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Morpho-biochemical and molecular insights of fibre quality in jute: A review update

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ABSTRACT

Jute fibre is an inexpensive, biodegradable and eco-friendly natural bast fibre. Jute fibre has both traditional and industrial applications. The commercial demand for improved jute fibre is gaining importance to replace the synthetic fibres. The use of jute fibre is restricted because of its high lignin content and low cellulose content. As evident from published literatures, both the classical and molecular approaches have been used to improve the fibre quality. The strength, fineness, and luster of the fibre are considered as the fibre quality parameters. During the recent past, researchers reported the key genes and enzymes that are playing a major role in the lignin pathways like Monolignol pathway, Shikimate-aromatic amino acid pathway and cellulose biosynthesis pathway. A total of 38 isoforms of 16 genes in upstream of Shikimate-aromatic amino acid pathway and 43 isoforms of 10 genes in the downstream of Monolignol pathway have been reported. Down regulations of cinnamyl alcohol dehydrogenase, coumarate 3-hydroxylase, ferulate 5-hydroxylase, cinnamate 4-hydroxylase and caffeic acid O-methyltransferase genes associated with lignin biosynthesis have been reported in substantial reduction of the lignin content in jute. In cellulose biosynthesis, the major identified gene families are Sucrose synthase, Uridine diphosphate glucose pyrophosphorylase and Cellulose synthase (CesA), having important roles in fibre formation. The present review is aimed to present a detailed morpho-biochemical and molecular insights of jute fibre quality that will help the breeders to fix the breeding plan in enhancing the quality of jute fibre.

***Keywords*:** Cellulose, fibre quality, jute, Monolignol, Shikimate-aromatic amino acid.

Jute is a dicotyledonous plant which is the second most important cultivated fibre crop after cotton (Begum *et al*., 2013). It was previously classified to Tiliaceae family but presently reclassified into Malvaceae family (Adeyinka and Akintade, 2015). Jute belongs to genus *Corchorus* and the only two cultivated species are *Corchorus olitorius* and *Corchorus capsularis* (Finlow, 1939). The chromosome numbers of these two species are same, 2n=14 (Datta *et al*., 1975; Maity *et al*., 2012), but the observed ranges of the mitotic chromosome sizes in *Corchorus olitorius* and *Corchorus capsularis* are 1.3-2.7 µm and 1.7-3.7 µm respectively (Maity and Datta, 2009). Though jute is mainly a self-fertilized crop (Fryxell, 1957), sometimes natural outcrossing happens (Basak and Paria, 1975; Mir *et al*., 2009). The estimated genome size of *Corchorus olitorius* is ~448 Mb and *Corchorus capsularis* is ~404 Mb (Islam *et al*., 2017). The major jute producing countries are India, Bangladesh, China, and Thailand. India contributes more than 50% raw jute and more than 40% jute goods of the global need (https://www.jute.com). In India, West Bengal accounts for nearly 75% of total raw jute production (Price Policy for Jute, 2018-19). Jute is produced in the tropical, subtropical and equatorial zones in the hot – rainy season (Roy and Lutfar, 2012). 70-74% relative humidity (Maity *et al*., 2012) and 24°C-37°C temperature are favorable for jute cultivation (Roy and Lutfar, 2012). In recent past, cheap, environmental friendly, biodegradable and renewable jute fibre has been replaced by petrochemical synthetic fibre which is more costly and produces greenhouses gases (Meshram and Palit, 2013a). The lignocellulosic jute fibre (Chakrabarti *et al*., 1991) is mainly used for making clothes, ropes, packaging materials, gunny bags, jute mats, carpets, jute yarn etc. (Maity *et al*., 2012; Islam, 2019). Other than the traditional uses, jute fibres are also used for making the jute geotextiles for controlling the soil erosion, for making composites, pulps and papers (Ranganathan, 1994). Jute leaves are utilized as food in different countries. Due to some medicinal properties, the products of jute leaf have beneficial effects in the treatment of several diseases (Islam, 2013). The primary by-product jute stick is used for producing charcoal (Banerjee and Mathew, 1985) besides being used as fuel in rural areas.

Corchorus olitorius is commonly known as *"tossa* jute" where the word *"tossa"* indicates "lustrous golden shine" (Kundu, 1956; Roy *et al*., 2006). *Corchorus capsularis* is called as "*White* jute" because of it's white

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colour fibre (Kundu, 1956). The common name of *Corchorus capsularis* is also "Tita (bitter) pat" because of the presence of bitter glucoside which causes bitterness and it is not found in *Corchorus olitorius* (Finlow, 1939; Ghose *et al*., 1948). There are some controversies on the origin of the two jute species (Kundu *et al*., 2013). Earlier, it was believed that the centre of origin of "*tossa*" jute was Africa and the centre of origin of white jute was Indo-Burma region, including South China (Kundu, 1956). Later, based on the chloroplast and nuclear microsatellites of the two species, it has been assumed that both species have originated in Africa (Kundu *et al*., 2013). The *"tossa"* jute produces stronger, softer and more lustrous fibre (Kundu, 1956) which is more preferred (Maiti *et al*., 2010). It was reported that the lignin content of *Corchorus capsularis* fibre was lesser than *Corchorus olitorius* fibre and the cellulose content of *Corchorus capsularis* fibre was more than *Corchorus olitorius* fibre (Islam *et al*., 2017). Moreover, *"tossa"* jute is also more tolerant to pest and diseases than white jute (Roy *et al*., 2006).

The improvement of the fibre crops mainly focuses on the yield and quality of the fibre (Maiti and Chakravarty, 1977). Jute fibre is classified under the group of bast fibre together with kenaf, hemp, ramie and flax (Zimniewska and Wladyka-Przybylak, 2016; Guerriero *et al*., 2017). It is basically sclerenchyma cell type with secondary cell wall developed in the bast of the stem (Rowell and Stout, 2007) which provides mechanical support to the plant (Meshram and Palit, 2013a). The fibre cell development is genetically controlled (Sengupta and Palit, 2004) and phenotypic evaluation is crucial for understanding of the genetic variation of the fibre crops (Ghosh *et al*., 2013). The jute fibre is composed of cellulose, hemicelluloses, lignin, pectin and fat/wax (Zimniewska and Wladyka-Przybylak, 2016). The higher (11.8-12.9%) lignin content makes the jute fibre course and stiff (Zimniewska and Wladyka-Przybylak, 2016) which also creates negative effect in the separation of fibre and in the quality and it is also negatively correlated with fibre fineness (Chakraborty *et al*., 2015). The cellulose content (59-71%) (Zimniewska and Wladyka-Przybylak, 2016) of jute fibre is also lower than other natural fibre (Zhang *et al*., 2015) and low cellulose content restricts the raw jute fibre from spinning (Wang *et al*., 2008).

