

Chapter II

REVIEW OF LITERATURE

Jute fibre obtained from the bark of the stem which originated from primary and secondary phloems (Maiti, 1997). The industrial term for jute fibres are raw jute in the industrial and engineering uses of textiles, jute fibre is used more than any other single fibre. The fibres of *C capsularis* L. are off-white and slightly weak but *C olitorius* L. produces comparatively stronger fibre with brown or golden in color (Roy *et al.* 2006). The length of jute fibre is generally ranged from 1 to 4 meter.

The genus *Corchorus* belongs to the family Malvaceae (formerly under Tiliaceae) which is composed of approximately 100 species (Saunders, 2001). Of these, two species (*Corchorus capsularis* L. and *Corchorus olitorius* L.) were selected and domesticated in the wake of civilization and commercially important cultivated species of *Corchorus*. The others were found wild in nature, but most of them are now extinct or in endemic condition.

The cultivated jute species are diploid in nature. Cytologically it contains 14 chromosomes ($2n= 14$) and the basic chromosome number of the cultivated jute is seven (Banerjee, 1932; Alam and Rahman, 2000). Alam and Rahman (2000) found that *Corchorus capsularis* L. and *C. olitorius* L. had two satellite chromosome.

2.1 Morphology, Floral Biology and Pollination

Jute is highly photoperiod sensitive short day plant requiring long days for its vegetative growth and short days for seed production (Chawdhury and Mia, 1962) *C. olitorius* L. is more photoperiod sensitive than *C. capsularis* L. (Ali, 1961). Jute plant is a tap rooted annual shrub (Ghosh, 1983). Stem erect, cylindrical, branched or unbranched usually 1.5-4.5 m long, the color of the stem varies from full green to dark red. Leaves are stipulate, alternate in arrangement, glabrous, usually 5 to 18 cm $\times$ 2.6 to 8.2 cm ovate, ovate-lanceolate, lanceolate or oblong in shape with coarsely toothed. Stipule usually 0.5 to 2.0 cm or more; tip colored or green. Petiole 4 to 9 cm; varies in color, green to dark red in different genotypes.

Jute flower is perfect and small in size. The inflorescences occur on the terminal or lateral branches. Flower yellow or pale yellow in color, sepal 5 to 6, colored or green; petals 5 to 6 yellow, entire or split, stamen 30 to 60, anther yellow. Ovary elongated 5 rarely 6 or more, carpelled, syncarpus; ovule axile, usually 40 in each loculus in one row giving about 200 ovule in each ovary; style 3 to 5 mm; stigma globular. Anthesis period an hour or less before

sunrise. The fruit (pod) of *Corchorus capsularis* L. is roughly globular, while that of *Corchorus olitorius* L. is cylindrical (Ghosh, 2003). The seeds of *Corchorus olitorius* L. are different in color such as greenish blue, blackish blue, green to steel grey in cultivated varieties and steel grey to black in wild varieties that in *Corchorus capsularis* L. is copper brown or dark brown (Kundu, 1951).

Jute is generally a self-pollinated crop, but cross pollination of up to 8-12% occur in *Corchorus olitorius* L. and 3-4% in *Corchorus capsularis* L. (Ghosh and Gupta, 1945). The pollination mainly occurs by insects depending upon the genotype and environment. The flower is open before sunrise and close by noon of the same day.

2.2 Genetic diversity

Information on genetic divergence among the parental materials is vital to plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute to desirable segregants and, or to produce high heterotic crosses. More diverse the parents the greater are the chances of obtaining high heterotic F₁s and broad spectrum of variability in segregating generation (Murty and Arunachalam, 1966). The parents identified on the basis of divergence analysis would be more promising. In both cross and self-pollinated crops genetic diversity is one of the most important tools to quantify genetic variability. Evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm (Tomooka, 1991).

Many authors worked on genetic divergence by using D² statistics which provided for grouping of genotypes in several clusters. The clustering pattern of the genotypes was often not related to their geographical origin. It is suggested that genetic drift and selection in different environments cause greater diversity (Pandit *et al.*, 1997).

Ghosh *et al.* (2017) investigated 138 jute genotypes of *C. olitorius* and characterized by un-weighted pair-group method with arithmetic average cluster analysis of the 138 jute genotypes depicted a dendrogram using DARWIN, 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.

Das *et al.* (2016) evaluated the 18 released and common varieties of Tossa jute for genetic divergence and association of different component characters associated with fibre yield. The experimental materials were grown in Randomized Block Design with three replications at Central Research Institute for Jute & Allied Fibres, Baarrackpore, India during 2009-10 for recording data on eight yield and quality contributing characters viz., plant height, basal diameter, node no., fibre weight, stick weight, fibre strength, fibre fineness and fibre percentage. All the varieties irrespective of their origin were grouped into 5 different clusters. The clustering pattern revealed meager amount of genetic diversity between the varieties studied in tossa jute. Inter-cluster distance was maximum between I and IV. Fibre fineness, fibre %, stick weight and basal diameter were the potent characters that influence the genetic diversity.

Sawarkar *et al.* (2015) studied genetic divergence of 60 genotypes of Tossa jute (*Corchorus olitorius* L.) which included 16 standard varieties to identify the most diverged genotypes under moisture stress condition. On the basis of Mahalanobis D^2 analysis, genotypes were grouped into five clusters. Maximum inter-cluster distance was observed between cluster IV and V while cluster III showed the maximum intra-cluster distance. Cluster V exhibited the highest means for days to 50% flowering, plant height, number of node, internode length, base diameter, mid diameter, top diameter, bark thickness and fibre weight. The highest contribution (12.63%) was exerted by plant height of total divergence. The results of the present study suggested that hybridization between genotypes in cluster V and IV could provide a wide spectrum of variation in the segregating generation which could provide opportunity for isolation of drought tolerant with high fibre yielding lines.

Ghosh *et al.* (2013) observed the highest diversity (0.69) between clusters IX and IV, whereas clusters III and IV showed the greatest similarity (0.14). Principal component (PC) analysis revealed that the first five PCs having eigenvalues >1 explained 75.93% of the total variation. The variance explained by PC1 was mostly due to traits related to fiber and seed yield, whereas PCII was mostly related to color traits. Two-dimensional scatter plots supported the grouping patterns of cluster analysis. The accessions BRA/4792 and BRA/4794 and variety O-9897 of *C. olitorius* were identified as the most promising genotypes, based on their phenotypic variability and high yield performance, for use as genetic material for future jute breeding programs and for germplasm conservation.

Denton and Nwangburuka (2012) evaluated 15 accessions of leaf *C. olitorius* collected from two National Research Institutions and Biotechnological Center for genetic variability using Single linkage cluster analysis (SLCA) and Principal Component Analysis (PCA). The experiment was carried out at Babcock University Teaching and Research Farm during 2009. The experiment was carried out using a Randomized Complete Block Design (RCBD) with three replications. The contribution of number of leaves per plant height at maturity, fresh leaf weight, total plant weight and harvest index in the PCA leads to the conclusion that these traits contributes more to the total variation observed in the fifteen accessions of *C. olitorius* and therefore can be used in discriminating among the accessions of *C. olitorius*. BUC of 24 and BUC or 31, with high potential for number of leaves per plant, plant height at maturity, fresh leaf weight and total weight would make good parental stock material when breeding for *C. olitorius* leafy vegetative yield, while BUC or 31 and BUC or 05 are more distinct and diverse of all the accessions and can serve as source for variability in character for *C. olitorius* improvement. The accessions were grouped in four major cluster by the SCLA.

