DIVERGENCE STUDY OF WHITE JUTE

(*Corchorus capsularis* L.)

BY

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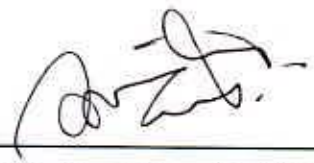

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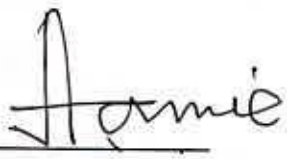

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*This is to certify that thesis entitled, "**DIVERGENCE STUDY OF WHITE JUTE (Corchorus capsularis L.)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **ABU SALEH MUHAMMAD YAHIYA**, Registration No. **00120** 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.

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DEDICATED TO
MY
BELOVED PARENTS

LIST OF ABBREVIATION AND SYMBOLS

Full Word	Abbreviation
Agro-Ecological Zone	AEZ
Assam Rice Collection	ARC
And others	*et al.*
Bangladesh Bureau of Statistics	BBS
Bangladesh Jute Research Institute	BJRI
Bangladesh Rice Research Institute	BRRI
Canonical Vector Analysis	CVA
Centimeter	cm
Cluster Analysis	CSA
Degree	^{0}(dg)
Degree Celsius	^{0}C
Degree of freedom	df
East	E
Et cetera	etc.
First filial	F_1
Figure	Fig.
Gram	g
International Jute Organization	IJO
Journal	J
Kilogram	Kg
Mean sum of square	MS
Meter	m
Millimeter	mm
Minute	"
Muriate of potash	MP
Negative logarithm of hydrogen ion concentration	p^H
North	N

Full Word	Abbreviation
Number	no.
Percent	%
Principal Component Analysis	PCA
Principal Coordination Analysis	PCO
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
That is	i.e.
Triple Super Phosphate	TSP
United Kingdom	UK
United States of America	USA
Univariate Analysis	UV

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DIVERGENCE STUDY OF WHITE JUTE
(*Corchorus capsularis* L.)

ABSTRACT

A field experiment was conducted with 42 genotypes of white jute (*Corchorus capsularis* L.) at the Jute Agriculture Experimentation Station, Jagir, Manikganj. Genetic divergence was estimated on the basis of thirteen different characters. Significant genotypic differences were observed for most of the characters studied. Multivariate techniques were used to classify 42 white jute genotypes, which computed by Mahalanobis's D^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 had the maximum of eleven genotypes while cluster II had the minimum of three genotypes. The highest inter-genotypic distance was found between G36 and G39 and the lowest distance between G4 and G23.The highest inter-cluster distance was observed between clusters I and II, and the lowest inter-cluster distance was observed between clusters I and VI. The highest intra-cluster distance was found in cluster I and the lowest in cluster II. Genotypes of cluster II had the highest values for base diameter, middle diameter, top diameter, core diameter, dry fibre weight and dry stick weight and that of cluster V had the highest values for technical height, leaf angle, leaf length and petiole length. Yield and yield contributing characters such as technical height, base diameter, dry fibre weight and dry stick weight contributed more towards genetic divergence considering diversity pattern. The clustering pattern indicated that geographic diversity was not a reliable guide to genetic diversity. Considering genetic diversity and other agronomic performances the genotypes G28 and G35 from cluster I; G7, G20, G22, G25, G30, G39 and G41 from cluster IV; G8, G19 and G24 from cluster V might be considered as suitable parents for future hybridization programme.

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Introduction

CHAPTER I

INTRODUCTION

Bangladesh is a homeland of quality jute production and the second largest producer of jute around the world. Jute is the principal cash crop of Bangladesh. It occupies 5th position after rice, pulses, oil seeds and wheat in respect of cultivated area (BBS, 2005). Bangladesh is not only the second largest producer of jute but she produces the best quality jute and leads the export market. Bangladesh produces 0.794 million tons of raw jute on about 0.392 million hectares of land with the national average production of 2.03 tons per hectare. It contributes about 6% of the total exporting earning and employs around 30 million people in different events such as cultivation, processing, carrying, marketing, research, trading and exporting jute (BBS, 2004). Jute fibre is extracted from the bark of the jute plant and is known as a bast fibre. About 95 percent of the world's jute is produced in Bangladesh, India and Pakistan. Jute fibre is the cheapest fibre and is used in the manufacture of cordage, gunny cloth, gunny bags and other packaging materials for agricultural and industrial products. Now a days, novotex, blanket, fabrics, shopping bags, knitwear, nursery sheets and pots, micro crystal cellulose for pharmaceutical products, geo-jute and photo stable dye are being made from jute (Islam, 1996). Jute constitutes an important source of employment and is of significant importance in the rural economy of Bangladesh.

Commercially jute is often referred to as the "golden fibre of Bangladesh", because of its immense contribution for the economy of this

country. A good part of the total population of our country is engaged directly and indirectly in production and processing of jute. Jute exports constitute an important source of foreign exchange (12-13%) earning in Bangladesh. During the year of 2004-2005, Bangladesh exported 619000 tons of raw jute and jute goods and earned about 16908 million taka (BBS, 2005).

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 species, which are distributed throughout the tropical regions of Africa, Australia, China and South-East Asia. Only two of the species, *Corchorus capsularis* L. and *Corchorus olitorius* L. are cultivated commercially for their fibre production. *Corchorus capsularis* L. has its center of origin in Indo-Burma (Singh, 1976) and *C. olitorius* L., however, originated in North Africa (Kundu *et al.*, 1959). *Corchorus capsularis* L. is called deshi pat or white jute and its fibre is ordinarily whitish.

White jute (*C. capsularis* L.) can grow both in low and high land and has better adaptability than the other cultivated jute 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-grown plants are tolerant to standing water. In general, *capsularis* shows flexibility in relation to drought and flood condition.

Although jute exhibits high socio-economic importance and its fibre is friendly to the environment for the producing countries, the global

situation is confronted with number of problems. The prices paid to the farmers are not remunerative and subject to annual fluctuations. The area under jute in Bangladesh is declining and the crop is also being pushed more and more to the marginal lands.

In our country, 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 insect pests, diseases, drought, water logging, low temperatures 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, selection of such parents is a long term and tedious job. Genetic diversity is the fundamental law of plant breeding which is major tool and being used in parent selection for efficient hybridization programme. Modern breeding work needs 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 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). Therefore, the availability of transgressive segregant in any breeding programme depends upon the divergence of the involving parents. The quantification of genetic diversity through biometrical procedures (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse 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). Thus the present work was undertaken under the following objectives:

Objective(s):

- To study the genetic divergence among the different white jute genotypes
- To study the factors influencing genetic divergence
- To select the desirable parents for hybridization

Chapter II

Review of literature

CHAPTER II
REVIEW OF LITERATURE

Jute (*C. capsularis* L. and *C. olitorius* L.) is one of the most important fibre crops grown in Bangladesh, India, Indonesia, China, Thailand, Nepal and some other Asian and South American countries. Unlike cereals or even cotton, the economic yield in the form of fibre is derived from the vegetative part (the bark of the stem) in green condition, and it is impossible to derive fibre and mature seeds from the same plant. The knowledge of genetic diversity in crop plants is the key to success of breeding programmes. For this reason, breeders are forced to exercise selection on the basis of highly correlated components of yield such as technical height, stem diameter, node number, dry fibre weight, dry stick weight and so on. In Bangladesh and elsewhere in the world research reports on diversity analysis of jute crop is scanty. Therefore, information related to the diversity of seed fibre crops and some other self-pollinated crops available in the literature are reviewed in this section. Moreover, literature related to the efficient multivariate technique for diversity analysis is also reviewed.

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. Selection of diverse parents belonging to distant groups leads to wide spectrum of gene recombination for quantitative traits. Divergence technique measures the forces of differentiation at two levels, intra and inter-cluster levels, and thus helps in the selection of genetically diverse parents for their

exploitation. The multivariate analysis using D^2 statistic can estimate the amount of genetic diversity in a given set of genotypes in respect of several morphological traits considered together.

2.1 GENETIC DIVERSITY

Islam (1996) conducted a field experiment to assess the genetic divergence by using Mahalonobis's 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 programme.

Shreshtha (1991) used 26 genotypes of *C. capsularis* L. based upon eleven quantitative characters and grouped into 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 ecogeographical region was similar to that of other regions, since genotypes from distinct centres were grouped together. Genotypes from one ecogeographical region and also belonging to different pigmentation grade were grouped into different clusters. It indicated the presence of substantial variability within themselves. It was also evident that there was no parallelism between genetic diversity and geographical distribution of genotypes.

Sixty varieties/strains of jute were studied by Sasmal (1978) using D^2 statistics. Varieties of *C. capsularis* L. and *C. olitorius* L. formed six and eleven distinct clusters, respectively. Recombinant types were found to be included in closely related groups instead of their parental groups. The genetic distance was found maximum between cluster IV and V while it was minimum between III and VI indicating that these two clusters were very close to each other. Intra-group distance ranged from 0 to 6.69. He also stated that the grouping pattern to the varieties and the relationship between the clusters were not in complete accordance with their pedigrees. He also pointed out that the clusters, which possess varieties having poor fibre yield, are close together indicating that an effective multitire hybridization programme for obtaining hybrids superior in fibre yield would include varieties from distance clusters.

A field experiment with 85 soybean genotypes was conducted by Chowdhury (1993) to study the diversity pattern. As per PCA, D^2 and cluster analysis the genotypes were grouped into five different clusters. Seed size, pod length and days to emergence have been found contributing maximum towards divergence. He also stated that diversity was influenced by the morphological characters, but not by the origin of the genotypes.

