 60 genotypes of roselle (Hibiscus sabdariffa L.). Partitioning of phenotypic correlation coefficients of various components upon seed yield plant-1 into direct and indirect contributions revealed that pods plant-1 bas maximum direct effect followed by seeds pod-1 and test weight. Selection for characters viz., pods plant-1, seeds pod-1, test weight, plant height and base diameter along with seed yield will be useful for improving seed yield in Roselle.

Pervin *et al*. (2012); a study has been conducted on 11 genotypes of jute based on Path coefficient analysis revealed maximum contribution of plant height to fiber yield per plant and this was followed by the contribution of base diameter.

Al-mamun *et al*. (2010); a study has been conducted based on 18 genotypes of white jute from different geographic origin with a view to find out the path analysis revealed maximum direct contribution towards yield through stick weight followed by nodes per plant and plant height.

Akter *et al*. (2005); highest direct effect was obtained for fresh weight without leaves on fibre yield in jute. Khatun and Sobhan (1992), revealed that plant height and bark weight exerted the greatest influence both directly and indirectly upon fibre yield of tossa jute.

Thirthamallappa and Sheriff (1991), reported that plant height had maximum direct effect on fibre yield in jute.Sardana*et al*. (1990); reported that plant height had the maximum direct effect on fibre yield followed by basal diameter in jute germplasm analysis. Moderate indirect effect was observed only in case of node number through plant height. The effect was negligible.

Alamgir and Seal (1989), reached to the conclusion that jute plant with maximum stem circumference produced maximum fibre. Banerjee *et al*. (1988); studied path coefficient analysis in *Hibiscus sabdariffa* and revealed that the highest direct vehicles for fibre yield were basal diameter, green weight and plant height in the order. Top diameter, node number and stick weight indicated negative direct effects. The indirect contribution to fibre yield of base diameter, node number and stick weight were through green weight.

Chaudhury *et al*. (1981); showed that the indirect effect via green weight which was positive and high, while time of flowering and plant height was negative. Mandal *et al*. (1980); observed plant height; stem diameter and stem node number had direct positive effects with the effects of plant height being greatest on fibre yield.

Biswas (1984), reported that node number and inter nodal length had negative direct effect on yield. Ghoshdastidar and Das (1984), reported that plant height and base diameter had high positive effect on fibre yield.

Sasmal and Chakraborty (1978), reported that the magnitude of genotypic correlation was much higher than the phenotypic correlation in mesta, showing the influence of environment in reducing the actual inherent association between various characters. They further observed that the number of nodes has high degree of relationship with fibre weight.

Singhamahapatra and Raksit (1977), have reported that fibre yield for plant was genotypically and phenotypically correlated with plant height, basal diameter, node number and intermodal length in tossa jute.

Sasmol and Chakraborty (1977), stated that stripped green weight, wood weight and fibre weight had genotypic and phenotypic coefficients of variability of about 30%, while for days to flowering, plant height and basal diameter these were 10%.Meiti *et al*. (1975); observed that stem diameter is significantly correlated with number of nodes in both *capsularis* and *olitorius* of Corchorus.

Sukla*et al*. (1967); reported that green weight contributed maximum degree of positive direct effects towards fibre yield followed by plant height and time of flowering.

Roy (1965), found negative association between plant height and fibre; wood ratio and fibre yield in jute. Gosh and Patel (1945), observed in a population of *capsularis* that plant height and basal diameter are strongly but positively correlated.

2.4 GENETIC DIVERSITY

Information on genetic divergence among the parental materials is vital to plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute to desirable segregants and or to produce high heterotic crosses. More diverse the parents the greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generation (Murty and Anand, 1966). The parents identified on the basis of divergence analysis would be more promising. In both cross and self pollinated crops genetic diversity is one of the most important tools to quantify genetic variability. Evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm (Tomooka, 1991).

Regarding genetic diversity an experiment has been studied on 18 released varieties of tossa jute(*C. olitorius* L.)by Arpita and Kumar, (2016); and reported that all the varieties irrespective of their origin were grouped into 5 different clusters. The clustering pattern revealed meager amount of genetic diversity between the varieties studied in tossa jute. Inter-cluster distance was maximum between I and IV. Fibre fineness, fibre %, stick weight and basal diameter were the potent characters that influence the genetic diversity.

The genetic divergences among 51 white jute (*C. capsularis* L.) genotypes were studied by Jahangir (2009) who grouped the genotypes into six different clusters according to principal component analysis (PCA) and D^2 statistics. The PCA indicated that branches per plant, leaf width, petiole length, dry fibre weight, plant technical height, base diameter and number of nodes were the important components of genetic divergence in the population. He concluded that there was no parallelism between genetic diversity and geographical distribution of genotypes.

Akter (2009), studied genetic divergence of 29 indigenous and exotic *C. olitorius* L. genotypes based on D^2 analysis and showed that the genotypes were grouped into five clusters. She also showed that geographic distribution or origin did not strictly confirm to the genetic diversity.

Sandip *et al*. (2005); studied with 15 tossa jute (*C. olitorius* L.) cultivars for 13 morpho-economic characters and obtained the highest cluster distance between cluster I and IV suggesting wide diversity among the four cluster groups. Cluster IV had the highest mean values for plant height, base diameter, nodes/plant, fresh plant weight, stick and fibre yield/ plant. Cluster I showed the highest total chlorophyll, and chlorophyll „a" and „b" contents. Cluster II showed the highest number of capsules (pods)/plant, seeds/pod and seed yield/ plant. Cluster III showed the maximum leaf area.

The genetic divergence in 26 genotypes of vegetable mesta was assessed by Shobha and Dharmatti (2004), using Mahalanobis D^2 statistics. These varieties were grouped into five clusters based on D^2 values. Leaf area had the maximum contribution to genetic diversity followed by total green yield, plant height, number of leaves, fresh weight of leaves, petiole length and fresh weight of stem/plant. Cluster I was the largest, consisting of 22 genotypes, while cluster II, III and IV had solitary ones. The average inter-cluster D^2 values ranged from 59.15 (cluster I to IV) to 81.62 (cluster IV to V). Cluster IV (HS-1) and cluster V (GKK), with one genotype each, were diverse from the rest of the clusters as evident from their high inter-cluster D^2 values (81.62). Based on cluster mean analysis, it was revealed that genotypes GKK and HS-1 were the most divergent and they can be used in future breeding programs.

Cheng *et al*. (2002); found that the characters, such as middle stem diameter, whole stalk weight, and days to 50% flowering vary significantly among kenaf varieties. Morphological differences in characters such as seed character, leaf shape, stem colour, and plant maturity were small. Most of the kenaf accessions

tested had red green stems, yellow flowers and large seeds, entire or palmate leaves, and four maturity types were observed.

Hussain *et al*. (1999); reported that the clustering pattern of 30 parents along with their 78 hybrids of *C. olitorius* L. showed no parallel relationship between genetic diversity and geographical origin. Relationship between divergence of the parents and hybrids indicated the medium divergence class provided the optimum level of parental divergence to obtain economic heterosis in F_1.

Islam (1996), conducted a field experiment to assess the genetic divergence by using Mahalanobis D^2 statistics among 38 tossa jute (*C. olitorius* L.) genotypes for ten different characters. All the genotypes were grouped into five clusters. The highest inter-cluster distance was observed between cluster II and IV, and the lowest between cluster I and III. The intra-cluster distance was the highest in cluster IV and the lowest in cluster V. The pattern of distribution of genotypes within various clusters was independent for geographical distribution. Based on the mean performance, genetic distance and clustering pattern, 13 genotypes were selected as better parents for future hybridization program.

Shreshtha (1991), used 26 genotypes of jute (*C. capsularis* L.) and found seven clusters with low intra- but higher inter- cluster distance, which indicated the presence of possible genetic divergence in the population. The clustering pattern revealed that the nature of selection forces operating under one eco-geographical region was similar to that of other regions, since genotypes from distinct centers were group together. Genotypes from one eco-geographical region and also belonging to different pigmentation grade were grouped into different clusters. It indicated the presence of substantial variability within them. It is also evident that there was no parallelism between genetic diversity and geographical distribution of genotypes.

Devi *et al.* (1991); studied genetic divergence in 51 kenaf genotypes of different eco-geographic origins by D^2 analysis of data on nine quantitative traits and found 8 clusters. They concluded that geographical isolation was not the only factor causing genetic diversity. Days to 50% flowering contributed most to total divergence (72.7%) followed by fibre length and plant height. Tall genotypes with high fibre yield length were included in cluster VI (MT 102 and AC 80-5) and VII (Pure green), while cluster III (AC 80-9, AC 81-3 and AMC15) contained dwarf, early maturing types. Crossing of genotypes from these 3 groups offers the potential for producing tall hybrids with high yield, greater fibre length and short duration.

Malik *et al*. (1985); studied the genetic divergence in mungbean found days to flowering, seed yield and plant height contributed maximum towards divergence. An investigation was carried out by Singh *et al*. (1976); utilizing D^2 analysis and reported that pod length, days to flowering and seed yield contributed maximum towards divergence in green gram.

In black gram, Sagar *et al.* (1976); studied the genetic diversity through Mahalonobis‟s D^2 and revealed that days to flowering, plant height, 100 seed weight and pod length contributed maximum towards diversity.

