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Poster Abstract – G.25

A SURVEY ON GENE EXPRESSION AFTER LOW TEMPERATURE STRESS IN WHITE POPLAR (*POPULUS ALBA*)

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Temperature is one of the abiotic factors limiting growth and productivity of plants. Exposure of plants to low temperature induces reduction of membrane fluidity and affects kinetic parameters and protein folding. Low temperature stress is one of the most serious problems for forest crops, since it affects yield, quality, and survival. Forest crops are especially susceptible to low temperatures in spring, after dormancy release, when the newly flushed shoots are vulnerable, and cold stress causes serious loss of biomass production.

During last years, an increased incidence of warm episodes has determined early onset of spring phenophases, so that it has been calculated that an anticipation of 6 days has occurred from the sixties to today. The predicted global warming should further induce earlier bud flushing. Due to earlier dormancy release, forest crops are more exposed to frost injury in spring. Hence, breeding for cold tolerance is based on the development of late flushing genotypes, for which the possibility to cope with spring frost is reduced. The aim of our study was to improve the knowledge of the genetical bases of low temperature tolerance in forest trees: such a knowledge can be useful to improve the selection process.

White poplar plants in the stage of leaf burst were maintained for two weeks at 25°C, then transferred to 4°C for 6, 12, 24, 48 hours, and mRNAs were isolated from leaves. Two differential SSH cDNA libraries were constructed, after short- (6 hours) or long- (48 hours) cold treatments. We have isolated 162 genes, that can be grouped into six categories: i) encoding stress and defence proteins (containing genes already associated to cold stress); ii) involved in signal transduction; iii) related to regulation of gene expression; iv) encoding proteins involved in cell cycle and DNA processing; v) encoding proteins involved in metabolism and energetic processes; vi) involved in the protein fate. Genes encoding not yet characterized proteins were also found.

Genes encoding proteins involved in signal transduction, in cell cycle and DNA processing and in protein fate were especially induced in the early stages of stress. On the contrary, stress and defence proteins encoding genes and genes related to regulation of gene expression were more represented after the long-term treatment. The percentage of genes encoding proteins involved in metabolism and energy processes remained constant in both treatments.

The expression of isolated genes was analysed at 6, 12, 24, 48 h of cold treatment and after 24 h of recovery by reverse northern hybridisation. Sixty percent of genes were transiently expressed (i.e. their expression ceased with recovery), indicating that their function should be crucial for stress response. Almost all genes involved in signal transduction and the majority of genes encoding cell cycle and DNA processing related proteins and involved in protein fate belong to this category. Stress and defence proteins encoding genes were early activated and expressed also after recovery. In conclusion, we have established a reference transcriptome that is being used for comparisons of *P. alba* genotypes from different altitudes and presumably differently tolerant to cold stress. This approach will allow to identify candidate genes to be used for the selection of cold tolerant poplar genotypes.