

VARIATION OF METABOLIC PROFILES IN DEVELOPING MAIZE KERNELS UP-AND-DOWN-REGULATED FOR THE *HDA101* GENE

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To shed light on the specific contribution of the histone deacetylases101 (HDA101) in modulating metabolic pathways in the maize seed, we have investigated changes in the metabolic profiles of kernels obtained from *hda101* mutant plants. In the field of metabolomics the analysis of metabolic changes in time is a fundamental aspect of understanding the biochemical response of an organism to an external perturbation (Lindon et al., 2001). As processes develop through time, the metabolic responses also exhibit dynamic variation. Therefore, monitoring these changes results in characteristic patterns for each type of perturbation. Principal component trajectories have been constructed from Nuclear Magnetic Resonance (NMR) data to investigate the changing multivariate biochemical profile during development of a toxic lesion (Keun et al., 2004). However, this kind of analysis, although effective for trajectory analysis, is not suitable to the simultaneous comparison of several parallel systems, and thus the use of alternate multi-way tools for optimally extracting metabolic trajectory and biomarker information have been investigated (Antti et al., 2002; Dyrby et al., 2005a). Multi-way analysis is the extension of the traditional multivariate analysis to array with more than two way, where data are characterised by several sets of variables that are measured in a cross fashion (Bro, 1997).

In this paper, we describe the application of multi-way Partial Least Square (N-PLS) to NMR spectra to evaluate the effect of the up- and down-regulation of HDA101 activity in terms of metabolites concentrations during maize seed development.