EVOLUTION OF PROTEOMIC TOOLS TO INVESTIGATE INSECT - PLANT INTERACTIONS: APHIDS AS A CASE STUDY

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Whether the biological observation remains the first step of the plant – insect interaction's, the understanding of the adaptations between both kinds of protagonists needs molecular approaches. Besides genomic tools providing huge amounts of data's for several years, 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, molecular entomologists have now a panel of tools to determine the proteome patterns related to adapted or sensitive insects toward several stress situations such as having to cope with plant defence mechanisms. To illustrate the usefulness but also the limits of available proteomic approaches, the aphid-plant relations will be used as a case study. Indeed, from a biological point of view, aphids represent a wonderful model and provide plenty of topics to investigate: the adaptation and metabolic changes of aphids toward a switch of a host plant to others from different botanical families, the role of the bacterial symbionts in the aphid adaptation, the impact of aphids in plant defensive responses due to the sucking feeding behaviour including the particular role of the injected saliva. Descriptive but also differential analysis of the complex protein mixtures related to the different aphid materials will be presented. The use of diverse methods including traditional two dimension electrophoresis, 2D-Differencial In Gel Expression, liquid chromatography (LC) coupled with mass spectrometry (ESI-MS-MS and Maldi-Tof-MS-MS) and data bank investigations will be developed. From broad proteome investigation and identification, particular proteins of interest can then be 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 - host plant interactions.

Keywords: proteins, adaptations, 2D electrophoresis, mass spectrometry, co-evolution