Sasmal and Chakraborty (1978), indicated that in wheat, potent factor like the diverse agro-ecological conditions in the areas of their adaptation, varied from agronomic practices adopted by man for the end product, could cause a substantial genetic divergence. It can be concluded that genetic drift and selection in different environment could cause greater diversity than geographical distance.

2.5 HERITABILITY AND GENETIC ADVANCE

Heritability is the amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences. In a general sense heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a character or trait in a population. So the estimation of heritability is of great interest to the plant breeders. A quantitative character having high heritability is transmitted from parents to offspring conveniently. Heritability value alone provides the indication of the amount of genetic progress that would result from selecting the best individual. Heritability and genetic advance have also been worked out for different quantitative characters in *Corchorus olitorius*.

Alam (2009), the high heritability values with moderate genetic advance in percentage of mean were obtained for leaf width, petiole length, nodes per plant.Analyzing the information about heritability of the characters, it is observed that yield and different yield contributing characters of jute had shown low, moderate and high heritability values. The difference of the heritability value for some characters of jute had shown low, moderate and high heritability values. The difference of the heritability value for some characters among the different authors as observed was due to differences in the genetic makeup of their populations as well as the environmental influence where they conducted the study.

Islam and Ahmad (2003), studied heritability in jute genotypes and revealed high heritability and genetic advance for stick weight and fibre weight. Plant height had heritability with moderate genetic advance and green weight had moderate heritability with high genetic advance. According to Ahmed *et al.* (1993); the highest genetic advance (35.5%) coupled with the highest heritability (52.9%) was observed for fibre yield.

Sardana *et al.* (1990); studied genetic parameters in jute. Plant height, basal diameter and dry fibre weight had high broad sense heritability estimate coupled with a moderate high genetic advance indicating the success of direct selection. Node number was found to have low heritability and genetic advance.

Ghoshdastidar and Das (1984), observed very high heritability (82.43%) and high genetic advance as percent of mean (39.09) for plant height but node number and base diameter showed low heritability (63.93% and 39.71%) and low genetic advances as percent of mean (20.68 and 15.25). Fibre yield also showed low heritability (53.93%) but high genetic advances as percent of mean (44.95).

Joseph (1974), studied genetic parameters in segregating population of C. capsularis and noted that green weight and fibre weight had higher genetic variability than plant height, basal diameter and node number.

Singh (1970), observed maximum heritability values for plant height (86.75%) followed by basal diameter (82.46%) and stick weight (68.04%). The highest genetic advance was observed in case of fibre weight (22.81%) followed by stick weight (19.31%), basal diameter (11.72%) and plant height (8.20%). Rahman (1968), observed only 25 percent heritability for fibre yield in jute.

Robinson (1966), have been categorized the heritability values into low (below 10%) moderate (10-30) and high (above 30%).Characteristics that possess high heritability can be improved directly through selection as they are less affected by environmental criteria and subsequently the magnitude of heritability indicates the effectiveness of selection based on phenotypic performance.

Nei (1960), reported maximum heritability estimates for the characters of days to flowering, plant height, fibre weight, basal diameter and internodal length.

According to Jhonson *et al*. (1955); heritability along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimate alone.

Robinson *et al*. (1949); defined heritability as the additive variance in percent of total variance in narrow sense.

CHAPTER III

MATERIALS AND METHODS

The experiment was carried out at the Jute Agriculture Experimentat Station, Jagir, Manikganj, Bangladesh Jute Research Institute (BJRI) during the period from April to August, 2017.

3.1 Experimental Site

The experimental site was situated at 23^0 53.95‟ N latitude and $90^0$04‟E longitude with an elevation of 8.8 m from the sea level (Appendix-I).

3.2 Climate and Soil

The experimental site was situated in the tropical climate zone, characterized by heavy rainfall during the month from May to September and scantly rainfall during rest of the year. Mean monthly temperature and rainfall for the growing season are presented in Appendices II.

The soil of the experimental field was sandy loam in texture having pH around 6.5 to 7.5. It belongs to the young Brahmaputra and Jamuna Floodplain Agro Ecological Zone (AEZ No 8). The land was medium high with uniform topography and almost homogenous with respect to soil fertilizer

3.3 Experimental Material

The material comprised of 21 genotypes of tossa jute (***C.****olitorius* L.) including two improved varieties, O-9897 and O-72. The genetically pure and physically healthy seeds of these genotypes were collected from the gene bank of Bangladesh Jute Research Institute (BJRI), Dhaka. Accession number and origin of the genotypes are shown in Table 1.

3.5 Design and layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each plot had a single row of 3.0 m length. Space between rows was 0.30 m and block to block distance was 1.0 m. The genotypes were randomly distributed to each row with in each block.

3.6 Land preparation

The experimental plot was prepared by deep plough followed by harrowing and laddering. The recommended doses of fertilizer such as 166 kg/ha of Urea, 25 kg/ha of TSP and 30 kg/ha MP. The whole amount of TSP, MP and half of the Urea were applied during final land preparation. The remaining half of the Urea was top dressed after 45 days of sowing.

3.7 Sowing and intercultural operation

Seeds were sown on 2nd April, 2017. Thinning and weeding were done twice after 15 and 45 days of sowing to maintain uniform plant population. Insecticide (komolas, mancojeb group) was applied for controlling mites. Hand picking was practiced to control the hairy caterpillar at larval and pupal stage.

Table 1. Accession number, origin and sources of the selected genotypes oftossajute (*C. olitorius*L.)

Genotype No.	Genotypes	Origin	Sources
G1	BJRI Tossa Pat-4	Bangladesh	Breeding division, BJRI
G2	A-1282	Bangladesh	Gene Bank, BJRI
G3	A-1283	Bangladesh	Gene Bank, BJRI
G4	A-1285	Bangladesh	Gene Bank, BJRI
G5	A-1331	Japan	Gene Bank, BJRI
G6	A-1335	Japan	Gene Bank, BJRI
G7	A-1337	Egypt	Gene Bank, BJRI
G8	A-1338	Philippine	Gene Bank, BJRI
G9	A-1341	India	Gene Bank, BJRI
G10	A-1344	India	Gene Bank, BJRI
G11	A-1345	India	Gene Bank, BJRI
G12	A-1346	India	Gene Bank, BJRI
G13	A-1349	Mozambique	Gene Bank, BJRI
G14	A-4568	Bangladesh	Gene Bank, BJRI
G15	A-4569	Nepal	Gene Bank, BJRI
G16	A-4570	Nepal	Gene Bank, BJRI
G17	A-4738	China	Gene Bank, BJRI
G18	A-4739	China	Gene Bank, BJRI
G19	A-4740	China	Gene Bank, BJRI
G20	A-5001	China	Gene Bank, BJRI
G21	O-9897	Bangladesh	Breeding division, BJRI

Plate 1: A partial view of preparing field experiment

Plate 2: A top view of tossa jute genotypes

Plate 3: A side view of tossa jute genotypes

Plate 4: A close view of tossa jute stem color with different stature

Plate 5: Field visit at the time of harvesting

Plate 6: Preparing of samples for data collection

Plate 7: Data collection of different tossa jute genotypes

Plate 8: Defoliating of jute Plant before retting

Plate 9: Retting of jute genotypes in the retting tank

Plate 10: Jutefibre are drying under the sun shine

3.8 Collection of data

The following data were recorded on 5 randomly selected plants from each row of each genotype.

3.8.1 Plant height (m):

It was measured from the base of the plant to the tip of the main shoot in meter.

3.8.2 Base diameter (mm):

Base diameter was measured at the base of the stem in mm using slide caliper.

3.8.3 Core diameter (mm):

Core diameter was measured at the base of the stem by removing the bark in mm using slide caliper.

3.8.4 Nodes per plant:

Total number of nodes per plant were counted and expressed in number.

3.8.5 Leaf length (cm):

The length of leaf was measured in cm.

3.8.6 Leaf width (cm):

The width of leaf was measured in cm.

3.8.7 Leaf angle (dg):

The leaf angle was measured in dg.

3.8.8 Petiole length (cm):

The length of petiole was measured in cm.

3.8.9 Green weight (g):

Fresh weight of the plant with branches and without leaves was recorded.

3.8.10 Fibre weight (g):

Weight of sun dried fibre per plant after retting, extraction and drying was measured in gram.

3.8.11 Dry stick weight (g):

Weight of sun-dried stick per plant was measured in gram after extraction of fibre.

3.9 Statistical Analysis

Mean values for each characters in each plot was used for statistical analysis.

3.9.1 Genetic diversity Analysis

3.9.1.1 Principal Component Analysis (PCA)

It is one of the multivariate techniques, is used to know the interrelationship among several characters and can be done from the sum of squares and products matrix for the characters. Therefore, principal components were computed from the correlation matrix and genotype scores obtained from the first component (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity .Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.9.1.2 Principal Coordinate Analysis (PCoA)

Principal Coordinate Analysis is equivalent to Principal Component Analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of p, it gives the minimum distance between each pair of the n points using similarly matrix (Digby *et al*., 1989).

3.9.1.3 Clustering

Clustering by D^2 statistics is useful to identify the diverse genotypes for hybridization purposes. It was done by using Mahalanobis‟s D^2 statistics. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improved the value of criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swapping two genotypes of different classes and so on.

