MACROARRAY EXPRESSION ANALYSIS OF TRANSGENIC AND WILD TYPE DURUM WHEAT PLANTS

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In order to investigate the eventual presence of differences in gene expression between genetically modified plants and their untransformed counterpart, we have utilized the DNA macroarray technology that allows a rapid and parallel analysis of many thousands of genes.

2200 individual sequenced cDNA clones of a durum wheat expression library were amplified and the PCR fragments were spotted on nylon filters by using the robotic workstation G3 (Genomic Solutions, PE).

The arrayed DNA fragments were then hybridised with $^{33}$P labelled cDNA prepared by retro-transcribing total RNA extracted from both durum wheat plants transgenic for the bialaphos resistance (BAR) gene and untransformed plants.

The analysis, performed with total rna prepared from three different developmental stages of grain revealed that there are no qualitative differences in gene expression between transgenic and wild type durum wheat plants.

Current investigations are being carried out to measure any quantitative differences in gene expression between the analysed samples.