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.

Shingh and Gupta (1968) stated that in upland cotton the genetic distance between two clusters including the varieties of same pedigree might be greater than the clusters having varieties derived from distinct types.

Saha (1993) reported the genetic divergence among 24 linseed (*Linum usitatissium*) genotypes on the basis of 13 quantitative characters and grouped into six clusters. D^2 values ranged from 9.02 to 746.89 and indicated the presence of possible genetic divergence in the population. He suggested that the clusters which were separated by the greatest statistical distance showed the maximum divergence and there was no relationship between genetic diversity and geographical distribution of the genotypes. He further indicated the availability of genetic diversity in types from same geographical origin.

Kumar and Asawa (1984) reported the results of multivariate analysis on three yield related traits in linseed. Forty four genotypes were grouped into 17 of which clusters; IX and X had the largest inter-cluster values; number of days to flowering and seed volume together accounted for 28 percent of the divergence. They also recommended varieties from different clusters to be hybridized to exploit genetic divergence.

In an experiment, Das and Gupta (1984) reported that in black gram, thousand grains weight and the branches per plant were found the main components of 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 linseed on the basis of multivariate analysis on 12 yield and quality components; 50 genotypes were grouped into 14 clusters by Chawala and Singh (1984). They showed that there was no relationship between genetic diversity and geographical origin of the genotypes.

Nadaf *et al.* (1986) studied the multivariate analysis of 83 genotypes of bunch groundnut from 18 countries on the basis of yield/plot and six other agronomic characters. Nine clusters were found which were not related to the grouping formed by geographical origin. They also observed that pod yield accounted for 88% of the total variation. They indicated that the number of developed pods, 50% flowering and 100 seed weight were also important in accounting for divergence.

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.

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.

Katiyar and Singh (1990) studied the genetic diversity of 40 indigenous and exotic strains of faba bean (*Vicia faba* L.). The genotypes were

grouped into 12 different clusters and no direct association was found between geographic distribution and genetic diversity.

With the genetic divergence study of 128 pea germplasm, and the whole population was divided into 16 broad based groups by Mian *et al.* (1991). The clustering pattern suggested no parallel relationship between genetic diversity and geographic distribution.

Sindhu *et al.* (1989) investigated diversity in twenty strains of black gram from different agro-ecological zones of India by Mahalonobis's D^2 statistics. They observed no parallelism between geographical and genetic diversity.

Thiagarajan *et al.* (1988) studied the genetic divergence among 7 parents and their 12 hybrids of cowpea. The genotypes were grouped into seven clusters. They stated that the characters namely 50% flowering, 100 grain weight and plant height contributed maximum towards genetic divergence. Similar reports were made by Ramanujam *et al.* (1974) in a study with 10 parents and their 25 F_1S in mungbean.

Divergence analysis was carried out by Natarajan and Palanisamy (1990) on 8 genotypes of mungbean and their 15 hybrids. The genotypes were grouped into 5 clusters. The canonical analysis confirmed to a large extent, the clustering patterns obtained by multivariate analysis. Canonical analysis identified harvest index as one of the source of 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.

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

A study on D^2 analysis in pigeon pea conducted by Bainiwal and Jatastra (1980) revealed that plant height, pod length and days to flowering were the principal components of diversity.

In blackgram, Sagar *et al.* (1976) studied 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.

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.

Days to flowering, pod length, pod girth and hundred grain weight contributed considerably towards diversity in cowpea (Kumar *et al.*, 1982).

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

An experiment was conducted by Kumar *et al.* (2004) to assess the genetic diversity among 50 restorers. They indicated that all the restorer lines were grouped into eight clusters indicating that the high level of variability exist among the lines. The biological yield contributed height

(32%) towards divergence followed by panicle length (28.7%) and plant height (27%).

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., spikelets/panicle, filled grains/panicle, single plant yield, yield and harvest index.

Reedy *et al.* (2004) conducted an experiment to assess the nature and extent of genetic divergence among 36 genotypes of rice for 14 quantitative characters using Mahalanobis's D^2 statistics. The genotypes were grouped into six different clusters adopting Tocher's method indicated the presence of wide range of genetic variability. Diversity in pedigree of the genotypes was conspicuously reflected in the clustering pattern. Cluster V was evolved as a largest cluster comprising of 10 genotypes followed by cluster I, III and IV each comprising 8 genotypes where as cluster II and VI were consisting one genotype each. Maximum genetic distance was observed between clusters I and VI. Hybridization between these clusters is expected to generate a wide range of variability and will facilitate the isolation of desirable genotypes.

An attempt was made to find out the nature and extent of genetic divergence and variability among a set of 54 standard rice varieties with the objective of selecting genetically divergent parental lines for

hybridization. The analysis of variance revealed that highly significant variation for plant height, panicle length, flag leaf length, tillers/hill, spikelets/panicle, days to 50% flowering, maturity duration and grain yield/plot. The genotypes were grouped into nine clusters employing Mahalanobis's D^2 analysis. This indicated the presence of wide genetic diversity in experimental material for majority of the characters. The pattern of clustering indicated no general association between ecological distribution of genotypes and genetic divergence. This might be due to differential adaptation, selection criteria, selection pressure and environment. Plant height contributed maximum towards genetic divergence (40.16%), followed by flag leaf length (20.12%), grain yield/plant (15.79%) and maturity duration (15.58%). Maximum inter cluster distance (7.93) was found between cluster number VI and VIII indicating that hybridization between these two clusters could produce progeny with desirable characters (Devi *et al.* 2004).

Dass *et al.* (1993) reported that genetic divergence among 30 rice genotypes measured by Mahalanobis's D^2 statistics based on plant height, effective tiller per plant, panicle length, fertile spikelet per panicle, 1000 grain weight, days to 50% flowering, days to maturity and grain yield per plant. They were grouped the genotypes into twelve different clusters. No parallel relationship between genetic and geographical divergence was observed. Of the 9 different characters only five viz., days to 50% flowering, days to maturity, plant height, effective tiller per plant and 1000 grain weight contributed as much of the total divergence.

Chauhan and Chauhan (1994) evaluated 44 breeding lines and two improved cultivars under rainfed upland conditions. They grouped the genotypes into twelve clusters using D^2 statistics. Thousand grain weight

contributed maximum (43.3%) to the total divergence. Other traits with appreciable contribution to total divergence were to 50% flowering, panicle weight and spikelets/panicle.

Sony *et al.* (1999) conducted an experiment to assess the genetic divergence among 132 rice genotypes for 18 quality traits. They grouped the genotypes 10 clusters. Grouping of genotypes in different clusters indicated the existence of significant amount of variability among the genotypes for the quality traits studies. Higher order of divergence was recorded between cluster VI and VII. Based on the mean performance, genetic distance and clustering pattern, hybridization of selected 10 genotypes are likely to give desirable segregants for grain quality.

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, intervarietal crosses are identified which may be useful in creating wider variability for early maturity, dwarf and high yielding segregants.

Vivekananda and Subramanian (1993) reported the nature and magnitude in 28 genotypes of rain fed rice using Mahalanobis's D^2 statistics. The population was grouped into five clusters. Plant height and grain yield contributed considerably, accounting for 85% of total divergence. The geographical diversity has not been found related to genetic diversity.

Mahajan *et al.* (1981) pointed out the genetic diversity (D^2 statistics) for 11 characters related to yield in 60 clusters of rice developed from 14 crosses involving 23 parents. The 60 clusters were grouped into 18 clusters. Mostly the clusters in a cluster came from the cross. The geographical diversity was associated with genetic diversity, high yield component and multiple resistances utilized as parents in future rice breeding program.

A study on D^2 analysis in rice conducted by Balram *et al. (2004)* stated that the estimation of resulted in grouping the germplasm into 6 clusters. Maximum genotypes are in the cluster III followed by cluster II through the survey was conducted in geographically small area, existence of six clusters among these shows that they are not genetically related. Among the characters studied, days to 50% flowering and test weight with 35% and 33%, respectively contributed maximum to the total divergence. Panicle length exhibited least condition of 0.47% to the divergence. The cluster mean for each character indicated that days to 50% flowering was maximum in cluster VI, plant height in cluster II, panicle length in cluster I, productive tillers per plant in cluster V, grain/panicle in cluster IV, test weight in cluster I and grain in cluster VI. It would be logical to effect cross among the genotypes belonging to different clusters and selection within cluster with maximum inter- cluster distance to improve the rice grain yield.

Prasad *et al.* (2004) conducted an experiment with 49 genotypes of basmati rice in two consecutive years (1998 and 1999) using Mahalanobis's D^2 statistic to identify the genotypically diverse parental lines and also to study the stability of character expression from year to year. All the genotypes were grouped into four clusters in a year wise

analysis. However, only three clusters were formed by the pooled analysis of the data over years. Maximum intra-cluster distance was noted in cluster III (D=46.05) in 1998, cluster II (D=43.44) in 1999 and again in cluster II (D=34.87) in the pooled analysis. Cluster I showed minimum intra-cluster distance in both the (26.70 and 20.59 in 1998 and 1999, respectively) as well as the pooled analysis (D=19.69). Maximum inter-cluster was observed between clusters III and IV during both the years (D=209.54) and 140.2 in 1998 and 1999, respectively) while minimum inter-cluster distance was observed between clusters I and II in year wise analysis (D=37.44 and 34.94 in 1998 and 1999, respectively). However, in the pooled analysis, maximum inter-cluster distance was found between cluster II and III (D=84.99) and minimum between cluster I and II (D=29.24).