3.9.1.4 Canonical Vector Analysis (CVA)

By this method vectors or canonical roots are calculated to represent the varieties in the graphical form. Using canonical vector analysis a linear combination of original variability‟s that maximize the ratio in between group to within group variation to be found out and thereby giving functions of the original variability‟s that can be used to discriminate between groups. Therefore, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of the among groups to within group variations. The canonical varieties are based on the roots and vectors of W-IB, where W is the pooled within group covariance matrix and B is the among groups covariance matrix.

3.9.1.5 Computation of Average Intra-cluster Distances

The average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the Principal Coordinate Analysis (PCO) after the clusters were formed. The formula used was $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations and n is the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.9.1.6 Cluster Diagram

Cluster Diagram was drawn using the D^2 values between and within cluster i.e. the intra and inter-cluster distances. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.9.1.7 Computation of Average Inter-Cluster Distances

The procedure of calculating inter-cluster distance was first to measure the distance between cluster I and II, between I and III, between I and IV, between I and V, between I and VI, between II and III, between II and IV, between II and V, between II and VI and so on. The clusters were taken one by one and their distances from other clusters were calculated.

3.9.2.1 Analysis of variance

Analysis of variance for each character was computed following Pansi (1957).

The total variability was partitioned into treatments (genotypes), blocks (replications) and error components.

The analysis of variance for each character was carried out under the model Error component

Ho:ti=0

Yij= μ+ti+bj+eij

Where,

μ = over all mean

ti= ith treatment effect bj= jth replication effect

eij= random

3.9.2.2 Procedure of analysis

Analysis of variance was determined by the following procedures

$$\text{Correction factor (CF)} = \frac{(\text{Grand total})^2}{\text{Number of observations (N)}}$$

Source of variation	df	MS	SMS	F- ratio
Replication	r-1	MSr		
Varieties	v-1	MSv	$\sigma^2 e + r\sigma^2 g$	MSv/ MSe
Error	(V-1)(r-1)	MSe		

Where,

r= Number of replications

v= Number of varieties

MSr, MSv and Mse strand for mean squares due to replication, varieties and error respectively.

$\sigma^2 e$ = Environmental variance

$\sigma^2 g$ = Genotypic variance

Total sum of square (TSS) = Sum of square of individual observation – CF

$$\text{Variety sum of square (VSS)} = \frac{\text{Sum of square of varietal total}}{\text{No. of replications}} - \text{CF}$$

$$\text{Replication sum of square (RSS)} = \frac{\text{Sum of square of replication total}}{\text{No. of varieties}} - \text{CF}$$

Error sum of square (ESS) = TSS- (VSS+ RSS)

Mean sum of squares were obtained as:

$$\text{Varieties MS} = \frac{\text{Varieties sum of square}}{\text{Degree of freedom for varieties}}$$

$$\text{Error MS} = \frac{\text{Error sum of square}}{\text{Degree of freedom for varieties}}$$

$$\text{Replication MS} = \frac{\text{Replication sum of square}}{\text{Replication degree of freedom}}$$

$$\text{F-ratio} = \frac{\text{Mean sum of square for varieties}}{\text{Mean sum of square for error}}$$

If the F-ratio was significant critical difference (CD) was calculated in order to find out the superiority of one variety over other by the formula:

$$\text{Standard error of mean} = \sqrt{\frac{\text{Variance due to error}}{\text{No. of replication}}}$$

$$\text{SE (m)} = \sqrt{\frac{\sigma^2 e}{R}}$$

3.9.2.3 Critical differences (CD)

In order to compare any two treatment means, the CD was calculated as:

Critical differences (CD) = SE (m) x √2x„t‟ at error d.f. And 5% level of significance.

3.9.2.4 Parameters of variability Mean

Mean was determined by diving the total by corresponding number of observations

$$\bar{x} = \frac{\sum Xi}{N}$$

Where,

$\sum Xi$ = Summation of all observations

N= Number of observations

$\bar{x}$ = Mean

Range

It is the difference of the lowest and highest values of the observations.

Genotypic variance

The genotypic variances **(**σ^2 g) were derived by subtracting error MS from the genotypic MS and dividing by the number of replications as shown below:

Genotypic variance (σ^2 g) = (GMS-EMS)/r

Where,

GMS= the genotypic mean square

EMS= the error mean square

r= the number of replications.

Phenotypic variance

The phenotypic variances (σ^2 p) were derived by adding genotypic variances (σ^2 g) with error variances (σ^2 e) as given by the following formula:

Phenotypic variance (σ^2 p) = σ^2 g + σ^2 e

Where,

σ^2g = The genotypic variance

σ^2e= The error variance

3.9.2.5 Estimation of genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation was calculated by Burton (1952) as,

Genotypic coefficient of variation (GCV) =(σ_g / $\bar{x}$) x 100

Where,

σ_g = Genotypic standard deviation

$\bar{x}$ = Population mean.

Similarly, the phenotypic coefficient of variation was calculated from the following formula:

Phenotypic coefficient of variation (PCV) = (σ_p/ $\bar{x}$) x 100

Where,

σ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

3.9.2.6 Estimation of heritability

Broad sense heritability was estimated define by Lush(1943) by the formula suggested by Hanson *et al*. (1956) and Johnson *et al.* (1955).

Heritability (H_b) = (σ^2_g/σ^2_p) x 100

Where,

(H_b)=Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.9.2.7 Estimation of genetic advance in percentage of mean (GA%mean)

The expected genetic advance for different characters under selection was using the formula suggested Johnson*et al.* (1955).

Genetic Advance (GA) = $(\sigma 2g / \sigma^2_p) \times K x \sigma_p$

Where,

K = Selection differential, the value of which selection intensity

σ_p = Phenotypic standard deviation

3.9.2.8 Estimation of genetic advance in percentage of mean (GA%mean)

Genetic advance as percentage of mean was calculated from the formula by Comstock and Robinson (1952).

GA% = (Genetic advance/ Pop^n mean) x 100

3.9.2.9 Estimation of genotypic and phenotypic correlation of coefficient

For calculating the genotypic and phenotypic correlation coefficient for all possibleCombinations the formula suggested by Miller *et al.*(1958), Johnson *et al*.(1955) andHanson *et al* (1956) were adopted.

The genotypic covariance component between two traits and have the phenotypic covariance components. The covariance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation}(r_{gxy}) = \frac{\Sigma gxy}{\sqrt{(\sigma^2_{gx} . \sigma^2_{gy})}}$$

Where,

σgxy = Genotypic covariance between the traits x and y $\sigma^2 gx$ = Genotypic variance of the trait x $\sigma^2 gy$ = Genotypic variance of the trait y

$$\text{Penotypic correlation}(r_{pxy}) = \frac{\sigma gxy}{\sqrt{(\sigma 2_{px} . \sigma^2_{py})}}$$

Where,

σpxy = Phenotypic covariance between the traits x and y

σ^2px = Phenotypic variance of the trait x σ^2py =

Phenotypic variance of the trait

3.9.2.10 Estimation of path coefficient

Correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959) using the following simultaneous equation:

$$r_{15} = p_{15} + r_{12}p_{25} + r_{13}p_{35} + r_{14}p_{45}$$

$$r_{25} = r_{12}p_{15} + p_{25} + r_{23}p_{35} + r_{24}p_{45}$$

$$r_{35} = r_{13}p_{15} + r_{23}p_{25} + p_{35} + r_{34}p_{45}$$

$$r_{45} = r_{14}p_{15} + r_{24}p_{25} + r_{24}p_{35} + p_{45}$$

Where,

r_{12}, r_{13}, r_{14} etc. are the estimates of simple correlation coefficients between variable x_1 and x_2, x_1 and x_3, x_1 and x_4 etc. respectively and p_{15}, p_{25}, p_{35} and p_{45} are the estimate of direct effects of variables x_1, x_2,x_3 and x_4 respectively on the dependent variable x_5 (effect).

$$\text{Residual effect, } P^2R_5 = \sqrt{\{1 - (p15r15 + p25r25 + p35r35 + p35\ r45)\}}$$

Path coefficient was estimated for 10 characters related to fibre yield viz. plant height, base diameter, nodes per plant, green weight, leaf angle, leaf length, petiole length, branches, stick weight and fibre weight.

CHAPTER IV

RESULTS AND DISCUSSION

This portion comprises the presentation and discussion of the findings obtained from the study. The data pertaining to different characters such as Plant height (m), Nodes/plant, Base diameter (mm), Core diameter (mm), leaf angle (dg), leaf length (cm), Leaf width (cm), Petiole length (cm), Green weight (gm), Stick weight (gm) and fibre weight per plant (gm). The datawere computed and statistically analyzed and the results thus obtained were presented and discussed below step by step.

4.1 Analysis of variance and genetic parameters among 21 genotypes of tossa jute

Genetic variability among the traits is important for breeding and in selection of expected types. The existing variability in a population can be evaluated into genetic parameters such as coefficient of variation of genotypic and phenotypic, heritability and genetic advance to serve as basis for selection of desirable ones in further research work. The genotypes differed significantly for all the characters (Appendix II). The extent of variation among the genotypes in respect of 11 characters was studied and plant height (m), nodes/plant, base diameter (mm), core diameter (mm), leaf angle (dg), leaf length (cm), leaf width (cm), petiole length (cm), green weight (gm), stick weight (gm) and fibre weight per plant (gm) have been presented in Table 2. Variance of the genotypes, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), heritability and genetic advance have been presented in Table-3.

