

**COMPARATIVE TRANSCRIPTOMIC AND METABOLOMIC ANALYSES
OF TRANSGENIC “GOLDEN” POTATO TUBERS OVER-
ACCUMULATING BETA-CAROTENE**

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Potato (*Solanum tuberosum*) is one of the world's most important tuber crops. It constitutes the staple food for millions of people in many developing countries. Its tubers, while rich in certain micronutrients (e.g. vitamin C), contain only trace amounts of carotenoids. To overcome this nutritional deficiency, we have produced a set of transgenic lines by inserting three genes of bacterial origin driving the synthesis of β -carotene from its precursor molecule, geranylgeranyl pyrophosphate. A high-throughput metabolomic approach, consisting both of GC-ToF-MS and LC-MS, has been applied to the mature transgenic tubers to study the metabolite abundances and assess potential unintended effects following the accumulation of β -carotene. We have also carried out a transcriptomic analysis, using a high-density potato oligo array, in order to detect the consequences of the transgene expression on the tuber transcriptome. The gene expression values of several independent transgenic lines have been clustered with the relative abundances of selected tuber metabolites to identify genes whose expression is associated with the accumulation of nutritionally-important compounds.