

- Pandey, A., Andersen, J.S., Mann, M., Use of mass spectrometry to study signaling pathways. *Science's Stake* 2000, 37, 1-12.
- Santos, M., Villalobos, E., Carvajal-Vallejos, P., Barberá, E., Campos, A., *et al.*, Immunolocalization of maize transglutaminase and its substrates in plant cells and in *Escherichia coli* transformed cells, in: Mendez Vilas, A., Díaz Alvarez, J., (Eds.), *Modern research and Educational Topics in Microscopy* 2007, 1, 212-213.
- Schägger, H., Von Jagow, G., Blue native electrophoresis for isolation of membrane protein complexes in enzymatically active form. *Anal Biochem* 1991, 199, 223-231.
- Villalobos, E., Santos, M., Talavera, D., Rodríguez-Falcón, M., Torné, J.M., Molecular cloning and characterization of a maize transglutaminase complementary DNA. *Gene* 2004, 336, 93-104.

## Proteomics as a complementary tool for identifying unintended side effects occurring in transgenic maize seeds as a result of genetic modifications<sup>1</sup>

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In order to improve the probability of detecting unintended side effects during maize gene manipulations by bombardment, proteomics was used as an analytical tool complementary to the existing safety assessment techniques. Since seed proteome is highly dynamic, depending on the species variability and environmental influence we analyzed the proteomic profiles of one transgenic maize variety (event MON 810) in T5 and T6 generation with their respective isogenic controls (F5 and F6). Thus, by comparing the proteomic profiles of F5 with F6 we could determine the environmental effects, while the comparison between F6 and T6 seeds from plants grown under controlled conditions allowed us to investigate the effects of DNA manipulation. Finally, by comparing T5 with T6 seed proteomes it was possible to get some indications about similarities and differences between the adaptations of transgenic and isogenic plants to the

same strictly controlled growth environment. Approximately 100 total proteins resulted differentially modulated in the expression level as a consequence of the environmental influence (F6 vs. F5), whereas 43 proteins resulted up- or down-regulated in transgenic seeds with respect to their controls (T6 vs. F6), which could be specifically related to the insertion of a single gene into a maize genome by particle bombardment. Transgenic seeds responded differentially to the same environment as compared to their respective isogenic controls, as result of the genome rearrangement derived from gene insertion. To conclude, an exhaustive differential proteomic analysis allows to determine similarities and differences between traditional food and new products (substantial equivalence), and a case-by-case assessment of the new food should be carried out in order to have a wide knowledge of its features.

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