The morphological parameters *viz*. plant height, basal diameter, green weight, stick weight, nodes per plant and days to 50% flowering are positively correlated with fibre yield as evident from published literatures (Rahman *et al*., 2009; Al-Mamun *et al*., 2010; Pervin and Haque, 2012; Ghosh *et al*., 2013). On the contrary, fibre strength, fineness, and luster of the fibre were reported as quality parameters of plant fibre (Meshram and Palit, 2013a). It was reported that, fiber bundle with less cross sectional area was required for producing finer fiber (Maiti *et al*., 2010). The fibre fineness is negatively correlated with cell wall thickness (Meshram and Palit, 2013a). For the improvement of the physical properties of jute fibre fabric, different enzymes (like cellulase, pectinase, xylanase, laccase, laccase/mediator system) and different chemical treatments were performed (Chakrabarti *et al*., 1991; Chattopadhyay *et al*., 2000; Karaduman *et al*., 2013; Dong *et al*., 2016). Some factors like soil, jute genotypes and jute retting affect the quality of the jute fibre (Das *et al*., 2014). Quantitative trait loci (QTL) analysis was used for studying the genetics of different fibre yield and fibre quality traits of jute (Das *et al*., 2012). The morphological traits are quantitative and environment sensitive in nature (Satya and Chakraborti, 2015). So, the molecular insights in the fibre quality should be explored.

For improving fibre fineness, it is desired to develop the jute fibre with low lignin content (Chakraborty *et al*., 2015) coupled with high cellulose content (Zhang *et al*., 2015). It necessitates the identification of the genes involved for lignin and cellulose biosynthesis in jute. In lignin biosynthesis, expansions of four gene families [*4-Coumarate:CoA ligase* (*4CL*), *Cinnamoyl-CoA reductase* (*CCR*), *Caffeoyl-CoA O-methyltransferase* (*CCoAOMT*) and *caffeic acid O-methyltransferase* (*COMT*)] were observed in the genomes of jute compared to flax. It was reported that the genes encoding transcription factors like -*APL*, *HAT22*, *WOX4* and the *TD1F* signal peptide played significant roles in the differentiation of fibre (Islam *et al*., 2017). Monolignol pathway and Shikimate-aromatic amino acid pathway are the two pathways associated with the lignin biosynthesis (Chakraborty *et al*., 2015). However, very less genomic resources are available for jute, so a reference bast transcriptome is important. 43 isoforms of 10 genes of downstream Monolignol pathway and 38 isoforms of 16 genes of upstream Shikimate-aromatic amino acid pathway were identified. In case of Monolignol pathway, highest numbers of isoforms were discovered for *Hydroxycinnamoyl-CoA:shikimate/ quinate hydroxycinnamoyltransferase (HCT)* and *cinnamyl alcohol dehydrogenase* (*CAD*). In the Shikimate aromatic amino acid pathway, highest numbers of isoforms (6-9 each) were discovered for *3-dehydroquinate dehydratase/shikimate dehydrogenase* (*DHD-SDH*), *arogenate/ prephenate dehydratase* (*ADT-PDT*) and *phenylpyruvate aminotransferase* (*PPY-AT*). By quantitative reverse transcriptase polymerase chain reaction (qRT-PCR) analysis it was observed that,

Corchorus capsularis phenylalanine ammonia-lyase 1 (*CcPAL1*) was co-downregulated with different genes of the upstream shikimate pathway in the bast tissue of deficient lignified phloem fibre (*dlpf*) mutant at an early growth stage. It has been also stated that *CAD* will be a good target for the development of jute fibre with low lignin (Chakraborty *et al*., 2015). Down-regulations of monolignol biosynthetic genes of jute - *Coumarate 3-hydroxylase* (*C3H*), *ferulate 5-hydroxylase* (*F5H*) (Shafrin *et al*., 2015) and *cinnamate 4-hydroxylase* (*C4H*), *caffeic acid O-methyltransferase* (*COMT*) (Shafrin *et al*., 2017) showed lower lignin content in transgenic jute.

In the cellulose synthase complex, cellulose is synthesized. Up-regulations of two Secondary cell wall (SCW) synthesis specific genes *Cellulose synthase* A4 (*CesA4*) and *CesA7* in fibre cells suggested that these genes were associated with SCW cellulose deposition (Islam *et al*., 2017). Higher levels of expression of some unigenes of *CesA* complex in stem bast indicated that they might play potential role in cellulose biosynthesis in jute (Zhang *et al*., 2015).

The present review is aimed to present detailed morpho-biochemical and molecular insights of jute fibre quality that will help to breeders to fix the breeding plan in enhancing the quality of jute fibre.

CHEMICAL PROPERTIES OF JUTE FIBRE

Jute fibre is developed in the bast regions of the stem of the plant (Rowell and Stout, 2007). The fibre cells belong to sclerenchyma cell types with secondary cell wall which give mechanical support to the plant and there are some molecules (cellulose, hemicelluloses, lignin, proteins) found in the secondary cell wall and their proportion controls variation in the mechanical properties of the cells (Meshram and Palit, 2013a). From the protophloem, a layer of primary fibre is generated in the growing part of the stem. Due to cambial activity, secondary phloem fibre is developed (Rowell and Stout, 2007). Range of length of one fibre cell is 0.75-5 mm and range of width of one fibre cell is 10-25 µm (Meshram and Palit, 2013a). Jute fibre contains cellulose (59-71%), hemicelluloses (12-13%), pectin (0.2-4.4%), lignin (11.8-12.9%) and fat/wax (0.5%) (Zimniewska and Wladyka-Przybylak, 2016). One fibre bundle contains 8-9 lowest numbers of cells to 20-25 highest number of cells and this difference is a reason for the diversity of the fibre in respect of physical as well as mechanical properties and the quality. Jute fibre is harvested mostly 110 to 120 days from sowing when the plant becomes mature (Roy and Lutfar, 2012). When the jutes are in the small pods, that stage is the perfect stage for harvesting (Kundu, 1956). Jute fibre is separated and extracted from the stem by a process called jute retting which is carried out chemically or with the help of microorganisms (Das *et al*., 2014).

