GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY IN KENAF (*Hibiscus cannabinus*)

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CERTIFICATE

*This is to certify that the thesis entitled, "**GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY IN KENAF (Hibiscus cannabinus)**" 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 **JUBAYER AHMED; Registration No. 10-03831,** under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma.*

I further certify that any help or sources of information, as has been availed of during the course of this investigation have been duly acknowledged.

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ABSTRACT

Twenty five genotypes of Kenaf (*Hibiscus cannabinus* L.) from different geographic origins were grown at the Central Jute Agricultural Experiment station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikganj during 15 March to 30 September, 2015 to study their variability, correlation and diversity for nine morphological characters. Significant variation was found for all the characters among the genotypes. PCV was greater than GCV and high GCV values were observed for green weight with leaves, green weight without leaves, stick weight and fibre weight. The high heritability (more than 85%) coupled with high genetic advance in percent of mean were observed for most of the traits. All the characters except green bark thickness and internode length showed significant and positive correlation with fibre weight. Path co-efficient analysis revealed that green weight with leaves, green weight without leaves, green bark thickness and stick weight showed positive direct effect on fibre yield. The maximum and minimum cluster distance were observed between clusters I and V **(**13.566) and I and III **(**2.602), respectively. Plant height was found responsible for the maximum diversity. The genotypes of clusters I and V were more diversed as they could be used as parents for future breeding program to develop Kenaf variety. Considering cluster distance and other agronomic performance genotypes G22 and G25 might be suggested for future hybridization program.

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et al.*
Accesions	Acc.
Bangladesh Jute Research Institute	BJRI
Before Christians	B.C.
Canonical Vector Analysis	CVA
Centimeter	cm
Co-efficient of Variation	CV
Co-efficient of Racial Likeness	CRL
Days After Sowing	DAS
Deoxyribo Nucleic Acid	DNA
Etcetera	etc.
East	E
Environment Mean Square	EMS
Food and Agricultural Organization	FAO
Figure	Fig.
Genotype	G
Genetic Advance	GA
Genotype Mean Square	GMS
Genotypic Co-efficient of Variation	GCV
Ginning Out Turn	GOT
Gram	gm
Harvest Index	HI
Inter Simple Sequence Repeat	ISSR
Journal	*J.*
Kilogram	kg
Meter	m
Mean Sum of Square	MS
Mili equivalent	meq
Millimeter	mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV

SOME COMMONLY USED ABBREVIATIONS (cont'd)

FULL WORD	ABBREVIATION
Principle Component	PC
Principle Component Analysis	PCA
Poly Unsaturated Fatty Acid	PUFA
Randomized Complete Block Design	RCBD
Random Amplified Polymorphic DNA	RAPD
Replication	r
Sher-e-Bangla Agricultural University	SAU
Simple Sequence Repeat	SSR
Soil Resource Development Institute	SRDI
Triple Super Phosphate	TSP
That is	*viz.*
United State of America	USA

CHAPTER I

INTRODUCTION

Kenaf (*Hibiscus cannabinus* L.) is a plant under the Malvaceae family and *Hibiscus* genus which is one of the most economically important fibre crop in the world. It is locally known as Deccan hemp, Roselle, Saimi jute, Java jute and so on. It is probably native to southern Asia, though its exact natural origin is unknown. It has been cultivated in its native Africa since 4000 B.C. (Keshk *et al*., 2006). It is a close relative of Cotton and Jute. It is mostly grown in wide latitudinal range like 16° S to 41° N (Kumar, 1999). Kenaf is cultivated for its fibre mostly in China, India, Bangladesh, United States of America, Indonesia, Malaysia, South Africa, Viet Nam, Thailand, parts of Africa, and to a small extent in southeast Europe.

Kenaf is an allotetraploid plant (2n=4x=72). It is an annual or biennial herbaceous plant (rarely a short-lived perennial) growing to 1.5-3.5 m tall with a woody base (Dempsey, 1975). The stems are 1-2.5 cm diameter, often but not always branched. The leaves are 10–15 cm long, variable in shape and deeply lobed with 3-7 lobes. Kenaf is a dicotyledonous plant has two distinctive stem regions. The outer portion or bast which is about 34% of the stem by the weight and inner, woody core which is about 66% of the stem by the weight. Fibers from the bast portion of stem are about 2.48 mm in length and resemble softwood fibers while those from the core are shorter, 0.72 mm in length and resemble hardwood fibers. The yield (Dry fibre) per hectare varies considerably. The differences in yield are associated with different Kenaf cultivars, soil type, location, climate and the management practices that could be an important consideration in selecting the best cultivar (Mahapatra *et al*., 2007 and Webber and Bledose, 1992).

There are more than 50 *Hibiscus* species that occur in the tropical and subtropical environments of every continent but only two of these species, kenaf (*Hibiscus cannabinus* L.) and Roselle (*Hibiscus sabdariffa* L. var. *altissima*) have economic importance for the production of pulp and paper (Rowell *et al*., 1997). In Bangladesh, BJRI has developed 36 varieties of Jute, Tosha, Kenaf and Mesta so far. Among them 5 varieties of Jute, 4 varieties of Tosha, 2 varieties of kenaf named HC-2 (1977) and HC-95 (1995) and 1 varieties of Mesta are now cultivating in farmers field. Moreover BJRI has more than 6000 germplasm of Jute, Kenaf, Tosha and Mesta of both exotic and indigenous origin. The HC-2 variety yields up to 6.8 tons per hectare. In Bangladesh around 30,000 ha. land are being used under Kenaf cultivation which yields 60-70 tons (FAO, 2012).

Kenaf has a great importance like other fibre crops. Kenaf fibre is widely used in paper industry, construction sector and as raw materials of cosmetics products. It is also utilized as packaging materials for different agricultural and industrial products as well as raw materials for the production of paper and pulp (IJO, 1994). The other uses of kenaf fibre are in rope, twine, coarse cloth, engineered wood, insulation, clothing-grade cloth, soil-less potting mixes, animal bedding and materials that absorb oil and liquids (similar to that made from Jute). In one words, it has multipurpose uses other than fibre and paper. The paper made from Kenaf are stronger, brighter and cleaner with less detriment to the environment and less bleaching is required to create a brighter sheet of paper. Due to less lignin content, it needs 20% less energy than tree pulp. Pre-board can be made from Kenaf which is used as base material to make car's interior. The kenaf leaves enriched with protein can be consumed as human and animal diets. Kenaf seeds yield an edible vegetable oil. Kenaf oil is high in omega polyunsaturated fatty acids (PUFA's) which are expected to play a role in cardiovascular health. Its dried stems is also used as fuel, fencing, match sticks and climbing sticks of various vegetables (BJRI, 1993).

It can take part in economic development of a country through generating employment opportunities and earning foreign currency. Kenaf as an alternative source of wood pulp, it conserves the forest resources. Kenaf can absorb CO_2 which is 3 to 8 times higher than a tree. In one acre of land, it can absorb 10 tons CO_2 per season. Less pesticides are needed in Kenaf cultivation. Its root can uptake nutrient from deeper soil as it can be cultivated in less fertile soil. It absorbs heavy metals from the soil. Products of Kenaf can be recycled. It enriches biomass content of soil. It has a great contribution to reduction of greenhouse gases and energy savings.

Kenaf can be used as a substitute of Jute having some advantages. Kenaf can be grown on marginal land where Jute cannot be gown. Moreover it needs less weeding and less care. It can be grown in saline and drought affected areas. Kenaf plants rapidly produce a tremendous amount of biomass, meaning that it has an ample opportunity as an alternative source of raw materials for making paper and pulp (Mostofa *et al.*, 2002).

The genetic improvement of any crop is dependent upon the existence of initial genetic variability amongst population. Therefore knowledge of the initial variability and the degree and direction of correlation amongst yield attributes are necessary for genetic improvement of economic yield through selection approaches in a population of diverse genotype. The yield and quality of Kenaf fibre may varies if variation in environmental factors occurs. Therefore it is also important to know the genetic, phenotypic and environmental variance for various attributes. These will help to select suitable genotypes which can be used in crop improvement program. In cereal crops, reproductive part is the main concern for improvement while vegetative part (stem bark) which need to be improved in Kenaf.

Fibre yield in Kenaf is a complex character and its improvements is dependent on some yield contributing traits. Existence of genetic variation of various attributes are useful for effective selection. These yield contributing attributes

are correlated with fibre yield and also themselves. Path analysis helps to find out the real contribution of this traits to yield and desired genotypes can be traced through diversity analysis.

Considering the above discussion, this research is undertaken with the following objectives:

- To know the genetic variation presence among the genotypes,
- To know the contribution of genetic and environmental factors on the phenotypic expression of the character as well as type of gene action involved,
- To know the degree and direction of relationship between the yield and yield contributing characters,
- To know the direct and indirect contribution of yield contributing traits on yield and
- To find out the superior genotypes for utilization in future breeding program.

CHAPTER II

REVIEW OF LITERATURE

Kenaf (*Hibiscus cannabinus* L.) is an important fibre crop in Bangladesh. It is a member of the family Malvaceae. Significant efforts were given by many workers for improvement of Kenaf through manipulations of qualitative and quantitative characters all over the world. Fibre yield in Kenaf is a complex character and is dependent on some morphological and physiological characteristics. These yield contributing attributes are correlated with fibre yield and also among themselves. A few literatures are available on variability, correlation, path and diversity analysis of yield and yield contributing characters of Kenaf. An attempt has been made here to summarize the findings of these study relevant to the present investigation. The whole review has been divided into following sections, namely –

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation co-efficient and path analysis

2.3 Genetic diversity

2.1 Genetic variability, heritability and genetic advance

Sawarkar (2015), estimated the genetic variability, heritability, genetic advance for yield attributing traits in thirty genotypes of Tossa Jute (*Corchorus olitorius* L.). The analysis of variance showed significant differences among the genotypes for all the characters. The highest genotypic variance was for plant height (680.97) followed by green weight (123.59), stick weight (49.33), days to 50% flowering (12.05), fibre weight (1.31), base diameter (0.02) and the lowest genotypic variance was that of bark thickness (0.03). High values of heritability (>90%) were recorded for almost all characters like plant height (93.01%), bark thickness (98.33%), base diameter (94.82%), green weight (91.64%), stick weight (99.20%) and fibre weight (96.48%). The high heritability with moderate to high genetic advance over percentage of mean

were observed in bark thickness (98.33%, 38.86), stick weight (99.20%, 56.87) and fibre weight (96.48%, 25.02) which indicate preponderance of additive gene action. He finally concluded that effective selection would be made considering the stick weight, bark thickness, green weight, plant height and base diameter per plant.

Variability, heritability, genetic advance were studied for some anatomical characters in relation to fibre yield in White Jute. The cultivars revealed significant differences among them for all the characters with range of variability. The differences between PCV and GCV were little for all the characters indicating these characters were less influenced by the environment. Heritability and genetic advance (GA) were high for area of pyramid and bark thickness. Number of pyramid, number of fibre bundle, number of fibre layer, length and breadth of fibre cells had high heritability with moderate genetic advance. Emphasis should be given on bark thickness, number of pyramid, area of pyramid and number of fibre bundle during selection of high fibre yielding genotypes were suggested by Pervin and Haque (2012).

Echekwu and Showemimo (2004), conducted an experiment for evaluating fifty-seven diverse genotypes of Kenaf for two years in Samaru in the Nigerian Guinea (Savanna ecological zone) to study genetic variability of seed yield and its components. The results indicated a preponderance of genetic variance for seed yield, plant height, number of seeds per pod and 1000 seed weight. Thus selection for these traits should result in heritable improvements.

Chaudhury (1984), found that top diameter, plant height, internode length in Tossa Jute had the highest heritability estimates associated with moderate genetic advance. So genetic improvement was more effective for above three characters based on phenotypic selection.

Mostofa *et al*. (2002); studied 33 Kenaf's (*Hibiscus cannabinus* L.) genotypes of diverse origin to obtain information on genetic variability, heritability for fibre yield and various yield contributing characters. A substantial variability was found on eight characters. The dry stick weight showed highest GCV and PCV followed by the dry fibre yield and green weight. High heritability with high genetic advance were found for days to 50% flowering and green weight per plant.

Sabiel *et al.* (2014); assessed the genetic variability of Roselle for calyx production as a seasonal crop.

It was mentioned by Begum and Sobhan (1991) that the dried fibre yield and some other morphoagronomic characters such as plant height, base diameter, node number, internode length, leaf angle etc. showed higher genotypic co-efficient of variation.

