

PROTEOMIC ANALYSIS OF *EUCALYPTUS* SP TISSUES.

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Brazil is a higher worldwide producer of cellulose for paper production and others uses. The paper production required a range of chemicals treatments leading to lignin degradation and bleaching, however these treatments are extremely pollutant. Studies for identification of critical proteins in the wood formation can contribute to the development of industrial harmful processes. In the present report, proteomics studies were performed to identify differential patterns of proteins in *Eucalyptus* sp tissues (xylem and leaf). Differential proteins were identified by mass spectrometry (MALDI-ToF) and 2DE analysis. Differential proteins were detected after 2DE analysis, and 65% of these were identified using MALDI-ToF mass spectrometry. Moreover, one spot (identical molecular mass and pI) to the both tissues (leaves and xylem) were identified as an isoflavone reductase protein. Three heat shock proteins were also been identified to leaves and xylem using mass spectrometry. The understanding of differential protein pattern between tissues and species of *Eucalyptus* can be essential for plant improvement with low constitution of lignin and contributing for the reduction of chemicals use.

Key words: *Eucalyptus* sp, Plant proteome, Mass spectrometry, 2DE.

Financial support: Universidade Católica de Brasília, CNPq and MCT.