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Poster Abstract - A.01

BOOSTING THE PHENYLPROPANOID PATHWAY IN *N. TABACUM* PLANTS BY OVER-EXPRESSION OF THE *OSMYB4* TRANSCRIPTION FACTOR

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Plants produce a vast array of natural products, many of which are likely to be useful bioactive molecules. Unfortunately, these complex natural products usually occur at very low abundance and with restricted tissue distribution. Genes encoding transcription factors (TFs) known to control several genes involved in a specific metabolic pathway offer new possibilities to direct the metabolic cellular flux toward the production of desired metabolites in one step by over-expressing these TF genes in plants.

Osmyb4 is a new TF, isolated from *O. sativa*, able to increase cold and freezing tolerance and to activate several genes of the shikimate pathway when over-expressed in *A. thaliana* (1).

Osmyb4 over-expressing *N. tabacum* calli and plants were generated by *A. tumefaciens* -mediated transformation. *Kan*$^+$ calli and plants were selected and checked for their effective expression by semi-quantitative RT-PCR. Metabolic profiling by HPLC-DAD, LC-MS and H1-NMR analysis revealed that the observed metabolic changes correlate with the level of transgene expression. The most significant metabolic change in transformed tobacco calli and plants was an increase in the content of chlorogenic acid, a natural metabolite with known antioxidant and anti-tumoral activity (2). Expression analysis of up-stream (PAL, phenylalanine ammonia lyase) and down-stream (CCoAOMT, caffeoyl-CoA 3-O-methyltransferase) genes of the CGA biosynthesis is underway to have a direct evidence that *Osmyb4* is a primary regulator of the phenyl-propanoid pathway in *N. tabacum*.

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