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REVIEW ARTICLE

BIOTECHNOLOGICAL APPROACHES OF JUTE PRACTICED UP TO DATE IN BANGLADESH

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ABSTRACT

Jute is a fiber crop which is often referred to as "golden fibers". The fiber of jute has been used for hundreds of years. It has been used for different purposes for many years. As it is biodegradable in nature, now it is considered a valuable and eco-friendly product. Jute is the second largest bast fiber source in the world, while first one is cotton. Its fiber is natural, strong, long, and shiny which makes it useful for both domestically and commercially across the world. Nowadays is becoming popular of making value-added industrial goods, such as, Paper, curtain, furniture, building materials, home decor, mulching materials. Moreover, currently, people are becoming concerned about using eco-friendly jute fibers. In consequence, this review paper focuses on enhancement of jute fibers production through biotechnological approaches.

KEYWORDS

Jute Fiber, Mutation, Tilling, CRISPR-cas 9, Gene identification

1. INTRODUCTION

Recently, Jute fiber demand has been increasing, as it is biodegradable and contributes to the development of the environment (Pereira et al., 2019). Moreover, it is natural fiber, and it has many advantages, such as, biodegradability, affordability, lower use of fertilizers and pesticides, availability, renewability, as a result, it is often called "ecofriendly fiber" and "fiber for the future" (Pickering et al., 2016; Saha et al., 2010). Jute plants (Corchorus sp.) often have carbon sequestration ability and about 15 tons of jute leaves in their total growing season fall per hectare and can add organic matter for the next crop (Singh et al., 2015).

Furthermore, jute fiber has versatile uses from small handicrafts products, such as rope, burlap, course cloth to big geotextiles industries (Meena et al., 2022). As jute fiber is long and shiny, it attracts many paper and textile manufacturing industries. The jute geotextiles act as soil stabilizers; it has been proved that sandy soil with 20 mm pieces of jute can improve and strengthen the sandy soil characteristics and it is often usable as construction of embankments (Sharma et al., 2017). In India, soil health and crop productivity has been improved practicing crop diversification. The Jute-Rice-Baby corn cropping system has the highest productivity (Kumar, et al., 2021).

There are some *Corchorus capsularis* species that have high nutritional value and often they are used as leafy vegetables (Tareq et al., 2020). Some *Corchorus* species contain a great amount of lycopene which is a powerful antioxidant. Antioxidants often prevent us from oxidative stresses, chronic diseases. It neutralizes free radicals, reduces risks of heart diseases, and cancers. Lycopene amount in fresh jute leaves in 45 days is almost double the fresh red tomatoes (Nasreen et al., 2022).

Jute is one of the cultivated cash crops in Bangladesh. According to the data 2023-2024, A total of 25.43 lakh acres area is under jute cultivation and total jute production amount is 95.82 lakh bales (Hassan et al., 2025). Bangladesh's economy has significantly dependent on jute, as 30% of jute and related products sold throughout the world comes from Bangladesh (Ahad et al., 2018). Jute production has increased annually by 0.83%. Although, due to the other high value crops, such as vegetables, urbanization and industrialization, jute cultivation in some regions (Chittagong, Rangamati, Sylhet, and Cumilla) are limited (Hassan et al., 2025).

As a result, more short duration high yielding, year-round jute cultivated verities are improves. Conventional breeding is time demanding and sometimes it might be inaccurate. Biotechnological approaches have been untaken for the development of the jute fiber, such as, whole genome sequencing of both *Corchorus olitorius* and *Corchorus capsularis*, CRISPR cas-9 mediated gene transfer technology, Agrobacterium-mediated genetic transformation, mutation breeding, and various bioinformatics tools for the identification of genes. Furthermore, different *in vitro* regeneration protocols of both *Corchorus olitorius* and *Corchorus capsularis* have been developed.

This review paper focuses on improvement of jute fiber through different biotechnological approaches, such as, *in vitro* regeneration, CRISPR cas 9 mediated gene editing technology, *in silico* techniques in Bangladesh context. Moreover, it has comprised different varieties that have improved through conventional breeding methods.