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.

Zhang *et al.* (1987) reported that multivariate analysis for the genetic distance of 7 yield related characters between the maintainer line Qing B and 31 newly developed restorer lines was used to predict heterosis. The

results, which agreed with the heterosis indices actually determined, showed that 15 restorers were better than other crosses between Qing B and 9 restorer lines, had greater genetic distances, implying higher heterosis than those with similar genetic distances.

A field experiment was conducted by Islam *et al.* (2004) to estimate the genetic diversity of 62 genotypes of irrigated rice originating from BRRI, IRRI and China through Mahalanobis's D^2 statistics. They grouped the genotypes into five clusters. The cluster II and IV contained the lowest (7). The highest intra-cluster distance was noticed for cluster III. The highest inter-cluster distance was observed between cluster I and cluster IV, followed by cluster I and cluster V, cluster I and cluster III, cluster III and cluster IV and the lowest between cluster IV and cluster V. The highest cluster mean for yield and other three yield contributing characters were obtained from cluster I, six highest and two second highest means for yield contributing characters were found in cluster III but the lowest mean for yield. Therefore, more emphasis should be given on cluster I for selecting genotypes as parents for crossing with the genotypes of cluster III, which may produce new recombinants with desired traits.

Genetic divergence studies were conducted by Singh *et al.* (1999) using 42 genotypes of rice in the boro season of 1996-97 at Rajendra Agricultural University farm at Pusa. Eleven quantitative characters, including grain yield were considered for the study. Multivariate analysis revealed considerable genetic diversity in the material and led to their grouping into four clusters. No relationship between geographic origin and genetic diversity was observed. Harvest index, total number of grains

per panicle, number of fertile grains per panicle and standability accounted 90.6% of the total divergence.

Pradhan and Roy (1990) conducted a field experiment on 25 breeding lines of rice from diverse pedigree, undertaken in two levels of water regimes (shallow and intermediate water), revealed six and seven cluster of varying constellation. The composition of clusters differed in two situations due to produce genotype environment interactions. Under both the situations, 1000 grain weight showed the highest contribution to D^2 values.

The genetic diversity and heterosis were studied with 65 rice varieties grouped into 18 clusters by Sharathe and Perraju (1990). Eight varieties were selected from these clusters on the basis of diversity estimates and popularity of variety. The 28 possible hybrid along with 8 parents fall into as many as 9 clusters. Direct relationship between genetic distance and heterobeltosis did not occur but parental diversity seems to play an important role in expressing the positive heterobeltosis. Most of the crosses did not show any relationship with divergence estimates.

Ibrahim *et al.* (1992) investigated that the genetic divergence in upland rice population compromising nine morphologically different genotypes over the different genotypes over the different environment (E) has been assessed through Mahalanobis's D^2 analysis. The analysis revealed considerable genetic diversity among genotypes. The genotypes under study fall into 3 constellation in E1, E2 and E3 in D^2. Poonagor, an indigenous short duration tall stature genotype, consistently occurred either in the same or closely related cluster in both stress (E1 and E3) and non-stress condition.

Anandakumar and Subramanium (1989) carried out an experiment with 23 drought resistant varieties during the 1987 wet season, using Mahalanobis's D^2 analysis, for plant height, productive tillers, boot leaf length and breadth and yield. Using Tocher's clustering technique genotypes were grouped into 6 clusters. Clustering patterns failed to reveal any relationship between geographic divergence and genetic variability. Several clusters were highly divergent and use of these genotypes (E45, IR9575 Sel, Moongil Samba) in breeding programmes may result in a large degree of heterosis.

In the basis of D^2 analysis of 10 characters, 67 random genotypes from the Assam Rice Collection (ARC) together with 2 genotypes from each of the subspecies *indica, japonica, javanica* and *ponlai* were grouped into 13 clusters, with 100 grain weight and grains/panicle making the greater contributions to values. The genetic diversity of the ARC strains indicated the importance of the northwestern region of India as a source of diverse germplasm. It is suggested that *javanica* strains could be synthetic assemblages of *indica* and *japonica* genotypes (De *et al.*, 1988).

Singh *et al.* (1996) showed the nature and magnitude of genetic divergence in 40 genotypes of fine rice using Mahalanobis's D^2 statistics for ten characters. The population was grouped into six clusters. Grain yield contributed the most, 40.6% of total divergence and plant height contributed 16.5%. The genotypes belonging to cluster II and V having greater cluster distance are recommended for inclusion in a hybridization programme as they are expected to produce good segregants.

An experiment was conducted by Selvakumar *et al.* (1989) to estimate the genetic diversity with 8 yield traits in 40 accessions from various

geographical areas using the Mahalanobis's D^2 statistics. The clustering pattern indicated that geographic diversity was not a reliable guide to genetic diversity. A wide range of variation in intra-cluster mean values was found for each trait. Yield component traits such as number of grains/panicle and number of fertile tillers contributed most to the genetic divergence between genotypes. Genotypes were grouped in 11 clusters and those related by provenance or pedigree tended to fall into the same cluster. The data are tabulated. Gandakasala, in cluster XI, appeared useful as a parent in breeding programmes.

Biswas and Sasmal (1990) estimated genetic distance using Mahalanobis's D^2 statistics in 7 rice varieties and their 21 F1 hybrids. They were grouped 28 genotypes into 6 clusters. The grouping of parental genotypes did not follow a geographic pattern. Shoot fresh weight was the main factor contributing to genetic variance.

In the basis of D^2 analysis by Singh *et al.* (1987) grouped fifty lowland rice cultivars into 10 clusters in respect of 15 characters related to yield. Cluster I (23 cultivars), II (8) and III (7) were the largest and together accounted for more than two-thirds of the total population. Genetic diversity was not related to geographical diversity. Plant height, sheath length, grain length and breadth, test weight, panicle length and spikelet number were mainly responsible for the divergence. Cultivars Anandi, Adamchini, Bhatafool, Kanakjiri and Motibadam (cluster IV); Dehradoon and Kesar (cluster V); Lanwangchur (cluster VIII); and Jilhore (cluster X) were selected for hybridization on the basis of their genetic diversity and high yield potential.

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 6 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.

Multivariate analysis of data on 13 yield components in 25 breeding lines grown in shallow and intermediate depth water showed 6 and 7 clusters, respectively. The composition of the clusters differed under the 2 regimes due to pronounced genotype-environment interactions (Pradhan and Roy, 1990).

Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental site

The experiment was conducted at the Jute Agriculture Experimental Station, Jagir, Manikganj during March to October, 2006. Manikganj is situated about 70 km west from Dhaka. The location of the 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 scanty rainfall during the rest of the year. During the growing period of the crop the total rainfall from April to October ranged from (70-455) mm (Appendix I).

The textural class of the soil was sandy loam to silty loam. Soil p^H ranged from 6.5 to 7.5. It belongs to the Young Brahmaputra and Jamuna Floodplain Agro Ecological Zone (AEZ No.8). The land types consist of 37% medium high land, 20% medium low land, 8% low land and 5% high land. The organic matter contain was very low.

