

Aphid Adaptation to Plant Defence System

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Myzus persicae is one of the most generalist aphid species which is able to colonise around 400 host plant species. This capability to use a so large range of food sources has to be closely linked to high potential adaptation systems to cope with various defence mechanisms in host plant. On the other way, plants have evolved a variety of defence mechanisms, both constitutive and inducible, to cope with herbivore attacks. Here we studied the chemical ecology of *M. persicae* associated with plant species from Solanaceae and Brassicaceae family. The induction of detoxication enzymes such as GST in response to the presence of plant allelochemicals were first observed. To assess the differential expression of aphid proteome, a non restrictive proteomic approach was then developed to identify all the potential adaptation systems toward the secondary metabolites from host plants. The complex protein mixtures was separated by two dimension electrophoresis methods and the related spots of proteins significantly varying were selected and identified by mass spectrometry (ES-MS) coupled with data bank investigations. Aphid proteins involved in different metabolic pathways were either down regulated (proteins involved in glycolysis, TCA cycle, protein and lipid synthesis) or overexpressed (mainly proteins related to the cytoskeleton) according to aphid host plant switch. This proteomic approach is a very reliable tool to study the biologically involved proteins from organisms such as insects in response to environmental changes such as particular host plant defence mechanisms.

Key words: Detoxication enzyme, Plant allelochemical, Plant defence