Cytomorphological and biochemical characterization of nine species of *Corchorus* aiding to interspecific hybridization and induced mutagenesis in *C. olitorius* L. (Family: Tiliaceae).

Present investigation deals with morphological (including seed and seed-coat features following SEM analysis), anatomical (stem anatomy), palynological, physiological (stomatal characteristics), cytological (mitotic and meiotic analysis) and biochemical (quantitative and qualitative protein estimation) characterization of nine jute species (cultivated: *Corchorus capsularis* L. and *C. olitorius* L.- globally important for fibre yield; wild species: *C. aestuans* L., *C. fascicularis* Lamk, *C. pseudocapsularis* L., *C. pseudoolitorius* I. and Z., *C. tridens* L., *C. trilocularis* L., *C. urticaefolius* W. and A.- potential donor for fine fibre trait, disease resistance, drought tolerance amongst others) with an objective to ascertain interrelationship between/among the germplasms for their successful exploitation interspecific hybridization and crop improvement. Further, the methodology of induced mutagenesis (gamma irradiation and EMS) was adopted in *C. olitorius* var. JRO 524 to create genetic variations and to raise desirable “plant type” mutation, which may enrich jute trade in future. Interspecific hybridization between *C. trilocularis* (female parent, potential donor of fine fibre trait) and *C. capsularis* (male parent, fibre yielded) was performed to conserve the wild germplasms and to create genetic diversity. F₁ cross derivatives were cytomorphologically analyzed at F₂ and F₃ generations. An amphidiploid was also induced following colchicine treatment and evaluated. A concise account of the investigation performed is been presented below:

1. Petriplate (*C. capsularis*- 84.0%, *C. olitorius*- 80.0%; wild species- 24.0% to 64.0%) and field (16.0% to 48.0%) germination frequency were recorded in nine jute species. Survivality percentage of the species was 65.8% to 95.5%. Among the species, *C. tridens* had lower (65.8%) survivality percentage. Moisture content of seeds varied from 9.8% (*C. aestuans*) to 15.7% (*C. urticaefolius*). Moisture content was 14.6% in *C. capsularis* and 13.5% in *C. olitorius*. Seed weight (100 seed weight) was between 0.03gm and 0.31 gm among the species. *C. olitorius* had heavier seeds compared to other species. Seed viability was higher in the cultivated
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members (*C. capsularis* - 95.0%, *C. olitorius* - 100.0%) than those of wild species (35.0% to 85.0%).

2. Taxonomic characterization in jute species deciphered gross similarities and dissimilarities between / among themselves. Number of stamens, shape of leaf, shape of flower buds, style and stigma characteristics were given more emphasis for preparation of a key to the identification of the species. Based on morphological traits, a dendrogram was prepared and five prominent clusters were observed. From clustering analysis, a close relationship was noted between *C. trilocularis* and *C. tridens*, *C. pseudocapsularis* and *C. tridens* and *C. capsularis* and *C. pseudooolitorius*.

3. Seed and seed-coat surface analysis of *Corchorus* spp. revealed distinct variations and similarities among / between genotypes. The study was conducted on light microscopy and SEM analysis. Traits assessed were shape, size and colours of seeds, seed surfaces, cells of reticulation and lumen floor. A key was prepared to the identification of species. SEM analysis is been considered to be an additional constant for species characterization. A dendrogram prepared based on seed and seed-coat structures revealed four main clusters demonstrating close relationship among *C. aestuans*, *C. pseudooolitorius* and *C. fascicularis* and between *C. pseudocapsularis* and *C. tridens*, *C. trilocularis* and *C. urticaefolius*, and *C. olitorius* and *C. capsularis*.

4. A comparative study of pollen morphology (shape, size, colpi length, colpi margin, pore character, exine surface and cellular features) was made in the species of *Corchorus* following acetolysis technique and SEM analysis. Pollen grains in the species were subprolate (exception: *C. pseudocapsularis* - prolate) tricolporate (excepting *C. trilocularis* had both tricolporate - 90.0% and tetracolporate - 10.0% pollen grains), colpi margin normal or incurved, size of colpi medium to relatively longer and varied from 29.98±0.64 to 36.72 μm±0.92, pore lalongate with edges raised or inconspicuous, exine surface reticulate, reticulation indistinct or distinct,
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Tri- to pentagonal or variously gonals, shallow to alveolate or pitted, sometimes angular with raised irregularly walls, junction knobbed or unknobbed. Pollen size was variable among the species and it ranges from 38.30µm ± 0.54 X 30.45 µm±0.54 (*C. capsularis*) to 31.17µm ± 0.64 X 24.20µm±0.55 (*C. trilocularis*). Based on palynological characteristics a key to the identification of the species was prepared. Clustering analysis performed considering palynological traits revealed four main clusters and a very close interrelationship was ascertained between *C. aestuans* and *C. fascicularis*.