Alam *et al*. (2015); evaluated fifty-one genotypes of White Jute from different geographic origins to study their genetic variability of 11 morphological characters. Significant variation was observed among the genotypes for all the characters. Considering genetic parameters, high GCV was observed in branches per plant. High heritability values with moderate genetic advance in percentage of mean were obtained for leaf width, petiole length and nodes per plant.

High heritability coupled with high genetic advance (GA) for days to 50% flowering was recorded in Kenaf by Manjunatha and Sheriff (1991).

According to Singh (1970), less genetic variability were found for plant height and base diameter than fibre weight and stick weight in Jute. Maximum heritability values were for plant height (86.75%) followed by base diameter (82.46%) and fibre weight (68.04%). The highest genetic advance was observed in case of fibre weight (22.81%) followed by stick weight (19.31%), base diameter (11.72%) and plant height (8.20%).

Balogun *et al*. (2008); experimented fifty-one accessions of *Hibiscus cannabinus* L. and characterized 14 morphological parameters in Ibadan, southwestern Nigeria. The most widely varied traits were earliness, number of apical branches and leaf lobes per plant with 483.3, 97.9 and 60.6% coefficients of variation, respectively. The variation was seen as a manifestation of environmental response in addition to the genotypic constitution. They concluded that it would aid in parent selection during breeding programs.

High heritability for the character days to 50% flowering, plant height, green weight and fibre weight were reported by Sasmol and Chakraborty (1978) and Dutta *et al.* (1973) in *Hibiscus* species.

Phenotypic co-efficient of variation was observed higher for plant height, base diameter, node number and fibre weight than GCV in Jute by Sardana *et al*. (1990).

Wide and narrow differences between the GCV and PCV were found in stick weight and petiole length in Jute. Both GCV and PCV were higher for fibre yield followed by green weight with and without leaves. PCV was higher than GCV for all characters. High heritability (52.9%) with high genetic advance (35.5) were observed by Ahmed *et al.* (1993).

Morpho-agronomical characterization was done for 16 kenaf accessions from 4 different geographic origins to assess the variation and genetic relationships according to their origin. Clustering of the accessions with origin showed the association of genetic variability among the accessions with their source of origin. To evaluate the genetic variability among the accessions, fishers distance was calculated with significant p-value. Faruq *et al*. (2011) found that the highest distance was observed among the accessions originated from Australia and China.

Dahal (1991), carried out an experiment with various genotypes of Deshi Jute and reported moderate heritability value with low genetic advance for leaf area, petiole length, plant height, base diameter, dry stick weight, harvest index and dry fibre weight.

Agro-botanical characteristics of 33 kenaf genotypes were investigated and data were analyzed across two seasons. Wide variation was observed in the genotypes for plant height, green weight etc. by Ogunnian (2014).

Landraces of Roselle (*Hibiscus sabdariffa* var. *sabdariffa* L.) were evaluated in a randomized complete block design with three replications during summer 2013 at Vegetable Research Station, Rajendranagar to assess the production potential and the genetic variability for various agro-economic traits. The variation was recorded within the landrace germplasm for plant height, total biomass, leaf yield, stalk yield, leaf-stalk ratio and harvest index showing its potential for use in the genetic improvement. The landraces RNR-16, RNR-20 and RNR-27 were promising as indicated by the high leaf production potential of 14.22, 12.72 and 11.85 gm plant^{-1} respectively. High estimates of heritability coupled with high genetic advance as percent of mean were recorded for plant height, total biomass, leaf yield, stalk yield and leaf-stalk ratio indicating the possibility to improve these agro-economic traits through selection programs. Medagam *et al*. (2015) concluded that selection would be effective for plant height, leaf yield, stalk yield, leaf-stalk ratio and total biomass in vegetable Roselle.

Noori *et al*. (2012); worked with forty kenaf accessions *(Hibiscus cannabinus* L.) to estimate the variability, heritability and genetic advance in randomized complete block design with three replications. In general PCV was higher than that of the GCV. The highest PCV of 36.50% and GCV of 29.05% were recorded for stem dry matter yield. Broad sense heritability estimates ranged from 14.79% (stem diameter) to 97.26% (days to flowering). The highest expected genetic advance was recorded for stem dry matter yield (47.62%)

followed by leaf to stem ratio (43.11%). They indicated that the traits showed high heritability and high genetic advance could be effectively improved through selection.

Talukder and Haque (1992), carried out an experiment related to genotype x environment interaction, heritability, genotypic variation and genetic advance in Jute (*Corchorus capsularis* L.). They observed that the genetic variance for harvest index (HI) and plant height were significant at 1% level for fibre crops. For HI, the genotype x location x year interaction was significant at 1% level. Heritability for branches/plant and 1000-seed weight were 2.74 and 3.15 times greater respectively than that of seed yield/plant. The estimates of broad sense heritability and genetic advance were higher for biomass yield. The heritability for branches per plant was 2.74 and 1000 seeds weight was 3.15 times greater than seed yield.

Ali *et al*. (2002); performed an experiment where three cultivated varieties of *Corchorus capsularis* and *Corchorus olitorious* were studied to evaluate their performance of yield and yield contributing characters at harvest stages 50, 70, 90, 110 days respectively. Wide ranges of variation were observed in each harvest stages. Two morphological characters such as plant height and base diameter have been used for selection of Jute plants for high fibre yield.

Islam (2002), studied 23 germplasms along with three control varieties of *Chorchorus capsularis*. He observed highest plant height (3.37 m), base diameter (23.33 mm) and harvest index (32.79) which were found in the control variety CVL-1. Dry weight of leaf (12.45 gm), dry weight of stick (64.13 gm) and total dry matter were found maximum in the accession 2271. Genetic variations were observed among the germplasms for plant height, base diameter, harvest index and total dry matter. No high yielding germplasm having higher harvest index could be identified from the germplasm studied. For all characters, PCV was higher than GCV.

An experiment was carried out by Ghosh *et al*. (2013) where twenty-five morpho-agronomic traits of 63 jute genotypes, including two varieties with 37 accessions of *Corchorus capsularis* and 1 variety with 23 accessions of *Corchorus olitorius*, were evaluated to assess the extent and patterns of variability and their relationships. Seed traits exhibited a wider range of variation than fiber traits and the genotypes in *Corchorus olitorius* varied the most than those in *Corchorus capsularis*. Qualitative traits were also the most informative.

Ali (1994), noted that high GCV and PCV were noticed in fibre yield and bark thickness in Jute.

High heritability and high genetic advance were obtained for stick weight and fibre weight in Tossa Jute by Ahmed and Islam (2003).

Gray *et al*. (2006); investigated variability in kenaf (*Hibiscus cannabinus* L.) as part of an agroindustrial project in northwest Argentina. Six highly inbred photosensitive cultivars were crossed, namely, Endora, Pandora, Tainung 1, Line 42, Line 21, and Line 29. Significant differences among F_1 family were observed. A predominant additive effect was detected for the days to flowering, giving high heritability (0.69) suggesting the possibility of effective selection for earliness in these cultivars. Early flowering in Line 29 was highly heritable, and therefore, is important for breeding purposes. Line 42, despite being the earliest, did not transmit this characteristic to its progenies, possibly because of epistatic genetic effects.

Mostofa (2013), genetically analyzed the days to first flowering, the number of fruits per plant, the number of seeds per fruit and the 1,000 seed-weight using six-parent half diallel crosses in kenaf to determine the inheritance pattern and genetic behavior of these characters. Hayman's analysis of variance and components of variations related to gene actions indicated the involvement of both additive and dominance effects for all the traits, but the value of additive

(D) and dominance (H_1) of $(H_1/D)^{1/2}$ indicated predominant additive effects for the days to first flowering (0.91) and 1,000 seed-weight (0.81), while there were dominance effects for the number of fruits per plant (28.35) and the number of seeds per fruit (2.58). Variance and covariance graphs revealed a partial dominance for all the traits except the number of seeds per fruit which showed over-dominance. Parents Acc.5030, Acc.4197 and Acc.2922 possessed the most recessive genes, while parents Acc.4659 and Acc.2731 had maximum dominant alleles for all the studied traits. The value of heritability in the narrow sense was comparatively high for the days to first flowering (0.59) and 1,000 seed-weight (0.56), but it was low for the number of seeds per fruit (0.09) and the number of fruits per plant (0.01).

Helianto *et al*. (1998); reported wide differences between the GCV and PCV for different characters in Kenaf. They reported that selection on phenotypic basis would not be very effective for genetic improvement.

Faruq *et al*. (2013); recorded 15 morphological data and multivariate analysis was used to measure the genetic variation among the genotypes. There were significant differences among the genotypes in fibre weight, days to 50% flowering and days to maturity. Principal component analysis showed that days to flowering, days to maturity, plant diameter and leaf shape were the traits responsible for major variation among the genotypes.

Siepe *et al.* (1997); carried out an experiment where a collection of 103 genotypes belonging to nine species has been evaluated for 3 years at the Research Centre of Trisaia. A total of 15 morphological and yield parameters have been considered such as plant height, stem diameter and color, leaf form, fresh and dry biomass, bark/core ratio and flowering date. To evaluate the genetic variability, multivariate statistical analysis has been applied during three successive growing seasons. The germplasm under investigation could be divided in two main groups, one typically early-maturing and the other late-maturing type.

2.2 Correlation co-efficient and path analysis

Ahuja (2012), estimated the correlation coefficients and the direct and indirect effects of component traits in Cotton. Hence, the present investigation was carried out on these aspects by grouping the 20 F1 hybrids into 3 sets on the basis of fibre length and strength, (i) 10 hybrids of low fibre strength (20 gm) and medium staple length (25.0 mm), (ii) 10 hybrids of high fibre strength (>=24 gm) and longer fibre length (>=28 mm), and (iii) 20 hybrids, i.e. all the 10 hybrids of set 1 and set 2 of *Gossypium hirsutum* L. for agronomic and fibre quality traits. Significant genotypic difference existed among the hybrids in all the sets for all the characters studied. The direction of association, coefficient of the traits and direct effects on seed cotton yield differed for all the traits except for the number of bolls per plant, boll weight and fibre strength in set 1 and set 2. Set 1 gave the same direction of association with seed cotton yield as obtained in set 3 of usual practice except for the traits ginning out turn (GOT) and days to flowering, whereas set 2 gave similar information to the usual practice for the traits days to flowering, total bolls, boll weight and GOT, and differed for other traits. The study indicated that the hybrid population needs to be grouped on the basis of fibre length and fibre strength prior to estimation of correlation coefficients and direct and indirect effects of other traits on seed cotton yield.

Islam (2002), studied 23 germplasms along with three control varieties of *Chorchorus capsularis*. Plant height, base diameter and dry weight of bark were positively correlated with harvest index.

Pervin and Haque (2012), reported on eleven genotypes of Deshi Jute during April to August 2008. Fibre yield per plant was significantly positively correlated with plant height, base diameter, green weight and stick weight. Path coefficient analysis revealed maximum contribution of plant height to fibre yield per plant and this was followed by the contribution of base diameter.

In Jute, fibre yield was directly correlated with base diameter where plant height was not a dependable indicator were showed by Eunus (1969).

Ali (1994), showed that fibre yield was strongly and positively correlated with number of phloem wedges (0.97), area of phloem wedges (0.88), number fibre layers (0.92), dry stick weight (0.99), bark wood Ratio (0.37) and fibre/stick ratio (0.58).

Echekwu and Showemimo (2004), conducted an experiment where they noted that seed yield was positively and significantly correlated with plant height, number of seeds per pod and 1000 seed weight. Significant and positive correlations were also obtained between plant height and number of capsules per plant and between 1000 seed weight and number of seeds per pod. The path-coefficient analysis indicates that number of seeds per pod and 1000 seed weight had the highest direct effects on seed yield.

Chowdhury *et al*. (1981); reported that plant height, base diameter were positively correlated with fibre yield. But the correlation of node number and internodal length were non-significactory. They also found that genotypic correlation is higher than phenotypic correlation.

In 52 genotypes of Mesta, genotypic correlations were found to be higher than the phenotypic correlations. The results indicated that the associated traits were responsible for increasing the fibre yield and improving the fibre quality. So, selection should be based on plant height, green weight, top diameter and strength were suggested by Sinha *et al*. (1986).

Das (1987), reported that plant height, base diameter, leaf area and node number showed greater correlation coefficient with fibre yield. Where petiole length was negatively correlated with leaf area in Jute.

The characters associated with genotypic and phenotypic levels had strong association with fibre yield in Tossa Jute. Genotypic correlation is higher than

phenotypic correlation in case of all characters was reported by Islam and Ahmed (1991).

