

## EXPRESSION ANALYSIS OF DIFFERENT *EUCALYPTUS* SPECIES XYLEM USING cDNA MICROARRAY

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This work represents the preliminary data from cDNA microarray expression analysis of 384 genes selected from the GENOLYPTUS (*Eucalyptus* Genome Project) database. The goal of this study is to investigate xylem-specific gene profile of distinct *Eucalyptus* species, focusing genes involved with cell wall formation and lignin and cellulose biosynthesis. Microarrays were produced by spotting selected genes in glass slides, replicated three time per slide. Probes were synthesized by mRNA collected from *E. urophylla* and *E. globulus* xylem (xy), and compared to probes from mature leaf (ml) mRNA. After data analysis, 11 and 10 genes were determined as differentially expressed (fold change xy/ml > [2.0]) in *E. globulus* and *E. urophylla*, respectively. In *E. globulus*, genes upregulated in xylem includes a pectin-esterase, involved with cell division and expansion, and an exo-1-4-galactanase, involved in cell wall formation. In *E. urophylla*, it was upregulated an endo-b-xylanase, also involved with cell wall formation. These results show paths to understanding cell wall biosynthesis and will be target of others studies.