Benor *et al.* (2012) investigated the genetic diversity and relationships in *C. olitorius* by analyzing populations representing different distribution areas, and developed a hypothesis on the origin and spread of the species in the pantropic. They employed amplified fragment lengths polymorphism (AFLP) and morphometric analyses in a total of 101 *C. olitorius* accessions. Results of both data sets are mostly congruent. The molecular analysis indicated generally low genetic diversity within populations and the Nei's gene diversity (H_e) ranged from 0.0457 to 0.0955 with a mean of 0.0763. Qualitative traits, especially related to leaf morphology, branching habit and stipule color were the taxonomically most informative characters. The highest morphological variability occurred within African accessions, indicating that this species originally evolved in Africa. In both analyses, the Asian materials were nested within African populations, especially with those from North and East Africa. This indicates an African origin of the species and they hypothesize that dispersal occurred via the Mediterranean–Indian trade routes instead of natural migration along the coasts from western Africa to the Indian subcontinent. Both analyses revealed materials from Ethiopia to be quite distinct. The highest number of private bands ($N = 35$), percent polymorphism (29.29%), and gene diversity (0.0955) were also detected in wild accessions collected from Ethiopia, suggesting a long-term spatial isolation of *C. olitorius* populations in the country. Germplasm samples from this region could therefore be a useful source of genetic variation in jute breeding programs.

Substantial amount of genetic diversity was observed among 40 genotypes of jute. D^2 values ranged between 126.03 and 156.28. All 40 genotypes were grouped into seven clusters. Cluster I was the largest among all clusters with 19 genotypes followed by cluster II (7 genotypes), cluster III (5 genotypes), cluster IV (3 genotypes) and cluster V, VI and VII contained 2 genotypes each. The inter cluster distances (D^2) was ranged between 354.19 (clusters V and IV) and 7419.65 (clusters VII and VI). The variances of cluster means indicated that 1000 seed weight, fibre yield per plant and days to 50 per cent flowering has contributed towards the genetic divergence.

Nargis (2009) grouped 29 Tossa jute (*C. capsularis*) genotypes into five clusters based on D^2 analysis. The results on intra and inter cluster distance showed that geographic origin did not strictly conform to the genetic diversity. Seven genotypes namely var. O-9897, var.O-72, Acc.-1749, var. O-4, SDLT₂ var. JRO-534 and Acc.-4582 were chosen from different cluster on the basis of their special characteristics.

Reyazul *et al.* (2008) conducted a preliminary study involving the following: (i) analysis of nature and extent of the genetic variability for fibre yield and four other related traits in a set of eighty one genotypes belonging to two commercially cultivated *Corchorus* species (45 genotypes of *C. olitorius* + 36 genotypes of *C. capsularis*), (ii) development and analysis of a set of simple sequence repeat (SSR) markers from *C. olitorius*, and (iii) use of a sub-set of SSRs for assessment of genetic diversity in the above set of 81 genotypes. The results suggested quantitative nature of fibre yield and other related traits, with a preponderance of dominance component in genetic variance. A sub-set of 45 SSRs derived from *C. olitorius*, when used for a study of DNA polymorphism and genetic diversity, showed high transferability of these *C. olitorius* SSRs to *C. capsularis*. The average number of alleles for individual SSRs was surprisingly low (3.04 for both species, 2.02 for *C. capsularis* and 2.51 for *C. olitorius*), and so was the average polymorphic information content (PIC; 0.23 and 0.24 in two species). In the dendrogram obtained using a similarity matrix, the 81 genotypes were grouped into three clusters, which largely corresponded to the two species, Cluster I belonging mainly to *C. capsularis* and the other two closely related clusters (clusters II and III) belonging to *C. olitorius*. It was also shown that a minimum of 15 SSRs could give the same information as 41 SSRs, thus making many SSRs redundant. The SSR markers developed during the present study and to be developed in future will prove useful not only for evaluation of genetic diversity, but also for molecular mapping/QTL analysis, and for comparative genome analysis of the two *Corchorus* species.

Haque *et al.* (2007) reported on genetic diversity of eighteen jute genotypes of the two cultivated species *Corchorus capsularis* L. and *C. olitorius* L. which included released varieties and collected races, referred to as accessions were evaluated. DNA profiling was generated using sequence independent RAPD markers. A total of 140 scorable loci were observed and a dendrogram was constructed with these markers. The relationship that is portrayed by this clustering also agreed with the available pedigree information on jute. 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. However, more extensive molecular data are needed in order to reach a general conclusion about the relationship between jute genotypes.

The genetic divergence among 42 white jute genotypes were studied by Yahiya (2007), who grouped the genotypes into six different clusters according to PCA, D^2 statistics. The principal component analysis indicated that dry stick weight, dry fibre weight, plant technical height, base diameter and number of nodes were the important components of genetic divergence in the population. He concluded that there was no parallelism between genetic diversity and geographical distribution of genotypes.

An experiment was conducted at Jute Agriculture Experimental Station, Manikganj by Yahiya *et al.* (2006) to estimate genetic divergence of 32 deshi jute germplasm collected from different sources along with the check varieties CVL-1 and CVE-3. The experiment was laid out in RCBD design with three replications. Row to row distance was 30 and plant to plant distance was 5-6 cm in rows. Wide range of diversity was observed among the accessions. All the genotypes were grouped into six clusters. Diversification observed in leaf colour, stem colour, petiole colour, plant technical height, dry core weight and days to first flowering. Pigmentation data were collected at 60 days after sowing. Plants were harvested at 120 days after sowing and post-harvest data were collected. The accessions were characterized for their morph-agronomic attributes as per *Corchorus* descriptor. Considering genetic diversity and other major yield contributing characters viz. technical height, leaf angle, leaf length, leaf width, petiole length, node number, base diameter of stem, middle diameter of stem, top diameter of stem, core diameter, dry fibre weight and dry stick weight

accessions 936, 1347, 2134, 2415, 2679, 3047, 3484, 4536, 4619 and 5095 performed better in most of the cases than the control varieties CVL-1 and CVE-3.

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

Hussain *et al.* (1999) reported that the clustering pattern of 30 parents along with their 78 hybrids of *C. olitorius* L. showed no parallel relationship between genetic diversity and geographical origin. Relationship between divergence of the parents and hybrids indicated that medium divergence class provided the optimum level of parental divergence to obtain economic heterosis in F₁.

Islam (1996) studied the genetic divergence among 38 Tossa jute (*C. olitorius*, L.) genotypes for ten different characters by using Mahalanobis's D² statistics. All the genotypes were grouped into five clusters. The highest inter-cluster distance was observed between cluster II and IV, and the lowest between cluster I and III. The intra- cluster distance was the highest in cluster IV and the lowest in cluster V. The pattern of distribution of genotypes within various clusters was independent for geographical distribution. Based on the mean performance, genetic distance and clustering pattern, thirteen genotypes were selected as better parents for future hybridization programme.

Shreshtha (1991) grouped 26 genotypes of *C. capsularis* into 7 clusters based upon eleven quantitative traits and reported low intra- but higher inter-cluster distances in the population studied. The clustering pattern revealed that the nature of selection forces operating under one ecogeographical region was similar to that of other regions, since genotypes from distinct centers were grouped together. Genotypes from one ecogeographical region and also belonging to different pigmentation grade were grouped into different clusters. It indicated the presence of substantial variability within themselves. It was also evident that there was no parallelism between genetic diversity and geographical distribution of genotypes.

Sasmal (1978) carried out with 60 varieties/strains of jute using D^2 statistics. Varieties of *C. capsularis* L. and *C. olitorius* L. formed six and eleven distinct clusters, respectively. Recombinant types were found to be included in closely related groups instead of their parental groups. The genetic distance was found maximum between cluster IV and V while it was minimum between III and IV indicating that these two clusters were very close to each other. Intra-group distance ranged from 0 to 6.69. Grouping pattern to the varieties and the relationship between the clusters were not in complete accordance with their pedigrees. The clusters, which possess varieties having poor fibre yield, were close together indicating that an effective multitier hybridization programme for obtaining hybrids superior in fibre yield would include varieties from distance clusters.