Das and Rakshit (1988), observed that highly significant correlation was found for fibre yield with plant height, base diameter, node number and leaf area but non-significant in case of petiole length in *Corchorus olitorius* jute.

According to Ghosdastidar and Das (1984), plant height, base diameter and node number showed positive correlation with dry fibre yield per plant in *Corchorus olitorius* jute.

Das (1987), conducted an experiment where plant height followed by base diameter, leaf area had a positive effect on fibre yield. The remaining traits such as petiole length, node number had low and negative effects in fibre crops.

Akter *et al*. (2005); reported that fresh weight without leaves had highest direct effect on fibre yield in Jute.

2.3 Genetic diversity

Zhang *et al.* (2012); estimated genetic diversity of 84 kenaf accessions collected from 26 countries and regions. The analysis showed that kenaf germplasm had abundant genetic variation, with genetic dissimilarity coefficients ranging from 0.01 to 0.62. The in-group dissimilarity coefficient (0.29) was observed in 84 kenaf accessions, and all the accessions could be divided into three groups: cultivars (L_{1-1}), relatively wild species (L_{1-2} and L_{1-3}), and wild species (the others). Further in-group analysis in group L_{1-1} (0.19) revealed that the kenaf cultivars could be divided into five subgroups with distinct regional characteristics. They resulted that genes be exchanged among all kinds of tested varieties from different origins. The results provide a useful basis for kenaf germplasm research and breeding.

The fifty-one accessions of *Hibiscus cannabinus* L. was studied by Balogun *et al*. (2008). The correlation matrix of the quantitative parameters was used to perform principal components (PC) analysis to understand the relative contributions of each trait to the variation observed. The first three PCs explained 66.23% of the variation, with only number of apical branches not highly weighted by any of the PC. The five clusters were distinguished by earliness, plant height, fibre yield, stem spine density, stem girth and apical branching. The variation was seen as a manifestation of environmental response in addition to the genotypic constitution. These results would aid in parent selection during breeding programs.

Faruq (2013), experimented with 32 kenaf genotypes originated from different parts. In cluster analysis different kenaf genotypes produce three distinct groups which can be used for selection of parents in the breeding program. From total three clusters, high yielding late mature genotypes of the cluster 3 can be used to cross with middle flowering genotypes of cluster 2 to produce relatively photo insensitive variety with better fibre and stick yield in Malaysian tropical environment.

Alam *et al.* (2015); conducted an experiment where he evaluated 51 genotypes of White Jute from different geographic origin. All the genotypes were grouped into six different clusters. Principal component analysis, principal coordinate analysis and canonical vector analysis gave similar results to that of cluster analysis. The highest inter-genotypic distance (1.84) was found between G15, G50 and the lowest distance between G38 and G26. The highest inter-cluster distance (14.37) was observed between cluster I, IV and the lowest distance (2.46) was between cluster III and V. Regarding the cluster distance, inter-genotypic distance and other agronomic performance, the genotypes G47, G33, G48 from cluster I; G27, G17, G23 from cluster III and G13, G40, G45 from cluster II were considered to be better parents for future use in hybridization programs.

Ghosh (2015), conducted an experiment where 138 Jute genotypes of *Corchorus olitorius* were characterized with ten jute specific SSR markers. A total of 23 alleles were amplified with an average of 2.3 alleles per locus and the PIC value ranged from 0.13 to 0.76 with an average of 0.455. The un-weighted pair-group method with arithmetic average cluster analysis of the 138 jute genotypes depicted a dendrogram which divided the genetic resource into three major clusters. Based on cluster analysis the most divergent genotypes identified were OIJ 167 (from Indonesia), OIM 058 and OIM 059 (India), however based on the agronomic traits as maximum plant height, basal diameter and fibre weight they were OIJ 245, OIJ (153 and 161) and OIJ 040, respectively.

Haque *et al*. (2007); studied the genetic diversity of 18 jute genotypes of the two cultivated species *Corchorus capsularis* L. and *Corchorus olitorius* L. DNA profiling was generated using sequence independent RAPD markers. Two major clusters representing the two species were resolved among the genotypes that were examined in the study. This genetic distance information could be useful in breeding programs in order to introduce agronomically important traits such as short field duration, low temperature tolerance, snow

white fibre, higher harvest index etc. From the study one *C. olitorius* and two *C. capsularis* varieties were found more suitable for their selection as seed parent against different accessions for improvement because of their higher genetic distant relationship within species.

Guang *et al*. (2011); studied the genetic diversity and genetic relationship of some kenaf genotypes using ninety one ISSR molecular markers for amplification on 44 shares of kenaf germplasm resources, of which 21 that showed good diversity. The genetic diversities between cultivars and wild type or half-wild type varieties were 0.47-0.91, while that among 32 cultivars were 0.85-0.97, suggesting that genetic relationships among cultivars are relatively close and their genetic similarities were rather narrow.

Ogunbodede *et al*. (1997); estimated genetic diversity in kenaf. Fifty four accessions of kenaf of diverse eco-geographical origins were evaluated in an 8 x 8 lattice design in south-western Nigeria. Two multivariate techniques - the coefficient of Racial Likeness (CRL) and principal component analysis (PCA) were used to assess the extent of genetic divergence among the accessions. The CRL distances for the 1431 possible pairs of accessions were each less than 2.0. The first three principal axes accounted for 67.17% of the total variation among the accessions. From a two-dimensional ordination of the first two principal axes, six clusters can be identified. Clustering was closely related to average CRL values and there was no relationship between clustering and eco-geographical distributions. The analysis of CRL values showed that stem diameter and fiber yield each accounted for 13.0% of the variation detected in the accessions. Plant height and retting percentage each contributed 11.3% while core weight, number of leaves per plant, core percentage and fresh plant weight contributed 12.5, 10.3, 10.2 and 10.0%, respectively.

The characteristics of 33 kenaf genotypes were investigated by Ogunniyan (2014). First six principal component axes showed strong discriminating ability among the characters, and accounted for 81.5% of the total variance. Principal

component axes (PCAs) I and II had eigen values greater than unity and the difference between the 2 axes were 1.526. The discriminating ability of PCA I was strongest. It accounted for 26.7% due to basal, middle and top stem diameter. Principal component II which accounted for 16.5% described variation in the flowering pattern whereas PC III described variation due to yield components accounting for 13.0%. The basal, middle and top stem diameters, days to first, and 50%, flowering, bast and core dry weights respectively contributed large variability as 0.8832, 0.8866, 0.8963, 0.8413, 0.6761, 0.8063 and 0.8138 as eigen vectors. The genotypes were early maturing and plant height in four clusters ranged from 201.50 cm to 264.83 cm. Genotypes that clustered into groups I and II are good candidates for fibre production. PCAs I and II adequately distinguished 32 of the 33 genotypes suggesting a high level variability among the genotypes. Genotypes AU-245243, A-60-282-51, AC-313244, Tianung 2 and Exshika loaded the first 3 principal axes. Genotypes 2QQ 13 and AU-60-2826 were most distinct in all the 3 configurations.

Cheng *et al.* (2002); studied the genetic diverstity of Kenaf. DNA (RAPD) markers were analyzed among 14 kenaf varieties in Japan. The varieties could be divided into three major groups. The characters, such as middle stem diameter, whole stalk weight, and days to 50% flowering were highly responsible for the variation of the kenaf varieties.

Zhang *et al*. (2015); used 58 Jute accessions, including two control varieties (Huangma 179 and Kuanyechangguo) to analyze the genetic diversity. The 58 jute accessions were DNA-fingerprinted with 67 SSR markers from the 28 primer pairs. Their genetic similarity coefficients ranged from 0.520 to 0.910 with an average of 0.749, indicating relatively great genetic diversity among them. The 58 jute accessions were divided into four groups with the coefficient 0.710 used as a value for classification, consistent with their species and pedigrees.

CHAPTER III

MATERIALS AND METHODS

This chapter discusses with the major information regarding materials and methods that were used in conducting the experiment. It consists of a short description of experimental site's location, soil characteristics, climate, materials, layout and design of the experiment, land preparation, manuring and fertilization, intercultural operations, harvesting, data recording procedure and statistical analysis etc., which are presented as follows:

3.1 Experimental site

The research work relating to Genetic variability, character association and diversity in Kenaf (*Hibiscus cannabinus* L.) was conducted with 25 Kenaf genotypes at Central Jute Agricultural Experiment Station of Bangladesh Jute Research Institute (BJRI), Jagir, Manikganj during the time span of 15 March to 30 September, 2015.

3.2 Geographical location

The experimental area was situated at 23°53.95'N latitude and 90°04'E longitude at an altitude of 8.8 meter above the sea level. The experimental field belongs to the Agro-ecological zone named "Young Brahmaputra and Jamuna Flood Plain", AEZ-8 (Rahman M.M., 2006). This was a region of complex relief and soils developed through the floodplain sediment. It is located about 60 km west of Dhaka. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.3 Climate and soil

The experimental area were located in the tropical climate zone. It was characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-October) and low rainfall associated with moderately low temperature during the Rabi season (November-March). Weather

information regarding temperature, relative humidity and rainfall prevailed at the experimental site during the study period were presented in Appendix II.

Soil of the experimental site belongs to the general soil type. The soil was sandy loam in texture. Soil p^H ranged from 6.4- 6.8 (slightly acidic) and organic matter content is 0.87%. The land topography was uniform with medium highness and it was above the flood level. It was homogeneous in respect to soil fertility. Irrigation and drainage system were satisfactory. Physiochemical properties of the soil were presented in Appendix III.

3.4 Experimental materials

Twenty five genotypes of *Hibiscus cannabinus* L. were taken as experimental material. The seeds were collected from the gene bank of Bangladesh Jute Research Institute (BJRI), Dhaka. The seeds were physically healthy and genetically pure. The name and origin of these genotypes are presented in Table 1.

3.5 Design and layout of the experiment

The experiment was carried out in Randomized complete block design (RCBD) with three replications. The genotypes were distributed into the every plot of each block according to layout of the experiment. The individual plot was 3 m × 1 m in size. The twenty five genotypes of the experiment were assigned at random into plots of each replication. The spacing distance maintained as row to row 30 cm and plant to plant 5-7 cm. The distance maintained between two lines was 3 m.

3.6 Land preparation

The experiment plot was prepared by four ploughing and cross ploughing followed by two mowing with tractor and power tiller to bring about good tilth in the third week of March, 2015. Weeds and other stables were carefully removed from the experimental plot and leveled properly.

Table 1. Name and origin of 25 selected genotypes of Kenaf

Genotype No.	Accession	Origin/Country name
G1	BJRI Kenaf 3 (HC-3)	Check (Australia)
G2	Acc-1653 (HC 95)	Check (Iran)
G3	Acc-1583	USA
G4	Acc-1585	USA
G5	Acc-1589	USA
G6	Acc-1592	USA
G7	Acc-1593	USA
G8	Acc-1594	USA
G9	Acc-1611	Iran
G10	Acc-1612	Iran
G11	Acc-1626	Iran
G12	Acc-1633	Iran
G13	Acc-3741	Kenya
G14	Acc-3746	Kenya
G15	Acc-4622	USA
G16	Acc-4623	USA
G17	Acc-4627	USA
G18	Acc-4718	USA
G19	Acc-4750	USA
G20	Acc-4823	Kenya
G21	Acc-1575	Pakistan
G22	Acc-1607	Iran
G23	Acc-4415 (PI-329192)	Elsalvador
G24	Acc-1576	Pakistan
G25	Acc-1876	Kenya

3.7 Seed sowing

Seeds sowing were done on 09 April, 2015. Seeds were sown in line. First thirteen accessions were planted towards east to west direction and next twelve accessions were planted towards west to east direction. Maximum seeds were germinated within six days (15 April, 2015).

3.8 Manure and fertilizers application

The following doses of manure and fertilizers were applied to the plots for Kenaf cultivation. The whole amount of Cowdung, TSP (Triple Super Phosphate), MP (Muriate of Potash) and half of the Urea were applied as broadcast during final land preparation. Remaining Urea was top dressed twice one days after first and final weeding which was 24 DAS and 36 DAS respectively.

Table 2. Dose of manure and fertilizers used in the study

Sl. No.	Fertilizer/Manure	Dose
1.	Cowdung	4.5 ton/ha
2.	Urea	122 kg/ha
3.	TSP	18 kg/ha
4.	MP	32 kg/ha

3.9 Intercultural operation

Two weeding and thinning were done on same date which were 23 and 35 days after sowing. Acaricide named Nitrow was applied twice after 23 and 40 days of sowing to control the mite. Plants infected by Leaf curl virus were pulled out and burried when observed.