5. Anatomical characterization of nine jute species was made from cross sections of stem (basal zone: 1.5 cm. to 2.0 cm. above ground level; upper zone: 15.0 cm. to 20.0 cm. from apex) of uniformly matured plant (at fruit ripening stage, 175-180 days from sowing) considering the following aspects: fibre zone, appearance and shape of phloem fibre, number and area of fibre pyramid, number of bundles per pyramid, diameter of fibre cell, xylem area and nature of pith. Variations in anatomical features between the zones were evaluated. A key to the identification of the species was prepared and presented. Dendrogram constructed from clustering analysis based on anatomical parameters showed four clusters demonstrating interrelationship among (*C. olitorius*, *C. urticaefolius* and *C. capsularis*; *C. pseudocapsularis*, *C. trilocularis* and *C. pseudoolitorius*) and between (*C. fascicularis* and *C. tridens*) species. *C. aestuans* seems to be widely apart from the remaining species from anatomical point of view.

6. Stomatal parameters namely stomatal size variation including aperture size (area), the frequency of distribution, and conductance were studied in jute species in an attempt to characterize the germplasms. Stomata in jute species were paracytic, amphistomatic and anisostomatic. Among the *Corchorus* species, stomatal frequency (mm-²) ranged from 81.39 (*C. trilocularis*) to 176.43 (*C. olitorius*) in upper and 303.34 (*C. pseudocapsularis*) to 719.72 (*C. aestuans*) in lower epidermis. The ratio (upper/ lower) of stomatal frequency were minimum in *C. aestuans* (0.21), *C. urticaefolius* (0.25), *C. trilocularis* (0.26) and *C. pseudoolitorius* (0.26); thereby
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suggesting their utility as drought tolerant genotypes. *C. olitorius*, *C. urticaefolius* and *C. aestuans* had closely spaced stomata in both leaf surfaces. Site specific as well as random distribution of stomata were studied among the species. *C. capsularis* and *C. olitorius* had broader stomata; while, among the wild species *C. trilocularis* had larger sized stomata. Stomata conductance was higher in *C. pseudocapsularis*, *C. capsularis*, *C. olitorius* and *C. aestuans*.

7. Karyotyping through Image Analyzing System in nine species of *Corchorus* (2n=14) revealed the presence of three (*C. fascicularis*: 2Am$^{sc}$+ 8Bm+4Cm), two (*C. capsularis*: 2Bm$^{sc}$+2Bm$^{sm}$+4Bm+2Cm$^{sm}$+4Cm, *C. olitorius*: 2Bm$^{sc}$+6Bm+6Cm, *C. pseudocapsularis*: 2Bm$^{sc}$+6Bm+4Bm+2Cm$^{sm}$, *C. pseudoolitorius*: 2Bm$^{sc}$+8Bm+4Cm, *C. pseudocapsularis*: 2Bm$^{sc}$+4Bm+2Cm$^{sm}$+8Cm) and one (*C. tridens*: 2Cm$^{sc}$+12Cm, *C. trilocularis*: 2Cm$^{sc}$+12Cm, *C. urticaefolius*: 2Cm$^{sc}$+10Cm+2Cm, *C. fascicularis*: 1.77$\mu$m to 3.50$\mu$m, *C. pseudocapsularis*: 1.58$\mu$m to 2.74$\mu$m, *C. pseudoolitorius*: 2.00$\mu$m to 2.73$\mu$m, *C. tridens*: 1.37$\mu$m to 2.00$\mu$m, *C. trilocularis*: 1.50$\mu$m to 2.07$\mu$m and *C. urticaefolius*: 1.61$\mu$m to 2.25$\mu$m). Haploid chromatin length (11.97$\mu$m - 17.72$\mu$m) and S% (relative length of shortest chromosome compared to the longest) were also calculated. Relatively shorter sized chromosomes were found in *C. pseudocapsularis*, *C. tridens*, *C. trilocularis* and *C. urticaefolius*, mainly in the last three ones having chromosome size below 2$\mu$m was a frequent trait. *C. fascicularis* also showed 2n=28 (11.54%) chromosomes (karyotype formula 4Am$^{sc}$+16Bm+8Cm, absolute chromosome length 1.90$\mu$m to 3.74 $\mu$m, TF%=-45.37, S%-50.80). An identification key of the species has been formulated on the basis of karyomorphological data. Dendrogram was constructed from mitotic chromosome.
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Data based on clustering analysis and it revealed close relationship between *C. olitorius* and *C. aestuans* and among *C. pseudoolitorius, C. trilocularis* and *C. urticaefolius*, thereby suggesting a possible complex evolution in the genus. From karyomorphological point of view *C. capsularis* and *C. olitorius* may not be closely related.