There are noted limitations of jute fibre. The compatibility between the hydrophobic polymer matrix and the hydrophilic fibre is weak and due to these weak interfaces, low quality composites are produced. The jute fibre composites have less thermal stability (Gon *et al*., 2012). Jute fibre is coarse, stiff, the cellulose content and grip are low which restricts the raw jute fibre from spinning (Wang *et al*., 2008). Jute fibre contains more lignin than the other types of fibre like flax and ramie (Islam *et al*., 2017), for this reason jute fibre is more stiff and coarse than the other types of fibre (Zimniewska and Wladyka-Przybylak, 2016). The high lignin content is the limitation for not being utilized in non-textile products (Zimniewska and Wladyka-Przybylak, 2016). High lignin content creates negative effect in fibre separation and it decreases fibre quality (Chakraborty *et al*., 2015).

EFFECTS OF ENZYMATIC TREATMENTS ON JUTE FIBRE

Different types of chemicals are used to improve the physical properties of jute fibre. For making fine and pulpy fibre, some extracellular fungal enzymes are used which contain cellulase, pectinase and xylanase. It was reported that treatment of 1mM Ethylenediam inetetraacetic acid (EDTA) for 1 h at 30°C enhanced 5-8% brightness and 6-7% fineness of jute fibre. Fibre fineness was made better with the application of a mixed enzyme (including cellulase, pectinase and xylanase) on the fibre which was treated with EDTA. The combined application was less effective than the stepwise use of EDTA followed by enzyme because a part of tannin was removed for the pretreatment with EDTA which restricted the enzyme's function (Chakrabarti *et al*., 1991). The pure jute fabrics treated with cellulase enzyme (Biosoft-P) were reported to minimize the numbers of hair on the fabric and also produced better fabric in respect of softness (Chattopadhyay *et al*., 2000). The effects of treatment of pectinase, laccase, cellulase and xylanase enzyme solutions and Sodium hydroxide (NaOH) on the jute fiber fabrics were analyzed. These enzymes removed the pectin, hemicelluloses and lignin molecules from the bundle interface of the fibre which decreased the fiber diameter and thus enhanced the fiber aspect ratio. A greater fiber-matrix interface area was produced due to application of enzymes, which made better fiber-matrix adhesion and better mechanical properties of the composites (Karaduman *et al*., 2013). The fragments of fibre from jute fabrics were treated with laccase, laccase/mediator systems or multiple-enzyme synergisms prior to the fibre membrane preparation. It was observed that

the application of laccase enhanced mechanical properties as well as the surface hydrophobicity of the prepared fibre membranes. It happened because laccase mediated the cross-coupling of lignins with the ether bonds. The combination of xylanase/laccase and cellulase/laccase applications increased the mechanical properties and the surface hydrophobicity of the fibre membranes of jute (Dong *et al*., 2016).

MORPHOLOGICAL DESCRIPTIONS RELATED TO FIBER YIELD AND FIBER QUALITY

The fibre content in jute differs approximately 5-7% of overall weight of plants which are harvested (Chakraborty *et al*., 1996). The density of jute fibre is 1.3 g/cm^3 (Gon *et al*., 2012). It is important to study the yield as well as quality parameters of the fibre for improving the fibre crops through breeding programs (Maiti and Chakravarty, 1977). The fibre cell developmental process is controlled genetically (Sengupta and Palit, 2004). So characterization of genetic variation of the germplasm of the fibre crops is essential to improve the fibre crops genetically. Phenotypic evaluation helps to understand the genetic variation of the germplasm (Ghosh *et al*., 2013). Fineness of the fibre is the most important factors which affects spinnability of the fibre (Grishanov *et al*., 2006).

It was reported that the quality parameters of plant fibre were fibre strength, fineness, and luster of the fibre (Meshram and Palit, 2013a). A comparative study of the different components of fibre yield and quality was performed. Based on the quality parameters, the fibre quality of *"tossa"* jute and white jute were classified in the best quality groups (Maiti and Chakravarty, 1977). It was reported by many workers that the yield of the jute fibre is positively correlated with several morphological parameters *viz* plant height, basal diameter, green weight (green weight with leaves and green weight without leaves), stick weight and nodes per plant (Rahman *et al*., 2009; Al-Mamun *et al*., 2010; Pervin and Haque, 2012). The characterization of different agronomic traits of 63 jute genotypes was performed including both jute species. It was observed that fibre yield was positively correlated to plant height at average flowering (0.72), fresh weight (0.90), days to 50% flowering (0.60) and plant base diameter (0.74) but fibre yield was negatively correlated with leaf angle (-0.52) (Ghosh *et al*., 2013). It was stated that there was a positive correlation of fibre weight with plant height, node number, fibre fineness, basal diameter, stick weight and fibre percentage but fibre weight was negatively correlated with fibre strength (Das and Kumar, 2016).

It was reported that there was a positive correlation between the structural parameters of fibre bundles (number of cells/ fibre bundle, area of fibre bundle, area of fibre bundle minus lumen area) and fibre filament fineness (Majumdar, 2002). Some parameters were identified for improving the fibre quality of bast fibres of secondary origin like jute which were cross section area of fibre bundle, surface structure of the fibre bundle and ultimate fibre cells. For producing fine fibre, fibre bundle with minimal cross sectional area is required. Fibre bundle with uniform surface is needed for improving the textile quality. Long ultimate fibre cells and fibre cell tips increase the strength of the fibre (Maiti *et al*., 2010). By using a mutant library of *Corchorus olitorius* and JRO 632 as control, it was stated that, though lignin might be required for the fibre cell's maturation but the fibre quality characters like fibre strength and fibre fineness were not affected by lignin (Kundu *et al*., 2012). By using several jute varieties including low lignin mutant, *dlpf* [Indian National Germplasm Register (INGR) No. 04107] and its lignin sufficient parent (JRC 212) and by determining the lignin content as well as the fibre fineness, it was reported that, cell wall thickness was positively correlated with lignin and the fibre fineness was negatively correlated with cell wall thickness as well as lignin content (Meshram and Palit, 2013a).