Peer-reviewed articles, scientific reports, published between 2010 to 2025 were extensively reviewed in this review paper. This review sheds light on advanced biotechnological research that has been conducted for last 15 years and it provides a foundation for the breeding of jute plants up to date.

2. CONVENTIONAL BREEDING OF JUTE

46 improved varieties of jute, including 28 deshi jute (Table 1), 18 tossa jute (Table 2) types have been developed by Bangladesh Jute Research Institute, which helps us maintain sustainable jute cultivation throughout

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the year. At present, from the 46 types of jute varieties, 19 improved varieties—11 deshi, 8 tossa jute are quite popular among jute growers. O-9897 is a well-liked and very productive cultivar among jute growers. 2008 saw the development of BJRI Deshi Pat 7, a variety that yields bright golden fiber that is more valuable on the market than traditional kinds. BJRI Deshi pat 8 was created in 2013, which is a moderate (8 dS/m) salinity tolerant variety, and it was developed for the extension of jute cultivation in the southern part of Bangladesh. Later, in 2021, BJRI Deshi Pat 10 improved for highly saline (12 dS/m) soil. BJRI Tossa pat 4 and BJRI Deshi pat CC 45 have been developed for early sowing. Moreover, there are two early harvesting deshi jute varieties, such as, BJRI Tossa pat 6 and BJRI Deshi pat 7. Among other deshi jute varieties, a leafy vegetable named BJRI Deshi pat shak 1 was developed in 2014. A few years later, in 2020, BJRI Deshi pat shak 2 and 3, which are two more extremely nutrient-dense vegetable jute varieties, BJRI Deshi pat shak 2 and 3, developed (Bjri, 2023).

Table 1: List of White Jute (Corchorus capsularis L.) varieties using conventional breeding methods (Bjri, 2023).

Name of the Variety, White Jute (*Corchorus capsularis* L.)	**Pedigree**
Ocarpus, Kakya Bombai, R-85, D-154 (Dhaka-154), D-386, Funduk, C-212, C-13, C-412, C-1, C-2, C-3, C-4 (C320), C-5 (C-321), D-154-2, C-6 (C-322), CVL-1, CVE-3, CC-45, BJRI Deshi pat shak 2 (Mehra Red), BJRI Deshi pat shak 3 (Mehra Green), BJRI Deshi pat 10 (BJC-12221)	Pure line selection (PLS)
BJRI Deshi pat 5 (BJC-7370)	D-154 × CC-45
BJRI Deshi pat 6 (BJC-83)	CVL-1 × Fuleswari
BJRI Deshi pat 7 (BJC-2142)	CC-45 × BJC-718
BJRI Deshi pat 8 (BJC-2197)	CC-45 × FDR (Formusa Deep Red)
BJRI Deshi pat shak-1 (BJC-390)	Cap Dwarf Red × BINA Pat Shak-1
BJRI Deshi pat 9 (BJC-5003)	CVL-1 × Acc. 1831 (Blue Seeded)

Table 2: List of Tossa Jute (Corchorus capsularis L.) varieties using conventional breeding methods (Bjri, 2023).

Name of the Variety, Tossa Jute (*Corchorus olitorius* L.)	Pedigree
Chinsurah Green (D-38), R-26, R-27, O-620, O-632, O-753, O-1, O-2, O-3, O-4, O-5, BJRI Tossa pat 6 (O-3820), BJRI Tossa pat 7 (MG-1), BJRI Tossa pat 9 (Sobuj sona)	Pure line selection (PLS)
O -9897	O-5 × BZ-5
BJRI Tossa pat 3 (OM-1)	PLS (Uganda)
BJRI Tossa pat 4 (O-72)	(O-9897 × O-2012) × O-9897
BJRI Tossa pat 5 (O-795)	Uganda red × O-4

2.1 Genetic Engineering in Jute

2.1.1 Mutagenesis

As jute fiber's demand is growing significantly, most Bangladeshi breeder is trying to develop high yielding and early jute variety. Through mutation it can be achieved easily. JRO-524 was exposed to five doses of gamma radiation (700, 800, 900, and 1000 gy) to achieve desired variety. 25 M3 plants were selected at that time from bulked M2 plants. were originally chosen. After replicating trail for 2 years, two mutants, BJM-10-1-3 and BJM-10-1-5, were selected from among them for higher yield. These two mutants gave much more yield than their parents, which was about 4% to 6% respectively (khanam et al., 2024).

