

A METABOLOMIC STUDY OF TRANGENIC MAIZE (*ZEA MAYS*) SEEDS REVEALED VARIATIONS IN OSMOLITES AND BRANCHED AMINO ACIDS

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Aim of research was to investigate metabolic variations in the grains associated to genetic modifications of *Zea Mays*, using metabonomic techniques. Concerning this point, non-targeted characteristic of the technique is useful to identify metabolites peculiar to the genetic modification and initially undefined. The obtained results showed that the genetic modification, introducing *CryIAb* gene expression, induces metabolic variations involving primary nitrogen pathway. Concerning methodological aspects, the experimental protocol used has been applied for the first time in this field. It consists of a combination of Partial Least Squares-Discriminant Analysis and Principal Component Analysis (PCA). The most important metabolites for discrimination were selected and the metabolic correlations linking them are identified. PCA on selected signals confirms metabolic variations, highlighting important details about the changes induced on the metabolic network by the presence of Bt transgene in the maize genome.