

Assessing Proteomic Variations Due to Genetic Modification of Tomatoes Using Three Complementary Approaches

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Abstract : Applying the profiling approach for the assessment of proteomic variations due to genetic modification of the Egyptian tomato cultivar "Edkawy", three complementary approaches were used. These methods are amino acids analysis, gel electrophoresis, and Gas chromatography coupled with mass spectrometry (GC/MS). The results of the present study Show evidence of proteomic variations between both modified tomato and its non-modified counterpart. Amino acids concentrations, and the protein patterns separation on the 1D SDS-PAGE were not similar in the case of transformed tomato compared to that of the non-transformed counterpart. These detected differences are most likely derived from the process of transformation. Results also revealed that the efficiency of GC/MS approach to identify a mixture of unknown proteins is limited. GC/MS analysis was only able to identify few number of protein molecules. Therefore, more advanced and specific technologies like MALDI-TOF-MS are recommended to be employed.

Keywords : GMOs, unintended effects, proteomic variations, 1D SDS-PAGE, GC/MS

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