Robi-1 is the high yielding variety developed in 2019 using EMS (Ethyl Methane sulfonate) through TILLING (targeted induced local lesions in genomes), which is a high throughput screening technology to identify mutant plants in a randomly mutagenized population (BARJ, 2021).

Furthermore, jute is only grown in Bangladesh from March-July. As a result, long growing season hampered year-round jute fiber production. By using chemical mutagenesis, the 150 mM LD50 (Lethal Dose) of EMS (Ethyl Methane Sulfonate) after incubating deshi jute seed for four hours, new mutant named Komola was developed. It flowered for only 70 days. Moreover, it has other differences such as, petiole and stem color, which is coppery red. In m4 generation, were found stable when molecular analysis was done, two clade deletions in the ELF3 (Early Flowering 3) gene and four SNPs in the PMIR1 (Plastid Movement Impaired 1 Related 1) (Hossen et al., 2020).

The process of mutagenesis is illustrated in Figure 1.

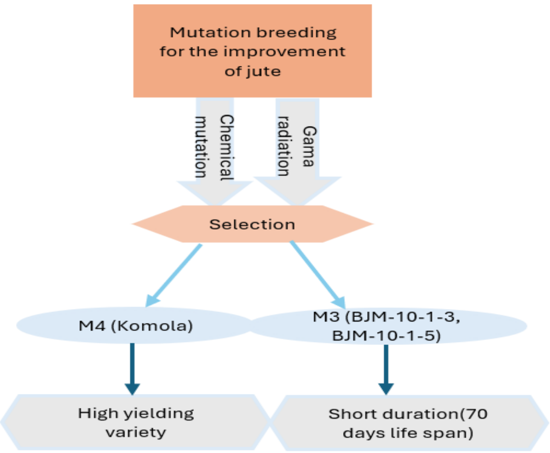

Figure 1: The steps of mutation breeding.

2.1.2 Genetic Transformation

Agrobacterium-mediated genetic transformation was performed in white jute using marker genes and gene constructs (CIPK and Gly-1), which gives drought and salt tolerance (Figure 2). The two cultivars (CVL-1 and Tricap-1) induced callus in MS medium supplemented with 2.0 mg/l BAP and 0.5 mg/l IAA and in the same media full plants were regenerated. Regenerated plants were submerged in bacterial cultures for a minute and in co-cultivation media, plants were left for whole night. Higher shoot regeneration was observed from Agrobacterium-infected cotyledon was observed in the case of CVL-1 cultivar which is 5% higher than Tricap-1 cultivar. After co-cultivation and selection, histochemical GUS analysis was performed among different varieties (vars. Tricap-1, CVE-3 and CVL-1). The GUS reporter gene was expressed as blue color in transformed plant CVE-3. Then, it was transferred into drought and saline conditions for further assessment (Amin *et al*., 2012).