FACTORS AFFECTING THE FIBER QUALITY

Some factors were identified which affect the quality of the fiber of jute which were quality of soil, jute genotype and retting of jute (Das *et al*., 2014). It was stated that sandy soil provides the coarser and light body fibers and superior quality fiber is produced from clay-loam soils with silt (Ahmed and Nizam, 2008; Das *et al*., 2014). Two types of retting process are practiced for separating and extracting the fiber from plant tissue which are chemical retting and microbial retting. For producing good quality fiber, proper retting process is essential prerequisite (Ahmed and Akhter, 2001). Xylanase, pectinase and cellulase are the three enzymes which are the major factors for affecting the fiber quality. Polygalacturonase and pectine lyase are the two pectinolytic enzymes which play crucial roles in retting process. Cellulase breaks down the strength of the fiber. Fiber becomes smooth by the activity of xylanase. It is important to choose the microorganisms for retting with low cellulase activity and high pectinase and xylanase activity for improving the fiber quality (Das *et al*., 2014). It was stated that a microbial retting consortium along with bacterial strains having high pectinolytic efficiency was potential for lowering the time of retting and improving the quality of fibre. Genomic analysis of three bacterial strains (PJRB 1, 2 and 3) of the consortium was performed, the estimated sizes of the genome of the strains were ~3.8 Mb and the numbers of protein coding genes were 3729-4002. Based on the phylogenetic and structural characteristics of the pectate

Table 1: Genes and enzymes involved in monolignol pathway and shikimate-aromatic amino acid pathway of jute

No.	Name of the gene/ enzyme	Function of the enzyme	Effect of the gene on the fibre	References
1.	*PAL*	Deamination of phenylalanine is catalyzed by *PAL* for producing cinnamic acid.	In the bast tissue of *dlpf* mutant jute, co-downregulation of *CcPAL1* was reported along with different genes of upstream shikimate pathway at an initial growth stage and at the later stage of growth, the expression level was deteriorated to the normal level.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Islam *et al*., 2017).
2.	*C4H*	*C4H* catalyzes the first hydroxylation of *trans*-cinnamate. *C4H* helps cinnamate to convert into *p*-coumarate.	Using hp-RNA based vector, *C4H* gene was downregulated and lower lignin content was observed in the transgenic jute plants compared to the non-transgenic lines.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Islam *et al*., 2017; Shafrin *et al*., 2017).
3.	*C3H*	*C3H* helps to form caffeoyl shikimic/quinic acid from *p*-coumaroyl shikimic/quinic acid.	Using artificial microRNA method, *C3H* gene was downregulated in jute and lignin content observed in transgenic lines was lower than the non-transgenic lines.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Shafrin *et al*., 2015; Islam *et al*., 2017).
4.	*4CL*	Hydroxycinnamate is activated by *4CL* which is used to form *p*-coumaroyl CoA.	In the normal jute plant, depletion in the expression level of *4CL* was observed at the non-fibre forming (non-FF) stage compared to the fibre forming (FF) stage. In the 'soft stem' mutant plant, the expression levels at the two stages were insignificant compared to the normal jute plant.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Samanta *et al*., 2015; Islam *et al*., 2017).
5	*HCT*	*HCT* creates an influence whether *p*-coumaroyl CoA will be used in flavonoid or lignin biosynthesis.	Expressions of the *HCT* genes were observed in both *Corchorus olitorius* and *Corchorus capsularis*.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Islam *et al*., 2017).

Contd..

Table 1 Contd..

No.	Name of the gene/ enzyme	Function of the enzyme	Effect of the gene on the fibre	References
6	*CCR*	*CCR* is used to convert the feruloyl CoA and *p*-coumaroyl CoA into coniferaldehyde and *p*-coumaraldehyde respectively.	It was reported that the *CCR* was expressed more in the normal jute than the 'soft stem' mutant jute.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Samanta *et al*., 2015; Islam *et al*., 2017).
7	*CCoAOMT*	*CCoAOMT* forms feruloyl CoA from Caffeoyl CoA.	Full length of cDNA of *CCoAOMT* gene from jute was cloned, modified and transformed in *Arabidopsis thaliana*. The lignin content of transgenic plants was higher than the non-transgenic.	(Zhang *et al*., 2014; Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Islam *et al*., 2017).
8	*CAD*	The final reduction of cinnamaldehydes is catalyzed by *CAD* to their corresponding alcohols, which are then oxidized and used to produce lignin polymers.	In the bast tissue of *dlpf* mutant jute, downregulation of *CcCAD7* was observed and *CAD* was predicted to be as a target for generating jute fibre with low lignin content.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Islam *et al*., 2017).
9	*F5H*	Coniferaldehyde is converted to 5-OH-coniferaldehyde by *F5H*.	*F5H* gene was downregulated in jute using artificial microRNA method and the transgenic lines showed lower lignin content than the non transgenic lines.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Shafrin *et al*., 2015; Islam *et al*., 2017).
10	*COMT*	*COMT* plays an important role for producing S lignin.	*COMT* gene was downregulated using hp-RNA based vector and the transgenic jute plants showed lower lignin content than the non-transgenic lines.	(Hao and Mohnen, 2014; Chakraborty *et al*., 2015; Shafrin *et al*., 2017; Islam *et al*., 2017).
11	*DAHPS*	It catalyzes an aldole condensation of PEP and E4P to form *DAHP*.	In the bast tissue of *dlpf* mutant jute, overexpression of *CcDAHPS2* was observed at 30 days after germination (DAG), whereas at 60 DAG, it was underexpressed.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).

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Table 1 Contd..

No.	Name of the gene/ enzyme	Function of the enzyme	Effect of the gene on the fibre	References
12	*DHD-SDH*	The dehydration of 3-dehydroquinate to 3-dehydroshikimate occurred where the first double bond in the ring is made and the reversible reduction of 3-dehydroshikimate into shikimate occurred using Nicotinamide adenine dinucleotide phosphate hydrogen (NADPH) and these two reactions are catalyzed by *DHD* and *SDH*.	Under expression of *CcDHD-SDH2* was reported in the bast tissue of *dlpf* jute at 30 DAG.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
13	*ADT –PDT*	Decarboxylation and dehydration of prephenate to phenylpyruvate is catalyzed by *PDT* and arogenate is converted to Phe by *ADT*.	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
14	*PPY-AT*	A reversible transamination between phenylpyruvate and Phenylalanine is catalyzed by PPY-AT where PLP is used as a cofactor.	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
15	*DHQS*	DAHP is converted to 3-dehydroquinate by *DHQS*.	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
16	*EPSPS*	It transfers the enolpyruvyl moiety of PEP to the 5-hydroxyl position of shikimate 3-phosphate and formation of EPSP is catalyzed by *EPSPS*.	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
17	*SK*	The phosphorylation of the C3 hydroxyl group of shikimate is catalyzed by *SK* to form shikimate 3-phosphate where ATP is used as cosubstrate.	In the bast tissue of *dlpf* fibre mutant jute, under expression of *CcSK1* was observed at 30 DAG whereas at 60 DAG, *CcSK1* was over expressed.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).

