

From Lipid Profiling to Lipid Fingerprinting. New Lipidomic Techniques for Metabolomic Analysis

Amina Ibrahim¹, Kirstin Feussner², Alexander Kaefer³, Peter Meinicke³, Martin Fulda¹,
Cornelia Göbel¹ and Ivo Feussner¹

¹Department of Plant Biochemistry, Albrecht-von-Haller-Institute, Georg-August-University, Göttingen, Germany; ²Department of Molecular Microbiology and Genetics, Institute of Microbiology and Genetics, Georg-August-University, Göttingen, Germany; ³Department of Bioinformatics, Institute of Microbiology and Genetics, Georg-August-University, Göttingen, Germany

The wound response of *Arabidopsis thaliana* is a well described model to investigate plants defence in case of herbivore attack. Fatty acid derived signals, like jasmonic acid and its derivatives, as well as other oxygenated fatty acid metabolites play a crucial role in mediating this response. We use this model system to analyze the underlying metabolic changes by directed and unbiased profiling techniques to extend the knowledge on global metabolic changes at early time points after wounding.

As an example for a directed approach a LC/MS method will be discussed that analyzes galactolipid species. It uses solid phase extraction and reversed-phase LC separation coupled to ion trap mass spectrometry detection. Using differential MS/MS conditions either the head group or the side chain structure of unknown galactolipid species can be determined. This method was used to identify more than 100 different galactolipid species in *Arabidopsis* leaves and to analyze their differential accumulation upon wounding in different lipid biosynthesis mutants. For the unbiased approach metabolite intensity profiles of aqueous and non-polar extracts from a wounding time course consisting of eight different experimental conditions were generated and subjected to a comparative analysis resulting in the identification of several thousand marker candidates. Advanced methods of data mining like metabolite-based clustering and visualization by one-dimensional self-organizing maps (1D-SOM) were developed to overview datasets of such a high complexity and to identify relevant groups of wound markers. A significant number of oxylipins was identified as expected from the current literature. In particular our approach also supports the discovery of so far unknown markers on the basis of their location in the 1D-SOM array with respect to the previously identified markers.