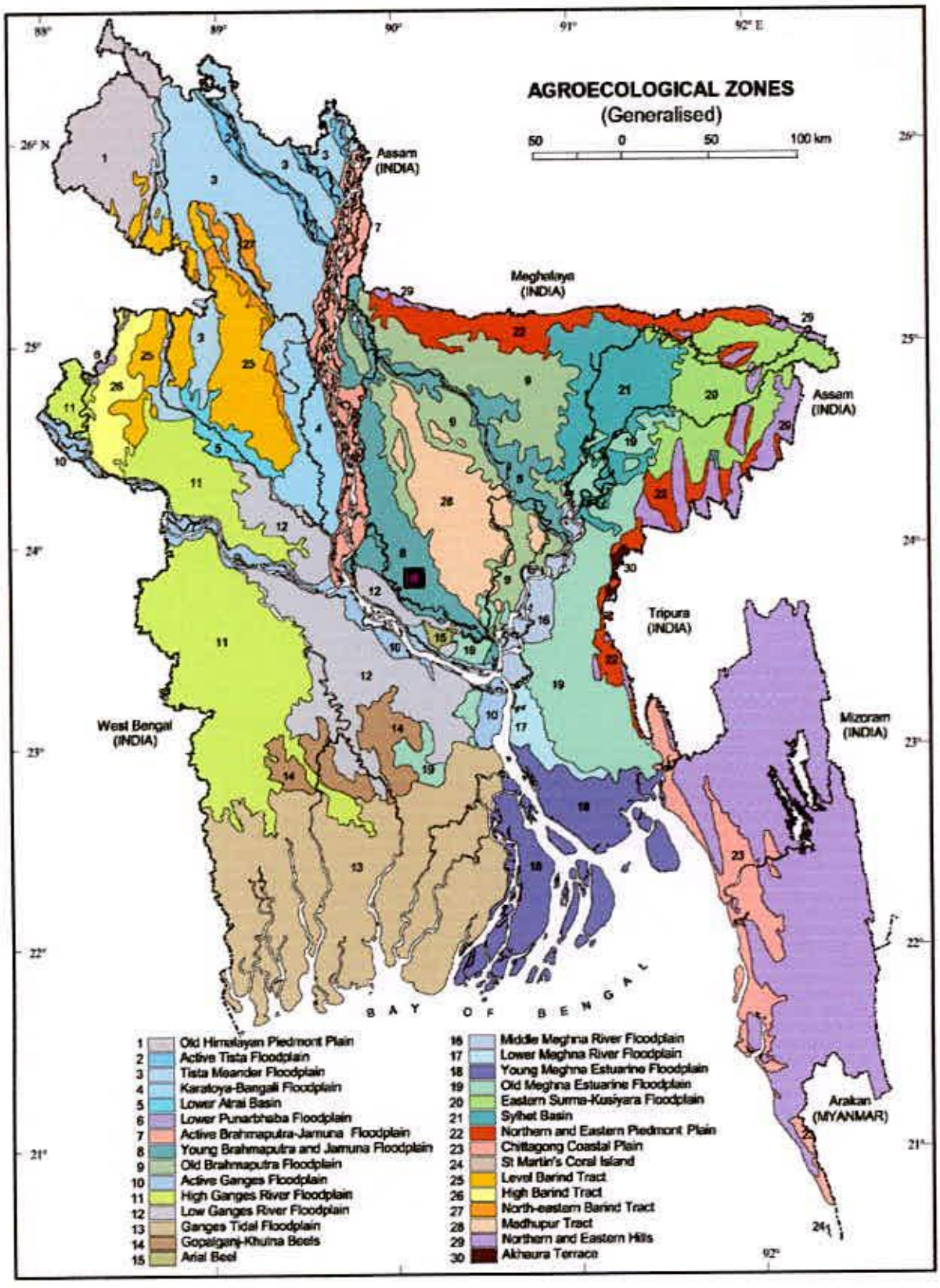

Figure 1. Location of experimental field ■

3.3 Crop materials

The crop materials consisted of 42 genotypes of white jute *(C. capsularis* L.*)* collected from the Gene Bank of Bangladesh Jute Research Institute (BJRI), Dhaka. These genotypes were collected from different regions of Bangladesh and from different countries (Table 1).

3.4 Design and layout

The experiment was laid out in Randomized Complete Block Design with three replications. Each plot had a single row of 3.0 m length. Space between rows was 0.3 m and block to block distance was 1 m. Plant to plant distance within a row was maintained at 6-7 cm. The genotypes were randomly distributed to each row within each block (Plate 1).

3.5 Land preparation

The experimental plot was prepared by deep ploughing followed by harrowing and laddering. The recommended doses of fertilizers such as 100 kg/ha urea, 25 kg/ha triple super phosphate (TSP) and 45 kg/ha muriate of potash (MP) were used. 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 twice after first and final weeding.

3.6 Sowing and intercultural operation

Seeds were sown on 29 March, 2006. Thinning and weeding were done twice after 15 and 35 days of sowing to maintain uniform plant population. Insecticide was sprayed twice and hand picking was practiced to control the jute hairy caterpillars at larval and pupal stage. Diseased plants were wiped out from the field timely.

Table 1. Sources of 42 white jute (*C. capsularis* L.) genotypes

Genotype No.	Accession No.	Source of collection	Stem Pigmentation
1	862	Bangladesh	Green
2	863	India	Red
3	864	Taiwan	Green
4	880	Japan	Green
5	890	Bangladesh	Green
6	924	China	Green
7	927	China	Green
8	928	Brazil	Green
9	941	Thailand	Green
10	945	Egypt	Green
11	957	-	Green
12	1482	-	Green
13	1483	-	Green
14	1489	Taiwan	Green
15	1490	-	Green
16	1491	Bangladesh	Light Red
17	1520	Bangladesh	Green
18	1800	Bangladesh	Green
19	1920	Bangladesh	Green
20	1939	Bangladesh	Green
21	1947	Bangladesh	Green
22	1958	Bangladesh	Green
23	1973	Taiwan	Green
24	2040	Cuba	Green

Table 1. (Cont'd)

Genotype No.	Accession No.	Source of collection	Stem Pigmentation
25	2344	Bangladesh	Green
26	2389	Bangladesh	Green
27	2390	Bangladesh	Green
28	2408	Bangladesh	Green
29	2581	Bangladesh	Red
30	2593	Bangladesh	Green
31	2699	Bangladesh	Green
32	3311	Bangladesh	Green
33	3332	Bangladesh	Green
34	3484	Bangladesh	Green
35	3564	Bangladesh	Green
36	4456	Thailand	Green
37	4484	USA	Green
38	4618	Brazil	Green
39	4619	Brazil	Green
40	4940	China	Light Red
41	5066	Nepal	Green
42	5125	Bangladesh	Green

Plate 1. Over all field view of white jute stem colour with differential stature

Plate 2. A close view of field experiment on white jute germplasm

3.7 Collection of data

The following data were recorded from 10 randomly selected plants of each genotype from each replication. Pigmentation of stem was recorded at 60 days after sowing.

3.7.1 Pigmentation spectrum: The pigmentation on different parts of the plant bodies and midribs of the leaves were recorded on the basis of IJO Report, 1988 and genotypes classified into O-VII grades.

3.7.2 Technical height (m): The height of the main stem was recorded from the soil surface to the point of forking.

3.7.3 Leaf angle (dg): The angle of leaf was measured in degree.

3.7.4 Leaf length (cm): The length of leaf was measured in cm.

3.7.5 Leaf width (cm): The width of leaf was measured in cm.

3.7.6 Petiole length (cm): The length of petiole was measured in cm.

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

3.7.8 Basal diameter (mm): Basal diameter of stem was measured at the base of the stem in mm using slide callipers.

3.7.9 Middle diameter (mm): Middle diameter of stem was measured at the d point between base and top of the stem using slide callipers.

3.7.10 Top diameter (mm): Top diameter was measured at the point of stem forking i.e. at the point of the technical height.

3.7.11 Core diameter (mm): The core diameter of stem was measured at the base of the stem after removing the outer bark using slide callipers.

3.7.12 Dry fibre weight (g): Weight of dry fibre per plant was measured in gram after retting and drying.

3.7.13 Dry stick weight (g): Weight of sun-dried stick per plant was measured in gram after extraction of fibre.

3.8 Statistical Analysis

3.8.1 Genetic Variability

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATE software. For both univariate and multivariate analysis, mean data for each character was used. In case of Univariate Analysis (UV), analysis of variance was done individually by F-test (Panse and Shukhatme, 1978). Multivariate analysis viz. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CSA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 software programme (Copyright, 1987, Laws Agricultural Trust, Rothamasted Experimental Station. UK).

3.8.1.1 Estimation Phenotypic and Genotypic Variance

Genotypic and phenotypic variances were estimated by Johnson *et al.* (*1955*). Genotypic variance (δ^2_g) was obtained by subtracting error mean sum of square from the genotype mean sum of square and dividing by the number of replications as shown below:

$$\delta^2_g = \frac{GMS - EMS}{r}$$

Where,

GMS= Genotypic mean sum of square

EMS=Error mean sum of square

r= Number of replication

The phenotypic variances (δ^2_p) were derived by adding genotypic variances (δ^2_g) with error variances (δ^2_r) as given by the following formula:

$$\delta^2_p = \delta^2_g + \delta^2_e$$

3.8.1.2 Estimation Genotypic and Phenotypic Coefficient of Variation

Genotypic and phenotypic coefficient of variations were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\delta_g}{\overline{X}} \times 100$$

Where,

δ_g=Genotypic standard deviation

$\overline{X}$=Grand mean

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\delta_p}{\overline{X}} \times 100$$

Where,

δ_g= Phenotypic standard deviation

$\overline{X}$= Grand mean

3.8.1.3 Estimation of Heritability

Broad sense heritability was estimated by the formula suggested by Johnson *et al.* (1955).

$$\% \, h^2_b = \frac{\delta 2_g}{\delta 2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense

$\delta 2_g$ = Genotypic variance

$\delta 2_p$ = Phenotypic variance

3.8.1.4 Estimation of Genetic Advance

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

$$\text{Genetic Advance (GA)} = \frac{\delta^2_g}{\delta^2_p} \times K \times \delta_p$$

Where,

K= Selection intensity, the value of which is 2.06 at 5% selection intensity

δ^2_p= Phenotypic stander deviation

δ^2_g= Genotypic variance

δ^2_p= Phenotypic variance

3.8.1.5 Estimation of Genetic Advance in Percentage of Mean

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

$$\text{Genetic advance in percentage of mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

3.8.2 Genetic Diversity Analysis

3.8.2.1 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.

3.8.2.2 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 similarity matrix (Digby *et al.* 1989).

3.8.2.3 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 examine the effect of swapping two genotypes of different classes, and so on.

3.8.2.4 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 variabilities that maximize the ratio in between group to within group variation to be found out and thereby giving functions of the original variabilities 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.

3.8.2.5 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.

3.8.2.6 Cluster Diagram

Cluster diagram was drawn using the D^2 values between and within clusters 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.

3.8.2.7 Computation of Average Inter-Cluster Distances

The procedure for 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.

Chapter IV

Results and Discussion

CHAPTER IV
RESULTS AND DISCUSSION

The results of the genetic divergence of white jute genotypes are presented in Table 2 to 7 and in Figures 2 to 4. The summery results of the analysis of variance for the attributes are given in Appendix II. The range and mean are presented in Appendix III.

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 83.14% (Table 2). A two dimensional chart (Z_1-Z_2) of 42 white jute genotypes are presented in Appendix IV. The scatter diagram showed six arbitrary clusters. The genotypes were distantly located from each other (Figure 2).

