GENETIC DIVERGENCE, VARIABILITY, CORRELATION AND PATH ANALYSIS IN WHITE JUTE (*Corchorus capsularis* L.)

A THESIS

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CERTIFICATE

This is to certify that thesis entitled, "Genetic divergence, variability, correlation and path analysis in white jute (Corchorus capsularis 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 bonafide research work carried out by Muhammad Jahangir Alam, Registration No. 08-03213 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 duly been acknowledged by him.

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Supervisor

Dated: December, 2009
Place: Dhaka, Bangladesh

DEDICATED TO

MY

BELOVED

PARENTS

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GENETIC DIVERGENCE, VARIABILITY, CORRELATION AND PATH ANALYSIS IN WHITE JUTE (*Corchorus capsularis* L.)

MUHAMMAD JAHANGIR ALAM

ABSTRACT

The experiment was conducted with fifty one genotypes of white jute from different geographic origin were evaluated to study their genetic divergence, variability, correlation and path analysis with 11 morphological characters. The experiment was carried out at the Central Jute Research Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikgonj during the period from April to August, 2010. Analysis of variance revealed significant variation among the genotypes for all the characters. Multivariate techniques were used to classify 51 genotypes, which computed by MahalanobisD^{2}statistics. All the genotypes were grouped into six different clusters. Principal component analysis, principal coordinate analysis, canonical variate analysis and cluster analysis gave similar results. Cluster V and VI had the maximum ten genotypes while cluster I had the minimum of seven genotypes. The highest inter-genotypic distance (1.8441) was found between G_{15}, G_{50} and the lowest distance between G_{38} and G_{26} . The highest inter-cluster distance (14.367) was observed between cluster I, IV and the lowest distance (2.458) was found between cluster III and V. The highest intra-cluster distance was found in cluster I and lowest in cluster V. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed for branches per plant. High heritability values with moderate genetic advance in percentage of mean were obtained for leaf width, petiole length, nodes per plant. Correlation studies showed positive correlation between fibre yield and its most components. Path analysis showed highest positive direct effect of stick weight on fibre weight followed by base diameter, leaf width and petiole length. Considering the cluster distance, inter-genotypic distance and other agronomic performance, the genotypes G_{47},G_{33}, G_{48} from cluster I; G_{27}, G_{17}, G_{23} from cluster III and G_{13},G_{40},G_{45} from cluster II were considered to be better parents for future use in hybridization programme.

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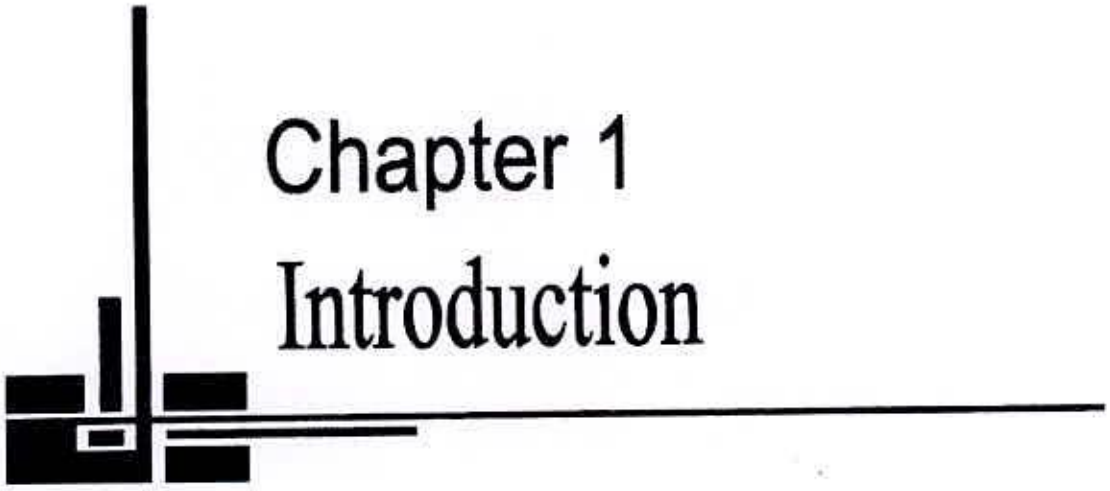
SYMBOLS AND ABBREVIATIONS

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
G	Gram
h^2b	Heritability in broad sense
J.	Journal
Kg	Kilogram
M	Meter
MSS	Mean Sum of Square
Mm	Millimeter
MP	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 1
Introduction

CHAPTER 1

INTRODUCTION

Jute is a biodegradable natural fibre and leading crop of Bangladesh. Bangladesh is the second largest and the best quality jute producer around the world. It is singly earns foreign exchange equivalent to sixteen thousand, three hundred and thirty six million taka annually to our national economy (BBS, 2008). It is also the most important natural fibre crop next to cotton (Singh, 1976). Presently; jute is growing in about 1089 thousands acres producing 839 metric tons in Bangladesh (BBS, 2008). The average yield of jute in our country is only 0.77 metric tons which is very low as compared to other countries of the world like India and China. Jute constitutes major sources of employment such as cultivation, processing, carrying, marketing, research, trading and exporting of jute. Commercially jute is often referred to as the "golden fibre of Bangladesh", because of its immense contribution for the economy of this country.

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). The genus *Corchorus* contains about 50-60 genotypes 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, the bast fibre, is obtain from the bark of two cultivated species of the genus namely *Corchorus capsularis* L. and *Corchorus olitorius* L. of the family Tiliaceae . *C. olitorius* is called tossa pat or mitha pat whereas *C. capsularis* is called deshi pat or tita pat or white pat. The fibre of *C. capsularis* is ordinarily whitish. The fibre of jute is obtained the green bark of the stem.

White jute (*C. capsularis* L.) can grow both in low and high land and has better adaptability than the other cultivated species. *Capsularis* varieties in general, are suitable for early sowing from March onwards and perform better in low lying areas. A moist heat is more favorable for the growth of the *capsularis* jute and nearly full

growth plants are tolerant to standing water. In general, *capsularis* shows flexibility in relation to drought and flood condition.

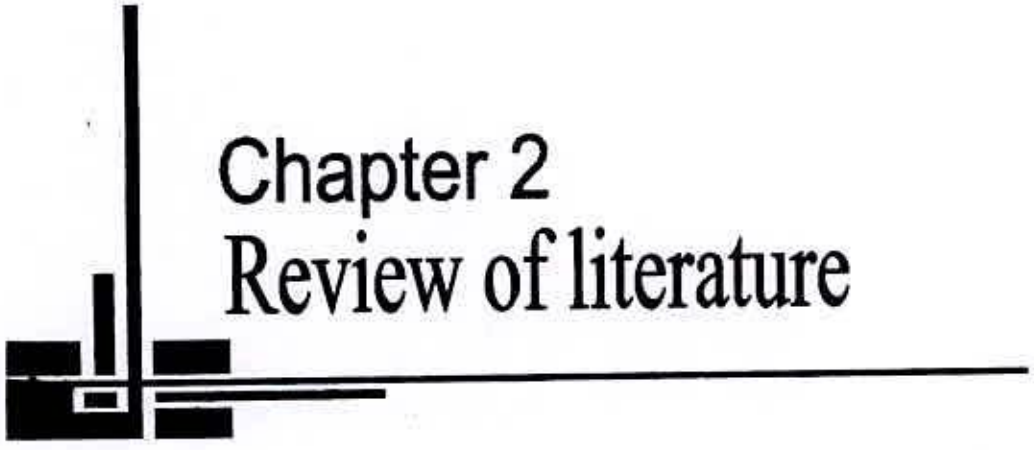
In Bangladesh, the number of recommended jute varieties is limited in terms of meeting the requirements of wide agro-ecological conditions. Most of these varieties are quite old and have narrow genetic base and susceptible to various biotic and abiotic stresses such as insects, pests, diseases, drought, water logging, and low temperature and so on. 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 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 with in the available germplasm (Tomooka, 1991).

Under the present context of global environment prospective, jute is getting 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 white jute genotypes.
2. To asses the variability present in different genotypes.
3. To asses the characters association and contribution of characters towards fibre yield in different genotypes. and
4. To select the desirable parents for hybridization.



Chapter 2
Review of literature

CHAPTER 2

REVIEW OF LITERATURE

Fibre yield in white jute (*C. capsularis* 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).

Scientists are trying hard into 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. The relevant literature available on *Corchorus capsularis* L. has been reviewed and here under being presented.