3.10 Harvesting

The crop was harvested on 28 October, 2015. Five plants were selected randomly from each replication for harvest. After harvesting, the plants were kept on land for 2-3 days. The harvested stems were retted in a concrete retting tank. After retting, fibres were extracted and dry fibre weight and dry stick weight were recorded.

3.11 Data Collection

The following data on nine morphological characters were recorded from 5 randomly selected plants of each genotype from each replication during the experiment.

3.11.1 Plant height (m)

It was measured from the base of the plant to the tip of the main shoot in meter and average data was recorded.

3.11.2 Base diameter (mm)

Base diameter was measured at the base of the stem in mm using slide calipers and average data was recorded.

3.11.3 No. of nodes per plant

Total number of nodes per plant was counted and expressed in number and average data was recorded.

3.11.4 Internode length (cm)

Internode length was measured from the middle portion of the plant which is expressed in centimeter and average data was recorded.

3.11.5 Green weight with leaves (gm)

Green weight with leaves per plant was weighed in gram unit and average data was recorded.

3.11.6 Green weight without leaves (gm)

Green weight without leaves per plant expressed in gram was measured and recorded.

3.11.7 Green bark thickness (mm)

Green bark was extracted from the plant after removing the leaves. Then it was measured in millimeter.

3.11.8 Dry stick weight (gm)

The sundried sticks were weighed in gram after retting and drying. Then average data was recorded in gram.

3.11.9 Dry fibre weight (gm)

The weight of the dried fibre was taken after extraction, retting and drying in gram and average data was recorded.

Plate 1a: A photograph during seed sowing

Plate 1b: Field view of the experiment (Vegetative growth stage)

Plate 1c: Field view of the experiment (Harvesting stage)

Plate 1d: Field view of the experiment during inspection by my supervisor

3.12 Statistical analyses

3.12.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955). Genotypic variance (σ^2_g) were obtained by subtracting Error MS from Genotypic MS and dividing by the number of replication (r) as shown below:

$$\text{Genotypic variance } (\sigma^2_g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

The phenotypic variance (σ^2_p) were derived by adding genotypic variance (σ^2_g) with error variance (σ^2_e) as given by following formula-

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

3.12.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952).

$$\text{Genotypic co-efficient of variation (GCV \%)} = \frac{\sigma_g}{\overline{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

$\overline{X}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula-

$$\text{Phenotypic co-efficient variation (PCV \%)} = \frac{\sigma_P}{\overline{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

$\overline{X}$ = Population mean

3.12.3 Estimation of heritability

Broad sense heritability was estimated by Lush (1943) through the following formula, suggested by Johnson *et al.* (1955).

$$\text{Heritability } (H_b\,\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

H_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.12.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = K \times \frac{\sigma^2 g}{\sigma^2 p} \times \sigma_p$$

Where,

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

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.12.5 Estimation of genetic advance mean's percentage

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

$$\text{Genetic advance (\% mean)} = \frac{\text{Genetic Advance}}{\text{Population mean}} \text{ X } 100$$

3.12.6 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient 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 co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters are presented as follows:

Genotypic correlation (r_{gxy}) = $\frac{\sigma^2_{gxy}}{\sqrt{\left(\sigma^2_{gx} \times \sigma^2_{gy}\right)}}$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

Phenotypic correlation (r_{pxy}) = $\frac{\sigma^2_{pxy}}{\sqrt{\left(\sigma^2_{px} \times \sigma^2_{py}\right)}}$

Where,

σ_{pxy} = Phenotypic covariance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.12.7 Path co-efficient analysis:

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) are required to be formulated as shown below:

$r_{yx1} = p_{yx1} + p_{yx2}\, r_{x1x2} + P_{yx3}\, r_{x1x3}$

$r_{yx2} = p_{yx1}\, r_{x1x2} + p_{yx2} + p_{yx3}\, r_{x2x3}$

$r_{yx3} = p_{yx1}\, r_{x1x3} + p_{yx2}\, r_{x2x3} + p_{yx3}$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

p_{yx1} = The direct effect of x_1 on y.

$p_{yx2}\ r_{x1x2}$ = The indirect effect of x_1 via x_2 on y

$p_{yx3}\ r_{x1x3}$ = The indirect effect of x_1 via x_3 on y

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$P^2_{RY} = 1 - \sum p_{iy} \cdot r_{iy}$

Where,

$P^2_{RY} = (R^2)$; and hence residual effect, $R = (P^2_{RY})^{1/2}$

p_{iy} = Direct effect of the character on yield

r_{iy} = Correlation of the character with yield

3.12.8 Estimation of Genetic diversity

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952), suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis *viz*. Principal component analysis, Principal coordinate analysis, Cluster analysis and Canonical vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.12.8.1 Principal component analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.12.8.2 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.* 1989).

3.12.8.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows; starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.12.8.4 Canonical vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variability that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.12.8.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ------ to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.12.8.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = The sum of distances between all possible combinations (n) of genotypes included in a cluster

n = Number of all possible combinations between the populations in cluster

3.12.8.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible Combinations of the populations in cluster i and j

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

3.12.8.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data on yield and its contributing characters of 25 Kenaf genotypes were statistically analyzed and the results thus obtained are discussed below under the following heads:

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Genetic diversity analysis

4.1 Analysis of variance

The analysis of variance indicated higher amount of significant variability among the genotypes for all the characters studied such as plant height, base diameter, number of nodes per plant, internode length, green weight with leaves per plant, green weight without leaves per plant, green bark thickness, dry stick weight and dry fibre weight (Table 3). The variation due to replication was non-significant for all the characters studied. This variation might be due to the diverse geographic origin and distribution of genotypes.

4.2 Genetic variability, heritability and genetic advance

The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance in percent mean for all the characters were studied and the results are presented in Table 3 & 4 and depicted in Fig. 1 and 2. The mean performance of Kenaf genotypes for various growth characters and yield components are presented in Appendix IV.

Table 3. Analysis of variance for different characters of Kenaf genotypes

Source	Df	Mean sum of square								
		PH	BD	NPP	IL	GWL	GWWL	GBT	SW	FW
Replication	2	0.000	3.539	11.853	0.004	91.240	79.053	0.012	2.520	1.213
Treatment	24	0.148**	15.751**	191.835**	0.577**	21,318**	12,649**	0.150**	330.60**	41.858**
Error	48	0.001	0.853	3.867	0.014	44.017	31.039	0.002	4.783	0.352
CV%		1.24	4.81	2.94	3.00	2.57	2.64	2.53	6.20	4.23

**** indicate significant at the 0.01 level**

PH = Plant height (m), BD = Base diameter (mm), NPP = Number of nodes per plant, IL = Internode length (cm), GWL = Green weight with leaves per plant (gm), GWWL = Green weight without leaves per plant (gm), GBT = Green bark thickness (mm), SW = Stick weight (gm) and FW = Fibre weight (gm).

4.2.1 Plant height (m)

Mean sum of square for plant height was highly significant (Table 3). The minimum plant height was found 1.89 m in G11 and the maximum plant height was recorded 2.99 m in G25 with the mean value 2.39 m (Appendix IV). The PCV and GCV were 9.36 and 9.28 percent, respectively (Table 4). High heritability (98.23%) with moderate genetic advance over percentage of mean 18.94 percent were observed for this trait (Table 4). High heritability was found for the plant height were reported by Dutta *et al*. (1973). Variation of plant height among different genotypes of Kenaf was shown on following photograph (Plate: 2a, 2b, 2c).

The highly significant MS value indicates existence of considerable difference for this trait. A narrow range of difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicating less environmental influence on the phenotypic expression of plant height and it is mostly governed by genetic factors. Hence, selection will be effective on phenotypic basis. High heritability coupled with moderate genetic advance for plant height indicating the predominance of additive gene effects on plant height. So we have scope to improve this trait before using it in breeding program.

4.2.2 Base diameter (mm)

Mean sum of square for base diameter was highly significant (Table 3) indicating existence of considerable difference among the genotypes for this trait. The maximum base diameter was found 24.37 mm and the minimum base diameter was recorded 14.87 mm with the mean value 19.20 mm. The value ranged from 14.87 mm to 24.37 mm, in the genotype G11 and G25, respectively (Appendix IV). The PCV and GCV were 12.56 and 11.61 percent (Table 4). The heritability estimates were high (85.33%) with high genetic advance over mean of 22.08 percent (Table 5). Mostofa *et al.* (2002) also reported the highest heritability for base diameter in Tossa Jute. Photographs of

Table 4. Estimation of genetic parameters for nine characters in 25 Kenaf genotypes

Characters	σ^2_p	σ^2_g	σ^2_e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	0.05	0.05	0.00	9.36	9.28	1.24	98.23	0.45	18.94
BD	5.82	4.97	0.85	12.56	11.61	4.81	85.33	4.24	22.08
NPP	66.52	62.66	3.87	12.21	11.85	2.94	94.19	15.82	23.69
IL	0.20	0.19	0.01	11.41	11.01	3.00	93.08	0.86	21.88
GWL	7135.4	7091.3	44.02	32.76	32.65	2.57	99.38	172.94	67.06
GWWL	4237.1	4206.0	31.04	30.89	30.78	2.64	99.27	133.11	63.17
GBT	0.05	0.05	0.00	10.72	10.42	2.53	94.42	0.44	20.86
SW	113.39	108.61	4.78	30.18	29.54	6.20	95.78	21.01	59.55
FW	14.19	13.84	0.35	26.85	26.52	4.23	97.52	7.57	53.95

PH = Plant height (m), BD = Base diameter (mm), NPP = Number of nodes per plant, IL = Internode length (cm), GWL = Green weight with leaves per plant (gm), GWWL = Green weight without leaves per plant (gm), GBT = Green bark thickness (mm), SW = Stick weight (gm), FW = Fibre weight (gm), PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation and ECV = Environmental coefficient of variation.

Plate 2a: Photograph showing variation in plant height among different genotypes of Kenaf

Genotype 25

Genotype 11

Plate 2b, 2c: Photographs showing the genotypes having the highest and the lowest plant height

Genotype 25

Plate 3a: Photograph showing the genotype having the highest base diameter

Genotype 11

Plate 3b: Photograph showing the genotype having the lowest base diameter

the genotypes having the highest and the lowest base diameter were depicted in plate 3a, 3b. A narrow range of difference between the PCV and the GCV indicating less environmental influence. Here, selection will be effective on the basis of phenotype. High heritability coupled with high genetic advance for base diameter indicates that the selection of such character may be useful for improvement of the crops.

4.2.3 Number of nodes per plant

The analysis of variance revealed highly significant differences among the genotypes with respect to number of nodes per plant. The maximum number of nodes per plant (81.67) was recorded by the genotype G22 and the lowest number of nodes per plant (50) was recorded by G11 (Appendix IV). The PCV and GCV were 12.21 and 11.85 percent (Table 4) respectively. Narrow difference between GCV and PCV for this trait indicated the less environmental influence. High heritability (94.19%) with high genetic advance in percent mean (23.69) were observed for this character (Table 4). Similar findings were reported by Ghosdastidar *et al*. (1984) and Johnson *et al*. (1955). This value notifies that the character is governed by additive genes and selection will be rewarding for improvement of such trait.

4.2.4 Internode length (cm)

The internode length was ranged from 3.30 cm to 5.03 cm with the average value 3.94 cm (Appendix IV). Highly significant differences among the genotypes were observed for internode length. The maximum internode length (5.03 cm) was recorded by the genotype G11 and the lowest internode length (3.30 cm) was recorded by G25 (Appendix IV). The PCV and GCV were 11.41 and 11.01 percent, respectively. The estimates of heritability were high at 93.08 percent with genetic advance over mean also moderately high 21.88 (Table 4). So selection is ineffective without improvement of this character. Chaudhury *et al.* (1984) observed the same findings in Tossa Jute.

4.2.5 Green weight with leaves per plant (gm)

Significant differences were observed in green weight with leaves per plant due to diverse origin and distribution of genotypes. The green weight with leaves per plant were ranged from 118 to 500 gm with mean of 257.88 gm. The minimum green weight with leaves were observed in genotype G11 while the maximum green weight with leaves were found in the genotype G25 (Appendix IV). The coefficients of variability at phenotypic and genotypic level were 32.76 and 32.65 percent respectively. High heritability (99.38%) with high genetic gain (67.06%) provided better opportunity for selection of this parameter (Table 4).