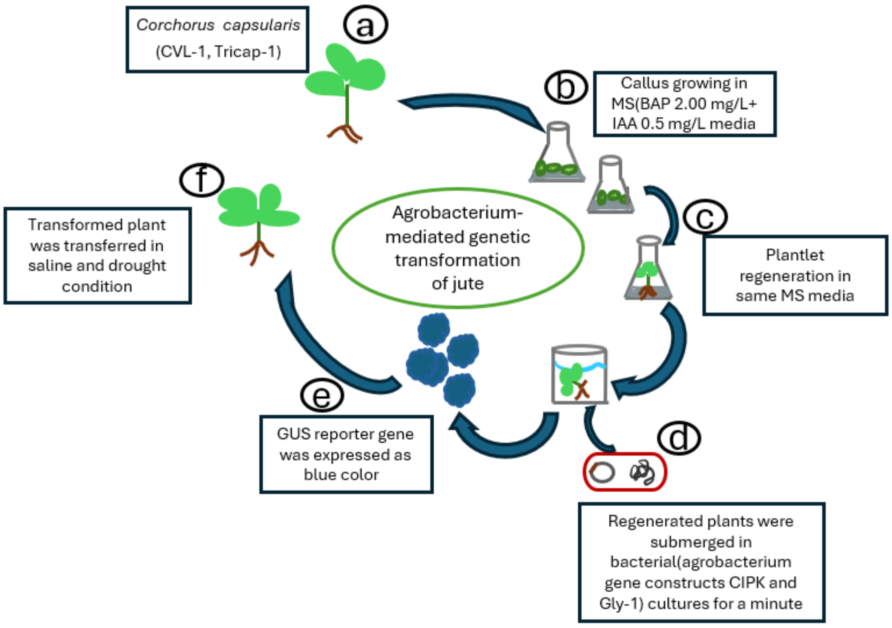

Figure 2: (a) Experimental materials *Corchorus capsularis* (CVL-1, Tricap-1) were taken for Agrobacterium-mediated genetic transformation of jute. (b) Callus were grown in MS media supplemented with (BAP 2.0 mg/L + IAA 0.5 mg/L). (c) Plantlets were regenerated using same media. (c) Regenerated plants were submerged in bacterial (agrobacterium gene constructs CIPK and Gly-1) cultures for a minute. (d) GUS reporter gene was used and expressed as blue color. (f) Finally, transformed plant was transferred in saline and drought conditions.

2.1.3 Genomics of two jute species

The high-quality draft genomes of two species, *Corchorus olitorius* and *Corchorus capsularis* along with functional genomics comparisons were performed to facilitate customed designed breeding. The assemblies span 91.6% and 82.2% of the projected genome sizes, for *Corchorus olitorius* and *Corchorus capsularis*, respectively. cDNA and RNA-seq data confirmed thirty-nine percent of the 30,096 *Corchorus capsularis* and 37,031 *Corchorus olitorius* genes. Clustered gene families and gene collinearity were analyzed about 18.66 million years ago; jute underwent shared whole-genome duplication. The major structural and regulatory genes involved in the creation of fiber were identified by the investigation of the RNA expression of isolated fiber cells (Islam et al., 2017).

2.1.4 Genomic investigation for improving fiber quality

As lignin is an important component of jute fiber, which reduces the quality of jute fiber unsuitable for use in the textile industry for the biofuel generation. As the genome sequence of the jute fiber (*Corchorus olitorius*) is available, it was possible to identify fourteen genes and eleven transcription factors from different species that are involved in lignin production. After phylogenetic analysis and expression analysis, it was confirmed that these genes may involve the lignin manufacturing of jute fiber (Hossain et al., 2024).

2.1.5 Whole transcriptome sequencing and analysis of jute

Conventional breeding often takes time to develop jute varieties and molecular mechanism for jute formation is mostly unknown. The entire transcriptome of the RNA in fiber cell was sequenced. A total of 66 genes linked to fiber were discovered and they are involved in the start and elongation of fibre cells and creation of secondary cell walls (Ahmed et al., 2020)

2.2 GA biosynthesis pathway

Gibberellic acid (GA) is a phytohormone which is essential for plant growth and height. As a result, bast fiber production in jute (*Corchorus sp.*) is significantly dependent on GA. A total of 22 candidate genes has been identified through genome-wide analysis. At the initial stage, four genes CoCPS, CoKS, CoKO, and CoKAO are functional. Eight GA2ox genes, three CoGA3ox genes, and seven CoGA20ox genes are functional in the later stages of jute growth. After further analysis eleven GA oxidase were found highly active in the production of the jute GA. The four important genes for jute GA production may be CoGA20ox7, CoGA3ox2, CoGA2ox3, and CoGA2ox5 based on their expression. CesA1/10, CesA3, CesA4, CesA5/6/2/9, CesA7, and CesA8 (Honi *et al*., 2020).