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Table 1 Contd..

No.	Name of the gene/ enzyme	Function of the enzyme	Effect of the gene on the fibre	References
18	*CS*	Chorismate is produced from EPSP by *CS*.	*CcCS1* was under expressed at 30 DAG in the bast tissue of *dlpf* mutant jute.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
19	*PPA-AT*	A reversible transamination between prephenate and arogenate is catalyzed by this enzyme with *PLP* as a cofactor.	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
20	*ADH*	Arogenate is converted to Tyrosine by *ADH*.	In the core tissue of Hemp (*Cannabis sativa* L.) Chamaeleon variety, higher expression of *ADH* isoform 2 was observed.	(Van Den Broeck *et al*., 2008; Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).
21	*IGPS*	The irreversible conversion of 1-(*o*-carboxyphenylamino)-1-deoxy-ribulose 5-phosphate (CdRP) to indole-3-glycerol phosphate is catalyzed by *Indole-3-glycerol phosphate synthase* (*IGPS*).	Not characterized for Jute Fibre.	(Maeda and Dudareva, 2012; Chakraborty *et al*., 2015).

Table 2: Genes involved in cellulose biosynthesis of jute

No.	Name of the gene	Function of the gene	Effect of the gene on the fibre	References
1	*UGPase*	*UGPase* is a precursor of catalytic cellulose-uridine diphosphate glucose synthesis.	Higher level of expression was observed in the stem bast of jute.	(Zhang *et al*., 2013; Zhang *et al*., 2015).
2	*CesA*	In the development of plant cell wall cellulose, the catalytic subunits of *CesA* act as central catalysts.	Expression level was high in the stem bast of jute.	(Zhang *et al*., 2015).
3	*SuSy*	*Susy* is an integral component of the cellulose synthesis machinery which is also required for starch and sucrose metabolism.	Highly expressed in stem bast of jute.	(Zhang *et al*., 2015).

Contd..

Table 2 Contd..

No.	Name of the gene	Function of the gene	Effect of the gene on the fibre	References
4	*CSL*	There is a similarity between *CSL* and *CesA* gene. *CSL* consists conserved motifs required for nucleotide-sugar binding and catalytic activity of processive glycosyltransferases.	The expression level of the unigenes of *CSL* displayed low expression in stem bast compared to *CesA*.	(Delmer, 1999; Zhu *et al*., 2003; Zhang *et al*., 2015).
5	*KOR*	*KOR* provides the chains of cellulose for the termination of microfibrils.	The expression level of the unigenes of *KOR* was lower than the unigenes of *UGPase*, *SuSy* and *CesA* in stem bast of jute.	(Zhang *et al*., 2015).
6	*COBRA*	In the orientation of deposition of cellulose microfibrils, *COBRA* participates.	Maximum unigenes of *COBRA* showed lower level of expression in the stem bast than the other gene families involved in cellulose biosynthesis.	(Zhang *et al*., 2015).

lyase proteins, it was revealed that the PJRB strains were closely related with *bacillus* (Datta *et al*., 2020).

IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) FOR YIELD AND FIBRE QUALITY TRAITS IN JUTE

The first QTL interval mapping of jute (*Corchorus olitorius*) was conducted for fibre yield and fibre quality traits in jute where using single locus analysis, 21 QTLs for fibre yield and 1 QTL for fibre fineness were identified and using two locus analysis, 22 QTLs for fibre yield, 5 QTLs for fibre fineness; 6 QTLs for Fibre strength were recognized. However, 7 of the QTLs for fibre yield and 1 QTL for fibre fineness were identified by both methods, so the numbers of QTL identified were 36 QTLs for fibre yield, 5 QTLs for fibre fineness and 6 QTLs for Fibre strength. The molecular markers associated with the identified traits may be used in marker assisted selection for developing jute cultivars with high fibre yield and good quality (Das *et al*., 2012). The first complete microsatellite genetic map of *Corchorus olitorius* were reported using an F_6 recombinant inbred population. Screening of 403 microsatellite markers were performed and 82 microsatellite markers were mapped on the 7 linkage groups (LGs) covering a total genetic distance of 799.9 cM, with an average marker interval of 10.7 cM. 26 definitive QTLs for bast fibre quality, yield and yield-related traits were identified by Genome wide non parametric single marker analysis along with multiple QTL models (MQM) mapping (Topdar *et al*., 2013). RAD (restriction-site associated DNA) sequencing strategy was used for identifying genome wide Single nucleotide polymorphisms (SNP)s and for constructing a dense linkage map using an intercross F_2 population in *Corchorus olitorius*. QTL mapping based on the $F_{2:3}$ phenotypes identified 9 QTL across the 2 environments. The QTL for Fibre content was coincident with 1 QTL each for Fibre yield, Plant height, Root weight and Stem base diameter on top of a single SNP (C/T) marker at 40.2 cM on Linkage group 1, each accounting for around 7–11 % of the phenotypic variance. 2 QTL associated in repulsion one each for Plant height and Stem base diameter with varying degrees of over-dominance, were linked with 2 single SNP (C/T) markers on Linkage group 2, each accounting for around 17–18 % of the phenotypic variance (Kundu *et al*., 2015). Five QTLs were identified for bast fibre cellulose in *Corchorus capsularis* (Niyitanga *et al*., 2019)

