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Poster Abstract – G.21

GM POPLAR CULTIVATION: EVALUATION OF AGRONOMIC PERFORMANCE, MOLECULAR AND BIOCHEMICAL INVESTIGATIONS, TRANSGENE- SOIL INTERACTIONS.

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In vitro grown GM poplar plants (*Populus alba* L.) expressing the *bar* and *StSy* transgenes and the *nptII* marker gene (Confalonieri et al., 2000; Giorcelli et al., 2004) were transferred to the greenhouse and cultivated in pots containing soil collected from agricultural land. We studied the stability of *StSy* transgene expression over different seasons by evaluating the susceptibility of the *StSy* GM poplars to different leaf diseases and the amount of resveratrol-like compounds produced by different plant tissues. We also investigated the tolerance of *bar* GM poplars to a non selective herbicide (BASTA) during three years. Plants from each transgenic and control line were monitored to evaluate the steady-state level of the *bar* and *StSy* transcripts in apical and basal leaves under conditions of full vegetative growth and dormancy. The evaluation of the i*n planta* expression pattern over a two-year period showed significant fluctuations in the steady-state level of the *bar* and *StSy* transcripts. Investigations are currently in progress to check the methylation state of the transgenic sequences, in order to find out the molecular processes responsible for the transient silencing of both transgenes. From the agronomic point of view, neither *bar*-transformed line showed any damage due to the application of the herbicide, either with the field standard concentration and with the double concentration. The analysis of leaf extracts showed the presence of resveratrol-like glucosides in all the tested tissues (leaves, stems and roots) in the *StSy* GM poplars. The concentrations of the *cis* and *trans* isomers in the leaves are alike, whereas the total concentration varies, from 150 up to 1300 mg/kg, in different plantlets of the same transgenic line. The same results were found in all *StSy* lines.

Different soil samples from *bar* and *StSy* pots were collected to monitor the persistence of recombinant DNA sequences in soil and to assess the possible occurrence of horizontal gene transfer from GM poplars to soil microrganisms. Molecular analysis allowed the detection of recombinant DNA sequences derived from GM poplar tissues. On the same soil samples the total culturable bacterial population and the fraction of kanamycin-resistant bacteria were also analysed. No significant variation was detected in the microbial flora of the soil cultivated with GM poplars in comparison with the soil before GM poplar cultivation.

The reported data will contribute to a better understanding of the agronomical response and environmental impact of different classes of GM white poplars cultivated on a large scale, as a result of detailed analyses carried out at biochemical, molecular and cellular level.