2.1 Genetic diversity

Somayajulu *et al.* (1970) and Sasmal (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.

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.

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 pea (*Pisum sativum* L.) Narshighani *et al.* (1978) studied the genetic diversity through Mahalanobis's D^2 and found that seed size, plant height and days to maturity contributed maximum to the total divergence. But major role of days to flowering was found by Ranalli in 1982.

An experiment was conducted by Kanwal *et al.* (1983) to assess the genetic diversity on 100 strains using Mahalanobis's D^2 statistics and canonical analysis revealed that panicle weight, days to maturity, height and grain size contributed most towards divergence. The strains were grouped into nine clusters, which were not correlated geographical diversity.

Julfiquar *et al.* (1985) observed divergence among 100 elite lines (67 R and 33 M from 68 cross made at IRRI) and concluded that these maintainers and restorers, which were grouped under different clusters could be used in crossing programme to produce heterotic F_1 hybrids.

Malik *et al.* (1985) studied the genetic divergence in mungbean found days to flowering, seed yield and plant height contributed maximum towards divergence.

Sharma and Luthra (1987) studied the genetic diversity in lentil and reported that pod per plant, seed per plant and yield per plant contributed maximum towards the diversity.

Biswas and Sasmal (1990) estimated genetic divergence using Mahalanobis's D^2 statistics in seven rice varieties and their 21 F_1 hybrids. They were grouped 28 genotypes into six clusters. The grouping of parental genotypes did not follow a geographic pattern. Shoot fresh weight was the main factor contributing to genetic variance.

Murthy and Dorairaj (1990) studied the genetic diversity and canonical analysis of 60 early genotypes of pigeon pea. Genetic diversity was found independent of genotypic origin and the genotypes were grouped into three clusters V.

Sinha *et al.* (1991) studied genetic divergence in indigenous upland rice on the basis of the Mahalanobis's D^2 statistics calculated for 10 growth and yield related traits. They assigned 30 traditional varieties to one of six clusters. Cluster I combined 66.6% of genotypes while IV, V and VI were mono-genotypic. Varieties from the Northeastern region showed the greatest diversity, being represented in all clusters except cluster VI.

Thirty five genotypes of Virginia runner groundnut were studied by Golakia and Makne (1992) through D^2 statistics. The genotypes were grouped into seven clusters and there was no parallelism between geographical and genetic diversity.

Islam (1995) carried out his research with 90 groundnut genotypes and found five different clusters. He stated that shelling percentage and plant height contributed maximum towards divergence and indicated that geographic diversity is not related to genetic diversity.

A field experiment was conducted by Bansal *et al.* (1999) and they reported the genetic diversity in 34 rice stocks using D^2 analysis of 10 economic traits. Thirty four genotypes from seven countries were grouped into 15 clusters. The pattern of distribution of genotypes within various clusters was independent of geographical distribution. Based on the mean performance, genetic distance and clustering pattern, inter varietal crosses are identified which may be useful in creating wider variability for early maturity, dwarf and yielding segregants.

Sreedhar *et al.* (2004) conducted a field experiment during rabi season in 2002 for genetic diversity of 114 germplasm of rice and concluded that the maximum inter cluster distance (23.73) was observed between cluster V and cluster X, followed by cluster III and cluster IX (22.27). Based on the divergence estimates and clustering pattern in the present genetic material, cross could be made between the genotypes of cluster V and cluster X for yielding good recombinants for the character viz., spike lets/panicle, filled grains/panicle, single plant yield, yield and harvest index.

2.2 Variability

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.

Charles and Smith (1939) separated the genetic variance from the total variance by the use of estimates of environmental variance based on non segregating population and also established possible relations between mean and variance.

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.

Shukla and Singh (1967) studied different plant characters of ten varieties of *C. capsularis* which is enable to compare the amount of variability present in different characters.

Eunus (1968) reported that increased fibre yield in jute is mainly based on two morphological characters namely plant height and base diameter.

Singh (1970), observed plant height and base diameter were found to have less genetic variability than stick weight and fibre weight respectively.

Dutta *et al.* (1973) observed that the genetic coefficient of variability was only 2.64 percent for fibre yield in two improved varieties of *C. capsularis* and two improved varieties of *Hibiscus cannabinus*.

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.

Ghosdastidar and Das (1984) revealed that the genetic coefficient of variance was higher for fibre weight (33.01) whereas it was low for node number (12.55) and base diameter (11.75) in tossa jute.

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.

Dahal (1991) observed the phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation for all characters.

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.

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.

2.3 Heritability and genetic advance

Heritability is the degree to which variability of quantitative characters is transmitted from parents to offspring. 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 capsularis*.

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

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.

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

Robinson (1966) have been categorized the heritability values into low (below 10%) moderate (10-30) and high (above 30%).

Rahman (1968) observed only 25 percent heritability for fibre yield in jute.

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%).

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.

Ghosdastidar 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).

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.

According to Ahmed *et al.* (1993) the highest genetic advance (35.5%) coupled with the highest heritability (52.9%) was observed for fibre yield.

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.

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.

2.4 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. capsularis* were studied with a view to find out suitable basis for selection that are likely to be correlated with the yield of fibre.

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.

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.

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

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.

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.

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.

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.

Manjunatha and Sheriff (1991) observed high genotypic and phenotypic coefficients of variation were observed for dry fibre yield, green weight and stick weight.

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.

2.5 Path analysis

Path analysis helps to find out the direct and indirect causes of association. 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.

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.

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.

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.

Ghoshdastidar and Das (1984) reported that plant height and base diameter had high positive effect on fibre yield.

Biswas(1984) reported that node number and internodal length had negative direct effect on yield.

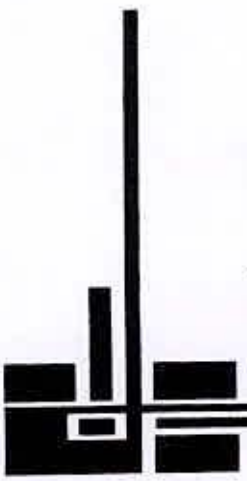
Banerjee *et al.* (1988) studied path coefficient analysis in *Hibiscus sabdariffa* and revealed that the highest direct vehicles for fibre yield were basal diameter, green weight and plant height in the order. Top diameter, node number and stick weight indicated negative direct effects. The indirect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

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 incase of node number through plant height. The effect was negligible.

Thirthamallappa and Sheriff (1991) reported that plant height had maximum direct effect 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.

Akter *et al.* (2005) highest direct effect was obtained for fresh weight without leaves on fibre yield in jute.



Chapter 3

Materials and Methods

CHAPTER 3

MATERIALS AND METHODS

The experiment was carried out at the Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikgonj during the period from April to August, 2009.

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 (Figure 1).