4.1.1 Plant height

Significant differences were observed among the genotypes for plant height. The highest plant height was observed in G11 (3.64m) followed by G21 (3.55m), G15 (3.41m) and G18 (3.36m) (Table 2). The lowest Plant height was observed G16

(2.62m) followed by G14 (2.82m),G17 (2.87m) and G1 (2.98m). Similar results were also revealed the same variation by Sawarkar *et al.*, (2014).

The phenotypic coefficient of variation (PCV) (13.14) and the genotypic coefficient of variation (GCV) (10.90) were indicated presence of considerable variability among the genotypes for this traits (Table 3).

The high heritability (68.82) together with considerable genetic advance (18.63%) indicated the effectiveness for selection of this character (Table 3). Similar results were observed by Chaudhury *et al.* (1984) in jute.

4.1.2 Nodes per plant

The variance due to node number showed that the genotypes differed significantly. The maximum node number was found at G5 (81.30) followed by G11 and G15 (80.73) and minimum was found atG16 (59.13) followed by G13 (59.37) (Table 2).The phenotypic coefficient of variation (16.00) and genotypic coefficient of variation (9.58) respectively in the (Table 3). The PCV and GCV indicated that less influenced by the environment. So the breeders should go for the high heritability for these traits to make improvement. Alam *et al*., (2016) found high difference between GCV and PCV for this trait but less difference found by Nayak*et* and Baisakh (2007). Moderate high heritability (35.84) with considerable genetic advance (11.82%) (Table 3), indicating that this trait might be taken into consideration while selecting a suitable line as suggested by Johnson *et al*. (1955). Similar results were found in Ghosdastidar and Das (1984).

Table 2. Mean performance of different characters of twenty one different genotypes of tossa jute (*C. olitorius*)

Genotype	PH	NN	BD	CD	LA	LL	LW	PL	GW	FW	SW
G1	2.98	71.1	13.89	10.45	30	12.82	6.5	5.65	146.75	10.4	24.3
G2	3.04	68.7	12.87	9.95	28.3	16.39	5.93	5.76	121.5	8.2	21.3
G3	3.06	68.5	13.83	11.05	30	15.53	6.04	5.58	176.00	10.5	27.27
G4	3.09	68.9	13.46	10.17	30	16.39	6.35	6.56	144.27	10.6	27.57
G5	3.06	81.30	13.37	10.89	30	16.32	6.68	7.33	167.97	10.8	27.5
G6	3.25	70	13.4	10.9	28.33	15.95	6.02	5.96	180.9	11.47	29.4
G7	3.29	66.33	15.47	12.37	30	16.08	5.79	5.72	220.23	13.57	36.03
G8	3.16	68	12.12	10.03	28.33	16.11	6.61	6.19	153.47	9.8	27.77
G9	3.11	66.5	13.01	10.57	28.33	15.31	6.28	6.39	177.57	11.77	28.47
G10	3.09	72.1	12.64	10.94	26.67	16.39	6.07	5.94	160.87	10.6	25.8
G11	3.64	80.73	15.98	12.71	28.33	15.95	6.17	6.4	201.33	15.17	34.47
G12	3.17	70.67	13.73	11.24	30	15.29	5.94	6.05	180.56	11.47	27.67
G13	2.98	59.37	12.25	9.42	30	15.11	5.69	6.16	125.2	8.367	20.23
G14	2.82	61.67	11.04	8.76	26.67	15.44	6.14	6.72	107.53	8.27	19.37
G15	3.41	80.73	14.63	12.35	28.33	16.15	6.19	6.13	195.33	15.23	37.43
G16	2.62	59.13	11.23	8.46	26.67	15.33	6.06	6.35	184.73	9.43	21.63
G17	2.87	67.03	11.83	9.68	30	14.89	6.15	6.25	177.83	9.77	22.97
G18	3.36	77.47	14.75	9.01	28.33	15.53	6.23	6.63	182.1	12.87	30.37
G19	3	77.03	11.92	9.54	28.33	16.28	6.3	6.97	137.9	11.2	29.1
G20	3.33	75.63	13.97	11.51	26.67	15.35	6.16	6.35	162.23	11.53	44.37
G21	3.55	73.87	17.5	13.82	30	15.71	6.03	5.71	168.73	17.63	36.73
Mean	3.14	70.70	13.47	10.66	28.73	15.63	6.16	6.23	165.38	11.36	28.56

PH= Plant height (m), NP= Nodes/plant, BD= Base diameter (mm), MD= Mid diameter (mm), TD= Top diameter (mm), Core diameter (mm), LA= Leaf angle (dg), LL= Leaf length (cm), LW= Leaf width (cm), PL= Petiole length (cm), GW= Green weight (gm), StW= Stick weight (gm) and FW= Fibre weight per plant (gm).

Table 3. Estimation of genetic parameters of eleven different characters of twenty one different genotypes (*C. olitorius* L.)

Characters	$\sigma^2 g$	$\sigma^2 p$	$\sigma^2 e$	GCV	PCV	ECV	$h^2 b$	GA in % Means (5%)
Plant height (m)	0.117	0.170	0.053	10.90	13.14	7.34	68.82	18.63
Number of nodesper plant	45.89	128.03	82.14	9.58	16.00	12.82	35.84	11.82
Base diameter (mm)	7.805	80.030	72.225	20.74	66.41	63.09	9.75	13.34
Core diameter (mm)	3.319	5.632	2.313	17.10	22.28	14.28	58.93	27.05
leaf angle (dg)	0.298	4.921	4.623	1.90	7.72	7.48	6.05	0.96
leaf length (cm)	0.663	1.837	1.174	5.20	8.67	6.93	36.09	6.44
Leaf width (cm)	0.052	0.236	0.184	1.46	3.11	2.74	22.03	1.41
Petiole length (cm)	0.115	0.754	0.639	5.44	13.94	12.83	15.25	4.38
Green weight (gm)	131.69	2382.23	2250.54	6.94	29.51	6.94	5.53	3.36
Stick weight (gm)	2.11	120.77	118.66	5.08	38.48	38.14	1.75	1.38
Fibre weight per plant (gm)	4.082	17.343	13.261	17.79	36.66	32.05	23.54	0.18

4.1.3 Base diameter

Analysis of variance showed significant differences among the genotypes for base diameter. The height base diameter was observed in G21 (17.50mm) followed by G11 (15.98mm) and G7 (15.47mm).The lowest base diameter was observed G14 (11.04mm) followed by G16(11.23mm),G17 (11.83mm)in Table-2.This trait showed higher differences of phenotypic coefficient of variation than corresponding genotypic coefficient of variation (Table-3). The higher differences of PCV and GCV suggest that the expression of character was mostly under the control of environment. With low (9.75) heritability and greater (13.34) genetic advance indicated selection for this character would be effective. The results of this experiment support the findings of Dahal (1991) who found higher PCV than the corresponding GCV value and heritability coupled with low genetic advance for basal diameter.

4.1.4 Core diameter

Core diameterranged from G16(8.46mm) to G21 (13.82mm) (Table-2). The phenotypic (5.632) and genotypic (3.319) variance were close to each other. A minimum difference between phenotypic coefficient of variation (22.28) and genotypic coefficient of variation (17.10) indicate less influence of environmental factors on expression of this character (Table-3).Therefore, selection based on upon phenotypic expression of this character would be effective for the improvement of this crop.

4.1.5 Leaf angle

Significant differences among the genotypes were observed for leaf angles per plant. Maximum leaf angle was 30 dg and minimum leaf angle was 26.67 dg and mean value was 28.724 dg (Table 2).The phenotypic coefficient of variation (7.72) and genotypic (1.90) coefficient of variation were not close to each other indicating environmental influence in case of leaf angle (Table- 3).

4.1.6 Leaf length

The mean value of leaf length showed significant differences among the genotypes. The lowest and highest leaf length was observed G1 (12.82cm) and G2, G4, G10 (16.39cm) respectively (Table 2). The phenotypic variance (1.837) is higher than genotypic variance (0.663). Heritability was low (36.09) and genetic advance as percentage of mean was low (6.44) (Table 3). With such low heritability and low genetic advance, selection on leaf length would not be judicious.

4.1.7 Leaf width

The highest leaf width was observed in G5 (6.68cm) followed by G8 (6.61cm) and G1 (6.50cm).The lowest leaf width was observed G13 (5.69cm) followed by G7 (5.79cm), G2(5.93cm). (Table2).Significant differences among the genotypes were observed from the analysis of variance for leaf width. The mean value for leaf width was 6.16cm (Table 2). The phenotypic variance (0.236) and genotypic variance (0.052) were close to each other indicating negligible environment influence on leaf width. Low heritability (22.03) with low genetic advance (1.41%) for this trait might not be taken into consideration (Table3) while selecting a suitable line as suggested by Johnson *et al*. (1955). Similar results were found in Ghosdastidar and Das (1984).