8. Meiotic analysis performed in nine species of jute revealed that *C. olitorius* (mean/cell: 7II), *C. capsularis* (mean/cell: 6.98 II + 0.03I), *C. tridens* (mean/cell: 6.98 II + 0.03 I), *C. trilocularis* (mean/cell: 7 II) and *C. urticaefolius* (mean/cell: 7 II) formed 2n=14 chromosomes at metaphase I always with balanced (7/7) segregation at anaphase I; while, *C. fascicularis* (24.42%-MI; 1.79%-AI), *C. aestuans* (33.33%-MI; 28.57%-Al), *C. pseudoolitorius* (24.69%-MI; 15.73%-AI) and *C. pseudocapsularis* (2.56%-MI; 0.00%-AI) exhibited numerical variations in chromosome number (n= 1,2,3,4,5,6,9,10 and 14) in addition to normal (n=7). Average chromosome association per cell at MI was 0.002 VI + 0.006 IV + 6.98 II + 0.31I in *C. fascicularis*, 6.55 II + 0.60 I in *C. aestuans*, 6.60 II in *C. pseudoolitorius* and 7.08 II + 0.21 I in *C. pseudocapsularis*. Aneuploidy noted in jute species is been attributed to cytomixis. Chromosome in the species were mostly bivalents (6.55 – 7.08 mean/cell; random in distribution – p> 0.05) and rarely univalents (0.00 – 0.60 mean/cell; nonrandomly distributed – p<0.001); however, one PMC with a ring and a chain quadrivalent and one with a chain hexavalent were noted only in *C. fascicularis*. Bivalents in the species were of ring (1.44 ± 0.13 to 4.68 ± 0.14/cell) and rod (2.32 ± 0.14 to 5.44 ± 0.14/cell) configurations. Excepting *C. capsularis*, the species formed more of rod bivalents than ring. Ring and rod bivalents were nonrandom (p< 0.001); while chiasmata per cell (8.40 – 11.68) and per bivalent (1.20 – 1.67) was random (p> 0.50) in distribution among species. Pollen fertility in the species varied from 59.82% - 96.91%. Dendrogram constructed on the basis of clustering analysis from meiotic parameters revealed close proximity among *C. trilocularis, C. urticaefolius*, and *C. olitorius; C. aestuans, C. pseudoolitorius* and *C. fascicularis* and between *C. capsularis* and *C. tridens*. 

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9. Amount of total seed protein content among species varied from 11.1% (*C. pseudocapsularis*) to 17.1% (*C. pseudoolitorius*). *C. capsularis* and *C. olitorius* had 16.9% and 15.9% seed protein respectively. Among the wild species *C. urticaefolius* (15.1%) and *C. fascicularis* (13.5%) showed relatively higher protein contents. Estimated protein content from leaf tissue ranged from 2.8% (*C. trilocularis*) to 6.8% (*C. capsularis*). Total carbohydrate content was higher in cultivated species (*C. capsularis*-30.0%, *C. olitorius*-42.0%) than the wild species (13.5% to 28.5%).