BIOSYNTHESIS PATHWAYS RELATED TO FIBRE QUALITY IN JUTE

Lignin biosynthesis

Lignin belongs to a group of aromatic polymers which are responsible for the rigidness of the cell wall (Vanholme *et al*., 2010). For the production of bast fibre, lignification of the wall of the fibre is required (Kundu *et al*., 2012). Lignin is produced from the phenyl-

propanoid pathway of plants (Bonawitz and Chapple, 2010). The structure and composition of lignins are variable whereas cellulose or any protein consists a regular structure (Ralph *et al*., 2004). It was stated that formation of lignin polymer occurred through dehydrogenative polymerization of three hydroxycinnamyl alcohols (monolignols), namely *p*-coumaryl alcohol, sinapyl alcohol and coniferyl alcohol which further results in some units such as *p*-hydroxyphenyl (H), syringyl (S), and guaiacyl (G) units (Bonawitz and Chapple, 2010; Vanholme *et al*., 2010; Chakraborty *et al*., 2015). The biosynthesis of many lignins takes place by the incorporation of esterified monolignols into the lignification process (Sederoff *et al*., 1999). The three monolignols and the subunits of lignin can form bonds between them (Ralph *et al*., 2004). S/G/H ratio indicates the levels of the three lignin subunits. Mainly S/G ratio denotes the expression of lignin subunits because very inconsiderable amount of H subunit are found in woody species (Shafrin *et al*., 2017). The lignins made of S units are more susceptible to delignification than the lignins made of G units because the S unit rich lignins have less carbon-carbon bonds than the G unit rich lignins (Lapierre *et al*., 1999; Shafrin *et al*., 2017). If the S:G ratio is increased by changing the gene expression related to lignin biosynthesis, then cell wall will be easy to degrade (Lockhart, 2015).

There are associations of two pathways with lignin biosynthesis which are the Monolignol pathway and Shikimate aromatic amino acid (Chakraborty *et al*., 2015). Enzymes belonging to several large protein families with the members commonly known as isoforms (Wong *et al*., 2011) are recruited by these pathways (Chakraborty *et al*., 2015). The aromatic amino acids (L-Tryptophan, L-phenylalanine, and L-tyrosine) are acquired from shikimate pathway (Maeda and Dudareva, 2012). Shikimate pathway is also called chorismate biosynthesis pathway. In this pathway two metabolites, phosphoenolpyruvate (PEP) of the glycolysis pathway and D-erythrose 4-phosphate (E4P) of the non-oxidative branch of the pentose phosphate pathway are converted into chorismate (Tzin and Galili, 2010). The monolignol biosynthesis initiates with the deamination of phenylalanine, after that, hydroxylation reactions of the aromatic ring are occurred, followed by phenolic *O*-methylation and conversion of the side-chain carboxyl to an alcohol group (Boerjan *et al*., 2003). The enzymes involved in the shikimate aromatic amino acid pathway and monolignol pathways are 3-deoxy-D-*arabino*-heptulosonate *7-phosphate synthase* (*DAHPS*), *3-dehydroquinate synthase* (*DHQS*), *3-dehydroquinate dehydratase*/*shikimate dehydrogenase* (*DHD-SDH*), *shikimate kinase* (*SK*), *5-enolpyruvylshikimate 3-phosphate synthase* (*EPSPS*), *chorismate synthase* (*CS*), *anthranilate synthase* (*AS*), *chorismate mutase* (*CM*), *arogenate*/ *prephenate dehydratase* (*ADT-PDT*), *phenylpyruvate aminotransferase* (*PPY-AT*), *phenylalanine ammonia-lyase* (*PAL*), *cinnamate* 4-*hydroxylase* (*C4H*), *4-Coumarate*:*CoA ligase* (*4CL*), *prephenate aminotransferase* (*PPA-AT*), *arogenate dehydrogenase* (*ADH*), *Hydroxycinnamoyl-CoA*:*shikimate*/*quinate hydroxycinnamoyltransferase* (*HCT*), *Coumarate 3-hydroxylase* (*C3H*), *Caffeoyl-CoA O-methyltransferase* (*CCoAOMT*), *Cinnamoyl-CoA reductase* (*CCR*), *ferulate 5-hydroxylase* (*F5H*), *caffeic acid O-methyltransferase* (*COMT*), *cinnamyl alcohol dehydrogenase*/*sinapyl alcohol dehydrogenase* (*CAD*/*SAD*) (Maeda and Dudareva, 2012; Hao and Mohnen, 2014; Chakraborty *et al*., 2015). It was observed that *PAL* activity was more or less invariable in all the parts of the stem of *Corchorus capsularis* L. variety (JRC 212). In the lower part of the stem of the x-ray-induced mutant line (Accession number- CMU 0130), *PAL* content was not noticeable. In the wild type plant, the *PAL* activity was three to four times higher than the mutant plant in the middle and upper parts of the stem. The minimum *PAL* activity in the mutant jute than the normal plant indicated that there was a block upstream in the shikimate pathway, which reduced the lignin synthesis in the phloem parts of the plant. That mutant was named as *dlpf* (Sengupta and Palit, 2004).

Cellulose biosynthesis

Cellulose is a major component in secondary cell wall which is important for the strength of the fibre (Meshram and Palit, 2013b). Cellulose is a linear polymer of β-1,4-linked glucose molecules and the β-1,4-linked glucan chains made a crystalline microfibril by interacting with each other via hydrogen bond (Somerville, 2006; Meshram and Palit, 2013b). Cellulose biosynthesis occurs by some bacteria and prokaryotes (example: *Agrobacterium*, *Acetobacter*, *Rhizobium*), some fungi, cellular slime molds, amoebae, green algae and plants (Brown Jr., 2004). Though some organisms like some bacteria may live without synthesis of cellulose, but maximum vascular plants may need cellulose for living. Along with giving the strength, cellulose is also required to most of the plants to maintain the size, external form, division/differentiation potential of plant cells and direction of the plant growth (Saxena and Brown Jr., 2005). The synthesis of cellulose is occurred in the plasma membrane. The fibrils are built with plasma membrane complexes which are 30 nm diameter containing around of 36 subunits representing at least three types of related *CESA* proteins. The three

types of *CesA* proteins are needed for producing a functional complex (Somerville, 2006). A similarity was found between *CesA* gene and *cellulose synthase-like* (*CSL*) genes (Delmer, 1999). The cellulose content in bast fibre of jute is comparatively lower than other fibre like hemp, ramie and flax. For the improvement of jute fibre quality, it is required to increase the cellulose content (Zhang *et al*., 2015). 159 jute accessions were used and it was found that the mean cellulose content of *Corchorus olitorius* (52.17%) was lesser than the mean cellulose content of *Corchorus capsularis* (53.71%) (Zhang *et al*., 2017).

