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DIGE APPLICATION TO INVESTIGATE APHID ADAPTATION TO RESISTANT HOST PLANT

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Plant-insect relations are mainly regulated by the evolution of the defence mechanisms developed by plants and the ways herbivore insects adapt themselves to these defensive systems. Plant defence can be direct or indirect, localised or systemic. A common property of these mechanisms is the broad range of phytophagous agents, including insect pests, which are efficiently controlled by the produced defensive molecules. Nevertheless, some particular defence mechanisms only affect some herbivore species and show no effect on other pest. Here, one particular tomato mutant expressing the Mi gene was used and compared to sensitive control tomato as host plants for *Macrosiphum euphorbiae* aphid. To cope with the production of several direct defence molecules, herbivores developed several biochemical adaptations including enzymatic detoxification systems such as the glutathione S-transferases and monooxygenases. Using a 2D electrophoresis approach and DIGE staining method, here we studied: (1) the background proteomic difference between resistant and sensitive aphid clone from the *M. euphorbiae* species, and (2) the proteomic changes related to the switch of a resistant *M. euphorbiae* clone from sensitive control host plant to aphid resistant tomato mutant expressing the Mi gene. The complex protein mixtures generated from the different aphid materials were separated by two dimensional electrophoresis methods and the significantly varying spots of proteins were selected and identified by mass spectrometry (Maldi-Tof-MS-MS) coupled with data bank investigations. The down regulated or over-expressed aphid proteins are listed as they belong to different metabolic pathways. Moreover, as specific associations between aphids and their host plant were previously shown in biological experiments to depend on the presence of particular bacterial symbionts, the respective role of the aphid and their related symbionts in the adaptation to the host plant is discussed. This proteomic approach using the DIGE staining method is a very reliable tool to identify the proteins from aphids that are involved in their response to several environmental changes and particularly the insect - host plant interactions.