

## **A Metabolomic Approach for Analysing Plant-Herbivore Interactions**

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A metabolomic approach to uncover the complexity of the induced defense signaling networks that have evolved during the arms races between plants and their attackers is presented. Plants respond to herbivore attack by releasing defense metabolites. This study investigated how cabbages (*Brassica oleracea*.) respond to herbivore attack and subsequently how these defense metabolites chemically affect cabbage white (*Pieris rapae*) caterpillars which have been fed on the defense induced cabbages. Ultra Performance Liquid Chromatography Mass Spectrometry (UPLC/MS) was used to analyse the comprehensive chemical compositions of extracts made from both the plants and the caterpillars. MarkerLynx, a program which incorporates a peak deconvolution package and collects data into a single matrix by aligning peaks with the same exact mass/retention time along with their normalised intensities was used to identify the monoisotopic mass of the constituent components and perform PCA. The data table was exported to advanced statistical packages to enable univariate and multivariate statistical analyses to be performed. Online database searching was performed to tentatively identify metabolites of interest. Structural elucidation experiments were performed and MassFragment, a fragmentation interpretation tool which uses systematic bond disconnections to assign fragment ions to the precursor ion, was used to confirm the putative assignments.

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Proceedings of The Joint **2<sup>nd</sup> Pacific Rim International  
Conference on Protein Science** and **4<sup>th</sup> Asian-Oceania  
Human Proteome Organization**, Cairns- Australia, 22-26  
June 2008