GENES AND TRANSCRIPTION FACTORS ASSOCIATED WITH FIBRE BIOGENESIS

Genes and transcription factors linked with lignin biosynthesis including monolignol pathway and shikimate aromatic amino acid pathway

The information of the genes which are related to fibre biogenesis of jute is not available enough but it is essential to improve the quality of the fibre. The functions of different genes and enzymes involved in monolignol pathway and shikimate-aromatic amino acid pathway of jute and their effects on jute fibre were described in Table 1. RNA-seq data from both seedlings and fibre cells of *Corchorus olitorius* and *Corchorus capsularis* revealed that the expressions of some genes, *Myb*/*SANT-like domain*, *PHD*-type, *Zinc finger* and *F-box domain cyclin-like proteins* were more in fibre cells than seedlings which specified that they had significant roles in the development of bast fiber. 6,077 upregulated and 6,809 downregulated genes for *Corchorus olitorius* and 7,695 upregulated and 7,809 downregulated genes for *Corchorus capsularis* were identified. The identified genes involved in the lignin biosynthetic pathway and phenylpropanoid pathway of jute fibre are- *PAL*, *4CL*, *C4H*, *C3H*, *CAD*, *F5H*, *HCT*, *CCR*, *CCoAOMT* and *COMT*. Among them, expansions of *4CL*, *CCR*, *CCoAOMT* and *COMT* gene families were observed in jute genomes based on the comparison with flax. It was stated that the genes which encode the transcription factors like - *APL*, *HAT22*, *WOX4* and the *TD1F* signal peptide, which are also involved in the starting process of vascular cambium and in the proliferation process, expressed greatly in fibre cell and these indicated that they play a significant role in differentiation of fibre (Islam *et al*., 2017).

Lower lignin content of jute is important for the commercial use of the fibre. Shikimate-aromatic amino acid and Monolignol pathway are linked with the biosynthesis of lignin. A transcriptome analysis of jute (*Corchorus capsularis* JRC-212) and its *dlpf* mutant were performed and the unigenes were annotated and mapped to 189 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. 38 isoforms of 16 genes of upstream shikimate-aromatic pathway with their sequence ranging from 515 to 2,749 bp and coding region lengths ranging from 73 to 670 aa in jute were identified. In the Shikimate-aromatic amino acid pathway, for *DHD-SDH*, *ADT-PDT* and *PPY-AT,* highest number of isoforms (6-9 each) were discovered. For *DAHPS,* two homologous isoforms were identified. Only one homologous isoform was identified for *DHQS*, *EPSPS*, *SK, CS*, *PPA-AT, ADH*, and *IGPS*. 43 isoforms of 10 genes of downstream monolignol biosynthesis pathway were also identified with their sequence ranging from 619-3567 bp and coding sequence length ranging from 119-778 aa. Six genes were found with more than one isoforms. Individually for *PAL* and *C4H*, three homologous isoforms were found. Highest numbers of isoforms were identified for *HCT* and *CAD*. For *CCoAOMT*, five isoforms and for *4CL*- two homologous isoforms were discovered. Only one homologous isoform was found for *CCR*, *COMT*, *F5H* and *C3H*. qRT-PCR analysis was performed and in the X-ray-irradiated true-breeding secondary phloic fibre-deficient mutant plants, co-downregulation of *CcPAL1* with various genes of the upstream shikimate pathway in bast tissues at early growth stage were observed. The downregulation of *CcCAD7* was observed in the secondary phloic fibre deficient mutant. Disruption of *CcCAD7* at the early growth stage was gone along with by co-upregulations of SCW specific genes *CcCesA7* and *Cc-fasciclin-like arabinogalactan 6* (*CcFLA6*) which was assumed to be involved in coordinating the S-layers' deposition in the xylan-type jute fibres. It was stated that for producing jute fibre with low lignin content, *CAD* could be used as target. Some bast related transcription factor families were also identified where *C3H*, *MADS*, *WRKY*, *NAC*, *FAR1*, *MYB-related*, *bHLH* and *PHD* were reported to be the most abundant and *C2H2*, *Orphans*, *SET*, *SNF2*, *HB*, *FHA*, *bZIP* and *AP2-EREBP* were the others (Chakraborty *et al*., 2015).

In monolignol biosynthesis pathway, which is one of the major biosynthesis pathway related with lignin biosynthesis, a number of genes are involved. It was reported that, by increasing few transgenic plants with the different gene constructs of monolignol pathway, genetic manipulation of lignin content could be done (Rastogi and Dwivedi, 2008). If the expression of any gene is reduced, then it is expected to have influence in the fibre development. Suppression subtractive hybridization was used and differentially expressed transcripts of white jute were identified which were associated with the bast fibre development. Cultivated variety *of Corchorus capsularis* L., JRC 321 and its 'soft stem' mutant were used. *WRKY* transcription factor was

reported to be most essential transcript. Among the transcripts, *COMT* (FK826456), *4CL* (JK714316) and *CCR* (FK826506) transcripts were identified to be linked with the formation of lignin in plants. The expressions of these three enzymes were observed to be higher in normal plant than mutant irrespective of their developmental stages which were found by Northern analysis. The expression levels of these enzymes were increased with the progression of the developmental stages in normal and mutant plant which indicated that these enzymes were developmentally regulated. The results showed that the expressions of these transcripts were positively correlated with the deposition of lignin in the jute fibre as displayed by histological analysis. By real-time PCR analysis, it was revealed that among the three transcripts, *4CL* had a major role during the accumulation of lignin in jute plant (Samanta *et al*., 2015).