10. Distinct polymorphism in electrophoretic banding patterns of seed protein following SDS-PAGE was noted in nine jute species and led to the detection of 52 polypeptide bands (cultivated members: *C. capsularis* -40; *C. olitorius* -42, wild species: *C. aestuans* - 28, *C. fascicularis* - 23, *C. pseudocapsularis* - 30, *C. pseudoolitorius* - 34, *C. tridens* - 30, *C. trilocularis* - , 26 and *C. urticaefolius*- 35) with molecular weight ranging between 13.0 kD to 122.5 kD. Polypeptide bands were mostly medium (25.0 kD to 49.9 kD: 8 to 17 bands) to low (<25.0 kD: 6 to 11 bands) molecular weights but very high (>80.0 kD: 1-6 bands) and high (50.0 kD to 80.0 kD: 5-11 bands) molecular weight bands were also noted. Band number 3 (97.5 kD), 8 (76.0 kD), 15 (57.5 kD), 20 (47.0 kD), 29 (35.0 kD) and 35 (28.0 kD) were common band in all the species. Species specific polypeptide bands (present or absent) were detected( no. 36-27.0 kD, *C. capsularis*; 17-53.5 kD, *C. olitorius*; 33-30.3 kD, *C. aestuans*; 30-34.0 kD, *C. fascicularis*; 22 and 45-41.0 kD and 20.0 kD respectively, *C. pseudocapsularis*; 7 and 42 -79.0 kD and 22.0 kD respectively, *C. tridens*; 39-24.0 kD, *C. trilocularis* and 43 -21.0 kD, *C. urticaefolius*). The clustering (Hierarchical cluster analysis; based on proximity matrix) of the species on un-weighted pair group method with arithmetic mean algorithm (UPGMA) analysis was made and 3 prominent clusters were noted (Cluster 1: *C. trilocularis* and *C. urticaefolius*; cluster 2: *C. fascicularis*, *C. tridens* and *C. pseudoolitorius* and cluster 3: *C. olitorius*, *C. capsularis* and *C. aestuans*).
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11. Dendrogram (cluster analysis based on UPGMA) constructed based on all the traits (morphological, Palynological, anatomical, cytological and biochemical) analyzed revealed three distinct clusters but a very close interrelationship was noted between C. urticaefolius and C. trilocularis and C. fascicularis and C. pseudoolitorius. C. capsularis seems to be widely apart from the other species.

12. Considering 76 parameters an unrooted tree was prepared using the software PHYLIP (v. 3.68, neighbor-joining method) in nine species of Corchorus and it revealed that the cultivated species were more primitive than those of the wild members under evaluation. C. capsularis seems to be most primitive; while, C. trilocularis and C. urticaefolius were advanced species. Among the wild germplasms, C. aestuans was most primitive. Phyllogenetic relationship among the species of Corchorus suggested a complex evolutionary trend.

13. Jute species were assessed for three consecutive years under a uniform agronomic conditions for different quantitative traits and the results indicated that C. olitorius was much taller plants but seed yield was higher in C. capsularis. Excepting C. urticaefolius, seed yield was more or less similar in the wild species. Number of branches and capsule per plant were much higher in C. aestuans compared to other species.

14. Days to maximum flowering was recorded to be 60 to 65 days in C. capsularis, 125 to 135 days in C. olitorius, 63 to 68 days in C. aestuans, 59 to 70 days in C. fascicularis, 78 to 90 days in C. pseudocapsularis, 58 to 66 days in C. pseudoolitorius, 92 to 95 days in C. tridens, 150 to 158 days in C. trilocularis and 152 to 165 days in C. urticaefolius.

15. A desynaptic mutant of Corchorus fascicularis showing distinctive morphological variations than normal was identified from the natural population (1 out of 27 plants scored) of jute species following male meiotic analysis. Self segregation of the desynaptic plant suggested that desynapsis (mutant trait) was monogenic recessive to normal. Compared to normal plants, the spontaneous desynaptic mutant (medium
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Strong type) demonstrated enhanced univalent frequency per cell (4.05, normal-0.31), reduced number of chiasma (6.67, normal-7.28) and bivalent (5.12, normal-6.99) per nucleus, few meiocytes (13.64%, normal-5.36%) with unequal separation at AI, cytologically near normal AII (94.83%, normal-100.00%) cells and high male fertility (81.77%, normal-92.06%). Cytomixis (prophase I/ metaphase I) was evident in both normal and mutant plants forming aneuploid (mutant: 2n<14-1.40%, 2n>14-2.80%; normal: 2n<14 - 14.20%, 2n>14 - 10.22%) PMCs predominantly at MI (mutant: 4.20%, normal: 24.42%) and rarely in AI (mutant: 1.52%, normal: 1.79%) cells.

