



Proteomic analysis of a genetically modified maize flour carrying Cry1Ab gene and comparison to the corresponding Wild-type

Aim of the study

A comparison between two maize flours was chosen as a model to verify proteomics capability in detecting unexpected differences between near-isogenic lines.

Analyte

Maize seedlings

Methodology

Protein expression in a maize hybrid flour (WT) and its corresponding transgenic version resistant to European corn borer (BT, carrying a gene encoding for the *Bacillus thuringiensis* insecticidal protein Cry1Ab) were analyzed by means of two-dimensional gel electrophoresis and mass spectrometry. Proteins were extracted from seedlings of the two types and analyzed by 2-DE (two-dimensional electrophoresis). After staining, gels were compared by image analysis and statistical analysis. Most abundant proteins, together with those evidenced by statistical analysis, were identified by mass spectrometry.

System Maize (*Zea mays*)

Customer This study was performed in collaboration with *Istituto Sperimentale per la Cerealicoltura* and Dipartimento di Chimica IFM, University of Torino.

Results

Some unpredictable differences were detected: i) glucose and ribitol dehydrogenase spot was unique of BT maize; ii) endochitinase A spot was unique of WT maize; iii) triosephosphate isomerase 1 and one spot of globulin-1 S were overexpressed while cytosolic 3-phosphoglycerate kinase and one spot of aldose reductase were down-regulated in BT maize with respect to WT. Moreover, a reference map for maize flour was built: forty spots, corresponding to twenty-five different proteins, were successfully identified.

Advantage of the methodology

Obtained results outline the potential of the non-targeted “-omics” technologies (in particular proteomics) in the detection of unexpected, unintended and unwanted variations in Genetically Modified (GM) versus non-GM food comparison and suggest the possible employment of these technologies in substantial equivalence evaluation.

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