4.1.8 Petiole length

The mean values for petiole length showed significant differences among the genotypes. Highest petiole length was observed in G5 (7.33cm) followed by G19 (6.97cm), G14 (6.72cm) and G4 (6.56m) (Table 2). The lowest petiole length was observed G3 (5.58cm) followed by G1 (5.65cm), G7 (5.72cm) and G21 (5.71cm).The phenotypic variance (0.754) was much higher than genotypic variance (0.115). The heritability (15.25) was low with a low genetic advance (4.38%) (Table3). With such low heritability and low genetic advance, selection on petiole length not is judicious.

4.1.9 Green weight

Significant differences were observed among the genotypes in respect of green weight. Green weight ranged from 121.50 gm to 220.23 gm (Table-2). The estimates of phenotypic variance were very high (2382.23). Heritability (5.53%) and genetic advance were low (3.36) (Table3). Difference between phenotypic and genotypic coefficient of variation were more. However low heritability and low genetic advance indicate that this trait might not be taken into consideration while selecting a suitable one.

4.1.10 Stick weight

The highest stick weight was observed in G20 (44.37gm) followed by G15 (37.43gm), G21 (36.73gm) and G7 (36.03gm) (Table2). The Lowest stick weight was observed in G14 (19.37gm) followed by G13 (20.23gm), G2 (21.3gm) and G16 (21.63gm) (Table2). The phenotypic (120.77) and genotypic (2.11) variance were higher then to each other. A difference between phenotypic coefficient of variation (38.48) and genotypic coefficient of variation (5.08) (Table 3) indicate that selection can be applied on the traits to isolate more promising line. Alam *et al*.,(2016) found PCV was higher than GCV. Low heritability (1.75%) with low genetic advance (1.38%) in percent of mean the trait was governed by non-additive and epistatic genes action and selection for this trait might be ineffective due to environmental effect.

4.1.11 Fibre weight

The maximum dry fibre weight was observed in G21 (17.63) followed by G15 (15.23gm), G11 (15.17gm) and G7 (13.57gm) (Table-2). The genotypic coefficient of variation (17.79) and phenotypic coefficient of variation (36.66) were close to each other indicated that less influenced by the environment. The heritability (23.54) was higher as well as genetic advance in percentage of mean (0.18%) was observed lower (Table3). The higher heritability with low genetic advance as percentage of mean provided low opportunity for selecting high valued genotypes for breeding programs.

4.2 Correlation coefficient analysis

For the development of desirable charactersin breeding programs can be achieved by indirect selection with other characters. The estimates of correlation of yield with other characters genotypes could be assessed visually.Yield is a complex product being influenced several interdependent quantitative characters. So the Phenotypic and genotypic correlation coefficients between yield and yield attributing characters of 21 tossa jute (*C. olitorius* L.) genotypes presented in (Table 4).

4.2.1 Fibre weight vs. yield contributing characters

Fibre weight plays a significant and positive correlation at both the genotypic and phenotypic correlation coefficient among characters themselves has been presented in Table 4. Among inter character correlation highly significant positive association were observed with core diameter per plant (0.418and 0.521) followed by base diameter (0.249 and 0.346), plant height per plant (0.136 and 0.222), nodes number (0.111 and 0.180) and stick weight (0.005 and 0.042). Similar findings were also reported byChaudhury*et al.*,(1981),Singh (1970) and Sanyal and Dutta (1961). That‟s why;selection for any of these characters will indirectly help in selecting the genotypes for higher fibre yield.The combination which showed negative correlation coefficient was leaf area (-0.017) at phenotypic level but positive correlation coefficient genotypic level (0.095).

Table4. Genotypic(G) and Phenotypic(P) correlation coefficient among seven quantitative characters intossajute (*C. olitorius*).

Parameters		NP	BD (mm)	CD (mm)	LA (cm^2)	SW (gm)	FW (gm)
PH(m)	G	0.231	0.189	0.323	0.131	0.417	0.136
	P	0.369	0.221	0.327	-0.011*	0.430	0.222
NP	G		0.099*	0.099*	0.617	0.419	0.111
	P		0.094*	0.089*	0.026*	0.303	0.180
BD(mm)	G			0.148	-0.164	0.298	0.249
	P			0.192	-0.006**	0.394	0.346
CD (mm)	G				-0.026*	0.431	0.418
	P				0.011*	0.453	0.521
LA (cm^2)	G					0.416	0.095*
	P					-0.011*	-0.017*
SW (gm)	G						0.005**
	P						0.042*

* Significant at 5% level
** Significant at 1% level

Note: PH= Plant height, NP= Nodes/plant, BD= Base diametere, CD= Core diameter, LA= leaf area, SW= Stick weight and FW= fibre weight per plant.

4.2.2 Correlation coefficient among yield contributing characters

Plant height had a positive and highly significant at genotypic and phenotypic correlation with stick weight (0.417 and 0.430), core diameter per plant (0.323 and 0.327) and nodes per plant (0.231 and 0.369) level (Table 4).Base diameter (0.189 and 0.221) showed moderate positive association which are highly significant with plant height. Similar result was reported by Manjunatha and Sheriff (1991) in Kenaf. Leaf area (0.131) showed positive correlation at genotypic level but negative (-0.011) at phenotypic level. The genotypic value is greater than the phenotypic value indicating the higher genetically association of this traits having low environmental interaction.

Nodes per plant positive and highly significant correlation with leaf area (0.617 and 0.026), stick weight (0.419 and 0.303) and fibre weight (0.111and 0.180) atboth genotypic and phenotypic level (Table 4). Nodes per plant showed positive but moderately significant correlation with base diameter (0.099 and 0.094) and core diameter (0.099 and 0.089). Number of leaf area, stick weight, fibre weight, base diameter and core diameter will increase with the increase of nodes number per plant.

Base diameter had a positive and highly significant correlation with stick weight (0.298 and 0.394), fibre weight (0.249 and 0.346) and core diameter (0.148 and 0.192) at genotypic and phenotypic level (Table 4). Leaf area (-0.164 and -0.006) had a significant negative association with base diameter (Table 4). In this case higher leaf area can decrease base diameter per plant. Similar findings were reported by Banerjee *et al*. (1988).

Core diameter had a positive and highly significant correlation with stick weight (0.431 and 0.453) and fibre weight (0.418 and 0.521) at the genotypic and phenotypic level. Core diameter also had a negative and significant correlation with leaf area (-0.026) at genotypic level but positive and significant correlation at phenotypic (0.011) level (Table

4). It had proportional relationship with core diameter with stick weight and fibre weight. The phenotypic value then the genotypic value indicates strong relationship among the traits.

Leaf area (0.416) showed positive correlation at genotypic level but negative (-0.011) at phenotypic level. The genotypic value is greater than the phenotypic value indicating the higher genetically association of this traits having low environmental interaction.

The character of plant height, nodes number per plant, base diameter, core diameter and stick weight seems to be predominant consideration for fibre yield as they exhibited highly significant correlation with fibre weight among themselves. Therefore selection based on these characters may improvement of fibre yield in tossa jute.

4.3 Path coefficient

In order to find out a clear picture of the interrelationship between fibre yield and other yield components direct and indirect effects were worked out using path analysis. Fibre weight considered as a resultant (dependent) variable and plant height, nodes per plant, base diameter, core diameter and stick weight were independent variables. The association of characters for the seven casual variables with fibre weight related to genotypic path coefficient analysis has been presented in (Table 5).

4.3.1 Plant height

Plant height had positive direct effect on fibre weight (0.6709) at genotypic level and it had positive correlation with fibre weight. Plant height has contributed indirectly through base diameter (0.0668), core diameter (0.1552), leaf area (0.0614), stickweight (0.0485) and fibreweight (0.4174) at genotypic level (table5). The indirect negative effect may be nullified by positive indirect effect. Direct positive effect of plant height on fibre weight was reported by several authors (Mandal*et al*., 1980, Chaudhury*et al*., 1981).

4.3.2 Nodes per plant

Nodes per plant had positive direct effect on fibre weight (0.5461) at genotypic level and it was also positive correlation with fibre weight at both levels. The positive indirect effect of nodes per plant through plant height (0.0396),base diameter (0.0354), Core diameter (0.0477), leaf area (0.2898) and stick weight (0.4189) at genotypic level while negative indirect effect through stick weight (-0.0398)(table5). Similar results were reported by Dahal(1991).

4.3.3 Base diameter

Base diameter had positive direct effect on fibre weight (0.7345) at genotypic level and it was also positive correlation with fibre weight at both levels. The positive indirect effect of base diameter through plant height (0.0323), core diameter (0.0711), stick weight (0.0892) and fibre weight (0.2978). Indirect effects of base diameter through nodes per plant were negligible. Indirect negative effect was (-0.0771) by leaf area(table5).

4.3.4 Core diameter

The direct effect of Core diameter on fibre weight (0.4598) was positive at genotypic level. It had also positive correlation with fibre weight at both levels. The positiveindirect effect of core diameter through plant height (0.0556), base diameter (0.0528) and fibre weight (0.4313 at genotypic level. Indirect positive effect of core diameter through nodes per plant (0.0046) is negligible while negative indirect effect through leaf area (-0.0120) and stick weight (-0.1493).

