

TWO DIMENSIONAL LIQUID CHROMATOGRAPHY TECHNIQUE COUPLED WITH MASS SPECTROMETRY ANALYSIS TO COMPARE THE PROTEOMIC RESPONSE TO CADMIUM STRESS IN POPLAR

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Plants are useful in studies of metal toxicity, because their physiological responses to different metals are correlated with the metal exposure dose and chemical state. Moreover a network of proteins and biochemical cascades that may lead to a controlled homeostasis of metals has been identified in many plant species. This paper focuses on the global protein variations that occur in a *Populus nigra* spp. clone (Poli) that has an exceptional tolerance to the presence of cadmium.

Using comparative proteomics, protein variations of the *Populus nigra* clone “Poli” grown without Cd, were compared to clones grown with a 50 μ M CdSO₄ treatment, which was sub-lethal treatment for this clone. Protein separation was based on a two dimensional liquid chromatography technique (2D-LC) (2). The protein patterns obtained from plant samples of the two experimental conditions were compared using the DeltaVue software. The combination of a software that could quantify protein differences after 2D-LC and identify proteins, with MS technique gave both qualitative and semi-quantitative evidence of some of the proteome changes due to Cd treatment in this particular poplar clone. Three sets of proteins were characterized: *i*) more abundant in the treated sample in respect to the control, *ii*) less abundant in the treated sample in respect to the control, *iii*) equally abundant in both treated and control samples. A subset of 20 out of 126 peaks regulated differently under cadmium stress were digested with trypsin and identified by Matrix-assisted LASER desorption/ionization time of flight mass spectrometry (MALDI-TOF/MS). Proteins that were more abundant in the treated samples were located in the chloroplast and in the mitochondrion, suggesting the importance of these organelles in the response and adaptation to metal stress.

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