4.2.6 Green weight without leaves per plant (gm)

Green weight without leaves per plant ranged from 98.00 to 386.67 gm with a mean value of 210.71 gm. The maximum green weight without leaves were recorded in the genotype G25 and minimum green weight without leaves in G11 (Appendix IV). The PCV and GCV observed were 30.89 and 30.78 percent (Table 5) respectively. Narrow difference between GCV and PCV value for this trait indicated the less environmental influence. This character can be selected on the phenotypic basis. High heritability (99.27%) coupled with high genetic advance over percentage of mean (63.17%) were found for this traits (Table 4). Selection is rewarding for this character and it can be used for further breeding program. Joseph (1974) noted that green weight and fibre weight showed higher genetic variability in *Corchorus capsularis* which is similar to this findings.

4.2.7 Green bark thickness (mm)

The mean green bark thickness (mm) was noticed 2.13 mm with a range of 1.69 mm to 2.64 mm (Table 4). Significant variation also observed for this trait was cited by Samsal and Chakrabarty (1977) in Kenaf. The genotype G24 showed the minimum green bark thickness and the maximum green bark thickness was recorded in the accession G22 (Appendix IV). The values 10.72 and 10.42 are noticed for PCV and GCV respectively (Table 4).

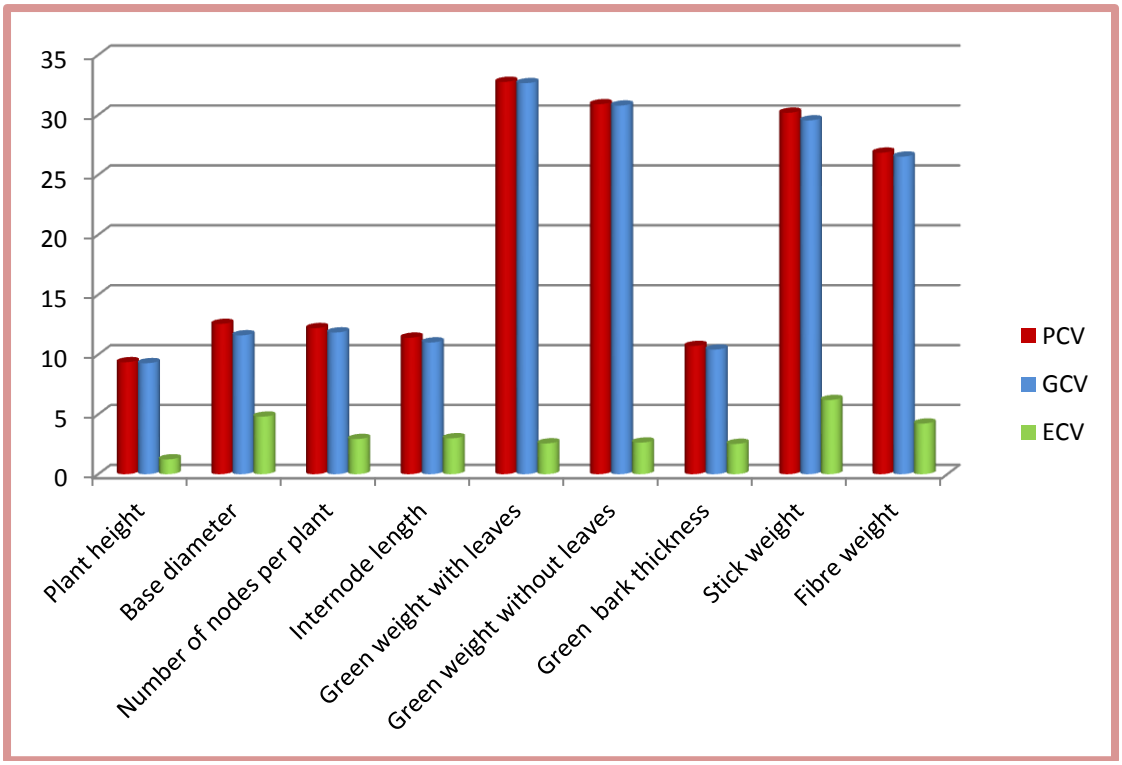

Fig 1. Phenotypic, genotypic and environmental variability in Kenaf

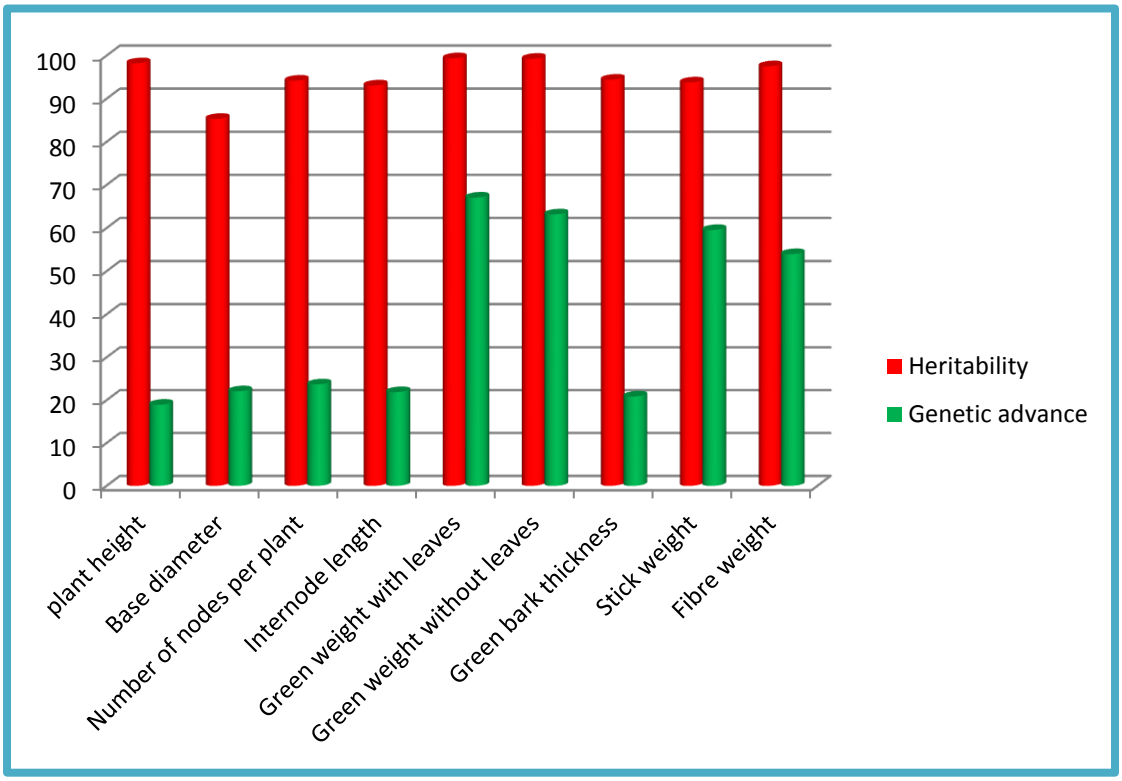

Fig 2. Heritability and genetic advance on percentages of mean in Kenaf

Narrow difference between GCV and PCV for this trait indicated the less environmental influence. The heritability estimate was high 94.42 percent with moderate genetic advance over mean of 20.86 percent could be noted (Table 4). This notifies that additive genes are predominant for green bark thickness. So we have to improve this trait before using it in breeding program.

4.2.8 Stick weight (gm)

A wide variation was found among the genotypes for the stick weight. It varied 22.33 to 59.33 gm significantly among the genotypes with an overall mean of 35.28 gm. The entry G10 showed the lowest stick weight and the highest stick weight was recorded by the entry G25 (Appendix IV). The PCV and GCV were 30.18 and 29.54 respectively (Table 4). Narrow difference between GCV and PCV for this trait indicated the less environmental influence. High heritability (95.78%) with high genetic advance in percent of mean (59.55%) were noticed for stick weight. Manjunatha and sheriff (1991) recorded similar findings in Kenaf. This character is highly efficient for selection.

4.2.9 Fibre weight (gm)

It ranged from 10.33 gm to 25.67 gm with a mean of 14.03 gm. The maximum fibre weight was recorded by the genotype G25 and the genotypes G10, G12, G13 and G19 showed the minimum fibre weight (Appendix IV). The PCV and GCV were obtained 26.85 and 26.52 percent respectively. Narrow difference between GCV and PCV for this trait indicating less environmental influence on the phenotypic expression of fibre weight and it is mostly governed by genetic factors. Hence, selection will be effective on phenotypic basis. The values of high heritability (97.52%) along with high genetic advance as percent mean (53.95%) were observed for this trait (Table 4). High values of broad sense heritability and genetic advance have recorded for this trait indicating that this character was controlled by additive genes and selection of this trait is highly promising. This findings was also supported by Sasmol and Chakrabarty (1978) and Dutta *et al*. (1973) in Kenaf.

4.3 Correlation analysis

The study of yield components and their inter relationship along with yield has immense importance. Yield is the result of combined effect of several components and environment. Understanding the interaction of characters among themselves and with environment have been of great use in the plant breeding. Correlation studies provide information on the nature and extent of association between only two pairs of metric characters. From this it would be possible to bring about genetic upgradation in one character by selection of the other of a pair, obviously, knowledge about character associations will surely help to identify the characters to make selection for higher yield with a view to determine the extent and nature of relationship prevailing among yield contributing characters. Hence, an attempt has been made to study the character association in the Kenaf accessions at both the levels.

4.3.1 Fibre weight vs yield components

A highly significant and positive association of fibre weight at both the genotypic and phenotypic levels was observed with base diameter (0.858** and 0.769**), green weight with leaves (0.854** and 0.848**), green weight without leaves (0.852** and 0.841**) and stick weight (0.0.909** and 0.897**) (Table 5). This results were supported by Chaudhury *et al.* (1981) and Singh (1970). Therefore, selection for any of these highly associated characters will indirectly help in selecting the plants for high fibre yield. Hence, it is worthwhile to have genotypes with high base diameter, higher green weight with leaves, higher green weight without leaves and high stick weight to get higher fibre yield. Plant height (0.665** and 0.0.643**) and number of nodes per plant (0.586** and 0.556**) showed moderate positive association which are highly significant with fibre weight. Similar results were reported by several authors like as Aruna (1998) in Roselle and Manjunatha and sheriff (1991) in Kenaf. Green bark thickness (-0.428** and -0.353**) and internode length (-0.556** and -0.523**) had significant negative association with fibre weight (Table 5).

Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters in Kenaf

Characters	r_g/ r_p	Base diameter (mm)	Number of nodes per plant	Internode length (cm)	Green weight with leaves (gm)	Green weight without leaves (gm)	Green bark thickness (mm)	Stick weight (gm)	Fibre weight (gm)
Plant height (m)	r_g	0.819**	0.831**	-0.943**	0.843**	0.869**	-0.016	0.800**	0.665**
	r_p	0.736**	0.794**	-0.909**	0.819**	0.835**	-0.001	0.761**	0.643**
Base diameter (mm)	r_g		0.766**	-0.837**	0.907**	0.920**	-0.175	0.894**	0.858**
	r_p		0.716**	-0.719**	0.830**	0.845**	-0.085	0.824**	0.769**
Number of nodes per plant	r_g			-0.899**	0.746**	0.791**	0.177	0.788**	0.586**
	r_p			-0.844**	0.737**	0.780**	0.235*	0.756**	0.556**
Internode length (cm)	r_g				-0.739**	- 0.779**	-0.079	-0.756**	-0.556**
	r_p				-0.703**	- 0.736**	-0.090	-0.702**	-0.523**
Green weight with leaves (gm)	r_g					0.993**	-0.225*	0.905**	0.854**
	r_p					0.991**	-0.147	0.884**	0.848**
Green weight without leaves (gm)	r_g						-0.184	0.928**	0.852**
	r_p						-0.091	0.902**	0.841**
Green bark thickness (mm)	r_g							-0.177	-0.428**
	r_p							-0.111	-0.353**
Stick weight (gm)	r_g								0.909**
	r_p								0.897**

**** indicate significant at 1%.** *** indicate significant at 5%.**

In this case higher green bark thickness and internode length can decrease the fibre weight per plant. Chaudhury *et al*. (1981) also found the negative correlation between the fibre weight and internode length in Jute.