4.1.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter-genotypic distances obtained from principal component analysis showed that the highest distance (1.4491) was observed between the genotypes G39 and G36 followed by G36 and G28 (1.4143), G36 and G7 (1.3364), G36 and G30 (1.3268), G36 and G22 (1.3166) and the lowest distance was observed between the genotypes G23 and G4 (0.1089) followed by G20 and G19 (0.1120), G37 and G13

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

Principal component characters	Eigen values	Percentage of total variation accounted for	Cumulative percentage
Technical height (m)	5.405	45.04	45.04
Leaf angle (dg)	1.972	16.44	61.48
Leaf length (cm)	1.592	13.27	74.75
Leaf width (cm)	1.007	8.39	83.14
Petiole length (cm)	0.636	5.30	88.44
Node per plant	0.407	3.39	91.83
Base diameter (mm)	0.300	2.50	94.33
Middle diameter (mm)	0.258	2.15	96.48
Top diameter (mm)	0.204	1.70	98.18
Core diameter (mm)	0.109	0.91	99.09
Dry fibre weight (g)	0.072	0.60	99.69
Dry stick weight (g)	0.037	0.31	100.00

Table 3. Ten of 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
1.4491	G39 & G36	0.1089	G23 & G4
1.4143	G36 & G28	0.1120	G20 & G19
1.3364	G36 & G7	0.1129	G37 & G13
1.3268	G36 & G30	0.1151	G34 & G16
1.3166	G36 & G22	0.1439	G13 & G4
1.3101	G36 & G27	0.1505	G34 & G4
1.2782	G35 & G33	0.1526	G13 & G11
1.2747	G35 & G14	0.1598	G41 & G15
1.1825	G36 & G25	0.1607	G22 & G7
1.1639	G36 & G24	0.1640	G37 & G2

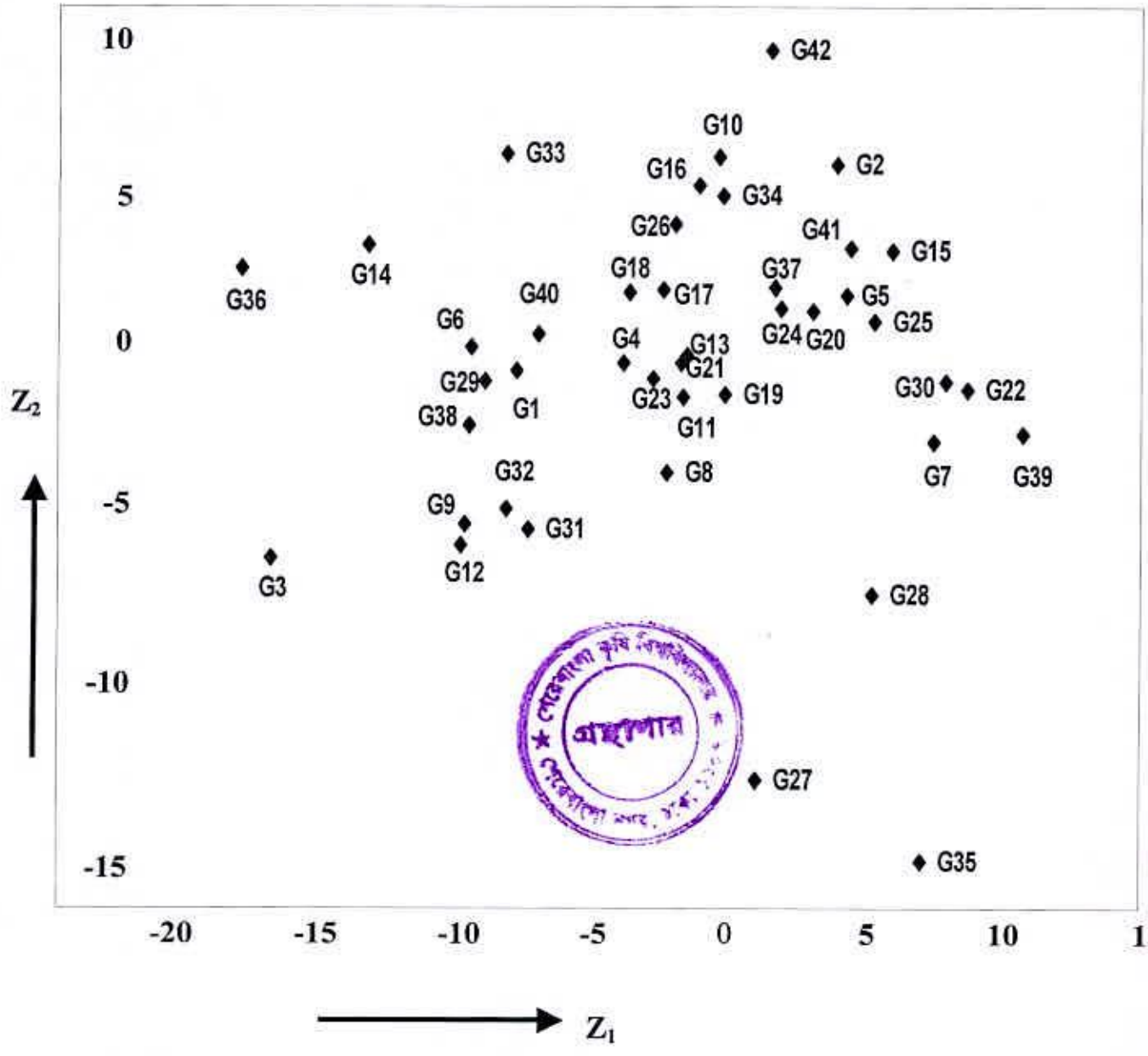

Figure 2. Scatter distribution of 42 white jute (*C. capsularis)* genotypes based on their principal component scores

(0.1129), G34 and G16 (0.1151), G13 and G4 (0.1439) (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 (1.3414), which was composed of seven genotypes followed by cluster V (1.3052) that was composed of eleven genotypes, cluster IV (0.9391) was composed of nine genotypes, both the cluster VI (0.8045) and cluster III (0.5506) were composed of six genotypes. The cluster II showed the lowest intra-cluster distance (0.3487) composed of three genotypes followed by cluster III (0.5506) composed of six genotypes and cluster VI (0.8045) composed of six genotypes. These results revealed that the genotypes in cluster I were distantly related. On the other hand the genotypes in cluster II were closely related.

4.1.3 Clustering

Forty two genotypes of white jute were grouped into six different clusters with the application of Mhalanobis'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 eleven genotypes were in cluster V, followed by nine in IV, seven in I, six in III and VI, three in II. There was seven genotypes in cluster I.

The genotypes of cluster I produced the lowest cluster mean for plant technical height (2.27), leaf length (14.51), leaf width (5.74), base diameter (16.37), middle diameter (8.80), core diameter (12.64), dry fibre weight (6.28) and dry stick weight (15.59) (Table 5).

Cluster II represented three genotypes. The genotypes of this group produced the highest cluster mean for base diameter (20.07), middle diameter (11.12), top diameter (4.80), core diameter (15.97), dry fibre weight (10.91) and dry stick weight (31.71). This group contained the second highest cluster mean value for petiole length (5.97) (Table 5).

Cluster III was composed of six genotypes (Table 4). The genotypes of this group produced the lowest cluster mean for top diameter (4.04). This group contained the second highest cluster mean value for leaf width (6.10) and node number (57.78).

Cluster IV contained nine genotypes. This cluster had the highest cluster mean values for technical height (2.73), leaf width (6.19) and number of node (58.74). This group contained the second highest cluster mean value for leaf angle (83.81), leaf length (14.87), base diameter (19.05), middle diameter (10..23), core diameter (15.27), dry fibre weight (9.92) and dry stick weight (24.42).

Cluster V was composed of the highest eleven genotypes. The highest cluster mean was observed for leaf angle (84.33), leaf length (15.15) and petiole length (6.00). This group contained the second highest cluster mean value for technical height (2.60). This cluster showed medium mean values for other characters.

Cluster VI contained six genotypes. The lowest cluster mean was observed for petiole length (5.64) and node number (44.41). This group contained the second highest cluster mean value for top diameter (4.54) of stem.

Table 4. Distribution of 42 genotypes of white jute (*C. capsularis* L.) germplasm in six clusters

Cluster	Number of genotypes	Name of genotypes	Accession No.
I	7	G1, G6, G14, G29, G33, G36, G40	862, 24, 1489, 2581, 3332, 4456, 4940
II	3	G27, G28, G35	2390, 2408, 3564
III	6	G2, G10, G16, G26, G34, G42	863, 945, 1491, 2389, 3484, 5125
IV	9	G5, G7, G15, G20, G22, G25, G30, G39, G41	890, 927, 1490, 1939, 1958, 2344, 2593, 4619, 5066
V	11	G4, G8, G11, G13, G17, G18, G19, G21, G23, G24, G37	880, 928, 957, 1483, 1520, 1800, 1920, 1947, 1973, 2040, 4484
VI	6	G3, G9, G12, G31, G32, G38	864, 941, 1482, 2699, 3311, 4618

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

Parameters/characters	Clusters					
	I	II	III	IV	V	VI
1. Technical height (m)	2.27	2.50	2.58	2.73	2.60	2.32
2. Leaf angle (dg)	83.62	80.89	82.27	83.81	84.33	82.28
3. Leaf length (cm)	14.51	14.80	14.59	14.87	15.15	14.83
4. Leaf width (cm)	5.74	6.05	6.10	6.19	6.02	6.05
5. Petiole length (cm)	5.84	5.97	5.78	5.92	6.00	5.64
6. Node per plant	48.05	50.56	57.78	58.74	53.06	44.41
7. Base diameter (mm)	16.37	20.07	17.37	19.05	18.03	17.38
8. Middle diameter (mm)	8.80	11.12	9.50	10.23	9.73	9.48
9. Top diameter (mm)	4.08	4.80	4.04	4.33	4.36	4.54
10 Core diameter (mm)	12.64	15.97	13.51	15.27	14.46	14.29
11 Dry fibre weight (g)	6.28	10.91	7.61	9.92	8.41	7.25
12 Dry stick weight (g)	15.59	31.71	17.83	24.42	20.78	19.66

