Studies on Character Association and Genetic Divergence in White Jute (*Corchorus capsularis* L.)

Sayan Jana, Nitesh Kumar, Subhra Mukherjee, Prabir Kumar Bhattacharyya, Gouranga Sundar Mandal, Sitanshu Ghoshal

**Abstract**

**Background:** In white jute, very limited success has been reported by researchers to break yield plateau due to the narrow genetic base of the genetic material available with the breeders. Evaluation of agronomic traits and information about genetic variance in the breeding population is essential for selection and in planning crosses to enhance the productivity and diversity in cultivars. Yield component traits are inherited and each one accounts for variations in yield, hence interrelated with each other. The current investigation was done to measure the genetic variability and genetic diversity of white jute genotypes for characters and interrelationship that contribute to yield and fibre quality.

**Methods:** In the present study, fifty-two white jute (*C. capsularis* L.) genotypes were assessed during the Pre-Kharif season of 2017 at the Teaching Farm of Bidhan Chandra Krishi Viswavidyalaya, Mandouri, Nadia, West Bengal. Plants were raised in randomized block design with three replications. Statistical analysis was done for the estimation of ANOVA variability, correlation and path analysis and genetic divergence.

**Result:** Plant height and bark thickness with high heritability and high genetic advance were identified as important selection parameters. Plant height, bark thickness and green weight per plant had a significantly high positive correlation with dry fibre weight per plant both at genotypic and phenotypic levels. Plant height had the highest contribution toward the dry fibre weight followed by bark thickness. Genotypes were grouped into 13 clusters and cluster I had the highest number of 23 genotypes. The inter-cluster distance was found maximum between cluster I and cluster VI. Cluster XI recorded the highest mean for the plant height. Ten genotypes identified from different clusters in this study can be incorporated as donors in hybridization to combine both yield and improved fibre quality.

**Key words:** Correlation analysis, Genetic diversity, Genetic variability, Heritability, Path coefficient analysis, White jute.

**Introduction**

Jute belongs to the second most important textile fibre next to cotton. It is a natural fibre with golden and silky shine hence called “The Golden Fibre”. Jute of commerce is obtained from the bast or bark of the plant’s stem of two cultivated species of the genus *Corchorus* namely *C. capsularis* L. (White jute/Desi jute) and *C. olitorius* (Tossa jute). The fibre of *Corchorus capsularis* is ordinarily whitish. White jute (*Corchorus capsularis* L.) can be grown both in low and high land and has better adaptability than the other cultivated species. In general, *C. capsularis* shows flexibility in relation to drought and flood conditions. Assessment of genetic variability among the genotypes of jute (*Corchorus sp.*) for quality improvement has been attempted by several workers at different places and times. Still, very limited success has been reported by researchers to break yield plateau in this crop due to the narrow genetic base of the genetic material available with the breeders. In this circumstance, success can be achieved if the available gene pool can be broadened by the collection of variable genotypes from diverse regions. Evaluation of agronomic traits and information about genetic variance in the breeding population is essential for selection and in planning crosses to enhance the productivity and diversity in cultivars. Yield character components are inherited and each one accounts for variations in yield, hence interrelated with each other. Heritability estimates, genetic gain, correlation and path analysis were used to assess the variability and relative importance of yield component traits. The path coefficient analysis (Wright, 1921) allows specific parameters to perform an important test to create a specific correlation and divides the amount of relationship into direct and indirect effects. The concept of D² statistics by Mahalanobis,1928 which is one of the potent techniques for measuring forces of differentiation at inter and intra-cluster levels determines the relative contribution of each component trait to total divergence. Considering this in view, the current investigation was done to measure the genetic variability and genetic diversity...
of white jute genotypes for characters and interrelationship that contribute to yield and quality to identify appropriate breeding methods and parents of choice in this species.