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

3.4 Experimental Material

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

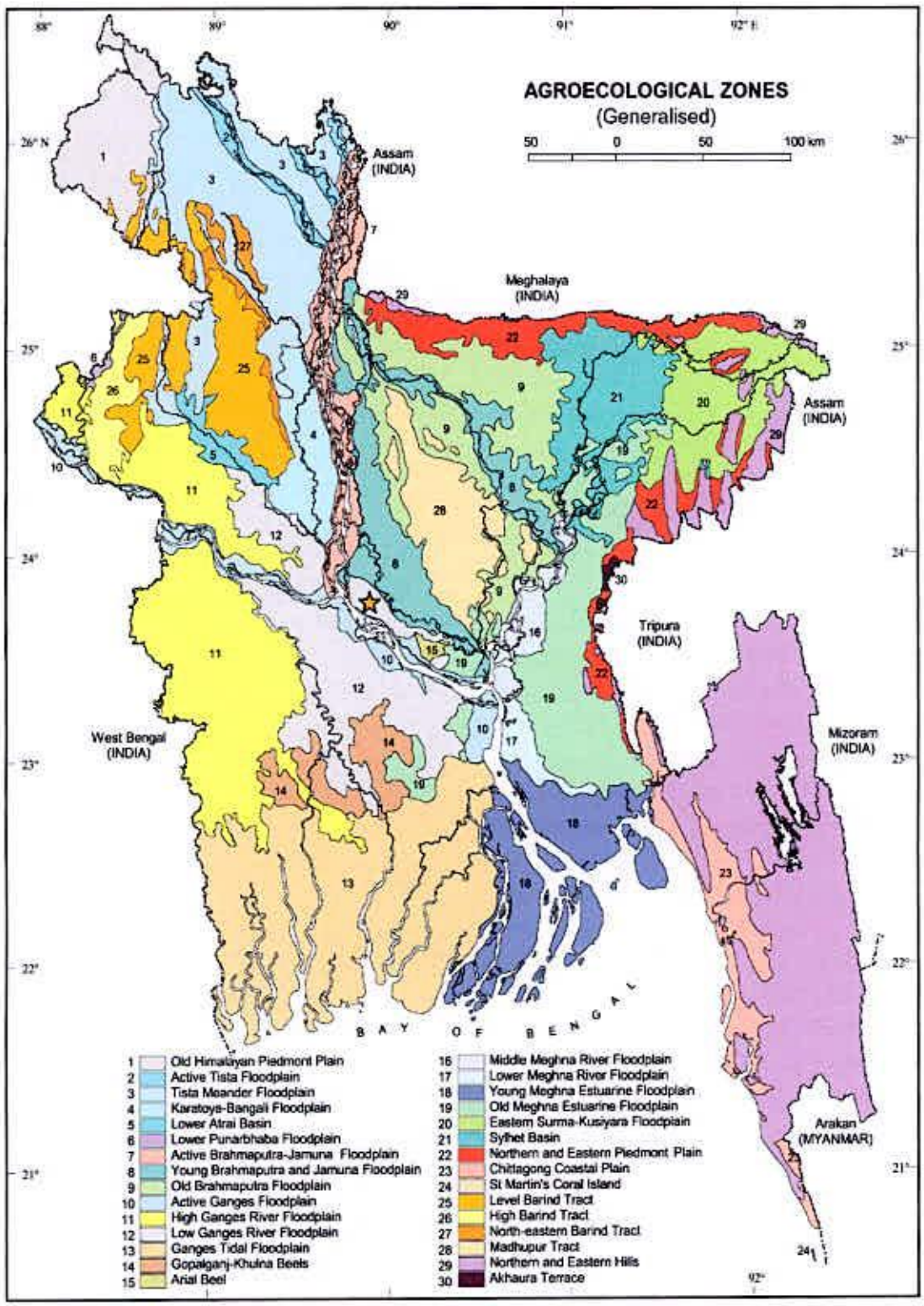


Figure 1. Location of experimental field

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

Genotype No.	Accession number	Country of origin/Place of collection
1	890(CVL-1)	Bangladesh
2	860	India
3	4616	Brazil
4	4591	Nepal
5	4872	Thailand
6	4926	China
7	72	Bangladesh
8	4617	Brazil
9	2212	USA
10	1513	India
11	4619	Brazil
12	4700	,,
13	4956	China
14	77	Bangladesh
15	4706	Brazil
16	4961	China
17	5125(BJC-7370)	Bangladesh
18	2214	USA
19	4474	Thailand
20	1514	India
21	858	,,
22	2215	USA
23	891 (CVE-3)	Bangladesh
24	80	,,
25	4468	Thailand
26	1832	Bangladesh
27	944	-
28	877	India
29	859	,,
30	2020	,,
31	2216	USA
32	4472	Thailand
33	78	Bangladesh
34	5060	-
35	4463	Thailand
36	4699	-
37	4710	Nepal
38	2219	USA
39	4879	Nepal
40	2019	India
41	1515	Nepal
42	4951	Nepal

Table 1 (Cont'd)

Genotype No.	Accession number	Country of origin/Place of collection
43	70	Bangladesh
44	947	India
45	74	Bangladesh
46	4871	Thailand
47	3693	China
48	865	India
49	75	Bangladesh
50	4615	Brazil
51	861	India

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 3.6 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 ploughing followed by harrowing and laddering. The recommended doses of fertilizer such as 166kg/ha of Urea, 25kg/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, 2010. Thinning and weeding were done twice after 15 and 45 days of sowing to maintain uniform plant population. Insecticide was not applied. Hand picking was practiced to control the hairy caterpillar at larval and pupal stage.

Plate 1: A partial view of field experiment of white jute genotypes

Plate 2: A close view of white jute stem color with different stature

3.8 Collection of data

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

1) Plant height (m): It was measured from the base of the plant to the tip of the main shoot in meter.
2) Base diameter (mm): Base diameter was measured at the base of the stem in mm using slide caliper.
3) Nodes per plant: Total number of nodes per plant were counted and expressed in number.
4) Leaf length (cm): The length of leaf was measured in cm.
5) Leaf width (cm): The width of leaf was measured in cm.
6) Leaf angle (dg): The leaf angle was measured in dg.
7) Petiole length (cm): The length of petiole was measured in cm.
8) Branches per plant: Total number of branches per plant was counted and expressed in number.
9) Green weight (g): Fresh weight of the plant with branches and without leaves was recorded.
10) Fibre weight (g): Weight of sun dried fibre per plant after retting, extraction and drying was measured in gram.
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 (Jager *et al.*, 1983). 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 (PCO)

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 Panse and Sukhatme (1967). 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

$Yij = \mu + ti + bj + eij$

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 varience

$\sigma^2 g$ = Genotypic varience

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:

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

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

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 $\sqrt{2}$x'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^2 g = The genotypic variance

σ^2 e= 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) = $(\sigma_p / \bar{x}) \times 100$

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, 1949) by the formula suggested by Hanson *et al.* (1956) and Johnson *et al.* (1955).

Heritability (H_b) = $(\sigma^2_g / \sigma^2_p) \times 100$

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 estimated using the formula suggested Lush (1949) and Jhonson *et al.* (1955)

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

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 possible Combinations the formula suggested by Miller *et al.*(1958), Johnson *et al.*(1955) and Hanson *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

$\sigma^2 px$ = Phenotypic variance of the trait x

$\sigma^2 py$ = 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 4

Results and Discussion

CHAPTER 4

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to 11 characters were computed and statistically analyzed and the results thus obtained were presented and discussed below section wise:

4.1 DIVERSITY OF WHITE JUTE GERMPLASM

4.1.1 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 90.81% (Table 2). A two dimensional chart (Z_1-Z_2) of 51 white jute genotypes are presented in Appendix III.

4.1.2 Principal Coordinate Analysis (PCA)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter-genotypic distances obtained from principal component analysis showed that the highest distance (1.8441) was observed between the genotypes G50 and G15 followed by G21 and G2 (1.8389), G41 and G2 (1.8273), G39 and G2 (1.8171), G31 and G2 (1.7973), and lowest distance (0.2328) was observed between the genotypes G36 and G26 followed by G42 and G26 (0.2527), G39 and G29 (0.2712), G34 and G25 (0.2729), G32 and G29 (0.2766) (Table 3). Inter cluster distances were calculated (Table 6) from these inter-genotypic distances followed by Singh and Choudhury (1979). The highest intra-cluster distance was observed in cluster I (0.835), which was composed of seven genotypes followed by cluster II (0.781) that was composed of eight genotypes, both the cluster III (0.737) and cluster IV (0.635) were composed of 8 genotypes.

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

Parameters	Eigen values	Percentage of total variation accounted for individual characters	Percentage of cumulative variation
Plant height(m)	7.963	46.10	46.10
Leaf angle(dg)	4.917	28.46	74.56
leaf length (cm)	1.434	8.30	82.86
Leaf width (cm)	1.373	7.95	90.81
Petiole length (cm)	0.607	3.52	94.33
Base diameter (mm)	0.365	2.12	96.45
Nodes /plant	0.231	1.34	97.79
Branch /plant	0.150	0.87	98.66
Green weight (gm)	0.114	0.66	99.32
Stick weight (gm)	0.088	0.50	99.82
Fibre yield /Plant.	0.032	0.18	100.00

The cluster V showed the lowest intra-cluster distance (0.609) composed of 10 genotypes followed by cluster IV (0.635) composed of eight genotypes and cluster VI (0.715) composed of 10 genotypes. These results revealed that the genotypes in cluster I were distantly related. On the other hand the genotypes in cluster V were closely related.

4.1.3 Clustering

Fifty one genotypes of white jute were grouped into six different clusters with the application of Mahalanobis's d^2 statistics (Table 4). Shrestha (1991) reported seven clusters in *C. capsularis* and eleven clusters in *C. olitorius* . Islam (1995) and Golakin and Makne (1992) found five and seven clusters in groundnut, respectively. These results confirmed the clustering pattern of the genotypes according to the principal component analysis.