2.3 Genetic variability

The genetic variability existing in genotype of a crop plant is an index of its genetic dynamism. Plant breeding revolves around selection, which can be effectively practiced only in the presence of variability of desired traits. Hence the success of breeding depends entirely upon the variability.

Biswas *et al.* (2018) measured considerable ranges of variability in plant height, base diameter, green bark thickness, dry fibre weight, dry stick weight, green weight with leaves and fibre percentage. The plant height ranged between 2.80 and 4.20m. Base diameter ranged between 14.90 and 20.74mm. Dry fibre weight ranged between 9.20 and 40.00g/plant. It was highest in accession 3730 (40.00 g/plant) which was followed by accessions 5086 (30 g/plant), 1076 (29.00 g/plant), 3724 (28.80 g/plant), 2966 (28.60 g/plant). The highest fibre % was recorded in accession 3730 (37.03 %/plant). Based on major yield contributing characters accessions 3730, 5086, 1076, 3724 and 2966 performed better in most of the cases than the control varieties O-9897 and O-795.

Biswas *et al.* (2018) reported highly significant genotypic differences for all the characters. The maximum coefficient was reported for green weight/plant (0.47) followed by fibre weight/plant (0.46), green bark thickness (0.44), stick weight/plant (0.39) and core diameter (0.39). The phenotypic and genotypic variance was found in green weight/plant 4203.63 and 4199.07 respectively. The high PCV and GCV values were estimated in green weight/plant (24.27 and 24.25). The maximum estimates of broad-sense heritability was recorded in green weight /plant (99.89) followed by stick weight/plant (99.77), fibre weight /plant (99.61) and green bark thickness (85.71).

Munguatosha *et al.* (2017) employed quantitative and qualitative traits to assess the morphological diversity of 90 accessions using univariate and multivariate analyses. Field experiments were conducted for two seasons to identify accessions suitable for leaf yield. The highest variability among accessions was found in harvest index, biomass yield, and weight of 1000 seeds. The traits that significantly correlated with biomass yield include plant height ($r=0.448$), petiole length ($r= 0.237$), primary branches ($r=0.319$), and number of leaves per plant ($r=0.333$). Principal component analysis showed that the first five PCs with eigenvalues ≥ 1 explained 72.9% of the total variability in the accessions. Pods per plant, primary branches, secondary branches, and number of leaves per plant accounted for the highest variability in PC1. Cluster analysis grouped 90 accessions into five major clusters mainly based on their origin. Thus, the collection displayed high variation in morphological traits, particularly those related to leaf yield.

Ghosh *et al.* (2014) evaluated 63 jute genotypes, including two varieties with 37 accessions of *C. capsularis* and one variety with 23 accessions of *C. olitorius*, for 25 morpho-agronomic traits 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 *C. olitorius* varied the most than those in *C. capsularis*. Significant positive correlations were recorded for fiber yield with days to 50% flowering (0.60), plant height at average flowering (0.72), plant base diameter (0.74) and fresh weight (0.90), whereas, leaf angle was negatively (-0.52) correlated. Seed yield was significantly positively correlated with pod length (0.72) and seeds per pod (0.79). The clustering patterns suggested that two jute species are distantly related. The highest diversity (0.69) was observed between clusters IX and IV, whereas clusters III and IV showed the greatest similarity (0.14). Principal component (PC) analysis revealed that the first five PCs having eigenvalues >1 explained 75.93% of the total variation. The variance explained by PC1 was mostly due to traits related to fiber and seed yield, whereas PC II was mostly related to color traits. Two-dimensional scatter plots supported the grouping patterns of cluster analysis. The accessions BRA/4792 and BRA/4794 and variety O-9897 of *C. olitorius* were identified as the most promising genotypes, based on their phenotypic variability and high yield performance, for use as genetic material for future jute breeding programs and for germplasm conservation.

Das and Kumar (2012) evaluated and characterized 32 jute (*Corchorus* spp.) varieties comprised of 18 *olitorius* and 14 *capsularis* for five quantitative and twelve qualitative characters. PCV and GCV were highest for 1000 seed weight (33.78 and 33.29%) followed

by fibre fineness (27.11 and 26.70%). Low variability was recorded in case of plant height. All qualitative characters exhibited more or less high heritability coupled with high genetic advance as per cent over mean. Out of 12 qualitative characters, in *C. capsularis* eight traits were monomorphic and four traits were dimorphic. However, in *C. olitorius* no trait was monomorphic, six traits were dimorphic and six traits were polymorphic among varieties indicating their potential for varietal characterization.

Phenotypic as well as genotypic coefficients of variability (PCV and GCV) were high for the trait pods per plant and seed yield; whereas, medium for base diameter and low for days to 50% flowering. Medium heritability coupled with high expected genetic gain was observed for pods per plant and seed yield. Seed yield was found to be highly significant and positive with pods per plant, base diameter and plant height both at genotypic and phenotypic levels; whereas, only at phenotypic level for seeds per pod and test weight.

Deshmukh (2010) recorded on ten characters viz., days to 50 % flowering, plant height, basal diameter, number of branches per plant, number of pods per plant, length of pod, girth of pod, 1000 seed weight, seed yield per plant and fibre yield per plant in jute (*Corchorus olitorius* L.). Significant treatment means sum of squares for all characters studied. The magnitude of GCV and PCV were high for number of branches per plant, seed yield per plant, fibre yield per plant, number of pods per plant and plant height, whereas, length of pod and girth of pod exhibited least GCV and PCV. The high magnitudinal differences between GCV and PCV were found for girth of pod, fibre yield per plant, seed yield per plant, length of pod and plant height. The characters plant height and days to 50 per cent flowering showed high broad sense heritability with high genetic advance, whereas the character number of pods per plant showed very high heritability with high genetic advance.

Palve and Sinha (2005) selected 80 accessions of nine *Corchorus* spp. including two cultivated species (*Corchorus capsularis* and *C. olitorius*) and grown in an augmented randomized complete block design. They observed highly significant differences among accessions for plant height, days to first flowering, and fibre strength. Among wild species, accession WCIJ-134 of *C. trilocularis* had the highest plant height (190.30 cm) and fibre yield (3.74 g). Accessions of *C. pseudo-olitorius* WCIJ-034 and WCIJ-092 had low mean values for basal diameter of 0.30 cm and 0.32 cm, respectively. *C. fascicularis* accessions, WCIJ-014 (126.55 days), WCIJ-025 (120.55) and WCIJ-029 (100.25) took more days to

flower whereas NYM-2846 (*C. aestuans*) and KBA-230 (*C. tridens*) flowered the earliest at 21.15 days.

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

Islam *et al.* (2002) studied genetic variability, genetic performance and correlation coefficients for yield and its components of four exotic varieties along with five strains/varieties at Bangladesh Jute Research Institute. The estimates of variance for all the characters showed significant differences among the nine genotypes. The improved variety 0-9897 of BJRI gave the highest plant height, base diameter, green weight, stick weight and fibre weight. The genotypic and phenotypic coefficient of variation, heritability and genetic advance were observed for fibre yield. Fibre weight showed positive significant correlation with plant height ($r=0.95$), base diameter ($r=0.92$), green weight ($r=0.98$) and stick weight ($r=0.93$).

Ahmed and Khatun (1997) observed the highest genetic and the lowest environmental coefficient of variation in jute for number of trapezoid, area of trapezoid per section, and bark thickness. They also found that the fibre yield had highly significant and positive correlation with number of trapezoid ($r=0.975$) followed by area of trapezoid ($r=0.882$) and bark thickness ($r=0.784$).