4.3.2 Correlation among yield components

Plant height had positive and highly significant correlation with base diameter (0.819** and 0.736**), number of nodes per plant (0.831** and 0.794**), green weight with leaves (0.843** and 0.819**), green weight without leaves (0.869** and 0.835**) and stick weight (0.800** and 0.761**) at both genotypic and phenotypic level (Table 5). It exhibited negative as well as nonsignificant association with green bark thickness (-0.016 and -0.001) at both the levels (Table 5). It also showed negative but highly significant association with internode length (-0.943** and -0.909**) at both the levels (Table 5). If plant height increases, base diameter, number of nodes per plant, green weight with leaves, green weight without leaves and stick weight will increase. But it will reduce the green bark thickness and internode length. The r_g value is greater than r_p signifying the strong genetical association of this traits having low environmental interaction.

Base diameter had a positive and highly significant correlation with number of nodes per plant (0.766** and 0.716**), green weight with leaves (0.907** and 0.830**), green weight without leaves (0.920** and 0.845**) and stick weight (0.894** and 0.824**) at both genotypic and phenotypic level (Table 5). It exhibited negative as well as nonsignificant association with green bark thickness (-0.175 and -0.085) at both the levels (Table 5). It also showed negative but highly significant association with internode length (-0.837** and -0.719**) at both the levels (Table 5). Number of nodes per plant, green weight with and without leaves and stick weight will increase and green bark thickness and internode length will decrease with the increase of base diameter.

Number of nodes per plant showed significant and positive correlation with green weight with leaves (0.746** and 0.737**), green weight without leaves

(0.791** and 0.780**) and stick weight (0.788** and 0.756**) at both genotypic and phenotypic level (Table 5). It exhibited positive nonsignificant correlation with green bark thickness (0.177) at genotypic level and positive significant association with green bark thickness (0.235*) at phenotypic level. It showed negative as well as highly significant association with internode length (-0.899** and -0.844**) at both the levels (Table 5). If number of nodes per plant decreases, green weight with leaves, green weight without leaves, green bark thickness and stick weight will decrease. But it has opposite relationship with internodal length. The greater r_g value indicating strong genetical association of this traits.

Internode length showed highly significant negative association with green weight with leaves (-0.739** and -0.703**), green weight without leaves (-0.779** and -0.736**) and stick weight (-0.756** and -0.702**) at both the genotypic and phenotypic level (Table 5). Moreover it had nonsignificant and negative correlation with green bark thickness (-0.079 and -0.090) at both levels (Table 5). Very minimum environmental effects were found for green weight with leaves, green weight without leaves and stick weight due to greater r_g value. But the r_g value was smaller than r_p value in case of green bark thickness showing that the apparent association between internode length and green bark thickness was not only genes but also the influence of environment.

Green weight with leaves had highly significant and positive correlation with green weight without leaves (0.993** and 0.991**) and stick weight (0.905** and 0.884**) at genotypic and phenotypic level. It had negative significant correlation (-0.225*) at genotypic levels and negative nonsignificant correlation (-0.147) at phenotypic levels with green bark thickness (Table 5). It had proportional relationship with green weight without leaves and stick weight but had inverse relationship with green bark thickness. The higher r_g value signifies the inherent relationship among the traits.

The correlation of green weight without leaves with stick weight (0.928** and 0.902**) was positive and highly significant at genotypic and phenotypic level.

It had nonsignificant and negative correlation (-0.184 and -0.091) with green bark thickness (Table 5). Furthermore If green weight without leaves increases, stick weight will increase. But it will reduce the green bark thickness. The r_g value is greater than r_p value signifying the strong genetical association of this traits.

Green bark thickness showed nonsignificant and negative correlation with stick weight (-0.177 and -0.111) at both genotypic and phenotypic level (Table 5). The r_p value is smaller than r_g value showing that the apparent association between the green bark thickness and stick weight was mainly for genes.

Thus the characters plant height, base diameter, number of nodes per plant, green weight with leaves, green weight without leaves, and stick weight appeared to be predominant consideration for fibre yield as they exhibited highly significant correlation with fibre weight and among themselves. Therefore selection based on this characters bring out improvement towards enhancing the fibre yield in Kenaf.

4.4 Path coefficient analysis

The technique of path coefficient analysis was developed by Wright (1921) and Dewey and Lu (1959) facilitated the partioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait on fibre weight and its indirect effect through other characters were computed and the results are presented in Table 6.

4.4.1 Direct effect

Four out of eight characters had positive direct effect on fibre weight. The characters which had positive direct effect were green weight with leaves (1.04), green weight without leaves (8.61), green bark thickness (0.16) and stick weight (1.71) suggesting direct selection based on these characters would be effective. However, character *viz.*, plant height (-10.63), base diameter (-7.49), number of nodes per plant (-5.56) and internode length (-13.08) had negative direct effect on fibre weight (Table 6). Path coefficient analysis revealed that fibre weight was directly influenced by green weight with leaves, green weight without leaves, green bark thickness and stick weight. Hence, selection for any of these independent traits leads to improve the genotypes for fibre yield. Plant height, base diameter, number of nodes per plant and internode length exhibited high and negative direct effects towards fibre weight, but their significant positive correlations with fibre weight per plant except internode length indicated that the indirect selection could be made for high yielding Kenaf genotypes. The residual effect (R) was 0.357, indicating there were also some other characters which may contribute more than 30% towards yield although not studied but influenced the yield of fibre weight.

Table 6. Path coefficient analysis of different characters of Kenaf

Parameters	Direct effect	Indirect effect via								Genotypic correlation with yield
		PH	BD	NPP	IL	GWL	GWWL	GBT	SW	
PH	-10.63	-	-6.14	-4.62	12.33	0.87	7.48	0.00	1.37	0.665**
BD	-7.49	-8.71	-	-4.26	10.94	0.94	7.92	-0.03	1.53	0.858**
NPP	-5.56	-8.84	-5.74	-	11.75	0.77	6.81	0.03	1.35	0.586**
IL	-13.08	10.03	6.27	5.00	-	-0.77	-6.71	-0.01	-1.29	-0.556**
GWL	1.04	-8.96	-6.79	-4.15	9.66	-	8.55	-0.03	1.55	0.854**
GWWL	8.61	-9.24	-6.89	-4.40	10.19	1.03	-	-0.03	1.59	0.852**
GBT	0.16	0.17	1.31	-0.98	1.03	-0.23	-1.58	-	-0.30	-0.428**
SW	1.71	-8.51	-6.70	-4.38	9.88	0.94	7.99	-0.03	-	0.909**

Residual effect: 0.357
**** indicate significant at 1%.**
*** indicate significant at 5%.**

PH = Plant height (m), BD = Base diameter (mm), NPP = Number of nodes per plant, IL = Internode length (cm), GWL = Green weight with leaves per plant (gm), GWWL = Green weight without leaves per plant (gm), GBT = Green bark thickness (mm), SW = Stick weight (gm).

4.4.2 Indirect effects

Plant height had negative indirect effect through base diameter (-6.14), number of nodes per plant (-4.62) (Table 6). However, its indirect effects through green weight with leaves (0.87), green weight without leaves (7.48), internode length (12.33) and stick weight (1.37) were positive. Plant height has no indirect effect via green bark thickness (0.00).

The effect of base diameter to plant height (-8.71), number of nodes per plant (-4.26) and green bark thickness (-0.03) were negative. Its indirect effect was remarkable and positive upon green weight with leaves (0.94), green weight without leaves (7.92), internode length (10.94) and stick weight (1.53).

Number of nodes per plant influenced the fibre weight indirectly through green weight with leaves (0.77), green weight without leaves (6.81), green bark thickness (0.03), internode length (11.75) and stick weight (1.35) positively (Table 6). It had negative indirect effect through plant height (-8.84) and base diameter (-5.74).

Internode length had positive indirect effect through plant height (10.03), base diameter (6.27), and number of nodes per plant (5.00). This trait showed negative indirect effect via green weight with leaves (-0.77), green weight without leaves (-6.71), green bark thickness (-0.01) and stick weight (-1.29) (Table 6).

The indirect and positive effect on fibre weight was exhibited by green weight with leaves via green weight without leaves (8.55), stick weight (1.55) and internode length (9.66). Whereas, through other traits, it had also negative indirect effects (Table 6).

Green weight without leaves showed positive indirect effect to fibre weight via green weight with leaves (1.03), internode length (10.19) and stick weight (1.59) (Table 6). It had a negative indirect effect through plant height (-9.24),

base diameter (-6.89), number of nodes per plant (-4.40) and green bark thickness (-0.03).

The indirect effect of green bark thickness on fibre weight was positive through plant height (0.17), base diameter (1.31) and internode length (1.03). Whereas, through other traits it had also negative indirect effects (Table 6).

Stick weight showed indirect positive effects on fibre weight by green weight with leaves (0.94), green weight without leaves (7.99) and internode length (9.88). It showed indirect negative effect on fibre weight through plant height (-8.51), base diameter (-6.70), number of nodes per plant (-4.38) and green bark thickness (-0.03) (Table 6).

From the present path analysis study in Kenaf, it may be concluded that improvement of fibre weight could be brought by selection for component characters like green weight with leaves, green weight without leaves, green bark thickness and stick weight.

4.5 Genetic diversity analysis

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding program. The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

4.5.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 25 Kenaf genotypes were grouped into five different clusters. It was observed that the highest percentage of (28%) genotypes were included in cluster II followed by cluster III, IV and V (20%). The remaining genotypes (12%) were in cluster I. The composition of clusters with different genotypes was presented in Table 7.

From Table 7, cluster II had the maximum number of genotypes (G3, G6, G7, G8, G15, G19, G21) followed by cluster III (G9, G10, G13, G14, G23), cluster IV (G4, G16, G17, G18, G20) and cluster V (G1, G2, G22, G24, G25) having five genotypes. Cluster I comprised with three genotypes (G5, G11, G12).

4.5.2 Principal component analysis (PCA)

Eigen values of principal component axis, percent of total variation and cumulative variation obtained from principal component analysis were presented in Table 8. The results showed that the first principal axis, plant height (m) largely accounted for the variation among the genotypes which alone contributed 74.07% of the total variation. The first two characters of the principal component axes with eigen values above one (01) unity accounted for 88.78% of the total variation among the nine characters. The rest seven characters contributed remaining 11.22% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Figure 3.

Table 7. Distribution of twenty five genotypes of Kenaf in different clusters

Cluster no.	No. of genotypes	Name of genotypes
I	3	G5, G11, G12
II	7	G3, G6, G7, G8, G15, G19, G21
III	5	G9, G10, G13, G14, G23
IV	5	G4, G16, G17, G18, G20,
V	5	G1, G2, G22, G24, G25,

Table 8. Eigen values and percentage of variation for corresponding nine component characters in 25 Kenaf genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	6.666	74.07	74.07
II	1.324	14.71	88.78
III	0.486	5.40	94.18
IV	0.186	2.07	96.25
V	0.150	1.67	97.92
VI	0.123	1.36	99.28
VII	0.045	0.50	99.78
VIII	0.015	0.16	99.94
IX	0.005	0.06	100.00

Z1-Z2 Graph

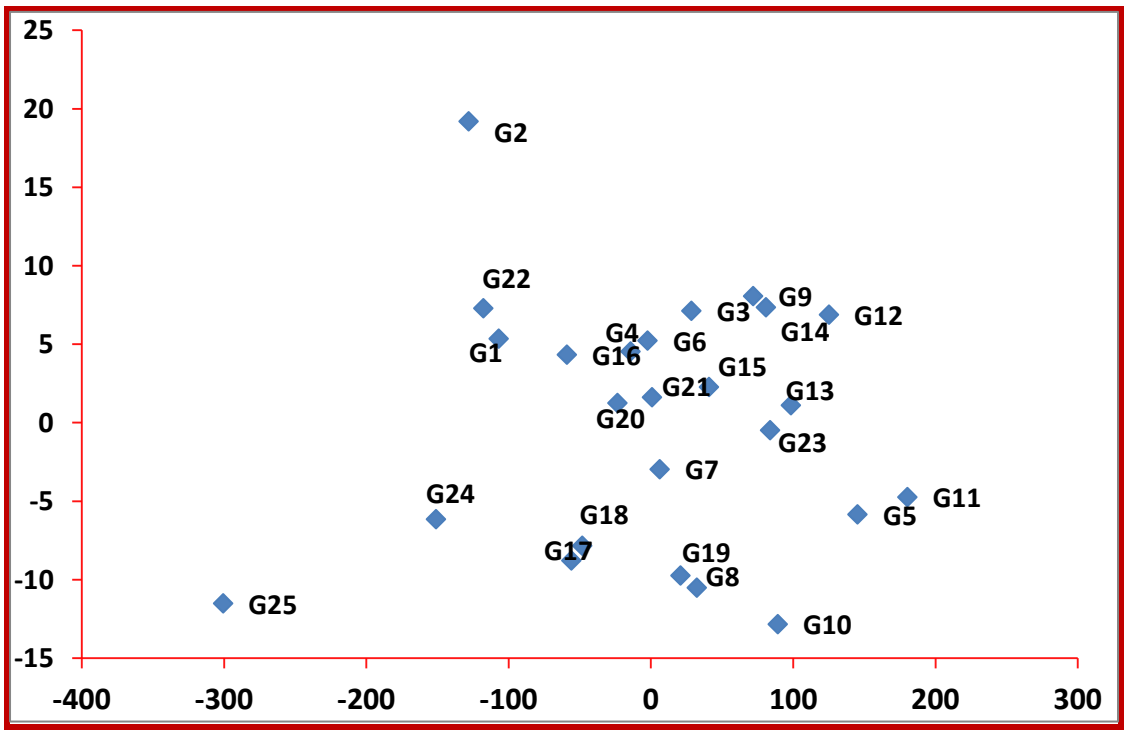

Fig 3. Scatter pattern of Kenaf genotypes on the basis of their principal component scores

4.5.3 Inter cluster distance

The inter cluster D^2 values were given in Table 9 and the nearest and farthest cluster from each cluster based on D^2 value was given in Table 10. The inter cluster D^2 value was maximum (13.566) between the cluster I and cluster V, followed by III and V (11.164), IV and I (9.398) and II and V (8.275). The higher inter-cluster distances indicate presence of wide spectrum variability in population. However, the highest inter cluster distance was observed between clusters I and V indicated the genotypes in these clusters were diverse than those other clusters. The minimum distance was observed between clusters I and III (2.602) indicated close relationship among the genotypes included. So the crossing between the genotypes derived from cluster V and I will bring desired result.