**Materials and Methods**

The present experiment was conducted during the Pre-Kharif season of 2017 at Bidhan Chandra Krishi Vishwa Vidyalaya, Mandauri, Nadia, West Bengal with 52 diverse genotypes of white jute (*Corchorus capsularis* L.) and two check varieties (JRC-517, JRC-698) (Table 1). Plants were raised in randomized block design with three replications. The gross plot was divided into three blocks and a spacing of 0.5 m width was left between the blocks. The blocks were considered as replications and each block, in turn, was divided into 52 equal plots. Each plot was of the size of 1.5 m × 0.9 m at a spacing of 30 cm between the rows for each genotype. Five randomly selected plants were considered per replication per individual genotype for recording data. Observations were made on eight characters viz. Plant height (cm) (PH), number of nodes/plant (NPP), basal diameter (mm) (BD), mid diameter (mm) (MD), top diameter (mm) (TD), bark thickness (mm) (BT), green weight/plant (mm) (GWP), dry fibre weight/plant (DFP). Statistical analysis was done for the estimation of ANOVA by Panse and Sukhatme (1989); Variability (Singh and Chaudhary, 1985); Correlation and path analysis (Dewey and Lu, 1959); and Genetic divergence by Mahalanobis D² statistics (Rao 1952).

**Results and Discussion**

Significant differences were observed among genotypes for all the eight characters studied in the present investigation indicating sufficient scope for further selection (Table 2).

**Studies on Variability**

The genotype CIN-107 reported the maximum variability for plant height (247.00 cm) and basal diameter (12.46 mm). The no of node per plant was found maximum in CIN-115 while the maximum dry fibre weight was reported in the genotype CIN-92 (Table 3). The phenotypic coefficient of variation (PCV) was approximately close to the genotypic coefficient of variation (GCV) for plant height, the number of nodes per plant, basal diameter and mid diameter, indicating less influence of environment on the expression of these characters. While for the characters like top diameter, bark thickness, green weight and dry fibre weight the PCV value was higher than GCV indicating the role of the environment in the expression of these characters. These are in accordance with findings reported by Ali (2003) and Senapati et al. (2006). Heritability estimates and the genetic advance were maximum for plant height (88.00% and 65.54) followed by basal diameter (82.60% and 52.08) respectively. It may, therefore, be suggested that the characters’ plant height and bark thickness can be considered for effective direct selection. Earlier studies indicate that high heritability coupled with high genetic advance will be more useful for selection, as reported by Johnson et al., 1985 and Das and Kumar (2016). Knowledge of variability and heritability (h²) is essential to identify the characters amenable to genetic improvement through selection. High heritability and high GA for plant height and bark thickness suggest the simple phenotypic selection for the traits.

**Studies on Character Association**

Correlation studies in the present experiment indicated the different degrees of association between characters both at genotypic and phenotypic levels. The correlation values at the genotypic level were slightly higher in magnitude than the phenotypic correlations indicating the inherent association between the characters (Table 4). The present findings are in conformity with Prakash et al. (2003) wherein, plant height, bark thickness and green weight per plant had a significantly positive correlation with dry fibre weight per plant at genotypic as well as at phenotypic levels, by Islam et al. (2002). The highest positive significant correlation was observed between plant height and green weight per plant at the genotypic level followed by plant height and number of nodes per plant. At the phenotypic level, the highest positive significant correlation was found between plant height and the number of nodes per plant closely followed by plant height and green wt. per plant and the lowest between dry fibre weight per plant and node number per plant. A similar relationship was also reported by Islam et al. (2001) and Das and Kumar (2016). The character also had a significant and positive correlation with dry fibre weight and dry stick weight.

**Studies on Path Coefficient**

The direct effects of plant height on dry fibre weight per plant were positive and maximum followed by basal diameter (Table 5). Similar findings were observed by Senapati et al. (2006). Hence these two traits should be considered as

