

## Abstract

Understanding of molecular mechanism associated with bast fibre development is of immense significance to achieve desired improvement in jute (*Corchorus* sp.). Thus, a comparative study was made to explore the gene expression pattern at fibre forming stage in normal *Corchorus capsularis* (as tester) with respect to its fibre-deficient mutant called 'soft-stem' mutant (as driver) following suppression subtractive hybridization. The subtraction resulted with 2685 expressed sequence tags which were assumed to represent the differentially expressed genes between two genotypes. The identified expressed sequence tags were assembled and clustered into 225 contigs and 231 singletons. Based on BLAST search analysis, among these 456 unigenes 377 were classified into 15 different functional categories while others were of unknown functional category. Reverse northern analysis of the unigenes showed distinct variation in hybridisation intensity for 11 transcripts between two genotypes tested. The transcripts included caffeic acid 3-O-methyltransferase, cinnamoyl-CoA reductase, 4-Coumarate CoA: ligase, arabinogalactan-protein, xyloglucan endotransglycosylase, pectin methylesterase, pectate lyase, glycine rich protein, homeodomain-leucine zipper, WRKY transcription factor and zinc finger protein. The differential expressions of these 11 genes between two genotypes at two different developmental stages, 'fibre-forming' and 'non-fibre forming', were documented by northern hybridization and real time PCR analysis. Variations in expression level of these transcripts between the genotypes at different developmental stages suggested their crucial involvement in fibre development in this species. The results were in agreement with the known role of WRKY transcription factor in other fibre producing plants in the regulation of the differentially expressed transcripts related to cell wall biosynthesis, cell expansion and lignification. It could be suggested that the information generated in this study would be useful for genetic improvement of fibre trait in this plant species. This report constitutes first systematic analysis of genes involved in fiber development process in jute.

**Keywords:** *Corchorus capsularis*, fibre-deficient mutant, expressed sequence tags, suppression subtractive hybridization, northern hybridization, real-time PCR.