According to Ali (1994) a high value of genotypic and phenotypic coefficient of variation was observed for fibre yield (24.8% and 35.4%) and bark thickness (11.2% and 15.7%).

Dastidar *et al.* (1993) observed that pod length, seeds per pod, seed weight per pod, 100 seed weight and days to 50% flowering were likely to be operated by non-additive gene action in olitorius jute.

Dahal (1991) reported the highest genotypic coefficient variation for dry fibre weight (21.89) followed by dry stick weight (18.73), green weight (18.29), leaf area (11.11), petiole length (11.02), plant height (11.02), harvest index (7.90), base diameter (7.09), node number (5.44) and internal length (3.28). He also observed higher phenotypic coefficient of variation than corresponding genotypic coefficient of variation for all characters.

Ahmed *et al.* (1993) observed that phenotypic coefficient of variation was relatively higher than genotypic one for all characters. Both genotypic and phenotypic coefficients of variation were the highest for fibre yield followed by green weight and the lowest for base diameter. Wide and narrow differences between genotypic and phenotypic coefficients of variation were observed in stick weight and petiole length.

Begum and Sobhan (1991) observed that the fibre yield and some other morpho-agronomic characters, viz. plant height, base diameter, leaf angle, petiole length and intermodal length showed high genotypic coefficient of variation (27.35, 12.53, 10.69, 14.63, 17.02 and 24.40).

Sardana *et al.* (1990) in their study with jute germplasm, reported higher phenotypic coefficient of variation than the corresponding genetic coefficient of variation for plant height, basal diameter, node number and fibre weight.

2.4 Heritability and genetic advance

Heritability is the degree to which variability of quantitative characters is transmitted from parents to offspring. So the estimation of heritability is of great interest to the plant breeders. A quantitative character having high heritability is transmitted from parents to offspring conveniently. Heritability value alone provides the indication of the amount of genetic progress that would result from selecting the best individual. Heritability and genetic advance have also been worked out for different quantitative characters in *C. olitorius*.

Biswas *et al.* (2018) studied the genetic parameters of variability for seven yield related characters in 47 genotypes of tossa jute. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Highly significant genotypic differences were reported for all the characters. The maximum co-efficient of range were reported for green weight (g/plant) and stick weight (g/plant) followed by fibre weight (g/plant), green bark thickness (mm) and core diameter (mm). The phenotypic and genotypic variances (PCV and GCV) were the highest in green weight (g/plant). High PCV and GCV values recorded in stick weight (g/plant). The maximum estimates of broad-sense heritability were recorded in stick weight (g/plant) followed by fibre weight (g/plant), green weight (g/plant) and plant height (m). The result from this study leads to the conclusion that green weight (g/plant), fibre weight (g/plant) and stick weight (g/plant) should be considered during selections for yield in *C. olitorius*.

Nargis (2001) found that high heritability value with high genetic gain in percent of mean observed in green weight with leaves, air dry weight without leaves, stick weight, fibre weight, and number of trapezoids and area of trapezoids.

Islam and Ahmed (2003) studied heritability in jute genotypes and revealed high heritability and genetic advance for stick weight and fibre weight. Plant height had heritability with moderate genetic advance and green weight had moderate heritability with high genetic advance.

Ali (1994) observed that the broad sense heritability was high for plant height (50%), bark thickness (50%), area of phloem trapezoids (55%), number of fibre bundle arcs (47%), but these exhibited low genetic gains. The fibre yield had a high heritability value (49%) coupled with high genetic gain (35.9%).

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

Talukder and Haque (1992) observed that the estimates of heritability (in broad sense) and genetic advance in biomass yield. Heritability for branches/plant and 1000-seed weight was 2.74 and 3.15 times greater, respectively than that of seed yield/plant.

Dahal (1991) reported that moderate heritability value with low genetic advance for the characters leaf area, petiole length, plant height, base diameter, dry stick weight, harvest index and dry fibre weight.

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

Chaudhury *et al.* (1984) reported high heritability value for plant height (64.85%) out of eight agronomic characters in tossa jute. They suggested that the phenotypic selection for these characters would be more effective to achieve high yield.

Ghosdastidar and Das (1984) observed very high heritability (82.43%) and high genetic advance as percent of mean (39.09) for plant height but node number and base diameter showed low heritability (63.93% and 39.71%) and low genetic advances as percent of mean

(20.68 and 15.25). Fibre yield also showed low heritability (53.93%) but high genetic advances as percent of mean (44.95).

Chaudhury (1984) observed that top diameter, internodal length and plant height had the highest heritability estimates coupled with moderate genetic advances. Therefore, phenotypic selection for making genetic improvement is expected to be more effective for those three characters.

In a study with *C. olitorious* L, Sobhan (1982) reported the highest broad sense heritability in tossa jute for seed yield (78.38%) followed by bark weight (63.92%) fibre yield (49.48%) plant height (38.97%) node number (38.72%) number of branches per plant (31.43%), stick weight (29.59%) and base diameter (15.03%).

According to Katiyar *et al.* (1974) heritability value alone provided the indication of the amount of genetic progress that would result from selecting the best individual.

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

Jana (1972) reported that the estimated heritability value in tossa jute was 39 percent for plant height, 15 percent for basal diameter, and nearly 40 percent for fibre yield.

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

Dudly and Moll (1969) reported that the improvement of a crop mainly depended upon the magnitude of genetic variability and the degree to which the yield and its components are heritable.

Rahman (1968) observed only 25 percent heritability for fibre yield in jute. The highest and the lowest heritability estimates were recorded for fibre weight and base diameter (Shukla and Singh, 1967). Robinson (1966) had been categorized the heritability values into low (below 10%) moderate (10-30) and high (above 30%).

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

Interpreting the information about heritability of the characters, it is observed that yield and different yield contributing characters of jute had shown low, moderate and high heritability values. The difference of heritability value for some characters of jute had shown low, moderate and high heritability values. The difference of heritability value for some characters among the different authors as observed was due to differences in the genetic makeup of their population as well as the environmental influence where they conducted the study.

2.5 Characters Association in Jute

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

Satya Narayana *et al.* (2018) reported partitioning of correlation coefficients of various components seed yield into direct and indirect contributions. The results revealed that pods per plant has maximum direct effect seed yield followed by seeds per pod and test weight at both levels. High positive correlation coefficients for plant height and base diameter were due to indirect effects of pods per plant. Hence, selection for the traits pods per plant, seeds per pod, plant height and base diameter may be successful for seed yield improvement in roselle.

Biswas *et al.* (2018) reported strong significant and positive correlation between plant height and base diameter (0.546); core diameter (0.492) green bark thickness (0.324); green weight/plant (0.363); fibre weight/plant (0.428) and stick weight/plant (0.418).

Hari *et al.* (2017) conducted an experiment during kharif 2013 and 2014 in North Coastal Zone of Andhra Pradesh at Agricultural Research Station, Ragolu, Srikakulam district to study the character association among quantitative traits and their direct and indirect effects on seed yield in a set of 60 genotypes of roselle (*Hibiscus sabdariffa* L.). The quantitative traits pods/plant, base diameter, seeds/pod, plant height, mid diameter, nodes/plant and test weight were found to be highly significant and positively correlated with the dependent variable, seed yield. Partitioning of phenotypic correlation coefficients of various components

upon seed yield plant⁻¹ into direct and indirect contributions revealed that pods/plant has maximum direct effect followed by seeds/pod and test weight. Selection for characters viz., pods/plant, seeds/pod, test weight, plant height and base diameter along with seed yield will be useful for improving seed yield in roselle.