Table 5. Partitioning of genotypic correlation coefficients into direct (bold faced) and indirect effects by path analysis

Parameters	PH	NP	BD	CD	LA	SW	Genotypic correlation with yield
PH	**0.6709**	-0.0016**	0.0668	0.1552	0.0614	0.0485*	0.4174
NP	0.0396*	**0.5461**	0.0354*	0.0477*	0.2898	-0.0398*	0.4189
BD	0.0323*	0.0045**	**0.7345**	0.0711	-0.0771	0.0892	0.2978
CD	0.0556	0.0046**	0.0528	**0.4598**	-0.0120*	-0.1493	0.4313
LA	0.0225*	0.0285*	-0.0584	-0.0123*	**0.7653**	-0.0339*	0.4158
SW	0.0233*	0.0051**	0.0887	0.2003	0.0446*	**0.7898**	0.0045**

R = .3109

* Significant at 5% level
** Significant at 1% level
Note: PH= Plant height (m), NP= Nodes/plant, BD= Base diameter (mm), CD= Core diameter (mm), LA= leaf area (cm^2), SW= Stick weight (gm) and FW= fibre weight per plant (gm).

4.3.5 Leaf area

The direct effect of leaf area on fibre weight (0.7653) was positive at genotypic level. It had also positive correlation with fibre weight at both levels (table5). The positive indirect effect of leaf area on fibre weight through plant height (0.0225), nodes per plant (0.0285) and fibre weight (0.4168) at genotypic level while negative indirect effect of leaf area on fibre yield through base diameter -0.0584), core diameter (-0.0123) and stick weight (-0.0339).

4.3.6 Stick weight

The direct effect of stick weight on fibre weight (0.7898) was positive at genotypic level.It had also positive correlation at both levels contributed indirectly through plant height (0.0233), base diameter (0.0887), core diameter (0.2003), and leaf area (0.0446). Other indirect effects were positive and negligible.

4.4 Genetic Diversity Analysis of TossaJuteGermplasm

4.4.1 Principal Component Analysis (PCA)

The principal component analysis gave Eigen values of each principal component axes of coordination of genotypes with the first axes totally accounting for the variation among the genotypes, whereas four of these Eigen values above unity accounted for 99.51% (Table 6). A two dimensional chart (Z_1-Z_2) of 21 tossa jute genotypes are presented in Appendix IV.

4.4.2 Principal Coordinate Analysis (PCoA)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter-genotypic distances obtained from principal component analysis showed that the highest distance (124.10) was observed between the genotypes G14 and G7 followed by G14 and G11 (117.852), G7 and G2 (111.95), G13 and G7 (109.020), G11 and G2 (106.89) and lowest distance (3.054) was observed between the genotypes G12 and G6 followed by G6 and G3 (6.412), G12 and G3 (6.423), G4 and G1 (6.587), G8 and G1 (9.246) (table 7). Inter cluster distances were calculated (table 7) from these inter-genotypic distances followed by Singh and Chaudhury (1985). The highest intra-cluster distance was observed in cluster II (78.799), which was composed of three genotypes followed by cluster IV (74.096) that was composed of five genotypes, cluster I (66.660) was composed of six genotypes, cluster V (43.492) was composed of two genotypes and the lowest intra-cluster distance was observed in cluster III (42.119) also composed of five genotypes in Table 8 and Table 10. These results revealed that the genotypes in cluster II were distantly related. On the other hand the genotypes in cluster III were closely related.

4.4.3 Clustering

Twenty one genotypes of tossa jute were grouped into five different clusters with the application of Mahalanobis‟s d^2 statistics (table8). Shrestha (1991) reported seven clusters in *C. capsularis* and eleven clusters in *C. olitorius* . Islam (1995) found five clusters in groundnut. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

The results presented in Table-8 represent the composition of different clusters with their corresponding genotypes and origin included in each cluster. Maximum six genotypes were in cluster I, followed by 5 in cluster III and IV. There were 3 genotypes in cluster II, followed by 2 in cluster V.

Table6. Eigen values and percentage of variation in respect of eleven characters of 21tossa jute (*C. olitorius* L.) genotypes.

Principal component axes	Eigen values	Percentage of variation	Cumulative % of percentage variation
I	5.96	83.33	94.58
II	4.917	11.25	98.42
III	1.534	3.84	99.51
IV	1.473	1.09	99.76
V	0.707	0.25	99.86
VI	0.465	0.10	99.91
VII	0.331	0.05	99.95
VIII	0.328	0.04	99.98
IX	0.214	0.03	99.99
X	0.158	0.01	100.00
XI	0.072	0.00	100.00

The genotypes of cluster V produced the highest cluster mean for plant height (3.47), base diameter (15.73),node per plant (73.53), green weight per plant (210.78), stick weight per plant (35.25) and fibre yield per plant (14.37) (Table 9).

Cluster I was composed of 6 genotypes (Table 8). The genotypes of this group produced the highest cluster mean for petiole length (6.36).This group contained the second highest cluster mean value for core diameter (10.96), leaf angle (28.89),leaf width (6.23), green weight (178.69) and fibre yield per plant (12.44) respectively (Table 9).

Cluster II was composed of 3 genotypes (Table 8). This group contained the lowest cluster mean value for most of the characters except leaf length and petiole length (Table 9).

Cluster III was composed of 5 genotypes (Table 8). The genotypes of this group produced second highest cluster mean for plant height (3.23), nodes/plant (72.45), base diameter (13.94) and stick weight (31.82) respectively (Table 9).

Cluster IV was composed of 5 genotypes (Table8). The genotypes of this group produced the highest cluster mean for leaf width (6.37) in Table 9.

Cluster V also contained 2 genotypes. This cluster had the highest cluster mean for Plant height (3.47), nodes per plant (73.53), base diameter (15.73), core diameter (12.54), leaf angle (29.17), leaf length (16.02), green weight (210.78), stick weight (35.25) and fibre yield (14.37). This group contained lowest cluster mean value for the petiole length (6.06) in (Table 9).

Table7. Ten each higher and lower Euclidean distance between pairs of tossa jute (*C.olitorius* L.) genotypes of different clusters

10 higher Euclidean distance				10 lower Euclidean distance			
SL	Genotypes	Genotypes	Values	SL	Genotypes	Genotypes	Values
1	G14	G7	124.10	1	G12	G6	3.054
2	G14	G11	117.852	2	G6	G3	6.412
3	G7	G2	111.95	3	G12	G3	6.423
4	G13	G7	109.020	4	G4	G1	6.587
5	G11	G2	106.89	5	G8	G1	9.246
6	G13	G11	105.759	6	G8	G4	10.265
7	G18	G14	98.859	7	G13	G2	10.391
8	G15	G14	93.883	8	G17	G9	11.439
9	G18	G2	88.880	9	G9	G3	13.449
10	G14	G6	86.793	10	G16	G9	14.683

The two economic important characters of jute plant are the fibre and stick yield per plant. In case of fibre yield, cluster V possess the highest mean values followed by cluster I, cluster III, cluster IV and cluster II (Table 9). The clustering pattern of genotypes did not follow geographical distribution. The genotypes evolved at one center even exhibited considerable amount of diversity and grouped into different clusters, including geographical diversity may not necessarily be related with genetic diversity. This result is in conformity with the findings of Chawla and Singh (1984). The probable cause of this situation might be due to frequent movement of plant material through introduction. Varieties developed at the same place have different genetic makeup. Certain entries also possessed similar characters even though they had their origin at different places. One of the reasons could be that the farmers from one place might have used different cultivars from various sources. That is why enormous variability in the materials even at single location might arise.

Table8. Distribution of 21 genotypes of tossa jute (*C. olitorius* L.) germplasm in five clusters

Cluster	Number of genotypes	Genotype number	Accession number
I	6	G5,G9,G15,G16,G17,G21	1331,1341,4569, 4570, 4738, O-9897
II	3	G2,G13,G14	O-72, 1349, 4568
III	5	G3, G6, G12, G18, G20	1283,1335,1346,4739,5001
IV	5	G1,G4,G8,G10,G19	O-72,1285,1338,1344,4740
V	2	G7,G11	1337,1345

Table 9. Cluster means for eleven characters in tossa jute (*C. olitorius* L.)