The full-length cDNA of the *CCoAOMT* gene from jute was cloned using homology clone and a modified Rapid amplification of cDNA ends (RACE) technique, and it was called as "*CcCCoAOMT1*". By Real-time PCR analysis, it was observed that the expression level of *CcCCoAOMT1* was highest in stem. For knowing the function of the gene, it was transformed into *Arabidopsis thaliana*. It was observed that the lignin content (20.44–21.26%) of the transgenic *Arabidopsis* plants were more than the non-transgenic plants (17.56%) which indicated that *CcCCoAOMT1* gene played an important role in the biosynthesis of lignin. These results suggested that reduction of *CcCCoAOMT1* gene would be efficient to minimize the lignin content in jute which would also improve the fiber quality (Zhang *et al*., 2014). By using artificial microRNA mediated gene silencing approach, two monolignol biosynthetic genes of jute - *C3H* and *F5H* were downregulated for decreasing the lignin content of jute (*Corchorus olitorius*). The gene expression levels were observed lower in the C3H- artificial microRNA and F3H- artificial microRNA transgenic lines and acid insoluble lignin content of the whole stem and fibre lignin content were reduced 25% and 12-15% respectively, compared to the non transgenic lines. The results gave an indication that these transgenes could be used for lowering the lignin content in jute (Shafrin *et al*., 2015). Two genes - *C4H* and *COMT*, involved in monolignoid biosynthesis pathway were downregulated by using hairpin RNA (hp-RNA) based vector in *Corchorus olitorius*. It was observed that the gene expressions were lesser in transgenic lines, the acid soluble lignin content decreased ~16-25% for the whole stem and fibre lignin content decreased ~13-14% in the transgenic lines compared to the control lines. Increase of cellulose content on an average of 3.5% in the *C4H*-hpRNA lines along with increase of cellulose/lignin ratio and in the *COMT*-hpRNA lines, increase of cellulose content up to 4% compared to the control plants with increase of cellulose/lignin ratio were observed (Shafrin *et al*., 2017).

Genes related to cellulose biosynthesis

Increasing the cellulose content is required for the improvement of fibre quality (Zhang *et al*., 2015). Analysis of gene expression of *CesA* genes were performed in different plants, including Maize (Appenzeller *et al*., 2004) and *Arabidopsis* (Hamann *et al*., 2004). The expressions of 10 *CESA* and 29 *CSL* genes were analyzed in *Arabidopsis.* It was observed that, in all of tissues used for analysis, expressions of various *CESA* genes were high but expressions of only few *CSL* genes were high (Hamann *et al*., 2004). Table 2 explained the functions of different genes involved in cellulose biosynthesis of jute as well as their effects on jute fibre. Full-length cDNA of the *Uridine diphosphate glucose pyrophosphorylase* (*UGPase*) gene from jute was isolated by homologous cloning and modified RACE techniques and the cloned gene- *CcUGPase* was constructed. Overexpressions of *CcUGPase* gene resulted transgenic lines were longer in height and showed more cellulose content than the non transgenic lines which indicated that *CcUGPase* gene played an important part in cellulose biosynthesis of jute and might be used for the betterment of jute fibre quality (Zhang *et al*., 2013). The cellulose synthesis is occurred in the cellulose synthase complex. 10 *CesA* and 32 *Csl* genes were recognized. Upregulations of two SWC synthesis genes, *CesA4* and *CesA7* were observed in fibre cells of jute which stated that these genes were linked with SCW cellulose deposition. *CesA1*, *CesA6* and *CesA3* were expressed significantly in seedlings which indicated that these genes were involved in primary cell wall cellulose deposition (Islam *et al*., 2017). Several genes required for cellulose biosynthesis of jute were identified. The identified gene families are *Sucrose synthase* (*SuSy*), *UGPase, CesA, CSL, KORRIGAN* (*KOR*) and *COBRA*. On the basis of transcriptome sequence, 5 *Susy*, 3 *UGPase*, 9 *CesA*, 18 *CSL*, 2 *KOR* and 12 *COBRA* unigenes were found and their expression patterns were observed. It was also observed that in the stem bast, the expressions of *CSL, KOR,* and *COBRA* were lower than the expressions of *SuSy, UGPase, CesA*, which predicted that *SuSy, UGPase, CesA* might have greater important roles than the others in fibre formation. Using RT-qPCR and FPKM, it was observed that among these unigenes which were involved in cellulose biosynthesis, the unigenes of comp11264_c0 (*SuSy*), comp24568_c0 (*UGPase*), comp11363_c0 (*CesA*), comp11363_c1 (*CesA*), comp24217_c0 (*CesA*) and comp23531_c0

(*CesA*) showed higher levels of expression in stem bast which predicted that they might play significant role in cellulose biosynthesis of jute (Zhang *et al*., 2015).

CONCLUSION

To reduce the use of synthetic fibre which is costly and also harmful, the use of natural fibres like jute fibre should be increased. The environmental friendly jute fibre has a great socio- economic importance for its versatile uses. But the higher lignin content and lower cellulose content create negative effects which should be minimized for improving the quality of the fibre. Increasing the fibre yield is also desirable and some morphological parameters including plant height, green weight, basal diameter, stick weight, nodes per plant and days to 50% flowering were identified which were positively correlated with fibre yield. The identified quality parameters of plant fibre are fibre strength, fineness, and luster of the fibre. Many QTLs were identified for fibre yield traits, fibre quality traits and bast fibre cellulose. Applications of different chemicals and some enzymes (like cellulase, pectinase, xylanase, laccase, laccase/mediator system) also produce better physical properties of jute fibre fabric. There are different enzymes and genes which play important role in the lignin biosynthesis and cellulose biosynthesis of jute fibre. With the help of molecular approaches, the genes could be identified and characterized. Many genes were identified, involved in the Monolignol pathway and Shikimate-aromatic amino acid pathway which are linked with the lignin biosynthesis. Downregulation of *CcCAD7* gene was seen in the bast tissue of *dlpf* mutant jute and the gene *CAD* was reported to be an important target for the developing jute fibre with less lignin content. The *CCoAOMT1* gene from jute was reported to play an important role in lignin biosynthesis in *Arabidopsis thaliana*. It was also observed that the downregulations of some genes including *C4H*, *COMT*, *C3H* and *F5H* showed less lignin content in the transgenic jute plants compared to the normal plants and these observations indicated that these transgenes can be used for improving the jute fibre quality by lowering the lignin content. In cellulose biosynthesis, the identified genes are *SuSy, UGPase, CesA, CSL, KOR* and *COBRA.* The higher expressions of some unigenes of *SuSy*, *UGPase*, *CesA* in the stem bast of jute indicated that these unigenes might be very important in cellulose biosynthesis of jute. Though, very limited amount information are available for the genes involved in these pathways of jute, it is required to further characterize different genes which will help in the betterment of the fibre quality of jute and also will be beneficial to get the superior alleles which are contributing to the fineness of fibre quality.

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