Hossain *et al.* (2014) observed that plant height, number of bolls/plant and boll weight were strongly associated with seed cotton yield both at genotypic and phenotypic levels, whereas number of secondary fruiting branches/plant and number of insect infested bolls/plant exhibited negative and significant relationship with seed cotton yield.

Deshmukh (2010) observed that seed yield per plant exhibited significant and positive correlation with plant height, basal diameter, number of branches per plant and number of pods per plant, whereas fibre yield per plant exhibited positive and significant correlation with days to 50 per cent flowering, plant height and basal diameter.

Alam (2009) reported that fibre yield was positively correlated with most of its yield components of *Corchorus spp.*

Palve and Sinha (2005) observed that correlation coefficients were of higher magnitude when all accessions (n=80) were compared to those of wild species only (n=63). The traits significantly correlated with fibre yield (n=80) were plant height (r=0.85), basal diameter (r=0.78), node number (r=0.61), stick weight (r=0.87), and fibre strength (r=0.59). However, in accessions of wild species (n=67), the significantly correlated traits were plant height (r=0.62), basal diameter (r=0.46) and stick weight (r=0.81).

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

Akter (2001) reported correlation studies and revealed that positive association of fibre yield exist with all the characters except breadth of fibre cell and length/ breadth ratio. Significant and high positive correlation were observed in fibre leaves, air dry weight with plant height, green weight with leaves, air dry weight without leaves, bark thickness, number of trapezoids and area of trapezoids.

Guo *et al.* (1994) reported negative correlation coefficient between fibre fineness and bark dry weight and positive correlation between fibre fineness and percentage and branching height.

Dastidar *et al.* (1993) reported in correlation study and indicated that the seeds of late flowering genotypes have higher volume than the early flowering genotypes. It is also suggested that good pod length is required for more number of seeds per pod as well as high seed weight per pod.

Character correlation's revealed that fibre yield was positively associated with lamina length, lamina breadth, canopy, petiole length and intermodal length (Begum and Sobhan, 1991).

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

Path analysis helps to find out the direct and indirect causes of association. It is a standardized partial regression coefficient analysis and as such measures the direct influence of one variable upon other and allows the partitioning of correlation coefficient into direct and indirect effects of component characters. So it is used to analysis the real contribution of individual characters on yield.

Hossain *et al.* (2014) observed that the highest positive direct effect (0.794) was exerted by number of bolls/plant, while cotton weight/boll and number of infested bolls/plant showed negative direct effects on seed cotton yield. Both positive and negative direct effects were not counteracted by sum total of indirect effects of other characters.

Pervin *et al.* (2012) studied correlation and path coefficient for plant height, base diameter, green weight, stick weight, number of pod per plant, number of seed per pod, 1000 seed weight, seed yield per plant and fibre yield per plant. Highly significant differences were observed among the genotypes for all the characters. Substantial amounts of genotypic variance were also obtained for all characters. 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.

Deshmukh (2010) observed that path analysis in number of pods per plant had the highest direct effect towards seed yield, whereas plant height had the highest direct effect towards

fibre yield. Along with number of pods per plant, plant height, basal diameter and number of branches per plant were good indicators of seed yield, whereas plant height, days to 50 per cent flowering and basal diameter were good indicators of fibre yield in jute.

Jahangir (2009) showed that path analysis highly positive direct effect of stick weight on fibre weight followed by base diameter, leaf width and petiole length.

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

Islam *et al.* (2001) studied the genotypic and phenotypic variances, correlations and path coefficients for plant height, base diameter, fresh weight, stick weight, number of pod per plant, number of seed per pod, 1000 seed weight, seed yield per plant and fibre yield per plant. Highly significant differences were observed among the genotypes for all the characters. Substantial amounts of genotypic variance were also obtained for all characters. Fibre yield per plant was significantly and positively correlated with plant height, base diameter, fresh 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.

Akter (2001) reported that path analysis indicated direct contribution towards yield through bark diameter, number of trapezoid, air dry weight without leaves, stick weight, base diameter, inter nodal length, length of fibre cell and also breadth of fibre cell. The analysis showed residual effect indicating that some more traits contribute on fibre yield, which were not considered in that experiment.

Dastidar *et al.* (1993) reported in path-coefficient analysis and suggested that a medium flowering genotype with high 100-seed weight, followed by seeds per pod and pod length is most suitable for better seed production in olitorius jute.

Khatun and Sobhan (1992) revealed that plant height and bark weight exerted the greatest influence both directly and indirectly upon fibre yield of Tossa jute.

Thirthamallappa and Sheriff (1991) reported that plant height had maximum direct effect on fibre yield in Tossa jute.

2.6 Combining ability

Roy *et al.* (2020) carried out a study with ten hybrids evolved from five lines of Tossa jute following half diallel mating design to ascertain gene action and combining ability in respect of fibre yield and yield attributing traits. Results revealed that the specific combining ability (SCA) components of variance (σ SCA) were larger than the general combining ability (GCA) JRO 524 was detected as the best general combiner considering the economically important trait. Finally, considering dry fibre and stick yield, three hybrids, namely OIN 24 $\times$ JRO 524, OIN 39 $\times$ OIN 46 and OIN 39 $\times$ JRO 524 has been identified to be superior over their better parent as well as standard check regarding these traits. Additionally, all these three hybrids exhibited positive and significant SCA effects. These three promising specific combiners can be advanced to get better Tossa jute lines for bolstering economic returns of the farming community in future.

Kumar *et al.* (2018) estimated combining ability of fifteen diverse genotypes using Line $\times$ Tester mating design. Analysis of variance revealed significant differences ($P < 0.01$) among the parents and their hybrids for fibre yield and its attributes traits. Three lines namely OIJ-268 (12.78), OMU-33 (3.22), OIJ-05 (0.28) and tester OIN-255 (4.61) revealed significant GCA effect for fibre yield and were identified as the best general combiners for the improvement of fibre yield and yield attributing traits. The crosses viz. OIJ-268 $\times$ S-19 (32.52; 27.1g/plant), OIJ248 $\times$ OMU-19 (19.52; 21.5g/plant), OMU-37 $\times$ OMU-27 (19.43; 18.7g/plant), OIJ-05 $\times$ JRO-204 (16.61; 20.1g/ plant), and OIJ-165 $\times$ OIN-255 (12.61; 20.9g/plant) were identified as best combinations for fibre yield based on SCA effects and per se performance.

Kumar *et al.* (2018) conducted a research on jute and allied fibers to estimate fiber yield of different jute varieties and evaluated the hybrids along with their parents at two plant growth stages viz., 30 and 60 days age of the crop. The results showed significant variation at both the dates of observation and it was conspicuous at 60 days age. Considering GCA effects, OMU-42 among the lines and JRO-204 among the testers were superior general combiners. There were 31 combinations exhibiting significant and desirable SCA effects with respect to different characters. Such SCA effects resulted from crosses between parents with high $\times$ high, high $\times$ medium, medium $\times$ low, high $\times$ low and low $\times$ low and medium $\times$ medium general combiners. Further, in the present experiment, only 4 combinations viz., OIM-45 $\times$ JRO-204 for total bark diameter, OMU-09 $\times$ JRO-524 and OMU-42 $\times$ JRO-8432 for average

length of fibre cell wedge and OIM-45 × JRO-average width of fibre cell wedge at middle produced significantly desirable SCA effects at both the ages.