The results presented in Table 4 represent the composition of different clusters with their corresponding genotypes and origin included in each cluster. Maximum ten genotypes were in cluster V and VI, followed by 8 in cluster II, III and IV. There were 7 genotypes in cluster I.

The genotypes of cluster I produced the highest cluster mean for plant height (2.66), base diameter (19.35),node per plant (54.11), green weight per plant (219.71), stick weight per plant (48.17) and fibre yield per plant (17.35) (Table 5).

Cluster II represented 8 genotypes. The genotypes of this group produced the cluster mean for plant height (2.51), base diameter (16.96), green weight per plant (180.37), stick weight per plant (38.04) and fibre yield per plant (11.99).This group contained the second highest cluster mean value for branches per plant (2.40) (Table 5).

Table 3. Ten each higher and lower inter- genotypic distance (D^2) between pairs of white jute (*C. capsularis* L.) genotypes of different clusters

10 higher D^2 values	Genotypes combination	10 lower D^2 values	Genotypes Combination
1.8441	50 & 15	0.2328	36 & 26
1.8389	21 & 2	0.2527	42 & 26
1.8273	41 & 2	0.2712	39 & 29
1.8171	39 & 2	0.2729	34 & 25
1.7973	31 & 2	0.2766	32 & 29
1.7944	17 & 2	0.2776	10 & 3
1.7914	40 & 2	0.2800	23 & 3
1.7816	15 & 2	0.2830	44 & 25
1.7587	44 & 2	0.2869	37 & 8
1.7296	50 & 2	0.2880	28 & 26

Cluster III was composed of 8 genotypes (Table 4). The genotypes of this group produced highest cluster mean for leaf length (14.12).This group contained the second highest cluster mean value for plant height (2.60),leafwidth (5.27), petiole length (5.04),base diameter (17.68),nodes per plant (52.29), stick weight per plant(40.71) and fibre yield per plant (13.97) respectively.

Cluster IV also contained 8 genotypes. This cluster had the highest cluster mean for leaf width (5.30) and petiole length (5.10). This group contained cluster mean value for plant height (2.54), base diameter (17.04) and fibre yield (8.71).

Cluster V was composed of the highest ten genotypes. The highest cluster mean was observed for branches per plant (2.78). This group contained the lowest nodes per plant (47.58). This cluster showed medium mean values for other characters.

Cluster VI also contained 10 genotypes. The highest cluster mean was observed leaf angle (78.83). This group contained second lowest cluster mean value for leaf width(4.92),branches per plant (2.03), stick weight (27.40) and fibre yield per plant (9.69) (Table 5).

Table 4. Distribution of 51 genotypes of white jute (*C. capsularis* L.) germplasm in six clusters

Cluster	Number of genotypes	Genotype number	Accession number
I	7	8, 12, 14, 15, 33, 47, 48	4617, 4700, 77, 4706, 78, BJC83, 865
II	8	7, 13, 16, 22, 37, 40, 43, 45	72, 4956, 4961, 2215, 4710, 2019, 70, 74
III	8	3, 6, 10, 17, 18, 23, 27, 46	4616, 4926, 1513, BJC7370, 2214, CVE3, 944, 4871
IV	8	11, 24, 28, 32, 35, 36, 49, 50	4619, 80, 877, 4472, 4463, 4699, 75, 4615
V	10	1, 2, 5, 20, 21, 29, 30, 31, 34, 51	CVL-1, 860, 4872, 1514, 858, 859, 2020, 2216, 5060, CVE3
VI	10	4, 9, 19, 25, 26, 38, 39, 41, 42, 44	4591, 2212, 4474, 4468, 1832, 2219, 4879, 1515, 4951, 947

Table 5. Cluster means for eleven characters in white jute (*C. capsularis* L.)

Parameters	Cluster					
	I	II	III	IV	V	VI
Plant height (m)	2.66	2.51	2.60	2.54	2.48	2.57
Leaf angle(dg)	77.94	78.77	75.96	76.37	75.10	78.83
leaf length (cm)	13.34	13.76	14.12	13.53	13.56	13.67
Leaf weidth (cm)	5.14	5.20	5.27	5.30	4.80	4.92
Petiole length (cm)	4.93	5.04	5.04	5.10	4.55	4.74
Base diameter (mm)	19.35	16.96	17.68	17.04	16.44	17.06
Nodes /plant	54.11	50.02	52.29	49.47	47.58	51.69
Branches/plant	2.21	2.40	2.19	1.88	2.78	2.03
Green weight (gm)	219.71	180.37	137.88	114.32	133.31	160.31
Stick weight (gm)	48.17	38.04	40.71	26.18	29.74	27.40
Fibre.yield /Plant (gm)	17.35	11.99	13.97	8.71	10.13	9.69

The two economic important characters of jute plant are the fibre and stick yield per plant. Incase of fibre yield, cluster I possess the highest mean values followed by cluster III, cluster II, cluster V, cluster VI and cluster IV (Table 5). 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 make up. 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.

4.1.4 Canonical Vector Analysis (CVA)

To compute the inter-cluster Mahalonobis's (D^2) values canonical variate analysis was used. The Table 6 indicates the intra and inter-clusters for distance (D^2) values. The highest inter-cluster distance (14.367) was between cluster I and IV indicating wider genetic diversity between these two clusters followed by the cluster I and V, I and III, II and IV, I and VI, II and V. The lowest inter-cluster distance (2.458) was observed between the cluster III and V suggesting the closer relationship among the genotypes followed by IV and V, II and VI, III and IV,V and VI, III and VI and so on included in these clusters. Similar distance was found between cluster III and V, IV and V, II and VI, III and IV reflecting a close relationship among these clusters (Figure 3 and Table 6). However, the maximum inter-cluster distance was recorded between cluster I and IV (14.637) compared to other clusters. Genotypes from the cluster I and IV having the highest distance if involved in hybridization might produce a wide spectrum of segregating population. It is the theoretical concept that 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 0.609 to 0.835, maximum being for cluster I which is composed of seven genotypes of diverse origin, while the minimum distance was found in cluster V which comprises ten genotypes (Table 6). Results of different multivariate techniques were superimposed in Figure 2. It mightbe concluded from this figure that all the techniques supplemented and confirmed the results of another one.

Table 6. Average intra (Diagonal) and inter cluster distances (D^2) for 51 white jute (*C. capsularis* L.) genotypes

Cluster	Cluster					
	I	II	III	IV	V	VI
I	**0.835**					
II	5.557	**0.781**				
III	10.920	5.587	**0.737**			
IV	14.367	8.838	3.775	**0.635**		
V	12.032	6.475	2.458	2.504	**0.609**	
VI	8.638	3.285	4.208	6.335	3.831	**0.715**