16. For induction of mutation, seeds of tossa Jute (*C. olitorius* L. var. JRO-524; Family: Tiliaceae; moisture content: 13.5%) were gamma irradiated (50, 100, 200 and 300 Gyre doses) and EMS (0.25, 0.50 and 1.00 per cent solution for 2 and 4 hour durations) treated.

17. As compared to control (96.0%), M1 seed germination frequency under petriplate condition seems not be affected by the mutagen doses (gamma rays: 96.0% to 100.0%; EMS: 94.0% to 100.0%). None of employed doses showed 50% reduction in germination and consequently LD50 could not be ascertained. Mean seedling length in control was 47.0mm ± 1.70 and in treatments (gamma rays: 38.7mm ± 1.38 to 44.9 mm ± 1.39; EMS: 36.4mm ± 1.32 to 46.2mm ± 1.79) it reduced mostly (excepting: 0.25%, 4h EMS-49.1mm± 1.20) but the reduction was significant only in 400Gy gamma irradiation and 1.0%, 2 and 4 hour and 0.5%, 4h EMS treatments.

18. Field germination frequency of control plants was 44.0% and it was 34.0% to 42.0% in gamma irradiations and 32.0% to 38.0% in EMS treatments. The control plants showed 95.45% survivality; while, in treatments it varied from 58.82% to 85.0% (gamma irradiations; 85.0% to 94.11%; EMS: 58.82% to 94.74%).

19. Capsule sterility in treatments was dose dependent and it varied from 5.56% to 22.22% in gamma irradiations and 0.00% to 18.18% in EMS treatments. Pollen sterility was recorded to be 3.86% in control plants and in treatments it ranged from
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2.91% to 51.88%. Pollen sterility was considerably higher in 0.50% and 1.0%, 4hour EMS treatments.

20. Mean seed yield in control was 0.87gm and in treatments it varied from 0.21 gm to 1.35 gm. Seed yield was found to enhance over control in 0.50%, 4h (1.35 gm) and 0.25%, 2h (1.10 gm) EMS treatments.

21. Biological damages namely lethality, injury and sterility were ascertained from M₁ parameters like seed germination frequency, seedling growth and seed yield per plant respectively. Results indicated variable response of the mutagen treatments in inducing biological damages.

22. As compared to control plants (52.50%), M₂ seed germination frequency was found to decrease markedly in all treatments of the mutagens (gamma-rays: 23.71% to 30.32%; EMS: 9.71% to 25.57%).

23. A total of eight macromutants (chloroxantha, viridis, pigmented stem, thick stem I and II, broad leaf, lax branching and late flowering) were recorded at M₂. All the mutants were viable.

24. Frequency of total mutation (viable mutation frequency) varied from 0.38% to 0.82% in gamma irradiations and 0.56% to 5.88% in EMS treatments. EMS treatments induced higher mutation frequency (1.49%) than gamma irradiations (0.52%). Total mutation frequency over the M₂ population was noted to be 0.89%. Spectrum of mutation was higher in EMS than gamma irradiations.

25. Over the M₂ population, the mutants occurred in the following order: viridis = chloroxantha = pigmented stem = thick stem II > late flowering > thick stem I = broad leaf = lax branching.

