

PROJECT PROFILE

Title: Identification of secondary xylem specific cellulose synthase genes from *Eucalyptus tereticornis*

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Start and Completion dates: Four years 1-4-2008 to 31-3-2012

Objectives:

1. In silico sequence analysis of cellulose synthase super family members to design gene specific primers.
2. Isolation of full length xylem specific cellulose synthase genes using RACE.
3. Expression profiling of cellulose synthase genes in *E. tereticornis* tissues.

Funding Agency: Indian Council of Forestry Research and Education (ICFRE)

Summary

- ❑ Six families of truncated cellulose synthase transcripts (*EtCesA1 – EtCesA6*) were isolated from different tissues of *E. tereticornis* and three developing xylem specific full length genes (*EtCesA1*, *EtCesA2* and *EtCesA3*) were isolated and characterized. ***This is the first report on isolation of full length cellulose synthase genes from E. tereticornis.***
- ❑ Seven reference genes were evaluated for normalization of RT-qPCR data and Actin (*EtAct2*) was found to be the most stable gene for gene expression across tissues. *EtAct2* and *EtSAND* were identified as the most stable genes in pair for expression profiling. ***This is the first report on selection of reference genes for normalization of RT-qPCR data in E. tereticornis.***

- The expression pattern of all the six families of *EtCesAs* revealed the presence of two groups of *CesAs* in *E. tereticornis*, including the three genes involved in cellulose biosynthesis during primary cell wall formation (*EtCesA4*, *EtCesA5* and *EtCesA6*) while the expression of *EtCesA1*, *EtCesA2* and *EtCesA3* were predominantly found in the developing and mature xylem tissues.