Bold figures denote intra-cluster distances

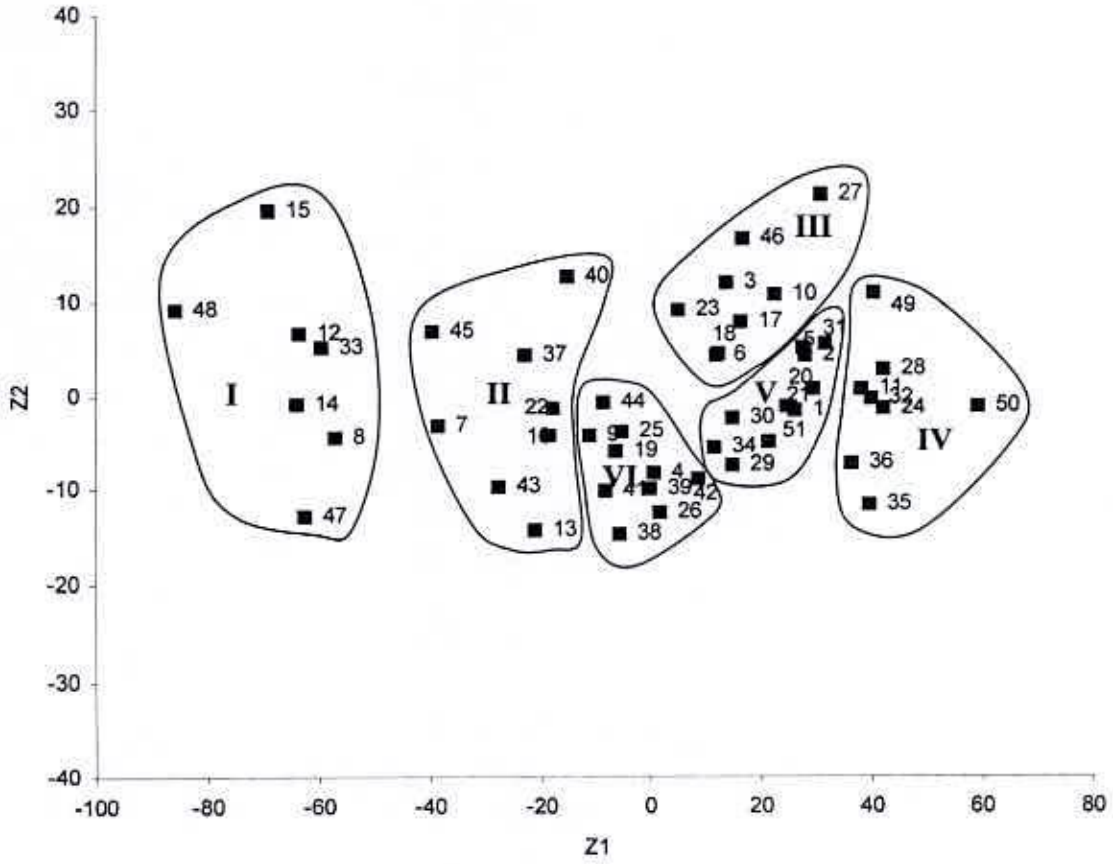


Figure 2. Scatter distribution of 51 white jute (*C. capsularis* L.) genotypes based on their principal component scores superimposed with clustering

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, Das and Gupta (1984) in black gram. 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 favour 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.

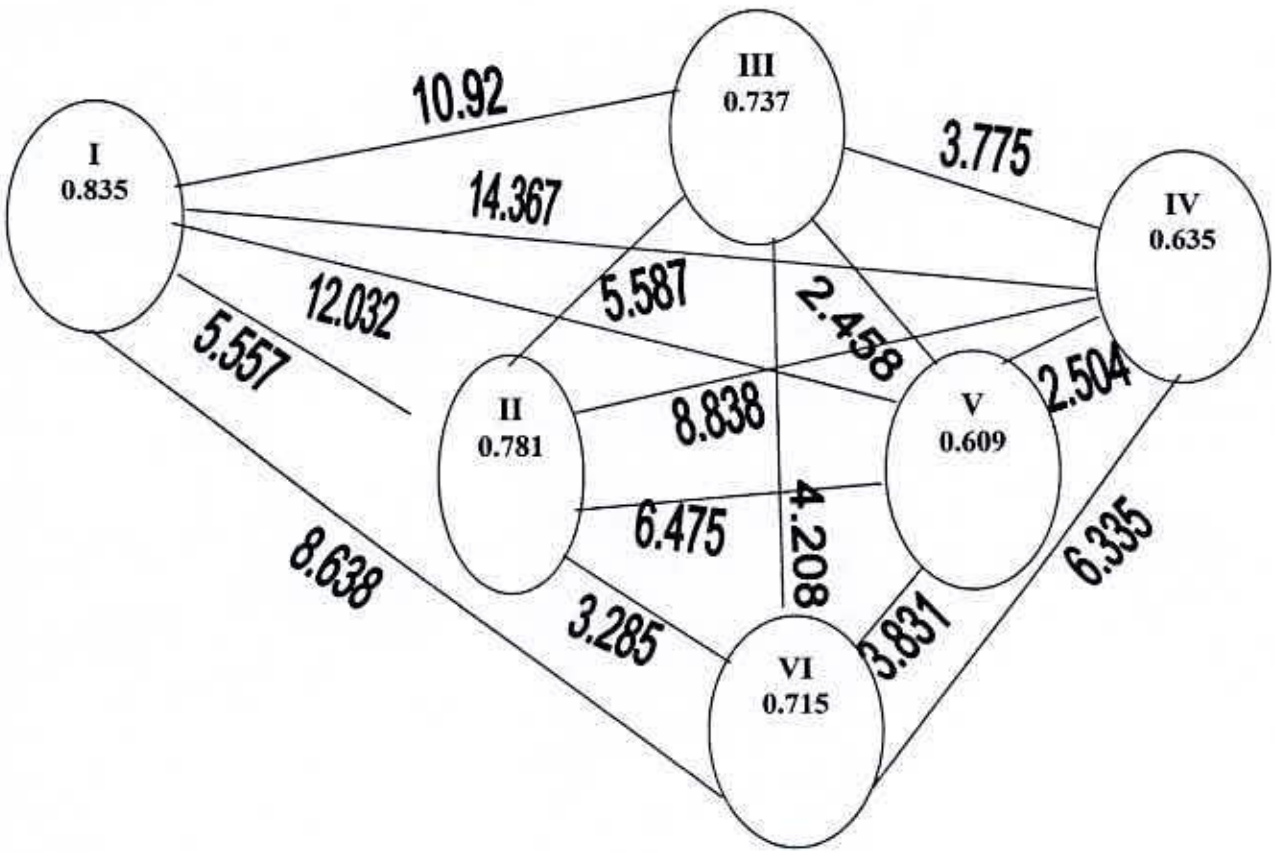


Figure 3. Diagram showing intra and inter-cluster distances ($\sqrt{D^2}$) of 51 white jute (*C. capsularis* L.) genotypes

4.2 CONTRUBUTION OF THE CHARACTERS TOWARDS DIVERGENCE OF THE GENOTYPES

Contribution of characters towards divergence is presented in Table 7. 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 plant height (0.6805), green weight (0.1280), fibre yield (0.0391), nodes per plant (0.0189) and base diameter(0.0146) were the major ones. In vector II (Z_2), the second axis of differentiation, plant height (0.2313), base diameter (0.1779), stick weight (0.1711) and fibre yield (0.0952) were more important for divergence but leaf angle, leaf width, petiole length, branches per plant played only a minor role in the second axis of differentiation (Table 7). The role of plant height, base diameter, green weight and fibre yield in both the vectors indicated the important components of genetic divergence in these materials.

Table 7. Latent vector for eleven morphological characters in white jute (*C. capsularis* L.) genotypes

Parameters	Vectors 1	Vectors 2
Plant height (m)	0.6805	0.2313
Leaf angle (dg)	-0.0229	-0.1594
leaf length (cm)	-0.0352	-0.0133
Leaf width (cm)	-0.2678	-0.3850
Petiole length (cm)	-0.3410	-0.0463
Base diameter (mm)	0.0146	0.1779
Nodes /plant	0.0189	0.0341
Branches /plant	-0.0549	-0.0760
Green weight (gm)	0.1280	0.0223
Stick weight (gm)	0.0199	0.1711
Fibre. Yield /Plant (gm).	0.0391	0.0952

4.3 Analysis of variance and genetic parameters

The genotypes differed significantly for all the characters (Appendix I). The extent of variation among the genotypes in respect of 11 characters was studied and means value, range and coefficient of variation have been presented in Table 8. 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 9.

4.3.1 Plant height

Significant differences were observed among the genotypes for plant height. Plant height ranged from 2.043m to 3.024 m and mean height is 2.556m.(Table 8). The moderate heritability (37.40) together with considerable genetic advance (8.77%) indicated the effectiveness for selection of this character (Table 9). Similar results were observed by Chaudhury *et al.* (1984) in jute.

4.3.2 Leaf angle

Significant differences among the genotypes were observed for leaf angles per plant. Maximum leaf angle was 84.08 dg and minimum leaf angle was 66.30 dg and mean value was 77.13 dg (Table 8). The phenotypic coefficient of variation (8.01) and genotypic (5.82) coefficient of variation were close to each other indicating less environmental influence incase of leaf angle (Table 9).

Table 8. Estimation of statistical parameters of ten different characters of fifty one different genotypes of white jute (*C. capsularis*)

Characters	Range	Mean	CV%
Plant height (m)	2.043 ----3.024	2.556	9.03
Leaf angle (dg)	66.30----84.08	77.13	5.50
leaf length (cm)	11.04----15.26	13.67	8.89
Leaf width (cm)	3.896----6.450	5.087	8.52
Petiole length (cm)	3.819----6.151	4.878	13.17
Base diameter (mm)	14.50----23.58	17.33	11.47
Nodes /plant	37.33----68.87	50.70	11.02
Branches /plant	1.00----10.67	2.26	27.89
Green weight (gm)	97.50----238.1	155.6	12.05
Stick weight (gm)	17.46----63.05	34.27	7.97
Fibre.yield /Plant (gm).	6.98----28.12	11.70	10.46

4.3.3 Leaf length

The mean value of leaf length showed significant differences among the genotypes. The minimum and maximum leaf length was observed 11.04cm and 15.26 cm respectively (Table-8). The phenotypic variance (2.08) is higher then genotypic variance (0.60). Heritability was low (28.96) and genetic advance as percentage of mean was low (6.29) (Table 9). With such low heritability and low genetic advance, selection on leaf length would not be judicious.