Sharma *et al.* (2017) crossed 11 parents in complete diallel fashion which resulted 55 F₁, 55 RF₁ (reciprocal F₁). Analysis of variance revealed significant differences ($P < 0.01$, $P < 0.05$) among the parents and their hybrids. The parents AMV 1, AMV 5, GR 27 and AHS 160 were identified as good combiners since they recorded significant general combining ability (GCA) effects for fibre yield and quality parameters. Further, For fibre yield only three crosses (AMV 1 × AMV 4, AMV 1 × GR 27, HS 4288 × JRR 07) showed significant specific combining ability (SCA) effects from them hybrid AMV 1 × GR 27 (fibre yield=27.37g/ plant) exhibited positively significant best parent (Non bris 4, Mean fibre yield=21.16g/plant) heterosis (29.35%). Similarly, for fibre tenacity, hybrid GR 27 × JRR 07 (fibre tenacity=23.47g/tex) exhibited positively significant best parent (HS 4288; fibre tenacity=20.35g/tex) heterosis (15.30%).

Kumar *et al.* (2016) carried out a study to estimate combining ability for fibre yield and yield attributing characters among diverse Tossa jute germplasm and in 21 F₁ hybrids were derived from 7 × 7 half diallel mating design. Analysis of variance revealed significance of parent's vs hybrids for most of the characters indicating variability among them. High GCA effects for fibre yield, plant height and green weight were recorded in OIN-255. High significant SCA effects for fibre yield were recorded in OMU-19 × OMU-27 (19.53**) and OIN-255 × OEX-32 (15.50*) crosses. Variances for general combining ability and specific combining ability were significant for few characters indicating additive and non-additive gene actions for those characters. Genetic parameters indicated that plant height, green weight and stick weight were controlled by additive gene action and basal diameter and fibre yield controlled by non-additive gene action.

Mostofa *et al.* (2012) estimated combining ability in 6 × 6 half diallel crosses for yield and yield contributing characters in kenaf (*Hibiscus cannabinus* L.). Combining ability analysis revealed that mean square due to general combining ability (GCA) and specific combining ability (SCA) were significant for all the characters studied, suggesting the presence of both additive and non-additive gene actions for the inheritance of the concerned characters. The magnitude of GCA variance was considerably higher than that of SCA variance for days to 1st flowering, fibre weight per plant and 1000-seed weight indicating the importance of additive gene action for these traits. The other characters were preponderantly controlled by

non-additive gene action. Ranking of parents on GCA performance indicated that parent P₆ (Acc.2731) was the best general combiner for fibre yield and yield attributes. On the other hand, parents P₂ (Acc.4197) and P₃ (Acc.2922) were found to be the best for seed related traits. On SCA performance, the crosses P₃ × P₅, P₁ × P₆, P₃ × P₆ and P₄ × P₅ were found to be the best for fibre related traits, while the best specific crosses for seed related traits were P₂ × P₃ and P₂ × P₄. For the development of high fibre or seed yielding kenaf varieties, either pedigree selection method or recurrent breeding is suggested depending on the genetic behavior of the trait.

Kumar *et al.* (2011) made diallel crosses among eight parents with high yield potential, good fibre quality, and resistance to biotic and abiotic stresses. A micro plot trial was conducted with four best F₇ lines along with two checks. Fibre yield, fibre percentage, and stick weight of all the four lines were higher than that of the checks. Analysis of variance revealed that differences in plant height, fibre yield, stick weight, and fibre percentage were significant. Line 2 derived from the cross combination CIJ 072 × CEX 045 was the best performer with regard to fibre yield, stick weight, and fibre % followed by line 1 derived from JRC 698 × CIJ 121. All four lines had fairly good fibre strength and fineness.

Khatun *et al.* (2010) made crosses between three varieties and seven accessions of white jute (*Corchorus capsularis* L.) in all possible combinations to establish 10 × 10 full diallel set. Variances for general combining ability (GCA) and specific combining ability (SCA) were significant or highly significant for all the characters indicating additive and non-additive gene actions played predominant role for expression of these characters. The magnitudes of GCA variance were higher than the corresponding SCA variance confirmed the predominance of additive genetic variations for these traits. The variety CVL-1 and Acc. 1831 were good general combiners for plant height, technical height, base diameter, number of nodes, bark weight, fibre weight and stick weight. Crosses, var. CVL-1 × Acc. 1831, Accs. 3695 × 4087, Accs. 1831 × 1833, Accs.1831 × var.CC-45, Acc. 2146 × var. A-38 and Acc. 2146 × var.CC-45 revealed significant positive SCA effect for fibre weight. Significant reciprocal SCA effect was observed in crosses, Accs.1832 × 3695, Acc. 1833 × 1831 and Acc. 4087 × var.CVL-1. Crosses, var. CVL-1 × Acc.1831, Accs. 3695 × 4087, Acc.1831 × var.CC-45, Acc.2146 × var.CC-45 and a reciprocal cross, Accs.1833 × 1831 were found to be good specific combiners for bark weight, fibre weight and stick weight.

Crosses were made between three varieties and seven accessions of white jute (*Corchorus capsularis* L.) in all possible combinations to establish 10 × 10 full diallel set by R.H and Sarker (2010). Variances for general combining ability (GCA) and specific combining ability (SCA) were significant or highly significant for all the characters indicating additive and non-additive gene actions played predominant role for expression of these characters. The magnitudes of GCA variance were higher than the corresponding SCA variance confirmed the predominance of additive genetic variations for these traits. The variety CVL-1 and Acc. 1831 were good general combiners for plant height, technical height, base diameter, number of nodes, bark weight, fibre weight and stick weight. Crosses, var. CVL-1 × Acc. 1831, Accs. 3695 × 4087, Accs. 1831 × 1833, Accs. 1831 × var. CC-45, Acc. 2146 × var. A-38 and Acc. 2146 × var. CC-45 revealed significant positive SCA effect for fibre weight. Significant reciprocal SCA effect was observed in crosses, Accs. 1832 × 3695, Accs. 1833 × 1831 and Acc. 4087 × var. CVL-1. Crosses, var. CVL-1 × Acc. 1831, Accs. 3695 × 4087, Acc. 1831 × var. CC-45, Acc. 2146 × var. CC-45 and a reciprocal cross, Accs. 1833 × 1831 were found to be good specific combiners for bark weight, fibre weight and stick weight.

Roy and Ghoshdastidar (2006) reported that analysis of variance for combining ability of 9 × 9 diallel cross without reciprocal showed highly significant variances in GCA and SCA in both F₁ and F₂ generations. The study included eight established macromutant genotypes such as, round leaf, long narrow leaf, ribbon leaf, stiff stem, crumpled leaf, tobacco leaf, drooping leaf and palmate leaf, and a cultivar, JRO-632. They observed that both additive and non-additive gene actions were important in the genetic control of all leaf characters.

Sengupta *et al.* (2005) studied fibre yield in Tossa jute (*C. olitorius* L.) from 11 × 11 diallel cross. The combining ability analysis revealed both additive and non-additive gene actions involved in the inheritance of all the characters studied. However, the additive variance was preponderant for basal diameter. Among the parents JRO-524 and KEN/DS/060C exhibited significant general combining ability (GCA) effects for fibre yield, plant height, node number, green weight, stick weight, fibre percentage and fibre fineness. Most of the SCA effects involved parents with high × high or high × low GCA effects. KEN/SM/024C × JRO-3670, JRO-524 × NPL/YPT/026C, KEN/DS/060C × TAN/X/112C crosses produced better quality fibre for textile purpose.