4.5.4 Intra cluster distance

The intra cluster D^2 values were given in Table 9. The intra cluster distance was observed in all the clusters. The intra cluster distance was higher in cluster I (0.518) followed by cluster V (0.092) and lowest in cluster III (0.067) (Table 10). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups.

4.5.5 Cluster diagram

The positions of the genotypes in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the genotypes (Fig 4).

Table 9. Average intra (Bold) and inter cluster distances (D^2) for 25 genotypes of Kenaf

Cluster	I	II	III	IV	V
I	**0.518**	5.557	2.602	9.398	13.566
II		**0.076**	3.443	4.214	8.275
III			**0.067**	7.194	11.164
IV				**0.087**	4.752
V					**0.092**

Table 10. The nearest and farthest clusters of 25 Kenaf genotypes based on D^2 values

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**III (**2.602)	**V (**13.566)
2	**II**	**III (**3.443)	**V (**8.275)
3	**III**	**I (**2.602)	**V (**11.164)
4	**IV**	**II (**4.214)	**I (**9.398)
5	**V**	**IV (**4.752)	**I (**13.566)

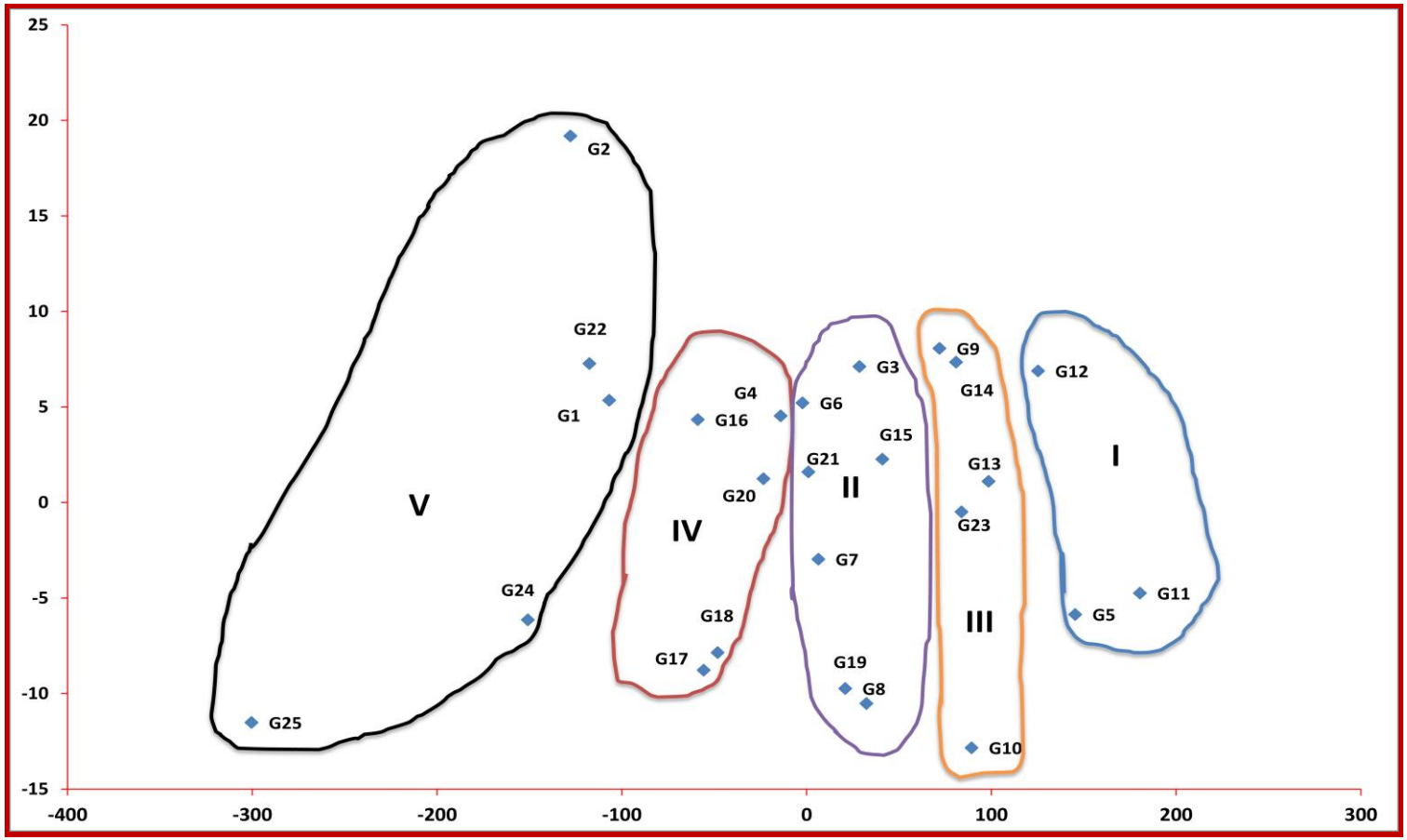

Fig 4. Scatter diagram of Kenaf genotypes based on their principal component scores

4.5.6 Cluster mean analysis

The cluster means of nine different characters (Table 11) were compared and found considerable differences between clusters. The maximum plant height was observed in cluster V (2.66), whereas the minimum plant height was observed in cluster I (2.13). The maximum (22.02) and minimum (16.18) base diameter were observed in cluster V and I respectively. Genotypes in cluster I showed the lowest number of nodes per plant (57.11) and in cluster V had the highest number of nodes per plant (77.00). The maximum internode length (4.44) was observed in the cluster I, whereas the minimum internode length (3.49) was observed in cluster V. The maximum (382.80) and minimum (140.11) green weight with leaves were observed in cluster V and I respectively. Maximum green weight without leaves were observed in cluster V (310.00), whereas minimum were observed in cluster I (118.67). Cluster IV had the maximum green bark thickness (2.20) and cluster V had the minimum green bark thickness (2.07). Stick weight was the highest in cluster V with a mean value of (50.60) and it was least in genotypes belongs to the cluster I (22.67). Highest fibre weight were recorded by the cluster V (19.00) while cluster I (10.33) showed the least fibre weight.

4.5.7 Contribution of characters towards divergence

Contribution of characters towards the divergence obtained from canonical variates analysis is presented in Table 12. The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same character given equal magnitude for both the vectors than the character was considered responsible for primary as well as secondary differentiation.

Table 11. Cluster mean for nine different characters of 25 genotypes of Kenaf

Characters	I	II	III	IV	V
PH	2.13	2.39	2.26	2.41	2.66
BD	16.18	19.36	17.17	20.00	22.02
NPP	57.11	64.81	62.00	70.07	77.00
IL	4.44	3.90	4.23	3.83	3.49
GWL	140.11	243.90	190.27	290.80	382.80
GWWL	118.67	199.19	160.53	232.93	310.00
GBT	2.09	2.12	2.15	2.20	2.07
SW	22.67	33.43	25.87	39.53	50.60
FW	10.33	13.09	11.27	15.33	19.00

PH = Plant height (m), BD = Base diameter (mm), NPP = Number of nodes per plant, IL = Internode length (cm), GWL = Green weight with leaves per plant (gm), GWWL = Green weight without leaves per plant (gm), GBT = Green bark thickness (mm), SW = Stick weight (gm) and FW = Fibre weight (gm).

Table 12. Relative contribution of nine different characters of 25 Kenaf genotypes to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Plant height (m)	-0.3510	0.1381
Base diameter (mm)	-0.3631	-0.0342
Number of nodes per plant	-0.3350	0.3323
Internodes length (cm)	0.3339	-0.2677
Green weight with leaves (gm)	-0.3687	-0.1125
Green weight without leaves (gm)	-0.3750	-0.0572
Green bark thickness (mm)	0.0299	0.8065
Stick weight (gm)	-0.3657	-0.0916
Fibre weight (gm)	-0.3318	-0.3505

The important characters responsible for genetic divergence in the axis of differentiation in vector 1 were green bark thickness (0.0299) and internode length (0.3339) because all these characters had positive signs. On the other hand, plant height, base diameter, number of nodes per plant, green weight with leaves, green weight without leaves, stick weight and fibre weight possessed the negative sign in the first axis of differentiation. All the characters except plant height, number of nodes per plant and green bark thickness possessed negative signs in the second axis of differentiation that meant it had minor role in the genetic diverse. Green bark thickness had positive signs in both the vectors, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied.

5.8 Salient feature of the genotypes of different cluster

The genotypes of cluster V was best in terms of higher plant height, high base diameter, more nodes per plant, greater green weight with and without leaves, lower green bark thickness, lower internode length, more stick weight and higher fibre weight. The genotypes of cluster II produced moderate plant height and moderate base diameter. The genotype of cluster III possessed moderate green bark thickness. The genotypes of cluster IV produced high bark thickness and medium stick weight and the cluster I generated highest internode length (Table 13).

Table 13. Salient features of genotypes belonging to five different clusters

Cluster	Salient features
I	Lowest plant height Lowest base diameter Lowest node per plant Highest internode length Lowest green weight with leaves Lowest green weight without leaves Lowest stick weight Lowest fibre weight
II	Moderate plant height Moderate base diameter
III	Moderate green bark thickness
IV	Moderate plant height Moderate base diameter Moderate green weight with leaves Moderate green weight without leaves Highest green bark thickness
V	Highest plant height Highest base diameter Highest node per plant Lowest internode length Highest green weight with leaves Highest green weight without leaves Lowest green bark thickness Highest stick weight Highest fibre weight

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was undertaken to study the variability, character association and diversity in 25 genotypes of Kenaf based on nine characters. The major findings of the present study have been concluded on the basis of the characters studied.

The analysis of variance showed significant differences among the genotypes for all the characters. The accession G25 has the highest plant height (2.99 m) while G11 has minimum plant height (1.89 m). The minimum and maximum base diameter were found in the genotypes G11 (14.87 mm) and G25 (24.37 mm), respectively. The maximum number of nodes per plant (81.67) were recorded by the genotype G22 and the lowest number of nodes per plant (50.00) were recorded by G11. The minimum internode length was recorded by the accession G25 (3.30 cm) and accession G11 (5.03 cm) showed the maximum internode length. The highest green weight with leaves was recorded in G25 (500.00 gm) and G11 (118.00 gm) genotype showed the lowest green weight with leaves. The maximum green weight without leaves was recorded in the genotype G25 (386.67 gm) and the minimum green weight without leaves was in the genotype G11 (98.00 gm). The maximum green bark thickness was recorded in the genotype G22 (2.64 mm) and the minimum green bark thickness in the genotype G24 (1.69 mm). The line G10 (22.33 gm) showed the minimum stick length and the maximum stick length were recorded in the accession G25 (59.33 gm). The highest fibre weight per plant was recorded by the accession G25 (25.67 gm) while accession G10, G12, G13 and G19 showed the lowest fibre weight per plant (10.33 gm).