4.3.4 Leaf width

Significant differences among the genotypes were observed from the analysis of variance for leaf area. The mean value for leaf width was 5.087 cm (Table-8). The phenotypic variance (0.51) and genotypic variance (0.33) were close to each other indicating negligible environment influence on leaf width. Moderate high heritability (63.42) with considerable genetic advance (18.41%) for this trait might be taken into consideration (Table-9) while selecting a suitable line as suggested by Jhonson et al. (1955). Similar results were found in Ghosdastidar and Das(1984).

4.3.5 Petiole length

The mean values for petiole length showed significant differences among the genotypes. The petiole length ranged from 3.819 cm to 6.151 cm with a mean value of 4.878 cm (Table-8). The phenotypic variance (0.62) was much higher than genotypic variance (0.20). The heritability (33.10) was low with a low genetic advance (10.98%) (Table-9). With such low heritability and low genetic advance, selection on petiole length not is judicious.

4.3.6 Base diameter

Analysis of variance showed significant differences among the genotypes for base diameter. Base diameter ranged from 14.50 m to 23.58 m and mean value was 17.33 m (Table-8). This trait showed higher differences of phenotypic coefficient of variation than corresponding genotypic coefficient of variation (Table 9). The higher differences of PCV and GCV suggest that the expression of character was mostly under the control of environment. With low (30.10) heritability and also low (8.50) genetic advance indicated selection for this character would not 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.

4.3.7 Nodes per plant

The variance due to node number showed that the genotypes differed significantly. The maximum node number was found (68.87) and minimum was (37.33) (Table 8). The phenotypic coefficient of variation (14.16) and genotypic coefficient of variation (8.89) closely related to each other. Moderate high heritability (39.46%) with

considerable genetic advance (11.51) (Table 9), 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).

4.3.8 Branches per plant

The mean value for number of branches per plant showed significant differences among the genotypes. The highest branches per plant was 10.67 and lowest was 1.00.The high heritability (84.13%) with high genetic advance (Table 9) indicating that this trait might be taken into consideration while selecting suitable genotypes for breeding program.

4.3.9 Green weight

Significant differences were observed among the genotypes in respect of green weight. Green weight ranged from 97.50 gm to 238.1 gm (Table-8). The estimates of phenotypic variance were very high (1507.85). Heritability (76.51%) and genetic advance were very high (39.19) (Table-9). Difference between phenotypic and genotypic coefficient of variation were small.However high heritability and high genetic advance indicate that this trait might be taken into consideration while selecting a suitable l

Table 9. Estimation of genetic parameters of ten different characters of fifty one different genotypes *(C. capsularis)*

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

Note: PH= Plant height (m), LA= leaf angle (dg), LL= leaf length (cm), LW= Leaf weidth (cm), PL= Petiole length (cm), BD= Base diameter (mm), BP= branches per plant, NP= Nodes/plant, GW= Green weight (gm), StW= Stick weight (gm) and FW= fibre weight per plant (gm).

4.3.10 Stick weight

Stick weight ranged from 17.46 gm to 63.05gm and mean weight was 34.27gm. (Table 8). The phenotypic (15.91) and genotypic (15.04) variance were close to each other. A minimum difference between phenotypic coefficient of variation (34.08) and genotypic coefficient of variation (33.13) indicate less influence of environmental factors on expression of this character (Table-9). Therefore, selection based on upon phenotypic expression of this character would be effective for the improvement of this crop.

4.3.11 Fibre weight

Dry fibre weight ranged from 6.98 gm to 28.12 gm showed significant differences among the genotypes (Table 8). The genotypic coefficient of variation (28.88) and

phenotypic coefficient of variation (29.99) were close to each other. The heritability (87.84%) as well as genetic advance in percentage of mean (54.27) was observed higher (Table-9). The higher heritability with high genetic advance as percentage of mean provided opportunity for selecting high valued genotypes for breeding programs.

4.4 Correlation coefficient

Yield is a complex product being influenced several interdependent quantitative characters. The Phenotypic and genotypic correlation coefficients between yield and yield attributing characters are presented in Table 10.

4.4.1 Phenotypic correlation coefficient among yield contributing characters

Phenotypic correlation coefficient among characters themselves has been presented in Table 10. Among inter character correlation highly significant positive association were observed, stick weight per plant vs. fibre weight per plant (0.814) followed by leaf width vs. petiole length (0.808), base diameter vs. nodes per plant (0.648), leaf angle vs. base diameter (0.534), green weight vs. stick weight (0.533), leaf angle vs. petiole length (0.513), green weight vs.fibre weight (0.508), leaf angle vs. leaf width (0.470), petiole length vs. base diameter (0.440), base diameter vs. fibre weight (0.426), leaf width vs. base diameter(0.417), leaf weidth vs. nodes per plant (0.415), plant height vs. nodes per plant (0.405), leaf angle vs. nodes per plant (0.393), leaf length vs. leaf width(0.387), plant height vs. Base diameter (0.383), petiole length vs. nodes per plant (0.343), plant height vs leaf angle (0.300), Similar findings were also reported by Sanyal and Dutta (1961). The combination which showed significant positive correlation coefficient at 5% level was as leaf angle vs. leaf length (0.288), base diameter vs. stick weight (0.263), nodes per plant vs. green weight (0.238), and plant height vs. leaf width (0.231). The combination which showed negative correlation coefficient was leaf length vs. green weight (-0.079). Rest of the combination had non significant correlation.

Table 10. Genotypic(G) and Phenotypic(P) correlation coefficient among nine quantitative characters in white jute (*C. capsularis*)

Parameters		LA(dg)	LL(cm)	LW (cm)	PL (cm)	BD (mm)	NP	GW (gm)	StW (gm)	FW (gm)
PH(m)	G	0.136	-0.142	0.067	-0.011	0.505**	0.541**	0.073	0.254*	0.219*
	P	0.300**	0.092	0.231*	0.213	0.383**	0.405**	0.157	0.181	0.180
LA(dg)	G		0.789**	0.529**	0.779**	0.383**	0.142	0.185	-0.031	0.012
	P		0.288*	0.470**	0.513**	0.534**	0.393**	0.145	0.057	0.122
LL (cm)	G			0.777**	0.868**	0.551**	0.425**	-0.127	-0.041	0.068
	P			0.387**	0.376**	0.126	0.121	-0.079	0.023	0.057
LW (cm)	G				0.999**	0.494**	0.567**	-0.057	-0.076	0.102
	P				0.808**	0.417**	0.415**	0.079	0.102	0.131
PL (cm)	G					0.519**	0.500**	-0.104	-0.133	0.049
	P					0.440**	0.343**	0.121	0.059	0.143
BD (mm)	G						0.241*	0.371**	0.448**	0.561**
	P						0.648**	0.370**	0.263*	0.426**
NP	G							0.231*	0.271*	0.162
	P							0.238*	0.148	0.190
GW (gm)	G								0.614**	0.542**
	P								0.533**	0.508**
StW (gm)	G									0.868**
	P									0.814**

* Significant at 5% level
** Significant at 1% level
Note: PH= Plant height (m), LA= leaf angle (dg), LL= leaf length (cm), LW= Leaf width (cm), PL= Petiole length (cm), BD= Base diameter (mm), NP= Nodes/plant, GW= Green weight (gm), StW= Stick weight (gm) and FW= fibre weight per plant (gm).

