

MICROARRAY ANALYSIS OF TRANSGENIC WHEAT OVER-EXPRESSING A GLUTENIN SUBUNIT RELATED TO TECHNOLOGICAL PROPERTIES

F. SCOSSA***, B. STAMOVA**, D. LAUDENCIA-CHINGCUANCO**, O.D. ANDERSON**,
D. LAFIANDRA*, R. D'OVIDIO*, S. MASCI*

*) Dipartimento di Agrobiologia e Agrochimica, Università della Tuscia, Viterbo, Italy - masci@unitus.it

***) U.S. Department of Agriculture, A.R.S., W.R.R.C., Albany, CA, USA

The effects of transgene expression in plants, whether direct or indirect, are relevant to basic research questions, industrial applications, and the issue of “Substantial Equivalence” of GM plants, because transgenes can affect other components of plant metabolism.

Wheat endosperm proteins are of major importance with regard to the nutritional and technological properties of wheat flours. Consequently, the potential effects of transgene introduction on these proteins deserve consideration. We focused our studies on a transgenic wheat line over-expressing a gene for a low-molecular-weight glutenin subunit (LMW-GS), which is correlated with dough quality. Proteomic data showed a high level of differential expression in most classes of wheat seed proteins. In order to identify the differentially expressed genes during the process of grain filling, and eventually provide insights about the metabolic pathways altered, we carried out microarray comparisons between the wild type cultivar, the “null genotype” (derived from the transgenic line, but has lost the transgene by segregation), and the transformed line expressing the transgenic protein.

During seed development, 543 candidate differentially expressed unigenes have been identified. Most of them are genes for seed-storage proteins, or coding for proteins involved in trafficking/secretion and amino acid biosynthesis.