The two economic important characters of jute plant are the fibre and stick yield per plant. In case of fibre weight, cluster II possessed the highest mean values followed by cluster IV, cluster V, cluster III, cluster VI and cluster I. Cluster II also possessed the highest stick weight followed by cluster IV, cluster V, cluster VI, cluster III and cluster I (Table 5). The clustering pattern of genotypes did not follow geographical distribution and also pigmentation pattern. In these clusters, genotypes were of diverse pigmentation grades. The genotypes evolved at one center even exhibited considerable amount of diversity and grouped into different clusters, indicating 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 of 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 (10.060) was between cluster I and II indicating wider genetic diversity between these two clusters followed by the cluster VI and IV, IV and III, IV and I, VI and III, V and II. The lowest inter-cluster distance (3.987) was observed

between the clusters I and VI suggesting the closer relationship among the genotypes followed by III and V, I and V, III and IV, IV and V and so on included in these clusters. Similar distance was found between clusters III and IV, I and V, III and V, IV and V reflecting a close relationship among these clusters (Figure 3 and Table 6). However, the maximum inter-cluster distance was recorded between cluster I and II (10.060) compared to other clusters. Genotypes from the cluster I and II having the highest distance if involved in hybridization might produce a wide spectrum of segregating population. It is a 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 0.3487 to 1.3414, maximum being for cluster I which is composed of seven genotypes of diverse origin, while the minimum distance was found in cluster II which comprises three genotypes (Table 6). Results of different multivariate techniques were superimposed in Figure 3. It might be concluded from this figure that all the techniques supplemented and confirmed the results of another one.

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 and therefore, it was not adequate as an index of genetic diversity. This might be due to continuous exchange of genetic materials in different places of the country even among the countries of the world. Similar results have

Table 6. Average intra (Diagonal) and inter cluster distances (D^2) for 42 white jute (*C. capsularis* L.) genotypes

Cluster	I	II	III	IV	V	VI
I	**1.3414**					
II	10.060	**0.3487**				
III	6.033	9.030	**0.5506**			
IV	8.785	6.950	4.660	**0.9391**		
V	4.599	7.476	4.198	4.673	**1.3052**	
VI	3.987	8.677	8.223	9.825	5.963	**0.8045**

Bold figures denote intra-cluster distances

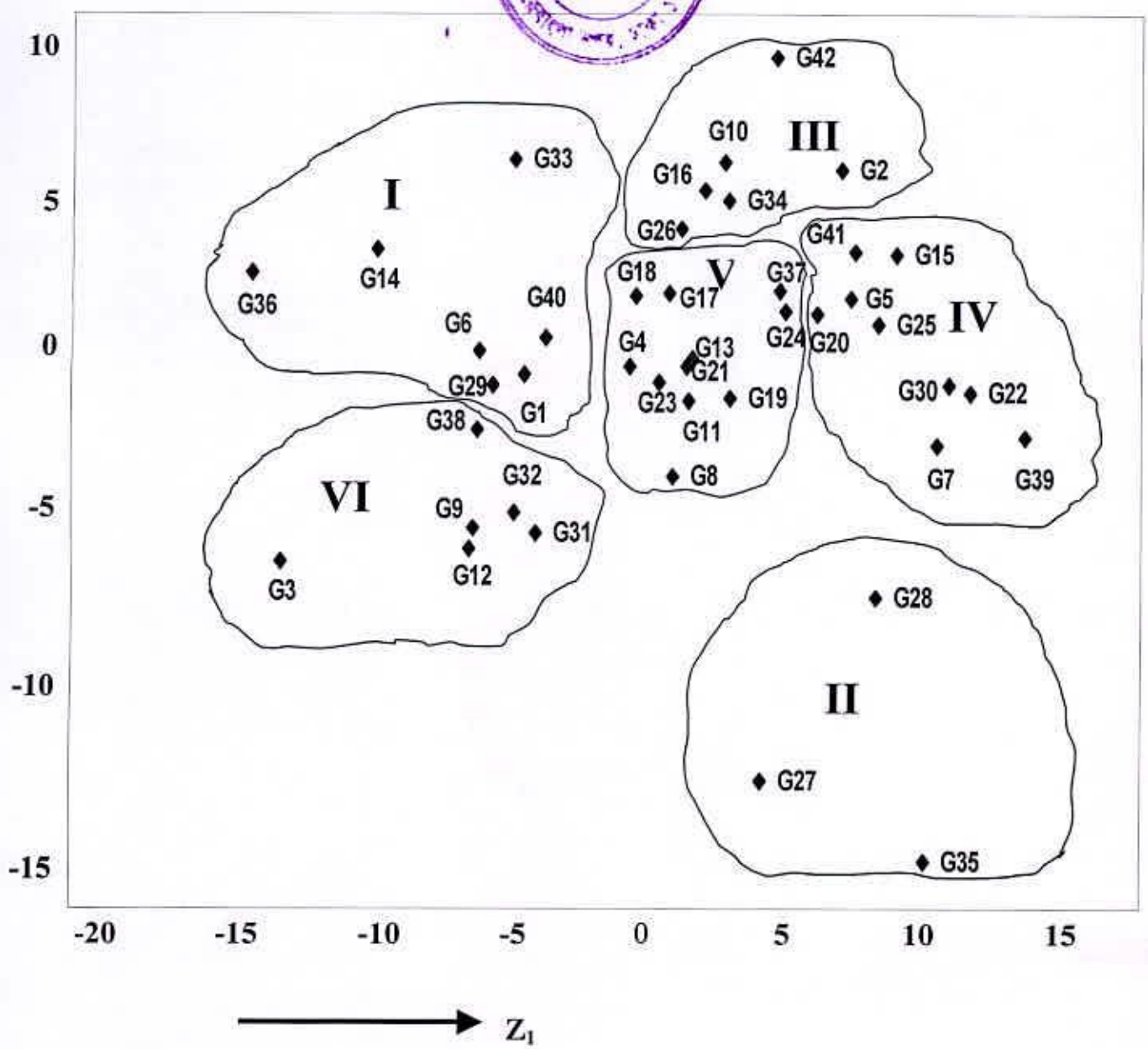

Figure 3. Scatter distribution of 42 white jute (*C. capsularis* L.) genotypes based on their principal component scores superimposed with clustering

been reported by Shreshtha (1991) in deshi jute, Mian *et al.* (1991) in field pea, Saha (1993), Murty and Anand (1966) in linseed flax, Golakia and Makne (1992) in virginia runner groundnut, Katiar and Singh (1990) in faba bean, Shewe *et al.* (1972) in groundnut, Verma (1970) in groundnut and soybean, Anand and Rawat (1984) in brown mustard and 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.