4.4.2 Genotypic correlation coefficient among yield contributing characters

Genotypic correlation coefficient among characters themselves has been presented in Table 10. Among inter character correlation highly significant positive association were observed incase of nine characters. The combination which showed highly significant positive correlation coefficient was observed in leaf width vs. petiole length (0.999) followed by leaf length vs. petiole length (0.868), leaf angle vs. leaf length (0.789), leaf angle vs. petiole length (0.779), leaf length vs. leaf width (0.777), green weight vs. stick weight (0.614), leaf width vs. nodes per plant (0.567), base diameter vs. fibre weight (0.561), leaf length vs. base diameter (0.551), green weight vs. fibre weight (0.542), plant height vs. nodes per plant (0.541), leaf angle vs. leaf width (0.529), petiole length vs. base diameter(0.519), plant height vs. base diameter (0.505), petiole length vs. nodes per plant (0.500), leaf width vs. base diameter (0.494), base diameter vs. stick weight (0.448), leaf angle vs. base diameter (0.383), base diameter vs. green weight (0.371). The combination which showed significant positive correlation coefficient at 5% level was nodes per plant vs. stick weight (0.271), plant height vs. stick weight (0.254), base diameter vs. nodes per plant (0.241), nodes per plant vs. green weight (0.231) and plant height vs. fibre weight (0.219).The combination which showed highly significant negative correlation coefficient was plant height vs. leaf length (-0.142). Rest of the combination had non significant correlation. Similar findings were reported by Banerjee *et al.* (1988).

4.5 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, leaf angle, leaf length, leaf width, petiole length, base diameter, nodes per plant, green weight and stick weight were independent variables.The association of characters for the nine casual variables with fibre weight related to genotypic path coefficient analysis has been presented in Table 11.

4.5.1 Plant height

Plant height had negative direct effect on fibre weight (-0.113) at genotypic level and it had positive correlation with fibre weight. Plant height has contributed indirectly through leaf

length (0.038), leaf width (0.011), base diameter (0.138) and stick weight (0.220) at genotypic level. 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).

4.5.2 Leaf angle

Leaf angle had negative direct effect on fibre weight (-0.026) at genotypic level. But it was positive correlation with fibre weight at both levels. The leaf angle contributed indirectly through leaf weidth(0.088), petiole length(0.127), and base diameter(0.104) at genotypic level. Other indirect effects were negligible.

4.5.3 Leaf length

Leaf length had negative direct effect on fibre weight (-0.268) at genotypic level. But it was positive correlation with fibre weight at both levels. The leaf length contributed indirectly through plant height (0.016), leaf width (0.129), petiole length (0.141), base diameter(0.150) and green weight(0.007) at genotypic level. The indirect negative effect may be nullified by positive indirect effect.

Table 11. Partitioning of genotypic correlation coefficients into direct (bold faced) and indirect effects by path analysis

	PH	LA	LL	LW	PL	BD	NP	GW	SW	Genotypic correlation with yield
PH	**-0.113**	-0.004	0.038	0.011	-0.002	0.138	-0.066	-0.004	0.220	0.2185*
LA	-0.015	**-0.026**	-0.211	0.088	0.127	0.104	-0.017	-0.011	-0.027	0.0118
LL	0.016	-0.021	**-0.268**	0.129	0.141	0.150	-0.052	0.007	-0.036	0.0676
LW	-0.008	-0.014	-0.208	**0.166**	0.163	0.135	-0.069	0.003	-0.066	0.1022
PL	0.001	-0.021	-0.233	0.166	**0.163**	0.141	-0.061	0.006	-0.115	0.0485
BD	-0.057	-0.010	-0.148	0.082	0.084	**0.273**	-0.029	-0.021	0.387	0.5612**
NP	-0.061	-0.004	-0.114	0.094	0.081	0.066	**-0.122**	-0.013	0.234	0.1616
GW	-0.008	-0.005	0.034	-0.010	-0.017	0.101	-0.028	**-0.057**	0.532	0.5419**
SW	-0.029	0.001	0.011	-0.013	-0.022	0.122	-0.033	-0.035	**0.866**	0.8683**

R= 0.405

*Significant at 5% level

** Significant at 1% level

PH= Plant height (m), LA= leaf angle, LL= leaf length (cm), LW= Leaf weidth (cm), PL= Petiole length (cm), BD= Base diameter (mm), NP= Nodes/plant, GW= Green weight (gm), SW= Stick weight (gm) and FW= fibre weight per plant (gm).

R= residual effects

4.5.4 Leaf width

The direct effect of leaf width on fibre weight (0.166) was positive at genotypic level. It had also positive correlation with fibre weight at both levels. The positive indirect effect of petiole length (0.163), base diameter (0.135) and green weight (0.007) at genotypic level while negative indirect effect through plant height(-0.008),leaf angle(-0.014), leaf length (-0.208) nodes per plant(-0.069) and stick weight(-0.066).

4.5.5 Petiole length

Petiole length had direct effect on fibre weight(0.163) was positive at genotypic level. It had also positive correlation with fibre weight at both levels. The positive indirect effect of petiole length through plant height(0.001),leaf weidth(0.166),base diameter(0.141),green weight(0.006) and negative indirect effect leaf angle(-0.021), leaf length(-0.233),nodes per plant(-0.061) stick weight(-0.115) at genotypic level on petiole length.

4.5.6 Base diameter

Base diameter had positive direct effect on fibre weight (0.273) at genotypic level and it was also positive correlation with fibre weight at both levels. The positive indirect effect of base diameter through leaf width (0.082), petiole length (0.084) and stick weight (0.387).Other highest indirect negative effect was (-0.148) by leaf length. Other indirect effects were negligible.

4.5.7 Nodes per plant

Nodes per plant had negative direct effect on fibre weight (-0.122) at genotypic level and it was also positive correlation with fibre weight at both levels. The positive indirect effect of nodes per plant through leaf width (0.094), petiole length(0.081), base diameter (0.066) and stick weight (0.234) at genotypic level while negative indirect effect through leaf length(-0.114). Other indirect negative effects were negligible. Similar results were reported by Dahal(1991).

4.5.8 Green weight

The direct effect of green weight was negative and negligible (-0.057) at genotypic level but it had positive correlation at both levels contributed indirectly through stick weight (0.532), base diameter (0.101). Other indirect effects were negative and negligible.

4.5.9 Stick weight

The direct effect of stick weight on fibre weight (0.866) was positive at genotypic level. It had also positive correlation with fibre weight at both levels. The positive indirect effect of leaf angle(0.001), base diameter(0.122) at genotypic level while negative indirect effect through plant height(-0.029),leaf width(-0.013), petiole length(-0.022), nodes per plant(-0.033) and green weight(-0.035). Path analysis indicated that stick weight was the most important character, which had maximum contribution to fibre yield as it exhibited highest direct effect.