Parameters	**I**	**II**	**III**	**IV**	**V**
Plant height (m)	3.10	2.95	3.23	3.06	3.47
Nodes /plant	71.43	63.25	72.45	71.43	73.53
Base diameter (mm)	13.60	12.05	13.94	12.81	15.73
Core diameter (mm)	10.96	9.38	10.74	10.23	12.54
Leaf angle(dg)	28.89	28.32	28.67	28.67	29.17
Leaf length (cm)	15.62	15.65	15.53	15.60	16.02
Leaf width (cm)	6.23	5.92	6.08	6.37	5.98
Petiole length (cm)	6.36	6.21	6.11	6.26	6.06
Green weight (gm)	178.69	118.08	176.36	148.65	210.78
Stick weight (gm)	29.12	20.30	31.82	26.91	35.25
Fibre yield /Plant (gm)	12.44	8.28	11.57	10.52	14.37

4.4.4 Canonical Vector Analysis (CVA)

To compute the inter-cluster Mahalonobis‟s (D^2) values canonical variate analysis was used. The Table-10 indicates the intra and inter-clusters for distance (D^2) values. The highest inter-cluster distance (111.429) was between cluster II and V indicating wider genetic diversity between these two clusters followed by inter-cluster distance (56.428) was between the cluster II and III, inter-cluster distance (47.354) was betweenthe cluster I and V, inter-cluster distance (37.850) was between the cluster II and IV, inter-cluster distance (37.836) was between the cluster IV and V and the inter-cluster distance (35.687) was between the cluster III and V. The lowest inter-cluster distance (26.538) was observed between the cluster I and III suggesting the closer relationship among the genotypes followed by inter-cluster distance (28.326) was observed between the cluster I and II and the inter-cluster distance (30.621) was observed between the cluster I and IV on included in these clusters (Table10). However, the maximum inter-cluster distance was recorded between cluster II and V (111.429) compared to other clusters. Genotypes from the cluster II and V having the highest distance if involved in hybridization might produce a wide spectrum of segregating population. It is the theoretical concept that the maximum amount of heterosis will be obtained in hybrids involving the genotypes belonging to the more divergent origins. However, for a plant breeder the objective is not only to get high heterosis but also to achieve high level of production by improving and utilizing the other yield contributing traits so that it could be adjusted in various types of cropping systems rather than getting only high heterosis. The intra-cluster distance varied from 42.119 to 78.799 maximum being for cluster II which is composed of three genotypes of diverse origin, while the minimum distance was found in cluster III which comprises five genotypes (Table10). Results of different multivariate techniques were superimposed in Figure 2. It might be concluded from this figure that all the techniques supplemented and confirmed the results of another one.

Table 10. Average intra (Diagonal) and inter cluster distances (D^2) for 21 tossa jute (*C. olitorius* L.) genotypes

Cluster	Cluster				
	I	II	III	IV	V
I	**66.660**				
II	28.326	**78.799**			
III	26.538	56.428	**42.119**		
IV	30.621	37.850	38.132	**74.096**	
V	47.354	111.429	35.687	37.836	**43.492**

Bold figures denote intra-cluster distances

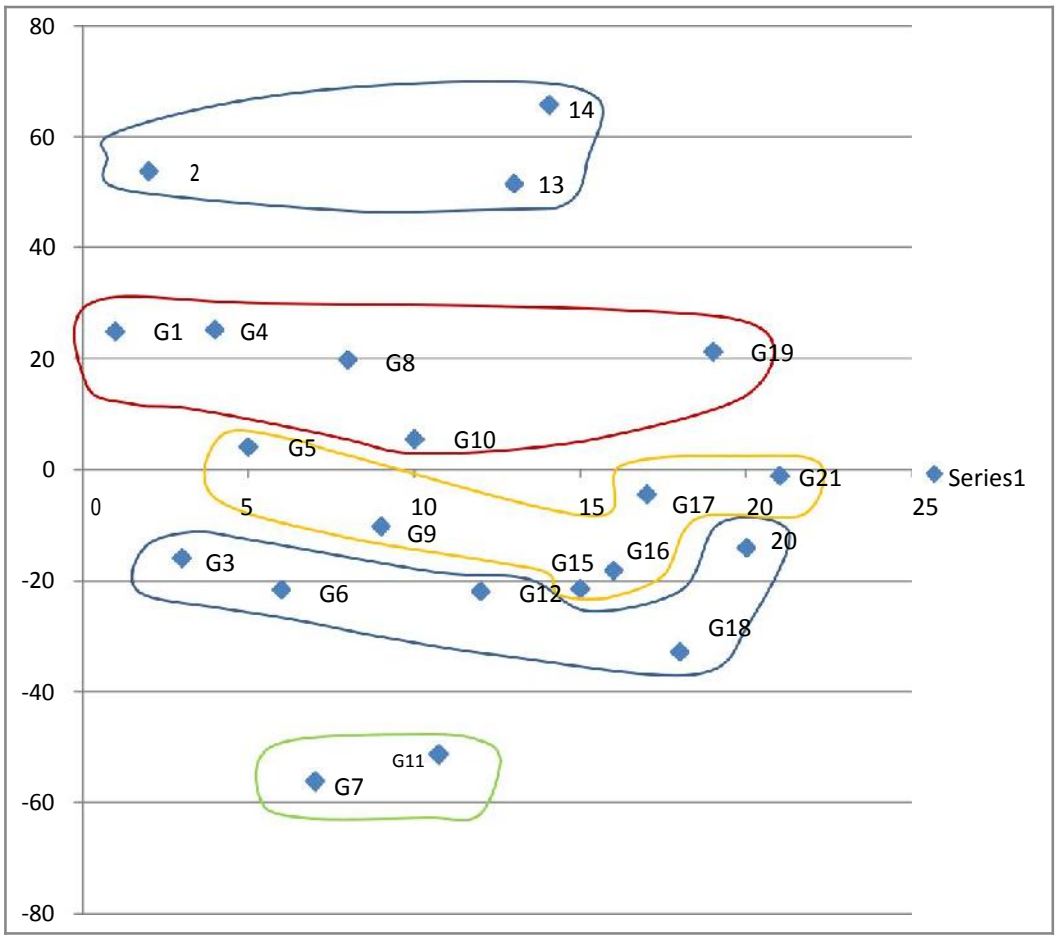

Figure 2. Scatter distribution of 21 tossa jute (*C. olitorius* L.) Genotypes based on their principal component scores superimposed with clustering

The pattern of clustering revealed that germplasm originating from the same country did not form a single cluster. The genotypes belonging to different countries were grouped in the same cluster. This indicated that geographic diversity was not always related to genetic diversity. This might be due to continues exchange of genetic materials in different places of the country even among the countries of the world. Similar results have been reported by Shreshtha (1991) in deshi jute. Mian*et al.* (1991) in field pea, Saha (1993), Murty and Anand (1996) in linseed flax,Katiar and Singh (1990) in faba bean. The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constancy of the associated characters and would thus form indiscriminate clustering. This would suggest that not to choose diverse parents from diverse geographic regions for hybridization.

4.5Contribution of the characters towards divergence of the genotypes

Contribution of characters towards divergence is presented in Table11. Principal Component Analysis (PCA) revealed that most of the characters in vector I (Z_1), the first axis of differentiation were important for genetic divergence of which important for petiolelength(0.00184) and leaf width (0.00080) were the major ones. In vector II (Z_2), the second axis of differentiation green weight (0.56070), leaf angle (0.04029),core diameter (0.01957),fibre yield (0.01340) and leaf width (0.00058) were more important for divergence but plant height, leaf length, petiole length, base diameter, nodes per plant and stick weight played only a minor role in the second axis of differentiation (Table11). If the same character given equal magnitude for both the vectors than the character was considered responsible for primary as well as secondary differentiation.

Table11. Latent vector for eleven morphological characters in tossajute (*C.olitorius* L.) genotypes

Parameters	Vectors 1	Vectors 2
Plant height (m)	-0.00396	-0.00322
Leaf angle (dg)	-0.00264	0.04029
leaf length (cm)	-0.00240	-0.00025
Leaf width (cm)	0.00080	0.00058
Petiole length (cm)	0.00184	-0.00899
Base diameter (mm)	-0.02764	-0.00104
Core diameter (mm)	-0.02151	0.01957
Nodes /plant	-0.07734	-0.11374
Green weight (gm)	-0.82401	0.56070
Stick weight (gm)	-0.12276	-0.09629
Fibre. Yield /Plant (gm)	-0.04833	0.01340

CHAPTERV

SUMMARY AND CONCLUSION

The research was carried out with twenty one genotypes of tossa jute from different geographic origin at the Central Jute Research Experiment Station, Jagir, Manikgonj, Bangladesh Jute Research Institute (BJRI) from April to August, 2016. Among all of the jute species tossa jute (*C. olitorius* L.) has several advantages such as more fibre strength, fineness, softness, brightness (golden) that attain the breeders concern. These features have made jute the second most important bast fibre crop after cotton. For this reason tossa jute cultivation is increasing at farmer‟s level. In Bangladesh there are nine BJRI released variety cultivated by the farmer, among them O-9897, BJRI tossa pat-4 (O-72) and BJRI tossa pat-5(O-795) popular are more popular. There are needs more high yielding and sustainable tossa jute variety for its increasing world‟s demand.With an objective to assess the genetic variability and correlation among the various yield attributing characters, the present investigation, “Genetic variability and character association of fibre yield and its component characters of tossa jute (*C. olitorius*L.)” was undertaken with twenty one genotypes of geographic origin. The observation was recorded on eleven yield contributing characters, viz. plant height, leaf angle, leaf length, leaf width, petiole length, base diameter, nodes per plant, green weight, fibre weight and stick weight. All the collected data of the study were subjected to statistical analysis.

Significant and non significant differences were observed among the genotypes. Multivariate analysis was performed through Principal Component Analysis (PCA), Cluster Analysis (CLA), Principal Coordinate Analysis (PCoA) and Canonical Vector Analysis (CVA) using GENSTATE 5.13 software programme. Results of different multivariate techniques indicated that all the techniques supplemented and confirmed the results of another one.