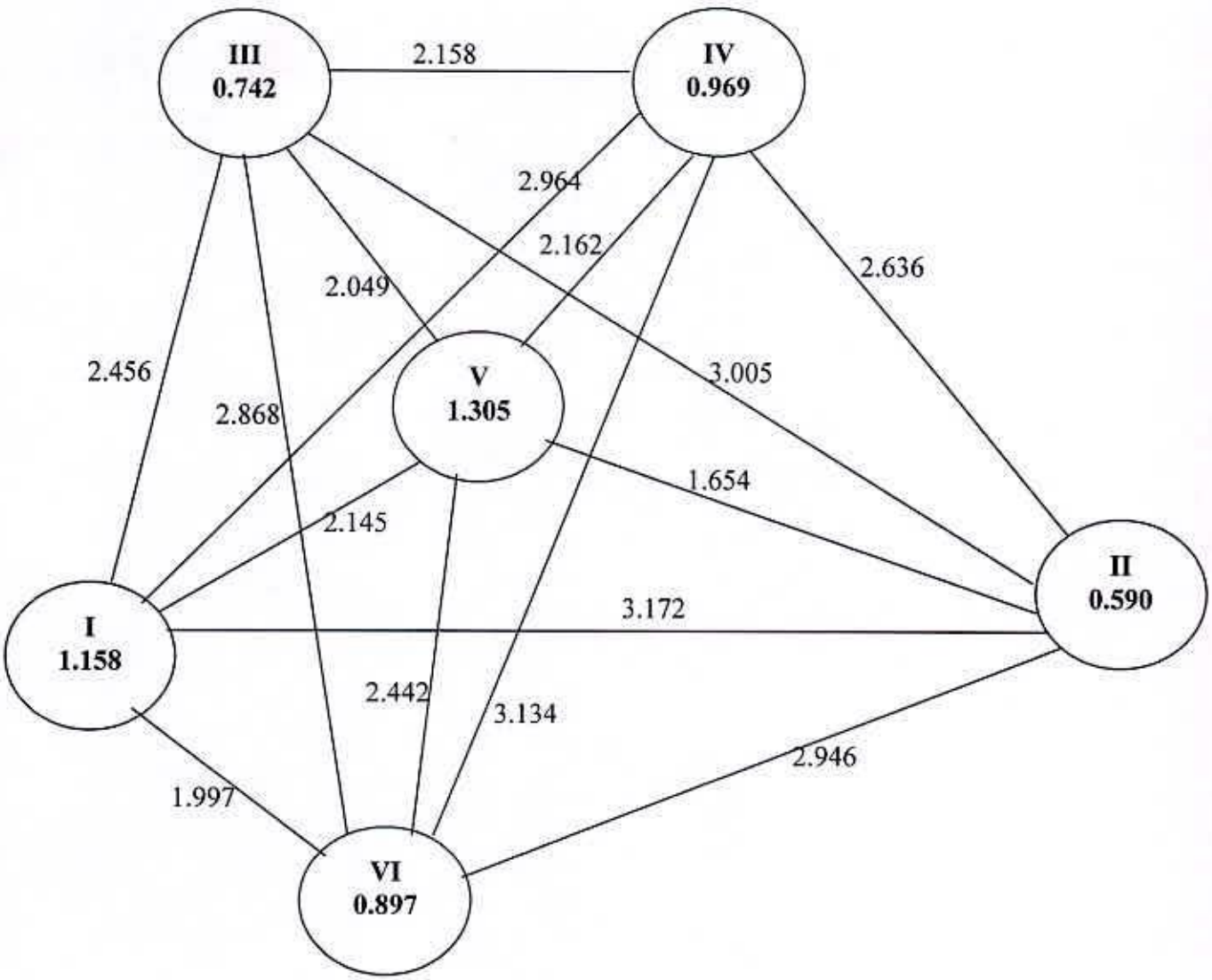

Figure 4. Diagram showing intra and inter-cluster distances ($\sqrt{D^2}$) of 42 white jute (*C. capsularis* L.) genotypes

4.2 CONTRIBUTION 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 base diameter of stem (0.3987), dry fibre weight (0.3762), dry stick weight (0.3651), technical height (0.2840), number of nodes (0.2184) were the major ones. In vector II (Z_2), the second axis of differentiation, plant technical height (0.2913), number of nodes (0.1829), dry stick weight (0.1676), dry fibre weight (0.1574) and base diameter (0.0567) were more important for divergence but leaf length, leaf width, petiole length, top diameter, leaf angle and core diameter played only a minor role in the second axis of differentiation (Table 7). The role of dry stick weight, dry fibre weight, base diameter, and plant height in both the vectors indicated the important components of genetic divergence in these materials.

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

Characters	Vector-1	Vector-2
1. Technical height (m)	0.2840	0.2913
2. Leaf angle (dg)	-0.0032	-0.1142
3. Leaf length (cm)	-0.1555	-0.5920
4. Leaf width (cm)	-0.1729	-0.4931
5. Petiole length (cm)	-0.1386	-0.4355
6. Node per plant	0.2184	0.1829
7. Base diameter (mm)	0.3987	0.0567
8. Middle diameter (mm)	-0.3969	0.0509
9. Top diameter (mm)	-0.2176	-0.1601
10. Core diameter (mm)	-0.3997	-0.0326
11. Dry fibre weight (g)	0.3762	0.1574
12. Dry stick weight (g)	0.3651	0.1676

4.3 COMPARISION OF DIFFERENT MULTIVARIATE TECHNIQUES

The cluster pattern of (D^2) analysis through non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the (D^2) has followed more or less similar trend of the Z_1 (principal component analysis) and Z_2 (principal component score II) vectors of the principal component analysis. Principal component analysis and (D^2) were found to be alternative methods in giving the information regarding the contribution of characters towards divergence of white jute. Similar results were reported by Chowdhury (1993) in soybean, Islam (1995) in groundnut, Islam (1996) in jute (*C. olitorius* L.) and Rahim (2006) in rice.

4.4 SELECTION OF PARENTS FOR FUTURE HYBRIDIZATION

Selection of genetically diverse parents is an important step for any breeding programme. Therefore, the genotypes were to be selected on the basis of specific objectives. Higher heterosis could be produced from the crosses between genotypically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ghaderi *et al.* 1984; Mian and Bhal,1989). Besides these Arunachalam *et al.* (1984) reported that in groundnut higher heterosis for yield and its component could be obtained from the crosses between the intermediate divergent parents than extreme ones. The same report was cited by Mian and Bhal (1989) that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters in chickpea. Sasmal (1978) reported that in jute,

the clusters which possessed varieties having higher fibre yield have wide inter-cluster divergence while those varieties having poor fibre yield were close together and an effective multitire hybridization programme was initiated for obtaining hybrids superior in fibre yield. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance, the genotypes G39, G24, G22, G8 and G7 had higher plant technical height, which had direct positive correlation with fibre yield (Shreshtha, 1991). These genotypes were also found better for other important yield contributing characters (Appendix V). On the other hand, the genotypes G36, G14, G33, G3 showed least performance in respect of plant technical height, dry fibre weight and dry stick weight. The highest and the lowest inter-cluster distances were observed between clusters I and II, cluster I and VI respectively. The next higher inter-cluster distances were observed between cluster IV and VI, II and III, I and IV, II and VI, III and VI, II and V, I and III, which indicated distantly related genotypes comprised these clusters. Therefore, hybridization programme among the genotypes of these clusters would give maximum heterosis.

Considering group distances, genetic distances and other agronomic performance the genotypes G35, G28, G39, G30, G7, G24, G22, G20, G25, G19, G41 and G8 might be selected as parents in future hybridization programme for better yield and stability.

Chapter V

Summary and Conclusion

CHAPTER V
SUMMARY AND CONCLUSION

An experiment was conducted with 42 genotypes of white jute (*C. capsularis*) at the Jute Agriculture Experimentation Station, Jagir, Manikganj (Central Research Station of Bangladesh Jute Research Institute), during March to October 2006 with a view to study the genetic diversity pattern on thirteen morphological characters. Seeds were sown in 3 meters single line in Randomized Complete Block Design (RCBD) with three replications. Pigmentation of stem and leaf, plant technical height (TH), leaf angle (LA), leaf length (LL), leaf width (LW), petiole length (PL), number of nodes (NN), base diameter of stem (BD), middle diameter of stem (MD), top diameter of stem (TD), core diameter of stem (CD), dry fibre weight (FW) and dry stick weight (SW) per plant were considered for the study.

Significant differences among the genotypes in the seven characters were observed and non- significant differences were observed in the rest five characters (leaf angle, leaf length, base diameter of stem, middle diameter of stem and top diameter of stem). Multivariate analysis was performed through Principal Component Analysis (PCA), Principal Coordinate Analysis (PCA), Cluster Analysis (CLA) 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 principal component axes accounted for 83.14% variation towards the divergence. According to PCA, D^2 and cluster analysis the genotypes were grouped into six different 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 was observed between cluster I and II followed by the cluster IV and VI, II and III, I and IV, II and VI, III and VI, II and V and so on. The lowest inter-cluster distance was observed between clusters I and VI followed by the cluster III and V, I and V, III and IV, IV and V. The highest intra-cluster distance was observed in cluster I contained seven genotypes. The lowest intra-cluster distance was observed in cluster II contained three genotypes. The principal component analysis revealed that dry stick weight, dry fibre weight, plant technical height, base diameter and number of nodes were the important components of genetic divergence in the population.

Genotypes of cluster II had higher base diameter, middle diameter, top diameter, core diameter, dry fibre weight, dry stick weight and other morpho-agronomic characters whereas some of the genotypes (G36, G14, G33) in cluster I had least performance in yield contributing characters.

The nature of selection forces operating under one ecogeographical region seems to be similar to that of other regions since genotypes from distinct centers were grouped together. Genotypes from one ecogeographical region and also belonging to different pigmentation grade were grouped in different clusters indicating substantial variation within themselves. Therefore, it is evident that there was no parallelism between genetic diversity and geographical distribution of genotypes. On the whole, the investigation revealed that no single quantitative trait had major contribution to the yield. Integrated approach of improving

quantitative traits would consequently help to increase yield potential of *C. capsularis* L. jute.

Considering cluster distance, inter-genotypic distance and other agronomic performance, the genotypes G28 and G35 from cluster II; G7, G20, G22, G25, G30, G39 and G41 from cluster IV; G8, G19 and G24 from cluster V were considered to be better parents for future uses in hybridization programme.