26. Desirable characteristics of the viable macromutants are: chloroxantha (seedling colour – Pea green 61 compared to Emerald green 758 in control; chlorophyll content: chlorophyll a = 0.003, b = 0.02, total = 0.03 compared to 0.19, 0.21 and
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0.41 respectively in control; recorded only from 0.5% and 1.0%, 4h EMS treatments); viridis (seedling colour Cyprus green 59, chlorophyll content: chlorophyll a – 0.02, b – 0.06, total – 0.08; spotted in 300Gy [0.51%] and 400 Gy [0.82%] gamma irradiations), pigmented stem (stem colour – Poppy red 16/1; only found in gamma irradiated samples; girth of the stem: basal 7.79cm ± 0.17, middle – 7.45 cm ± 0.22 and upper – 6.27 cm ± 0.08 compared to 7.62cm ± 0.47, 5.77 cm ± 0.85 and 4.00 cm ± 0.43 respectively in control plants; fibre weight – 18.33 g ± 1.67), thick stem I (only 1 plant was spotted in 0.50%, 4h EMS treatment; girth of the stem: basal – 14.2cm, middle – 12.2 cm and upper – 7.82 cm; yielded 82.0 gm fibre), thick stem II (noted in 0.50% and 1.0%, 2h EMS treatments; girth of the stem: basal – 11.85cm ± 0.42, middle – 8.21cm ± 0.37 and upper – 7.37cm ± 0.15; fibre yield – 73.33g ± 1.67), broad leaf (leaf colour – Scheeles green 80; frequency over the mutant population – 0.05%, spotted in 0.50%, 4h EMS treatment; leaf area: 9.66cm² ± 0.66 significantly higher than control – 1.93 cm² ± 0.15), lax branching (recorded only at 0.25%, 4h EMS; angle of divergence of primary branches in relation to main axis 50.8° ± 4.68 in comparison to 36.3° ± 3.34 in control) and late flowering (scored from 0.25%, 2h EMS treatment; flowering 160 days from sowing as compared to 75 to 90 days in control).

27. Mutagenic effectiveness was inversely related to the doses of treatments (excepting 0.5%, 4h EMS) mostly and it seems that EMS was more effective than gamma irradiation. Mutagenic effectiveness was higher in 0.50%, 4h and 0.25%, 2h EMS treatments compared to other doses of the mutagens. Mutagenic efficiency was lower in gamma irradiated materials based on injury and sterility. Relatively high (based on injury) mutagenic efficiency was recorded in 0.25%, 2h and 0.5%, 4h EMS treatments.

28. PMC squashes revealed 2n = 14 chromosomes in the plant types always. Predominant chromosomal associations recorded among the plant types was 7II (72.04% to 100.0%). Mean chromosomal association per cell at metaphase I in control was 7II and in mutants it varied from 6.60II +0.80I to 7II. Univalent
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... frequency per cell was relatively higher in viridis (0.80) as compared to other mutants. Anaphase I segregation of chromosomes was equal (7/7) mostly (100.0%) excepting viridis (96.67%) where occasionally 1 to 2 laggard(s) were observed. Pollen fertility in control was 95.91% and in the mutants it varied from 69.79% (chloroxantha) to 88.95% (broad leaf).

29. Inheritance of the mutant trait(s) were assessed from the segregation pattern noted in the M3 plants (M3 plants were raised from selfed seeds of M2 mutants), which indicated monogenic recessive (3:1/1:1) nature of the mutant trait(s).

30. Analysis of stem anatomical features (base, middle and upper portions) from suitable transverse sections in control and in 3 mutants (thick stem I and II and pigmented stem) in relation to control revealed that fibre zone, number of fibre pyramid/section and number of fibre bundles/pyramid enhanced significantly in mutants than control, however, diameter of fibre cell was random (excepting upper zone showed non-random distribution) among the plant types. Compared to upper and middle zones, basal zone had higher number of fibre pyramid/section and fibre bundle/pyramid in all the plant types ascertained. Thick stem I mutant seems to be the most useful plant type from anatomical point of view.

31. Stomatal parameters (stomatal size variation including aperture size, the frequency of distribution, and conductance) were studied in control and in eight morphological mutants (chloroxantha, viridis, thick stem I and II, pigmented stem, broad leaf, lax branching and late flowering) at M3 in an attempt to characterize the mutants in relation to control from physiological point of view and to screen genotype(s) with drought tolerance and photosynthetic efficiency. Thick stem I and broad leaf mutants were with high photosynthetic efficiency; while, thick stem I and lax branching mutants were promising for drought tolerant genotypes. Chloroxantha and viridis had relatively higher number of stomata, which were closely spaced.
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32. Seed protein content was 15.9% in control and among the mutants it varied from 11.9% to 18.1%. *Thick stem I* (18.1%) and *broad leaf* (17.2%) had relatively higher amount of protein content than the other plant types.

33. SDS-PAGE of seed protein of nine genotypes (control and 8 macromutants) resulted in 53 polypeptide bands of diverse molecular weights ranging from 20.0 kD to 122.5 kD. Out of 53 polypeptide bands, 42 in control, 20 in *chloroxantha*, 31 in *viridis*, 16 in *pigmented stem*, 21 in *thick stem I*, 24 in *thick stem II*, 38 in *broad leaf*, 30 in *lax branching* and 35 in *late flowering* were recorded. Mutant specific bands were detected.