On the basis of mean performance, the maximum plant height was observed in genotype G11 (3.64m) followed by G21 (3.55m), G15 (3.41m) and G18 (3.36m). The Maximum node number was found at G5 (81.30) followed by G11 and G15 (80.73).The Highest base diameter was observed in G21 (17.50mm) followed by G11 (15.98mm) and G7 (15.47mm). The maximum Core diameter ranged fromG14 (8.46mm) to G21 (13.82mm). The highest leaf length was observed in G1 (12.82cm) and G2, G4, G10 (16.39cm).The highest leaf width was observed in G5 (6.68cm) followed by G8 (6.61cm) and G1 (6.50cm). More green weight was observed in G7 (220.23gm) followed by G11 (201.33gm), G15 (195.33gm) and G16 (184.73gm). The Maximum stick weight was observed in G20 (44.37gm) followed by G15 (37.43gm), G21 (36.73gm) and G7 (36.03gm). The Highest fibre weight was observed in G21 (17.63) followed by G15 (15.23gm), G11 (15.17gm) and G7 (13.57gm) (Table 2).So these genotypes may be used for future breeding program.

The phenotypic coefficient of variation was higher for all the characters than their corresponding genotypic coefficient of variation. Among the characters the highest genotypic coefficient of variation was recorded for base diameter per plant followed by fibre weight, core diameter, Plant height, nodes per plant, green weight, petiole length, leaf length and stick weight in order of merit. The differences between the PCV and GCV for the characters were narrow indicating lesser influence of environment on these characters and could be improved by following phenotypic selection.

All the genotypes varied significantly with each other for all the characters studied. Among the characters studied comparatively high genotypic coefficient of variation, high heritability value and genetic advance were recorded for the characters of plant height, core diameter per plant, fibre weight per plant which suggests that these characters are under control of additive gene effects. High heritability value with moderate genetic advance were found for the characters number of nodes per plant,

leaf width and petiole length per plant indicated that this characters might be under the control of non additive gene effect.

Results of the present studies indicated significant variation among the genotypes for all the characters. High heritability coupled with genetic advance was observed in plant height, nodes per plant, core diameter, leaf length and petiole length. These characters were under control of additive gene effect and selection for genetic improvement for these might be effective. Correlation studies showed positive correlation between fibre yield and its most components. Fibre yield also reveled significant positive correlation with plant height, nodes per plant, base diameter, core diameter, leaf area and stick weight at genotypic level. Path analysis showed highest positive direct effect of stick weight on fibre weight followed by leaf area, base diameter,plant height, nodes per plant and core diameter.

The first four component axes accounted for 99.51 % variation towards the divergence. According to PCA, D^2 and cluster analysis the genotypes were grouped into six clusters. Five clusters were found from a scattered diagram formed by Z_1 and Z_2 values obtained from PCA. The highest inter-cluster distance (111.429) was observed between clusters II and V followed by cluster II and III, I and IV, III and IV, II and IV, IV and V. The lowest inter-cluster distance (26.538) was observed between the cluster I and III followed by I and II, I and IV. The highest intra-cluster distance was observed in cluster II contained three genotypes. The lowest intra-cluster was observed in cluster III contained five genotypes. The principal component analysis revealed that plant height, leaf angle and leaf length were the important components of genetic divergence in the population.

However, the investigation revealed that no single quantitative trait had major contribution to the fibre yield. Integrated approach of improving quantitative traits would consequently help to increase yield potential of jute. Considering the cluster,

inter-genotypic distance and other agronomic performance, the genotypes G9,G15,G21 from cluster I , G6,G12,G18,G20, from cluster III, G7,G11 from cluster V were considered to be better parents for future use in hybridization programme.

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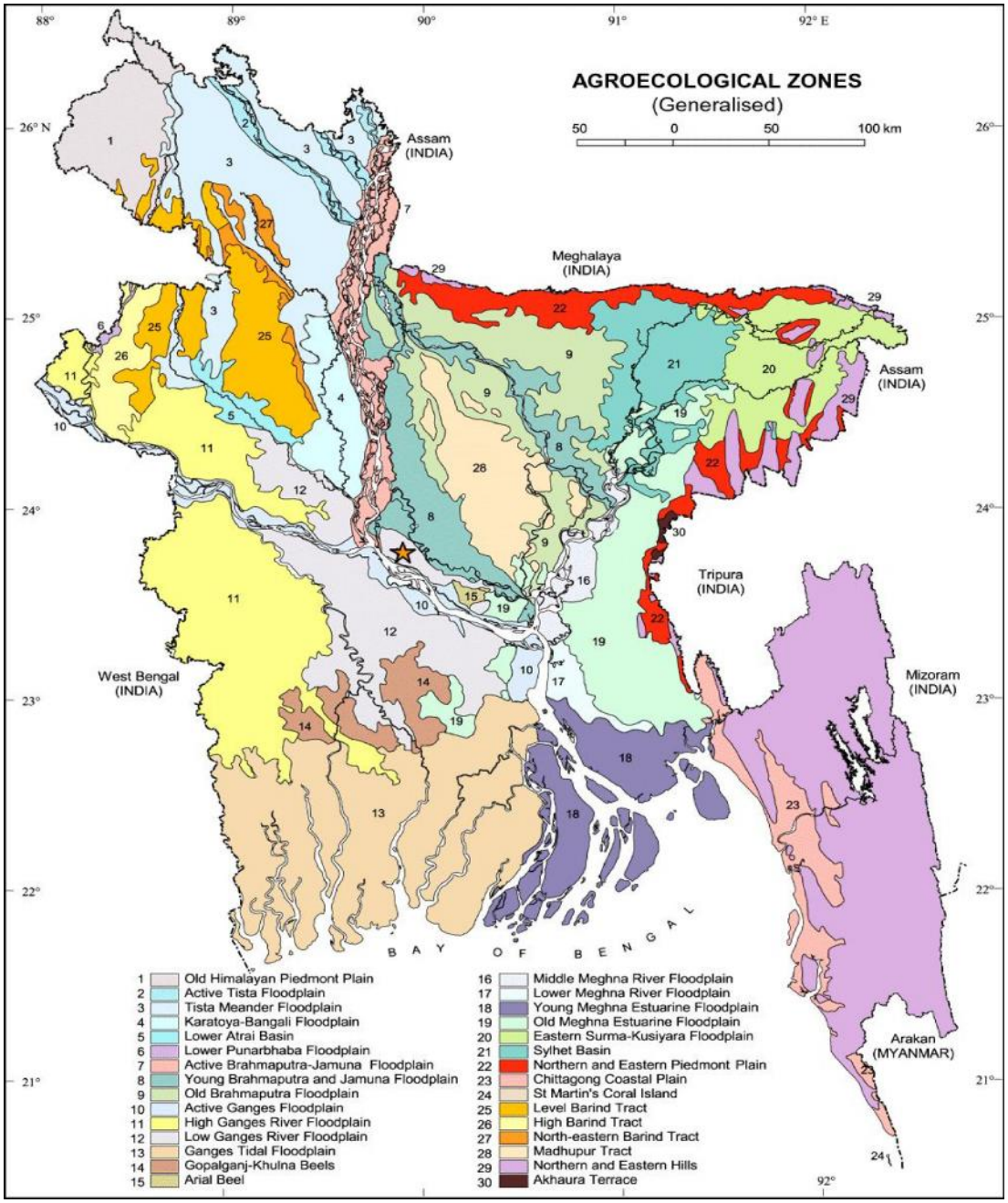
APPENDICES

Appendix I: Location of experimental plot



Appendix II: Analysis of variance of 11 different characters of 21 different genotypes of tossa jute (*C. olitorius*).

Source of variation	Df	Plant height (m)	Leaf angle	leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Base diameter (mm)	Nodes /plant	Core diameter	Green weight (gm)	Stick weight (gm)	Fr.yield /Pl.
Replication	2	0.523	7.540	2.653	0.236	0.832	12.831	676.534	10.072	6969.137	524.235	29.459
MSS	20	0.170	4.921	1.837	0.191	0.754	7.661	128.025	5.632	2382.232	120.777	17.343
Error	40	0.053*	4.623	1.174	0.184	0.639	1.875	82.138	2.313	2250.544	118.668	13.261

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

AppendixIII : Monthly summarized of mean daily maximum and minimum air temperature and monthly rainfall during the cropping season at Jute Agriculture Experimental Station, Jagir, Manikganj

Month	Mean daily temperature		Monthly rainfall (mm).
	Max(^{0}c)	Min(^{0}c)	
April/16	33.76	23.70	254.00
May/16	34.37	25.45	328.00
June/16	33.70	27.23	397.67
July/16	32.56	26.45	403.00
August/16	30.70	25.57	315.00

Appendix IV: Principal component scores for 21 tossa jute(*C. olitoriuss* L.) genotypes

Genotype No.	Z1	Z2
1	24.92	3.44
2	53.72	0.64
3	-15.93	-4.86
4	25.22	-0.26
5	4.13	10.73
6	-21.64	-4.45
7	-56.97	14.24
8	19.83	7.97
9	-10.22	6.54
10	5.49	-0.30
11	-52.29	-12.64
12	-21.94	-5.55
13	51.49	3.86
14	65.04	-7.88
15	-21.44	22.88
16	-18.15	6.44
17	-4.47	14.92
18	-32.85	-18.86
19	21.27	-17.56
20	-14.08	-25.30
21	-1.13	6.00