Sinha *et al.* (2004) studied the genetics of jute dry matter production and N uptake with 11 parental genotypes (indigenous lines JRO-524, JRO-3670 and JRO-3352; Tanzanian

accessions TAN/SM/040C, TAN/NYO 18C and TAN/X/112C; Kenyan accessions KEN/DS/060C, KEN/SM/024C and KEN/DS/053C; Thailand accession THA/YA/064C; and Nepal accession NPL/YPL/O26C) and resulting 55 F₁ hybrids grown in Barrakpore, West Bengal, India, during 2001 and 2002. The mean squares due to general (GCA) and specific (SCA) combining abilities were highly significant for both characters, indicating the importance of additive and non-additive gene actions in the inheritance of these traits. TAN/NY/018C exhibited superior mean performance and significant GCA effect for dry matter production. KEN/SM/024C also showed superior mean performance and significant GCA effects for total N uptake, and N content of bark and wood in terms of the N content of leaves, JRO-3670 showed superior mean performance and significant GCA value. Among the crosses, TAN/SM/040C × THA/YA/064C showed the highest SCA effect, coupled with high mean values for dry matter production and total N uptake, whereas KEN/DS/060C × TAN/SM/040C showed the highest SCA effect with high mean values for N concentrations in leaf and bark. For the N content of wood, JRO-524 × KEN/SM/024C was superior in terms of SCA and mean value for this trait. Most of the superior crosses, which were also good specific combiners, involved at least one high general combiner and superior parents. The results suggested that KEN/DS/060C, KEN/SM/024C, TAN/NY/018C and TAN/SM/040C had greater nutrient uptake than the other accessions.

Roy and Ghoshdastidar (2004) assessed with eight established macro mutants (round leaf, long narrow leaf, ribbon leaf, stiff stem, crumples leaf, tobacco leaf, dropping leaf and palmate leaf) and a standard cultivar (JRO-632) of jute (*C. olitorius* L.) and were used in a nine parent diallel cross without reciprocals. Five crosses, selected for showing residual heterosis in F₂ had consistently significantly specific combining ability effects in F₁ and F₂ generations. These crosses were: long narrow leaf × ribbon leaf for plant height; long narrow leaf × palmate leaf for leaf length; long narrow leaf × crumpled leaf for vertical separation of leaves; and crumpled leaf × stiff stem and palmate leaf × stiff stem for fibre yield. These crosses were expected to produce transgressive segregates which could be utilized for the development of superior pure line cultivars. The first three crosses stated above also produced fibre yield almost at par with the standard cultivar JRO-632.

Mondal and Sasmal (2003) reported that both additive non-additive gene effects played a major role in the expression of seed yield per plant and its components. General combining ability was high in JRO-632 for seed yield per plant and capsule length, yellow leaf for seed yield per plant, capsule length and seeds per capsule, elliptical leaf for capsule diameter, and

crumpled leaf for capsule diameter and seeds/capsule. Crosses derived from parents involving ribbon leaf or elliptical leaf registered high specific combining ability effects for most of the characters.

Ghoshdastidar *et al.* (2003) evaluated the inheritance of different seedling characters (root length, shoot length, root fresh weight and shoot fresh weight) at different growth stage (15, 30 and 45 days after germination) and of mature plant characters (plant height, base diameter, green weight, fibre weight and days to flower) of jute (*C. olitorius* L.). Both general and specific combining abilities (GCA and SCA) were highly significant for all seedling characters at all stages, except for root length at 30 days after germination. Both GCA and SCA were also significant for the plant characters at maturity. These results indicate that the inheritance of seedling and mature plant characters were controlled by both additive and non-additive gene actions.

Kumar and Palve (2002) reported high general combining ability (GCA) for fibre yield. Out of the 11 parental materials, only JRO-524 and JRO-7835 were the desirable combiners for fibre yield. SMC/024C also showed numerically high GCA effect though not significant. JRO-36E showed positive, though very low GCA effect, for this character.

Kumar *et al.* (2002) studied with 10 jute lines (Juta nonsoong, JRO 620, JRO 66, palmate leaf, KEN/SM/024, TAN/X/087, Selection-2, BC-3, JRO 3352 and JRO 524) and 4 testers (JRO 524, JRO 878, JRO 632 and JRO 7835) and obtained 40 crosses derived from the lines and testers. Genetic analysis showed the preponderance of additive gene action for all the studied characters. The lines TAN/X/087 and JRO 3352 were good combiners for high fibre yield and base diameter, respectively, whereas the testers JRO 524 and JRO 878 were good combiners for fibre yield, and plant height and stick weight, respectively. Ten crosses exhibited high general combining ability for higher fibre yield.

Chaudhury *et al.* (1999) stated that additive and non-additive gene actions were appeared as important in the inheritance of stem weevil (*A. corchori* L.) resistance through a nine parent diallel analysis in tossa jute (*C. olitorius* L.). Combining ability analysis showed that the general combining ability (GCA) effects of resistant parents (THA/Y/142 and KEN/DS/061) for weevil infestation were negative (desirable direction) and significant, while the susceptible parents (Tanganyika-1 and KEN/DS/060) had positive and significant GCA effects. The promising crosses for obtaining desirable segregants in subsequent generation were KEN/DS/061 $\times$ TAN/X/087, KEN/DS/061 $\times$ JRO-524, KEN/DS/061 $\times$ Tanganyika-1,

THA/YA/048 × JRO-524 and THA/Y/142 × Tanganyika-1 due to their low pest incidence and highly significant desirable specific combining ability (SCA) effects. Sinhamahapatra and Ghoshdastidar (1990) reported that plant height, node number, intermodal length are controlled by both additive and non-additive genes having predominant effect in a 9 parent diallel cross of *C. olitorius* L.

Alam and De (1995) reported that both GCA and SCA variances were highly significant for base diameter, plant height, green weight and node number, while SCA variance was significant for dry stick weight and fibre weight from a combining ability analysis of 5-parent half diallel cross in *C. olitorius* L. during 1990. They also observed that Tanganyika was a good combiner for base diameter, plant height, green weight and dry stick weight, and JRO-878 for plant height, green weight, node number and dry fibre weight. It was suggested that these 2 parents may be used profitably for future breeding programmes to improve yield and yield contributing characters. Combinations JRO-878 × Tanganyika, Sudan Green × Tanganyika and Russian Red × Tanganyika for base diameter, JRO-878 × Russian Red for plant height and green weight, and JRO-878 × Tanganyika for fibre weight may give rise to useful transgressive segregations in advance generations.

Kumar and Palve (1995) observed predominant role of additive gene action in the inheritance of all the characters studied, except basal diameter when studied diallel cross involving eleven genotypes of white jute (*C. capsularis* L.). The parents Tripura Cap. Brazil and Cap. Main Land China were identified as desirable combiners for fibre yield. Crosses JRC-212 × EC-4143, JRC-321 × Cap. Main L and China, EC-4143 × JRC-412, and Tripura Cap. × Liza were superior combinations for fibre yield and its attributes on the basis of their SCA effects.

Shah *et al.* (1994) recorded negative additive gene effects for plant height and stem base diameter. The best general combiner for plant height and stem base diameter was PARO-78, and FS-3 showed higher general combining ability for fibre yield. The best cross for fibre yield was in PARO-78 × FS-3.

Palve and Kumar (1994) obtained significant mean squares due to both GCA and SCA for fibre strength indicating the importance of both additive and non-additive gene effects in the inheritance of the trait studied. However, the magnitude of GCA variance was higher than that of SCA indicating the predominant role of additive gene action. The parents TJ-26, JRO-632 and JRO-524 were good general combiners. Four crosses were identified as potential on the basis of their specific combining ability effects. Of these, TJ-26 × JRO-632

and JRO-632 × JRO-524 exhibited the highest SCA effects. Bhaswati and Majumdar (1994) observed that the GCA and SCA were highly significant for eight characters studied in both the F₁ and F₂ generations, except for seed yield in *C. olitorius* L. and seeds per capsule in *C. capsularis* L. Estimates of GCA for the parents belonging to *C. olitorius* L. revealed that only JRO-7835 had significantly positive GCA effects for seed yield and its components in the F₁s which further increased in the F₂. None of the *C. capsularis* L. varieties showed consistency in GCA effects in either of the two generations. Additive variance was more important than non-additive variance in the inheritance of days to flowering, pod length, 100 seed weight and seed yield per plant in *C. olitorius* L. and for plant height and seeds/capsule in *C. capsularis* L. Narrow-sense heritability for these traits was generally high.