34. Control and mutants were assessed for nine quantitative characters (plant height, girth of stem, no. of primary branches and total branches per plant, no. of capsule on main axis, total number of capsule per plant, capsule length, seed per capsule and seed weight) after harvest and five traits (stick length, girth of stem, stick weight, fibre weight per plant and fibre colour) after retting at M2 and M3. Results obtained were discussed.

35. *Viridis*, *chloroxantha* and *pigmented stem* mutants may be used as genetic markers in efficient breeding programme in tossa jute not withstanding the significance of other desirable traits induced in the plant types. *Lax branching* mutant had enhanced fibre yield and also may be utilized as drought tolerant genotype; while, *broad leaf* mutant plants were with good photosynthetic efficiency. *Late flowering* mutant is always been a breeders choice in jute breeding. *Thick stem I* and *II* were the most promising mutant induced, which may enhance jute trade in future.

36. The mutants had lower amount of lignin content in fibre (3.5% - 8.5%) than control (11.0%).

37. Cytomorphological features of F1 hybrids (12 sets were analyzed; F1 plants raised from seeds of each crossed pod was considered as single set) between *Corchorus*
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capsularis* (male parent.-2n=14) and *C. trilocularis* (female parent.-2n=14) were studied in relation to parents. The hybrid plants looked morphologically alike in 12 sets. The F₁'s were intermediate to parents for few traits (stem colour, bud shape and flower colour); while, for other characters (pod colour, pod shape, seed colour and seed shape) they resembled the female parent. Average chromosome association per cell at diplotene and MI of F₁ plants was 0.007 VI + 0.007 IV + 6.74 II + 0.70 I [parents: *C. capsularis* L. – 6.98 II + 0.03 I /cell, *C. trilocularis* L. – 7II /cell] and it varied from 0.05 VI + 4.00 II + 2.00 I to 8.86 II + 0.00 I among the sets. F₁ plants formed bivalents (4.00 to 8.86 /cell, frequency – 0 to 14/cell) and univalents (0.00 to 2.00 /cell, frequency – 0 to 24/cell) mostly and very rarely quadrivalents (0.07/cell, set-7) and hexavalents (0.05/cell, set-5) in ring configurations. Predominant associations in F₁ plants were 7II (39.47% to 94.44%; average 70.17%) and 6II + 2I (0.00% to 30.77%, average 11.08%). PMC's (pollen mother cells) with aneuploidy (hypo- and hyperploid) and polyploidy (n=1, 2, 3, 4, 5, 8, 10, 12 and 14) were noted in some hybrid lines (set-1, 2, 5, 6, 7, 8 and 10) at diplotene and metaphase 1 only, which was attributed as the consequence of cytomixis. Cytomixis was evident from all hybrid lines including the female parent *C. trilocularis*. Anaphase I showed equal (7/7) segregation of chromosomes in 100.0% cells of both parents and in 96.5% cells of hybrid plants. Pollen fertility was high (F₁ plants: 79.7% to 95.6%, average – 89.1%; parents: *C. capsularis* – 91.2%, *C. trilocularis* – 73.3%) in the plant types. Results indicated close genetic relationship between the parents.

38. F₂ and F₃ plants (raised from selfed seeds of F₁ mother stock – *Corchorus trilocularis* L. used as female parent x *C. capsularis* L. male parent in crossings) were cytomorphologically assessed and estimates of qualitative and quantitative data including meiotic parameters suggested stability of F₁ cross derivatives at diploid level. An amphidiploid (0.5% colchicine, 6 hour, 2 consecutive days) was induced (1 out of 20 F₁ plants treated) which showed general polyploid traits (reduced growth, vigor and viability but with enhanced chlorophyll content in leaf and stomatal, pollen and seed sizes) but with near normal (2n=4x=28) pairing.
Cytomorphological and biochemical characterization of nine species of Corchorus aiding to interspecific hybridization and induced mutagenesis in C. olitorius L. (Family: Tiliaceae).

SUMMARY

behavior (12.95 bivalent/cell and 2.10 univalent/cell) and high pollen fertility (82.53%). The plant yielded a total of 32 seeds.