The phenotypic variance was higher than genotypic variance for all the characters studied except plant height and green bark thickness. The phenotypic coefficients of variation were higher than genotypic coefficients of

variation for all the characters studied. The differences between the PCV and GCV are negligible. High heritability were observed for all the characters. The high heritability coupled with high genetic advance in percent of mean were observed for all the characters except plant height and green bark thickness suggesting that effective selection may be done for these characters.

Plant height, base diameter, number of nodes, green weight with leaves, green weight without leaves and stick weight showed highly significant and positive correlation with fibre weight at both genotypic and phenotypic levels. Internode length and green bark thickness were negatively and significantly correlated with fibre weight. The genotypic correlation coefficient (r_g) is higher than the phenotypic correlation coefficient (r_p) in all characters indicating that there exists a strong association between these characters with fibre weight genetically. Highly significant and positive genotypic and phenotypic correlation were also observed between the green weight with leaves with green weight without leaves and green weight of leaves with stick weight. Internode length showed negative correlation with all parameters.

Fibre weight per plant showed the highest positive direct effect (8.61) with green weight without leaves per plant. Green weight with leaves, green bark thickness and stick weight also showed positive direct effect on fibre weight indicating that direct selection for this trait might be effective and there is a possibility of improving fibre weight through selection based on those characters. On the other hand, negative direct effect on fibre weight was showed by plant height, base diameter, number of node and internode length. The highest indirect effect of fibre weight was observed with plant height via internode length.

Genetic diversity of 25 Kenaf genotypes based on nine characters were measured through multivariate analysis. The 25 genotypes fell into five distant clusters. The cluster II comprised the maximum number (7) of genotypes followed by 5 genotypes in cluster III, IV and cluster V. The cluster I

comprised with 3 genotypes. The highest inter-cluster distance (13.566) was observed between the cluster I and V. The lowest inter-cluster distance (2.602) was observed between the cluster I and III.

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire five clusters was more or less low indicating that the genotypes within the same cluster were closely related. Green bark thickness was the important component characters having higher contribution to the genetic divergence.

Based on the results of the study, the following conclusions may be drawn:

- Significant variations were found for all the characters studied. The maximum variability were found for the parameters named number of nodes per plant, green weight with leaves, green weight without leaves and fibre weight. So selection based on these characters could be effective for the improvement of Kenaf yield.
- High heritability coupled with high genetic advance in percent of mean were observed in base diameter, number of, nodes per plant, green weight with leaves, green weight without leaves, stick weight and fibre weight. Hence, yield improvement in Kenaf would be achieved through selection of these characters.
- All the characters except green bark thickness and internode length showed highly significant and positive correlation with fibre weight at both genotypic and phenotypic levels with greater r_g value. This results suggested that fibre yield per plant can be increased by improving the characters such as plant height, base diameter, number of nodes per plant, green weight with leaves, green weight without leaves, stick weight.
- Green weight with leaves, green weight without leaves, green bark thickness and stick weight showed positive direct effect on yield while rest of the characters had negative direct effect. So yield improvement was associated with these characters having direct positive value.

- The maximum and minimum cluster distance were observed between clusters I and V as well as I and III respectively. The inter-cluster distances were larger than the intra-cluster distances. So, the genotypes of clusters I and V were more diversed. Plant height was found responsible for the maximum diversity.
- The genotypes of clusters I and V were more diversed. So the genotypes belonging to cluster I and V could be used as parents for future breeding program to develop Kenaf variety.

Recommendations

1) Selection based on the characters like as green weight with leaves, green weight without leaves, stick weight and fibre weight could be effective for the improvement of Kenaf yield.
2) The genotypes of cluster I and V could be used as parents in future breeding program to develop hybrid Kenaf variety.
3) Genotypes G22 and G25 could be included in the future study to improve fibre yield of Kenaf and develop hybrid variety.

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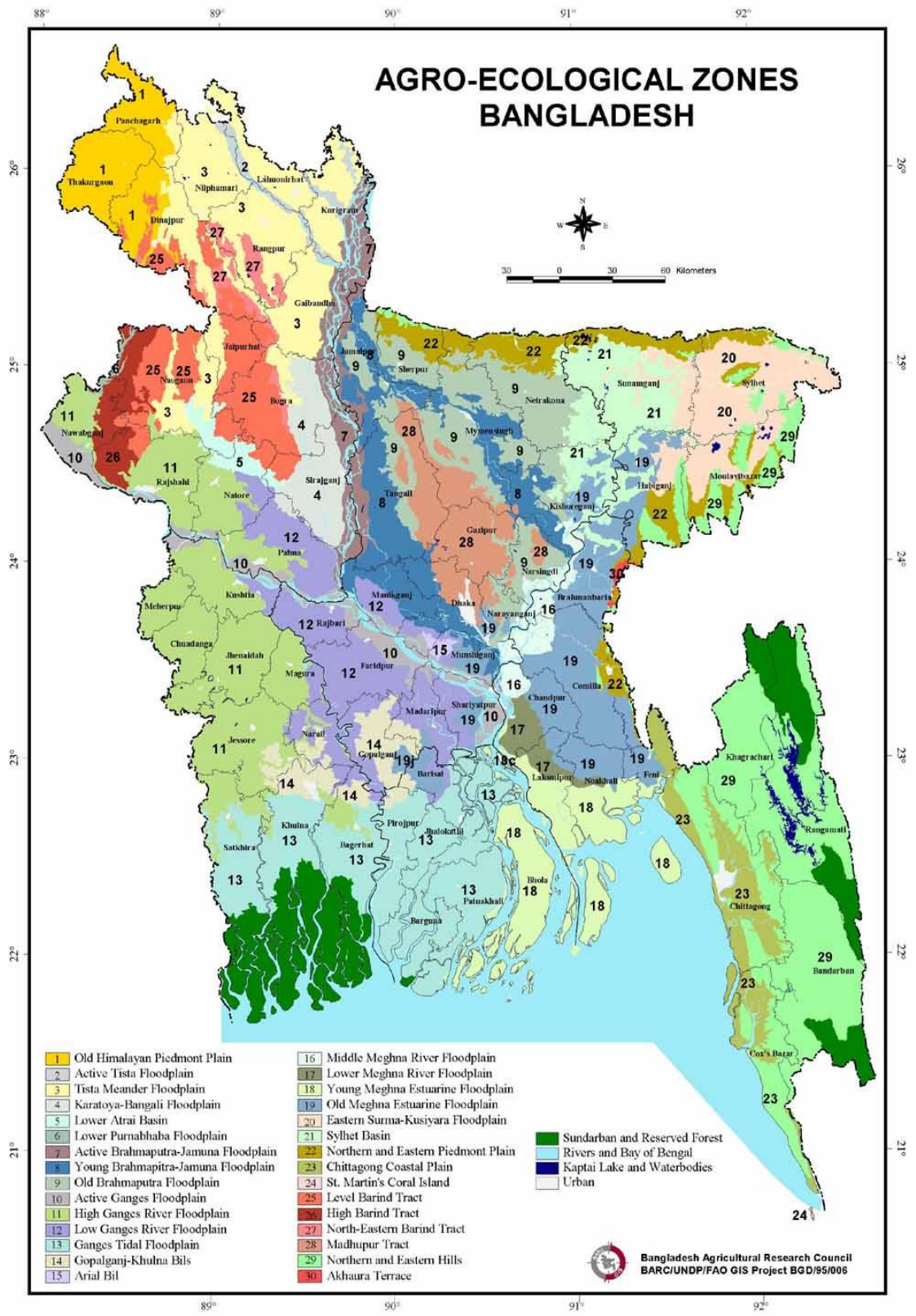
APPENDICES

Appendix I: Map showing the experimental site under the study (AEZ 8)



Appendix II: Monthly average record of temperature, rainfall and relative humidity of the experimental site during study period from April 2015 to September 2015

Month	Temperature (^{o}C)		Relative humidity (%)	Rainfall (mm)
	Maximum	Minimum		
April, 2015	36.25	25.32	74	36
May, 2015	37.87	26.61	76	115
June, 2015	34.67	27.05	79	587
July, 2015	34.28	29.91	80	796
August, 2015	33.02	27.48	77	261
September, 2015	31.90	26.37	76	154

Source: Physiology department, BJRI, Dhaka.

Appendix III: Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
AEZ	Young Brahmaputra and Jamuna Flood Plain
pH	6.4-6.8
Organic matter	0.87
Total N (%)	0.49
Available phosphorous	23 ppm
Exchangeable K	0.39 meq/100 g soil

Source: Physiology department, BJRI, Dhaka.

Appendix IV. Mean performance of different parameters of 25 Kenaf genotypes

Genotype	PH	BD	NPP	GWL	GWWL	GBT	IL	SW	FW
G1	2.53	21.07	77.33	340.00	277.00	1.75	3.66	48.67	17.67
G2	2.50	19.93	75.67	308.00	268.00	2.44	3.65	46.00	15.33
G3	2.46	19.67	72.67	282.67	239.33	2.35	3.75	44.00	15.00
G4	2.35	18.00	66.33	215.00	177.33	2.16	3.88	36.00	13.00
G5	2.45	18.27	64.67	224.00	183.00	2.16	3.88	32.33	12.00
G6	2.48	17.47	65.67	219.33	178.33	2.12	3.72	31.67	11.33
G7	2.40	20.07	64.33	251.33	204.67	2.05	3.91	35.67	13.33
G8	2.38	19.17	58.67	250.33	199.33	2.03	4.02	32.00	14.33
G9	2.32	17.53	63.00	194.67	176.33	2.06	4.06	24.67	10.67
G10	1.99	16.53	51.33	193.00	151.33	2.01	4.87	22.33	10.33
G11	1.89	14.87	50.00	118.00	98.00	1.99	5.03	25.33	12.33
G12	2.18	18.73	62.00	154.67	140.67	2.16	4.22	22.67	10.33
G13	2.36	15.87	62.33	179.33	152.67	2.37	4.21	23.33	10.33
G14	2.37	17.60	65.00	190.00	166.33	2.15	4.00	31.00	12.33
G15	2.29	19.93	65.33	224.33	187.00	1.90	3.98	33.00	16.33
G16	2.50	20.47	73.33	302.33	248.33	2.35	3.69	42.33	16.33

Appendix IV. (Cont'd.)

Genotype	PH	BD	NPP	GWL	GWWL	GBT	IL	SW	FW
G17	2.46	18.33	73.67	308.00	237.67	2.16	3.74	30.00	11.67
G18	2.31	21.00	63.00	299.33	236.00	2.17	3.96	38.33	15.33
G19	2.18	17.40	60.67	237.67	186.00	2.28	4.54	24.33	10.33
G20	2.29	20.73	70.33	276.67	223.33	2.14	4.00	41.67	17.33
G21	2.57	20.80	68.33	256.33	211.33	2.15	3.37	33.67	11.67
G22	2.69	22.53	81.67	348.00	284.33	2.64	3.31	47.00	15.67
G23	2.26	18.33	68.33	194.33	156.00	2.15	4.01	28.00	12.67
G24	2.55	21.40	70.67	379.67	298.67	1.69	3.65	48.67	19.33
G25	2.99	24.37	76.00	500.00	386.67	1.76	3.30	59.33	25.67
Mean	2.39	19.20	66.81	257.88	210.71	2.13	3.94	35.28	14.03
Min.	1.89	14.87	50.00	118.00	98.00	1.69	3.30	22.33	10.33
Max.	2.99	24.37	81.67	500.00	386.67	2.64	5.03	59.33	25.67

PH = Plant height (m), BD = Base diameter (mm), NPP = Number of nodes per plant, IL = Internode length (cm), GWL = Green weight with leaves per plant (gm), GWWL = Green weight without leaves per plant (gm), GBT = Green bark thickness (mm), SW = Stick weight (gm), FW = Fibre weight (gm).

Appendix V. Principal component score 1 & 2.

Genotypes	Z_1	Z_2
1	-106.79	5.35
2	-127.87	19.18
3	28.58	7.11
4	-14.08	4.53
5	145.42	-5.86
6	-2.17	5.21
7	6.39	-2.97
8	20.94	-9.74
9	71.92	8.06
10	89.29	-12.84
11	180.45	-4.75
12	125.25	6.88
13	98.53	1.11
14	80.92	7.34
15	40.99	2.26
16	-58.90	4.33
17	-55.65	-8.78
18	-48.10	-7.86
19	32.36	-10.52
20	-23.35	1.24
21	0.94	1.60
22	-117.60	7.27
23	83.82	-0.49
24	-150.84	-6.15
25	-300.44	-11.52