| Genotype | Sl. No. | Genotype | Sl. No. | Genotype |
|----------|---------|----------|---------|----------|
| CIN-84   | 19      | CIN-102  | 37      | CIN-122  |
| CIN-85   | 20      | CIN-103  | 38      | CIN-123  |
| CIN-86   | 21      | CIN-104  | 39      | CIN-124  |
| CIN-87   | 22      | CIN-105  | 40      | CIN-125  |
| CIN-88   | 23      | CIN-106  | 41      | CIN-126  |
| CIN-89   | 24      | CIN-107  | 42      | CIN-127  |
| CIN-90   | 25      | CIN-108  | 43      | CIN-128  |
| CIN-91   | 26      | CIN-110  | 44      | CIN-129  |
| CIN-92   | 27      | CIN-111  | 45      | CIN-130  |
| CIN-93   | 28      | CIN-112  | 46      | CIN-131  |
| CIN-94   | 29      | CIN-113  | 47      | CIN-132  |
| CIN-95   | 30      | CIN-114  | 48      | CIN-133  |
| CIN-96   | 31      | CIN-115  | 49      | CIN-134  |
| CIN-97   | 32      | CIN-116  | 50      | CIN-135  |
| CIN-98   | 33      | CIN-117  | 51      | JRC-517  |
| CIN-99   | 34      | CIN-119  | 52      | JRC-698  |
| CIN-100  | 35      | CIN-120  |         |          |
| CIN-101  | 36      | CIN-121  |         |          |

**Table 1: List of 52 White Jute genotypes used in the present experiment.**
important criteria for improving yield. The negative direct effect on dry fibre weight per plant was obtained by the characters like node number per plant, mid diameter and green weight at the genotypic level. The number of nodes per plant had direct negative effects on dry fibre weight per plant. The number of nodes per plant has the lowest positive effect on dry fibre yield per plant followed by mid diameter and top diameter. Thus, there was an indirect negative effect of the number of nodes per plant via other characters like plant height, basal diameter mid diameter and top diameter. This clearly shows the negative role of no. of node plant towards fibre yield. Pervin and Haque (2012) observed that there is a negative correlation between green weight and fibre yield.

### Studies on genetic diversity

The dry fibre weight contributed the maximum (62.59%) towards the degree of divergence followed by plant height (7.99%), bark thickness (6.63%). It is interesting to note that the other characters like the number of nodes per plant, basal diameter, mid diameter and top diameter had very little contribution to the degree of divergence. The grouping pattern of the genotypes observed due to geographical diversity and genetic divergence was unrelated. Based on

### Table 2: Analysis of variance in 52 genotypes of white jute (*C. capsularis* L.)

| Source of Variance | df | Mean Sum of Square |
|--------------------|----|--------------------|
| Replication        | 2  | 414.75             |
| Genotype           | 51 | 3608.55**          |
| Error              | 102| 156.95             |

### Table 3: Genotypic variability parameters of 52 genotypes of white jute (*C. capsularis* L.)

| Traits               | Range                  | GCV% | PCV% | H\(^2\) (BS) | GA | GA % of mean |
|----------------------|------------------------|------|------|--------------|----|--------------|
| Plant height (cm)    | CIN-107(247.00)        |      |      |              |    |              |
| No. of node/plant    | CIN-115(43.78)         |      |      |              |    |              |
| Basal diameter (mm)  | CIN-107(12.46)         |      |      |              |    |              |
| Mid diameter (mm)    | CIN-92(6.99)           |      |      |              |    |              |
| Top diameter (mm)    | CIN-92(5.68)           |      |      |              |    |              |
| Bark thickness (mm)  | CIN-133(1.08)          |      |      |              |    |              |
| Green weight (g)     | CIN-115(227.33)        |      |      |              |    |              |
| Dry fibre weight (g) | CIN-92(10.74)          |      |      |              |    |              |

### Table 4: Genotypic (G) and phenotypic (P) correlation among eight characters of white jute (*C. capsularis* L.)

| Characters          | G | P |
|---------------------|---|---|
| Plant height        |   |   |
| No. of node/plant   |   |   |
| Basal diameter      |   |   |
| Mid diameter        |   |   |
| Top diameter        |   |   |
| Bark thickness      |   |   |
| Green weight        |   |   |
| Dry fibre weight    |   |   |
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the Tocher value, fifty-two genotypes of white jute were grouped into 13 clusters of which cluster I had the highest number of 23 genotypes and all most all the remaining clusters accommodated 2 genotypes except cluster XI and XII had 3 and 6 genotypes respectively (Table 6). The results obtained with intra and inter-cluster divergence indicate variations for the parameters. When the clusters were compared for divergence, the inter-cluster distance was found maximum between cluster I and cluster VI indicating greater diversity between the genotypes falling under these clusters (Table 7). Among all the clusters the cluster XI recorded the highest mean for the character like plant height closely followed by cluster X for the same character. The number of nodes per plant, basal diameter and green weight recorded maximum means in cluster XI (Table 8). The mid and top diameter had a maximum mean in cluster V followed by cluster XI. All the characters studied contributed the maximum divergence which indicates the utility of