2.3 Identification of cellulose synthase family genes of jute

The bas fibers of jute (*Corchorus spp.*) support the stem mechanically and because of their high cellulose content, which is more than 65%, they are utilized in the textile and composite industries. Ten cellulose synthase genes (CesA1, CesA2, CesA3, CesA4, CesA5, CesA6, CesA7, CesA8, CesA9, CesA10) were identified from both *Corchorus capsularis* and *Corchorus olitorius*. According to the transcriptome and Real-time PCR analysis of fiber cells and seedling stage, the genes linked to fiber cells are significantly expressed in secondary cell wall associated genes, however, primary cell wall associated genes are highly expressed in seedling stages (Ahmed et al., 2023).

2.4 Identification of expansin, CDPK, FLAs, Co/ERF, PLD, SnRK2, SOD gene family

26 expansin genes were identified in *Corchorus olitorius* genome which are associated with cell wall loosening protein and essential for fibre cell development (Hossain et al., 2022). These genes are grouped into four subfamilies named 20 CoEXPA, 2 CoEXPB, 1 CoEXLA and 3 CoEXLB. Five expansin genes were permanently expressed in bark tissues that means they are associated with jute fiber biosynthesis.

CDPK genes (Calcium Dependent Protein Kinases) are essential for protective environmental stresses. Using different bioinformatics tools 16 and 18 CDPK genes were identified in both *Corchorus olitorius* and *Corchorus capsularis* respectively (Ahmed et al., 2020).

In addition, nineteen Fasciclin-like arabinogalactan proteins (FLAs) that play a significant role in plant growth and development genes are identified in *Corchorus olitorius* genome (Hossain *et al*., 2020). Moreover, 119 Co/ERF genes were identified in *Corchorus olitorius* genome that are essential for jute plant growth, development and stress response (Kabir et al., 2021). Again, 12 and 11 Phospholipase D (PLD) genes were identified in *Corchorus capsularis* and *Corchorus olitorius* respectively. These are crucial for plant stress responses (Sadat et al., 2022). Sucrose non-fermenting-1 (SNF1)-related protein kinase 2 (SnRK2) gene *Corchorus sp* (Ahmed et al., 2023). Superoxide dismutase (SOD) is an antioxidant, that was identified in jute (Mridula et al., 20240

The process of gene identification is demonstrated in Figure 3.