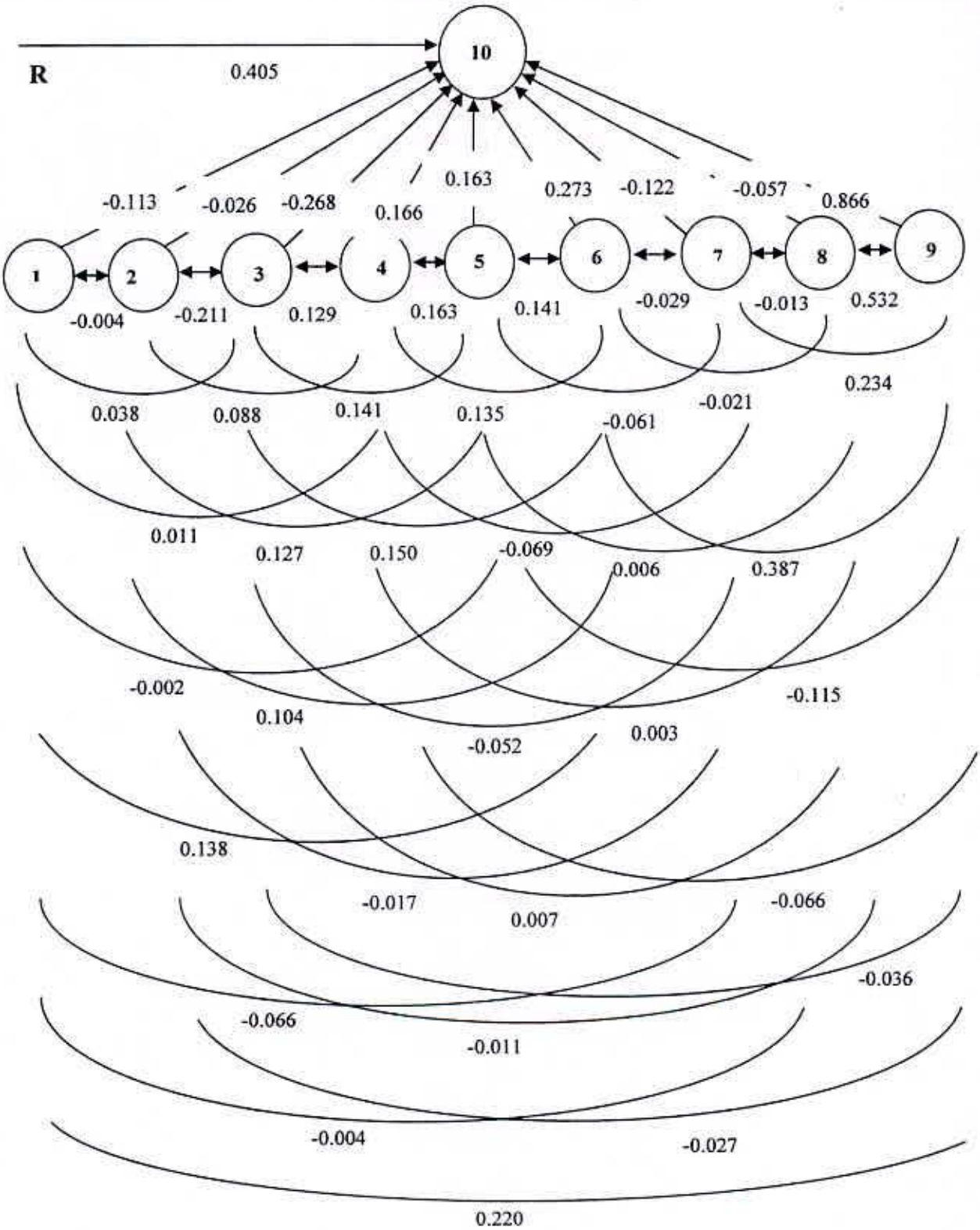


Fig. 4. Path diagram of 9 yield contributing traits in white jute
1= Plant height (m), 2= leaf angle, 3= leaf length (cm), 4= Leaf weidth (cm), 5= Petiole length (cm), 6= Base diameter (mm), 7= Nodes/plant, 8= Green weight (gm), 9= Stick weight (gm) and 10= fibre weight /plant (gm). R= residual effects.

Chapter 5

Summary and Conclusion

CHAPTER 5

SUMMARY AND CONCLUSION

With an objective to assess the genetic variability and correlation among the various yield attributing characters, the present investigation," Genetic divergence, variability, correlation and path analysis in white jute (*C. capsularis* L.)" was undertaken with fifty one genotypes of geographic origin. The experiment was conducted RCBD with three replications at the Central Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikgonj during the period April to August 2010. 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, branches 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 (PCA) 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.

The first four component axes accounted for 90% variation towards the divergence. According to PCA, D^2 and cluster analysis the genotypes were grouped into six clusters. Six clusters were found from a scattered diagram formed by Z_1 and Z_2 values obtained from PCA. The highest inter-cluster distance (14.367) was observed between clusters I and IV followed by cluster I and V, I and III, II and IV, I and VI, II and V and so on. The lowest inter-cluster distance (2.458) was observed between the cluster III and V followed by IV and V, II and VI, III and IV,V and VI, III and VI and so on. The highest intra-cluster distance was observed in cluster I contained seven genotypes. The lowest intra –cluster was observed in cluster V contained ten genotypes. The principal component analysis revealed that plant height, base diameter, nodes number, green weight and fibre weight were the important components of genetic divergence in the population.

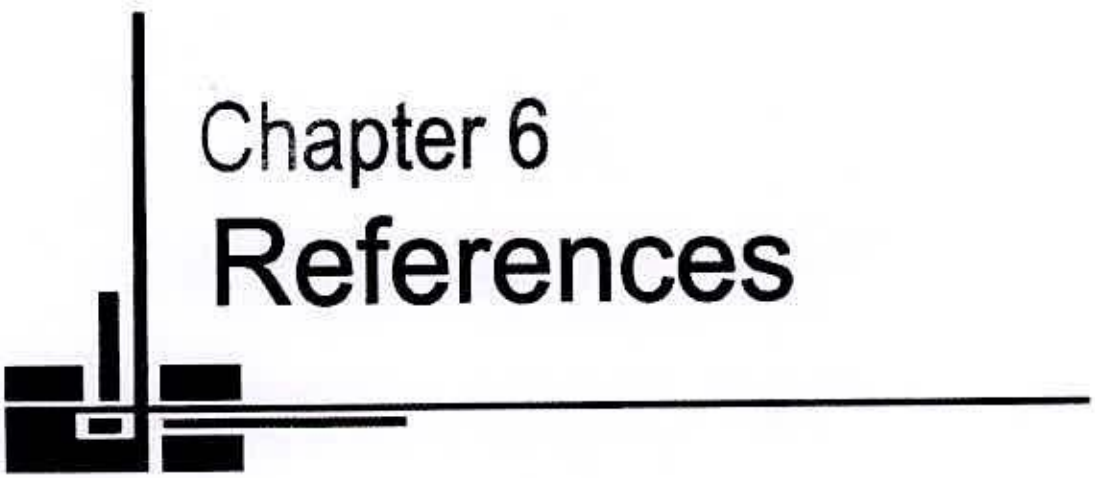
The phenotypic coefficient of variation was higher for all the characters than their corresponding genotypic coefficient of variation. Among the characters the highest genotypic coefficient of variation was recorded for branches per plant followed by stick weight, fibre weight, green weight, leaf width, nodes per plant, base diameter, petiole length, Plant hight, 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 characters branches per plant, stick weight, fibre weight and green weight which suggests 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.

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

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 G_{47},G_{33},G_{48} from cluster I ; G_{27},G_{17},G_{23}, from cluster III and G_{13},G_{40},G_{45}, from cluster II were considered to be better parents for future use in hybridization programme.



Chapter 6
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APPENDICES

Appendix I: Analysis of variance of nine different characters of 51 different genotypes of white jute (*C. capsularis*).

S0urce of variation	df	Plant height (m)	Leaf angle	leaf length (cm)	Leaf width (cm)	Petiole length (cm)	Base diameter (mm)	Nodes/plant	Branch /plant	Green weight (gm)	Stick weight (gm)	Fr.yield/Pl.
Replication	2	1.17**	281.573**	0.292	0.904**	0.047	0.155	355.343**	2.355**	11434.803**	582.803**	761.107**
MSS	50	0.148**	78.446**	3.279**	1.166**	1.026**	9.05**	92.209**	6.73**	3815.19**	45.986**	291.288**
Error	100	0.053	17.99	1.475	0.188	0.413	3.949	31.203	0.398	354.184	0.871	12.85

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

Appendix II. Monthly summarized of mean daily maximum and minimum air temperature and monthly rainfall during the cropping season at Jute Agricultural Experimental Station, Jagir, Manikgonj

Month	Mean daily temperature		Monthly rainfall (mm).
	Max(^{0}c)	Min(^{0}c)	
April/10	34.76	24.60	234.00
May/10	35.13	25.27	348.00
June/10	32.70	26.23	367.67
July/	32.36	26.76	303.00
August/10	31.34	25.96	295.00

Appendix III. Principal component scores for 51 white jute (*C. capsularis* L.) genotypes

Genotype No.	Z1	Z2
1	26.09	-1.58
2	27.86	4.22
3	13.68	11.96
4	0.70	-8.28
5	27.40	5.08
6	11.98	4.34
7	-38.30	-3.29
8	-56.96	-4.56
9	-11.24	-4.18
10	22.54	10.79
11	38.16	0.63
12	-63.43	6.57
13	-20.79	-14.33
14	-64.03	-0.97
15	-69.06	19.61
16	-18.21	-4.36
17	16.28	7.84
18	12.22	4.41
19	-6.27	-6.01
20	29.23	0.81
21	24.69	-1.12
22	-17.77	-1.29
23	4.79	9.10
24	41.94	-1.30
25	-5.20	-3.85
26	1.80	-12.35
27	30.68	21.10
28	42.08	2.91
29	14.89	-7.47
30	14.92	-2.31

Cont.d(Appendex-III)

Genotype No.	Z1	Z2
31	31.44	5.52
32	39.95	-0.34
33	-59.45	5.12
34	11.67	-5.47
35	39.55	-11.69
36	36.35	-7.31
37	-22.66	4.36
38	-5.51	-14.68
39	-0.34	-10.01
40	-15.08	12.58
41	-8.15	-10.18
42	8.70	-8.88
43	-27.56	-9.77
44	-8.65	-0.73
45	-39.68	6.71
46	16.59	11.61
47	-62.53	-12.82
48	-85.80	9.07
49	40.24	10.92
50	59.08	-1.14
51	21.18	-5.01