Sasmal and Biswas (1991) reported that the highest SCA effects were produced in hybrid from high × low GCA parents and from sweet × bitter cross combinations. Additive, additive × dominance and non-additive genetic control of characters was shown to be present.

De and Dastider (1991) reported that the crosses namely JRO-7835 × Tanganika, Sudan green × Russian red, JRO-632 × Tanganika and JRO-878 × Peking had good SCA for seed production. Population improvement approach in the form of diallel selective mating or mass selection with concurrent random mating was suggested for exploitation of both additive and non-additive gene actions for seed characters.

2.7 Handling of Segregating Population

Sanjoy and Jibon (2018) obtained high fibre yield and quality fibre from the variety, JRC 9057, derived from the cross, JRC 698 × CIJ 121 following pedigree method. The selection has been made for quality textile fibre coupled with high yield. For this purpose, pedigree of CIJ 121 was selected for quality and JRC 698 was used to incorporate high yield. This variety is mainly suitable for low and medium land rainfed situation and areas where jute is cultivated followed by transplanted aman paddy.

Mahdy *et al.* (2012) achieved two cycles of pedigree selection for lint yield trait in two segregating populations of Egyptian cotton (*G. barbadense* L.) under late planting condition. The genetic materials were the F₂, F₃, F₄ and F₅ generations of the crosses Giza 90 / Giza 85 (pop I) and Giza 85/Giza 70 (pop II). The phenotypic coefficient of variation (CV) of lint yield was large enough in the F₂ generation and accounted for 46.39 and 46.35 % in pop I and in pop II; respectively, However, the cv % of the respective parents were very low reflecting their purity. Broad sense heritability of lint yield was very high (0.99 and 0.99) and

unreliable in the F_2 generations, which results in high expected genetic advance of 79.01 and 80.60 % from the mean for pop I and pop II; respectively. After two cycles of selection the retained genetic coefficient of variability was 17.55 and 25.20 for pop I and pop II; respectively. However, the realized heritability and parent – offspring regression were 0.5509 and 0.3402 for pop I and 0.3016 and 0.3388 for pop II; respectively. In pop I, the direct observed gain was significant ($p < 0.01$) from the bulk sample (10.78 %) and from the better parent (18.20 %). four superior families were isolated from pop I and exceeded significant the better parent and bulk sample in lint yield and correlated traits. In pop II three superior families No. 58, No. 101 and No 130 showed significant direct gain in lint yield 34.96, 38.32 and 58.46 % from the bulk sample, and 48.30, 51.99 and 67.54 % from the better parent, respectively. Family No. 130, showed significant ($p < 0.01$) correlated gain from the better parent of 62.08, 35.92, 4.15, 9.63 and 6.70 % for seed cotton yield, number of bolls / plant, seed index, lint percentage and earliness index; respectively.

Hossain and Hossain (2002) observed the flower initiation of F_1 plants of white jute in almost same duration as in sensitive parent showing dominance of sensitiveness to insensitiveness when the photoperiod-insensitive mutant (D-18-7) and photoperiod sensitive cultivar (JRC-7447) of deshi jute (*C. capsularis* L.) were crossed to raise F_1 hybrid. From the segregating F_2 population, two selected recombinants (D-90 and D-110) flowered in 90 and 110 days, respectively. Pedigree selections were continued until the flowering habit was stable. These two selections and three sensitive cultivars (JRC-7447, JRC-212 and JRC-321) were sown every month round the year. The selections flowered almost in 90 and 110 days, respectively, while the sensitive cultivars had variation in flowering time for different sowing time. Yield trials twice in April and once in June registered the superiority of these two selections at 100 days harvest in April trials and that of D-110 at 120 days harvest over the control.

Roy and Ghoshdastidar (2002) suggested that long narrow leaf and round leaf producing parents were suitable in future breeding programmes for the improvement of fibre yield of jute. Each of the eight macro mutants, although originated from the same mother cultivar JRO-632, had different induced genetic background, confirming the possibility of creating a wide range of new genetic variability in tossa jute from a nine-parent diallel cross, and the genetic potentiality of eight established jute macromutants (round leaf, long narrow leaf, ribbon leaf, stiff stem, crumpled leaf, tobacco leaf, drooping leaf, palmate leaf) in terms of hybrid vigour for plant height, base diameter and fibre yield was determined. The crosses,

Long Narrow leaf × Tobacco leaf, JRO-632 × Long Narrow leaf, Long Narrow leaf × Palmate leaf, Crumpled leaf × Tobacco leaf, Crumpled leaf × Stiff stem, Ribbon leaf × Tobacco leaf, Ribbon leaf × Stiff stem and Palmate leaf × Stiff stem were expected to produced desirable transgressive segregates with improved fibre yield in future segregating generations.

Ali (2011) estimated the response to direct selection for grain yield/plant under normal and water stress conditions and study the correlated response of other studied traits. Two cycles of pedigree selection for grain yield/plant were practiced on a segregating population of wheat (Giza 168 × Sids 1) in the F₃-F₅ generations. Selection was practiced separately and over environments, at normal irrigation environment and drought stress irrigation environment. After the second cycle, the F₅ selected families were evaluated at the two environment. Pedigree selection for the two cycles at each environment showed 25.00 and 25.54% increase in grain yield/plant over the bulk samples for normal and drought stress selections, respectively, compared to 22.60% for selections over environments. The antagonistic selection was more efficient than synergistic selection in changing the mean. Selection for grain yield/plant was accompanied by late in heading date of 1.76, 4.07 and 0.13%, increase in plant height of 13.09, 9.79 and 7.38% and with decrease in 1000-gram weight of -2.01, -2.02 and -4.31% over the bulk sample when selection was practiced under normal, drought stress and over environment, respectively. Drought Susceptibility Index (DSI) was estimated for grain yield/plant. Four selected families i.e., No. 9 under normal environment, no. 71 under drought stress environment and no. 10 and 70 under over environments displayed DSI values less than one and the highest grain yield/plant. These families could be considered the best selected families resulted from selection for grain yield/plant. Pedigree selection for improving grain yield/plant was effective in isolating high yielding and drought tolerant genotypes.

Sinha *et al.* (2008) showed that progeny of 55 crosses (without reciprocals) were advanced through modified bulk method of selection (F₂ and F₃ generations) followed by single plant selection (F₄ onwards) for isolation of quality fibre with high yield. Three genotypes viz., JRO-3670, TAN/SM/040C, and NPL/YPY/026C were the highest combiners for fibre yield. Plant selection among advanced generations was confined to transgressive segregants which showed low lignin content and better fibre quality coupled with high fibre yield. The quality of jute fibre is usually judged by its suitability for

production of various types of yams and its behavior in the manufacturing process of end products. KEN/DS/053C $\times$ NPL/YPY/026C, TAN/X/112C $\times$ JRO-3352, JRO-524 $\times$ JRO-3352, KEN/DS/053C $\times$ JRO-3352, KEN/DS/060C $\times$ TAN/X/112C, THA/YA/064C $\times$ KEN/DS/053C, JRO-524 $\times$ JRO-3670, and KEN/SM/024C $\times$ KEN/DS/053C were selected in advanced generation. Thus far, two population from crosses JRO-524 $\times$ JRO-3352 and KEN/DS/053C $\times$ NPL/YPY/026C have out yielded JRO 524 by more than 13%. Because of lowest lignin and peroxidase activity with highest cellulose content, the KEN/SM/024C $\times$ KEN/DS/053C line is recommended to textile industries for blending its low lignin fibre with cotton and other synthetics.