Table 5: Path coefficient at genotypic level of 52 genotypes in white jute (*C. capsularis* L.).

| Character            | Plant height (cm) | No. of nodes/plant | Basal diameter (mm) | Mid diameter (mm) | Top diameter (mm) | Bark thickness (mm) | Green weight (g) | Dry fibre weight (g) |
|----------------------|-------------------|---------------------|---------------------|-------------------|-------------------|---------------------|------------------|---------------------|
| Plant height         | 0.84              | -0.203              | 0.022               | -0.039            | 0.024             | 0.224               | -0.124           | 0.744**             |
| No. of nodes/plant   | 0.306             | -0.213              | 0.014               | -0.035            | 0.021             | 0.261               | -0.114           | 0.240**             |
| Basal diameter       | 0.392             | -0.032              | 0.095               | -0.038            | 0.006             | 0.005               | -0.043           | 0.385**             |
| Mid diameter         | 0.361             | -0.084              | 0.041               | -0.09             | 0.028             | 0.181               | -0.047           | 0.390**             |
| Top diameter         | 0.463             | -0.102              | 0.013               | -0.057            | 0.044             | 0.044               | -0.062           | 0.343**             |
| Bark thickness       | 0.343             | -0.101              | -0.001              | -0.03             | 0.004             | 0.55                | -0.046           | 0.719**             |
| Green weight         | 0.767             | -0.178              | 0.03                | -0.031            | 0.02              | 0.185               | -0.136           | 0.657**             |

Table 6: Grouping of 52 genotypes of white jute (*C. capsularis* L.).

| Cluster | No. of genotypes | Genotype                          |
|---------|------------------|-----------------------------------|
| I       | 23               | CIN-84, CIN-85, CIN-86, CIN-87, CIN-88, CIN-89, CIN-90, CIN-91, CIN-92, CIN-93, CIN-94, CIN-95, CIN-96, CIN-97, CIN-98, CIN-99, CIN-100, CIN-101, CIN-102, CIN-103, CIN-104, CIN-105, CIN-106 |
| II      | 2                | CIN-112, CIN-124                  |
| III     | 2                | CIN-123, CIN-128                  |
| IV      | 2                | CIN-113, CIN-128                  |
| V       | 2                | CIN-116, CIN-124                  |
| VI      | 2                | CIN-119, CIN-120                  |
| VII     | 2                | CIN-122, CIN-125                  |
| VIII    | 2                | CIN-132, CIN-135                  |
| IX      | 2                | CIN-108, JRC-698                  |
| XI      | 3                | CIN-107, CIN-1 16, JRC-517        |
| XII     | 6                | CIN-129, CIN-130, CIN-126, CIN-121, CIN-1 17, CIN-1 14 |
| XIII    | 2                | CIN- 133, CIN-131                |

Table 7: Inter and intra cluster distance of 54 white jute genotypes.