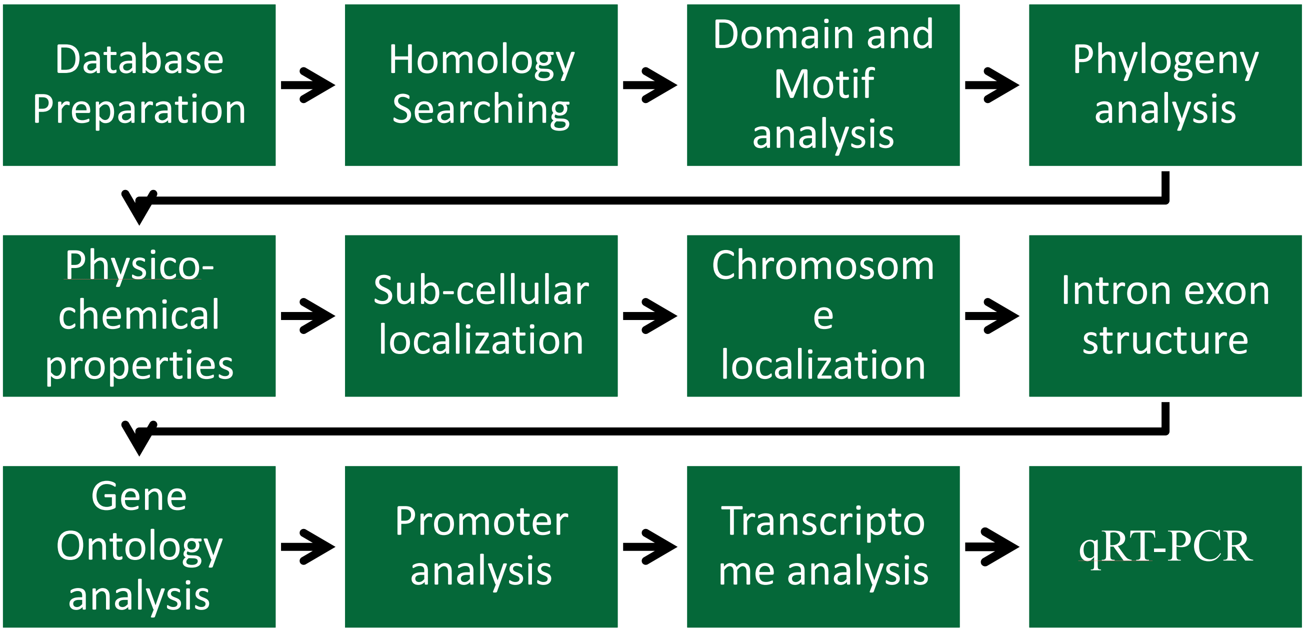

Figure 3: The prcess of genome wide identification of jute.

2.5 CRISPR cas-9 genome editing in both *Corchorus sp.*

Caffeoyl-CoA 3-O-methyltransferase (CCoAOMT) is a gene family responsible for lignin biosynthesis. Lignin is a component that lowers the fiber quality of jute species. 6 CCoAOMT genes were identified in both *Corchorus olitorius* and *Corchorus capsularis* through *in silico* approaches. Then identified genes were selected for knockout experiments using CRISPR cas 9 gene editing technology (Akhter et al., 2023).

2.6 *In vitro* regeneration protocol of *Corchorus sp.*

Using Murashige Skoog (MS) media supplemented with 2.5 mg/L BA + 0.5 mg/L IAA treatment, plantlets of *Corchorus olitorius var. O-4* were regenerated for further genetic improvement (Afroz et al., 2025). Furthermore, plantlets of *Corchorus olitorius var. O-9897 were* regenerated using MS media with 2.5 mg/L BA + 0.5 mg/L IAA (Hossain et al., 2024).

3. CHALLENGES

CRISPR cas 9 genome editing system, transgenesis, RNA interference suppresses specific gene expression, gene silencing, protein engineering, and using molecular marker in breeding process are several efficient methods for the development of different species (Gao, 2021). However, only a little work has been accomplished via this technique for the development of the jute in Bangladesh. Financial constraints and lack of improved infrastructure facilities are the common challenges for the adaptation of improved technologies. As a result, so many high yielding, short duration cannot be developed. As a result, farmers must depend on different inorganic fertilizers and pesticides to combat various abiotic stresses. In some regions of farmers are unwilling to cultivate jute due to its long cultivation period, farmers of southern region often can't grow much jute because of high salinity soil. Moreover, northern region suffers from drought while cultivating jute.

4. RECOMMENDATION AND CONCLUSION

Overall, Jute fiber is a biodegradable and ecofriendly fiber, which has immense potential. The integration of different conventional and biotechnological approaches such as, genome wide identification of different genes, mutation breeding, transgenesis, *in vitro* regeneration of plantlets, CRISPR cas 9 genome editing has been undertaken to enhance its cultivation. These approaches not just improve fiber yield, also it contributes to the development of a sustainable environment.

strong collaborative approach is needed among scientists, policymakers and stakeholders, which is essential for the further improvement of jute. It is also a necessary step to create awareness among farmers so that they become interested in cultivating modern jute variety and practicing conserved agriculture.

Authors contribution

This work was carried out in collaboration among all authors. All authors read and approved the inal manuscript.

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