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Appendices

Appendix I. 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	Year	Daily air temperature		Monthly rainfall (mm)
		Max (^{0}C)	Min (^{0}C)	
April	2006	33.92	23.21	83
May	2006	34.36	25.01	270
June	2006	32.65	26.79	334
July	2006	32.56	26.87	166
August	2006	32.96	26.38	219
September	2006	32.33	26.00	455
October	2006	32.40	24.24	70

Source: Physiology department, BJRI, Dhaka

Appendix II. Mean sum of squares from the ANOVA of 42 white jute (*C. capsularis* L.) genotypes in respect of 12 characters

Characters	df			Mean sum of square		
	Replication	Genotype	Error	Replication	Genotype	Error
Technical height	2	41	82	1.274**	0.203**	0.057
Leaf angle	2	41	82	394.987**	10.783 ns	12.007
Leaf length	2	41	82	19.895**	1.582 ns	1.314
Leaf width	2	41	82	2.041**	0.586*	0.325
Petiole length	2	41	82	3.969**	0.645*	0.389
Number of node	2	41	82	3.292 ns	89.437**	35.910
Base diameter	2	41	82	57.681**	6.286 ns	4.322
Middle diameter	2	41	82	12.487**	1.969 ns	1.758
Top diameter	2	41	82	0.965 ns	0.354 ns	0.322
Core diameter	2	41	82	40.577**	5.574*	3.307
Dry fibre weight	2	41	82	18.597*	8.431*	5.396
Dry stick weight	2	41	82	261.646**	63.959*	35.724

** Significant at 1% level of probability

* Significant at 5% level of probability

ns Not significant

Appendix III. Range and mean for 12 morphological characters in 42 white jute (*C. capsularis* L.) genotypes

Characters	Minimum	Maximum	Mean
1. Technical height (m)	1.64	3.07	2.52
2. Leaf angle (dg)	79.00	86.13	83.27
3. Leaf length (cm)	13.10	16.47	14.83
4. Leaf width (cm)	5.09	7.09	6.03
5. Petiole length (cm)	4.54	6.60	5.87
6. Node number	39.33	60.67	52.70
7. Base diameter (mm)	14.41	21.77	17.93
8. Middle diameter (mm)	7.40	11.89	9.17
9. Top diameter (mm)	3.40	5.140	4.32
10. Core diameter (mm)	9.94	17.57	14.28
11. Dry fibre weight (g)	4.27	11.83	8.28
12. Dry stick weight (g)	12.13	34.80	20.89

Appendix IV. Principal component scores for 42 white jute (*C. capsularis* L.) genotypes

Genotype No.	Z_1	Z_2
G1	-5.283	-0.121
G2	5.080	5.602
G3	-13.154	-5.339
G4	-1.765	0.099
G5	5.436	1.966
G6	-6.734	0.522
G7	8.261	-2.084
G8	-0.376	-2.923
G9	-7.099	-4.961
G10	1.272	5.791
G11	0.137	-0.806
G12	-6.944	-4.395
G13	0.245	0.324
G14	-10.063	3.353
G15	6.924	3.233
G16	0.638	5.037
G17	-0.513	2.127
G18	-1.586	2.021
G19	1.507	-0.786
G20	4.310	1.529
G21	0.084	0.118
G22	9.366	-0.604
G23	-0.806	-0.335
G24	3.289	1.583

Appendix IV. (cont'd)

Genotype No.	Z_1	Z_2
G25	6.338	1.225
G26	-0.130	3.953
G27	2.514	-11.430
G28	6.271	-6.341
G29	-6.317	-0.440
G30	8.634	-0.719
G31	-4.857	-4.517
G32	- 5.594	-3.922
G33	-5.572	5.881
G34	1.398	4.695
G35	7.868	-13.710
G36	-14.122	2.699
G37	3.067	2.206
G38	-6.796	-1.600
G39	11.157	-1.858
G40	-4.588	0.886
G41	5.549	3.266
G42	2.955	8.779

Appendix V. Mean per plant performance of 42 white jute (*C. capsularis* L.) genotypes for 12 characters

Genotype	Acc. No	TH (m)	LA (dg)	LL (cm)	LW (cm)	PL (cm)	NN	BD (mm)	MD (mm)	TD (mm)	CD (mm)	FW (g)	SW (g)
G1	862	2.25	85.00	15.05	5.99	5.73	48.33	17.99	9.6	4.45	14.35	7.67	17.60
G2	863	2.66	82.33	14.18	5.87	6.03	60.33	17.61	10.01	4.03	14.17	7.27	19.93
G3	864	2.06	82.67	13.13	5.57	4.54	39.33	15.87	8.49	4.56	13.07	5.93	17.93
G4	880	2.52	83.00	15.95	6.59	6.13	51.33	17.85	9.78	4.43	14.35	8.27	19.53
G5	890	2.74	84.00	15.59	6.31	5.88	58.00	20.13	9.66	4.14	16.64	8.47	21.93
G6	924	2.44	85.33	15.67	6.37	6.49	47.67	17.27	9.05	4.02	13.55	6.60	16.80
G7	927	2.75	85.33	14.89	5.88	6.07	57.67	19.58	10.97	4.24	15.31	10.47	27.13
G8	928	2.78	83.33	13.77	5.09	5.13	50.67	17.39	9.30	4.41	13.98	8.80	23.27
G9	941	2.21	83.00	16.13	6.39	6.09	44.00	18.15	9.67	4.78	14.21	8.00	20.20
G10	945	2.46	82.33	14.53	5.71	5.32	57.33	17.85	9.94	4.17	13.15	8.07	17.07
G11	957	2.51	86.13	15.39	6.20	6.53	52.00	18.61	9.89	4.54	15.64	9.27	21.07
G12	1482	2.12	85.53	15.25	6.23	5.19	44.33	17.99	10.21	5.01	14.54	8.33	19.80
G13	1483	2.55	84.00	15.11	5.82	6.17	53.00	18.59	10.13	4.46	14.73	8.20	20.53
G14	1489	2.17	83.33	15.16	5.96	5.78	47.00	16.03	8.88	4.45	12.40	5.80	12.73

Appendix V. (Cont'd)

Genotype	Acc. No	TH (m)	LA (dg)	LL (cm)	LW (cm)	PL (cm)	NN	BD (mm)	MD (mm)	TD (mm)	CD (mm)	FW (g)	SW (g)
G15	1490	2.64	84.33	14.41	5.60	5.29	60.00	19.90	10.11	4.36	14.99	9.00	22.13
G16	1491	2.55	83.67	14.45	6.61	5.82	56.33	17.56	9.55	4.14	13.43	7.67	17.53
G17	1520	2.46	84.00	15.27	5.74	6.49	53.67	17.61	9.81	4.56	14.35	6.87	19.20
G18	1800	2.29	86.00	15.80	7.09	6.29	52.67	17.11	9.71	4.75	14.39	6.80	18.80
G19	1920	2.73	83.67	14.79	6.35	5.37	53.33	17.67	9.37	4.01	14.21	9.60	22.40
G20	1939	2.76	84.67	14.63	6.08	5.47	57.00	16.71	9.41	3.98	13.49	9.93	22.73
G21	1947	2.57	85.87	14.87	5.43	5.65	52.67	18.18	9.65	3.97	13.94	8.80	20.93
G22	1958	2.81	82.33	14.40	6.45	5.65	59.67	19.75	10.81	4.70	15.31	9.73	26.60
G23	1973	2.41	81.33	16.47	6.37	6.13	52.00	17.13	9.25	4.43	13.91	8.27	20.80
G24	2040	3.03	84.67	14.28	5.61	5.90	56.00	18.98	10.41	4.15	14.81	9.87	21.00
G25	2344	2.55	85.00	15.21	6.24	6.45	58.33	17.67	9.70	4.50	14.68	9.99	23.83
G26	2389	2.58	79.27	14.29	6.07	5.27	55.33	17.14	8.52	3.97	13.09	7.80	17.93
G27	2390	2.22	84.00	14.17	5.53	5.81	47.67	19.19	10.74	4.87	14.84	9.13	31.67
G28	2408	2.59	79.67	14.99	6.37	6.05	53.67	19.24	10.72	4.40	15.51	11.83	28.67
G29	2581	2.47	84.67	13.10	5.26	5.36	47.67	15.17	9.24	4.19	11.43	7.07	18.73
G30	2593	2.57	81.00	15.00	6.51	6.60	59.00	18.62	10.05	4.29	14.99	11.40	26.07

Appendix V. (Cont'd)

Genotype	Acc. No	TH (m)	LA (dg)	LL (cm)	LW (cm)	PL (cm)	NN	BD (mm)	MD (mm)	TD (mm)	CD (mm)	FW (g)	SW (g)
G31	2699	2.43	80.67	13.91	5.53	5.89	46.33	17.40	9.63	4.38	14.46	7.07	21.67
G32	3311	2.43	80.00	14.99	5.94	6.53	46.00	18.09	9.44	4.33	14.85	7.60	20.20
G33	3332	2.33	80.67	14.17	5.26	5.15	52.33	15.73	8.17	3.76	12.17	5.93	13.80
G34	3484	2.54	83.67	15.58	6.45	6.07	56.67	17.79	10.07	4.20	14.27	7.73	18.00
G35	3564	2.69	79.00	15.24	6.24	6.06	50.33	21.77	11.89	5.14	17.57	11.77	34.80
G36	4456	1.64	83.33	14.13	5.82	6.28	43.67	14.41	7.40	3.40	9.94	4.27	12.13
G37	4484	2.72	85.67	14.95	5.94	6.20	56.33	19.25	9.77	4.25	14.79	7.80	21.00
G38	4618	2.68	81.80	15.57	6.65	5.58	46.50	16.80	9.43	4.17	14.64	6. 60	18.14
G39	4619	3.07	85.00	14.63	6.59	6.11	60.00	20.49	11.19	4.08	17.09	10.73	28.20
G40	4940	2.61	83.00	14.28	5.50	6.11	49.67	18.01	9.62	4.31	14.64	6.60	17.33
G41	5066	2.69	82.67	15.09	6.07	5.73	59.00	18.64	10.18	4.72	14.90	9.60	21.13
G42	5125	2.69	82.33	14.50	5.87	6.17	60.67	16.29	8.91	3.72	12.92	7.13	16.53
CV%		9.49	4.16	7.73	9.46	10.63	11.37	11.59	13.64	13.14	12.74	28.06	28.61

TH=Technical height, LA=Leaf angle, LL= Leaf length, LW=Leaf width, PL=Petiole length, NN=Number of node, BD=Base diameter of stem, MD=Middle diameter of stem, TD=Top diameter of stem, CD=Core diameter of stem, FW= Dry fibre weight, SW= Dry stick weight and CV= Coefficient of variation.

A. 2.1 (Agron) 03/04/08 38 992 15.3.15