| Cluster | I       | II      | III     | IV      | V       | VI      | VII     | VIII    | IX      | X       | XI      | XII     | XIII    |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| I       | 8.746   | 11.908  | 9.1     | 8.606   | 7.7758  | 87.005  | 10.413  | 10.182  | 7.785   | 10.296  | 11.123  | 9.064   | 10.383  |
| II      | 2.882   | 6.778   | 10.266  | 12.37   | 12.693  | 6.076   | 17.489  | 10.899  | 15.684  | 13.487  | 8.393   | 17.361  |
| III     | 2.899   | 6.761   | 9.516   | 8.694   | 7.732   | 13.332  | 5.858   | 12.167  | 11.467  | 7.312   | 13.739  |
| IV      | 3.313   | 9.371   | 6.944   | 7.844   | 9.914   | 6.893   | 10.118  | 12.219  | 8.591   | 10.61   |
| V       | 3.422   | 6.421   | 11.153  | 8.482   | 7.966   | 10.266  | 11.234  | 11.262  | 8.01    |
| VI      | 3.422   | 6.421   | 11.153  | 7.87    | 14.31   | 12.889  | 8.291   | 15.218  |
| VII     | 3.787   | 10.429  | 15.31   | 14.82   | 13.38   | 14.831  | 4.765   |
| VIII    | 3.86    | 4.06    | 7.795   | 13.38   | 14.831  | 9.57    | 10.386  |
| IX      | 4.172   | 9.94    | 11.061  | 9.57    | 10.386  |
| X       | 5.149   | 8.905   | 13.812  | 9.23    |
| XI      | 7.66    | 12.738  | 13.449  |
| XII     | 9.666   | 14.839  |
| XIII    | 6.969   |
### Table 8: Cluster mean of 52 white jute (*C. capsularis* L.) genotypes.

| Cluster | Plant height (cm) | Node no/plant | Basal diameter (mm) | Mid diameter (mm) | Top diameter (mm) | Bark thickness (mm) | Green-weight (g) | Dry fibre weight (g) |
|---------|-------------------|---------------|---------------------|-------------------|-------------------|--------------------|-----------------|-------------------|
| I       | 169.13            | 32.678        | 9.334               | 5.633             | 4.318             | 0.738              | 140.971         | 7.44              |
| II      | 131               | 22.538        | 9.768               | 5.037             | 3.593             | 0.498              | 122.833         | 4.185             |
| III     | 127.833           | 21.79         | 9.41                | 5.037             | 3.593             | 0.88               | 126.833         | 7.335             |
| IV      | 158.167           | 30.428        | 7.708               | 6.457             | 5.375             | 0.768              | 135.833         | 6.907             |
| V       | 175.167           | 34.667        | 9.217               | 6.457             | 5.375             | 0.825              | 136.667         | 8.07              |
| VI      | 149.333           | 30.165        | 11.663              | 5.688             | 4.043             | 1.007              | 134.5           | 9.183             |
| VII     | 138.333           | 26.553        | 9.127               | 5.115             | 3.835             | 0.538              | 124.833         | 7.56              |
| VIII    | 169.833           | 33.528        | 8.058               | 5.483             | 3.958             | 1.017              | 152             | 9.183             |
| IX      | 220               | 40.168        | 12.05               | 6.428             | 4.714             | 0.678              | 218.333         | 9.316             |
| X       | 242.444           | 43.509        | 10.585              | 5.788             | 4.172             | 0.642              | 128.056         | 6.247             |
| XI      | 138.722           | 24.332        | 10.585              | 5.788             | 4.172             | 0.982              | 151.5           | 8.942             |

Multivariate analysis in identifying potential parents combining high yield and other desirable characters. The genotypes from the cluster II and VI could be selected for hybridization program to produce highly heterotic or diverse genotypes due to higher inter-cluster distance. Cluster analysis for quantitative traits will be of direct use to breeders in planning crosses between diverse genotypes to create new variability. The clustering pattern revealed a meager amount of genetic diversity among the jute genotypes considered in the present study which indicates the presence of common ancestry and hence warrants for the collection of diverse genotypes to broaden the genetic base and an intensive hybridization program among new diverse genotypes. This result corroborated with the finding of Kar et al. (2009).

### CONCLUSION

Based on the present study, the hybridization program could be initiated by crossing among the genotypes CIN-84, CIN-85, CIN-86, CIN-119 and CIN-120 to create a new genetic base. The genotypes CIN-92, CIN-107, CIN-115 and CIN-132 were identified as promising for fibre production. The traits plant height, bark thickness, green weight per plant had a highly significant positive correlation with dry fibre weight per plant both at the genotypic and phenotypic levels. Plant height and bark thickness have significantly contributed to dry fibre yield and can be considered in the selection of superior genotypes of jute.

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