**Use of complementary "omic" approaches to identify bacterial symbionts in aphid and related impact in multitrophic interactions**

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Proteomics found recent developments due to significant improvement and availability of both protein separation and identification methods. Moreover, functional information’s linked to the studied proteins was brought when compared to genomic approach. For these reasons, a panel of tools is available to determine the proteome patterns related to differential adaptation of insects to cope with plant defence mechanisms or to transmit virus. The aphid-plant-virus relations represent interesting case studies. Indeed, aphids represent a wonderful model in the study of plant adaptation. The adaptation and metabolic changes of aphids in relation to host plants focusing on the role of the bacterial endosymbionts was investigated. Use of artificial diet including diverse antibiotics but also the comparison of proteomes related to whole aphid and respective purified bacterial symbionts were studied to identify the respective origin and function of proteins constituting the studied proteomes. Diverse methods including traditional two dimension electrophoresis, 2D-Differencial In Gel Expression (2D-Dige), liquid chromatography (LC) coupled with mass spectrometry (ESI-MS-MS and Maldi-Tof-MS-MS) and data bank investigations were developed. From the proteome investigation, characterisation of good and bad virus vectors were also performed in different aphid - plant - virus models. Particular proteins of interest were selected and accurately characterised with both fundamental but also applied views. This broad proteomic approach will be discussed as an interesting and reliable tool to study the biologically involved proteins from aphids in response to several environmental changes, and particularly the insect - virus - host plant interactions.