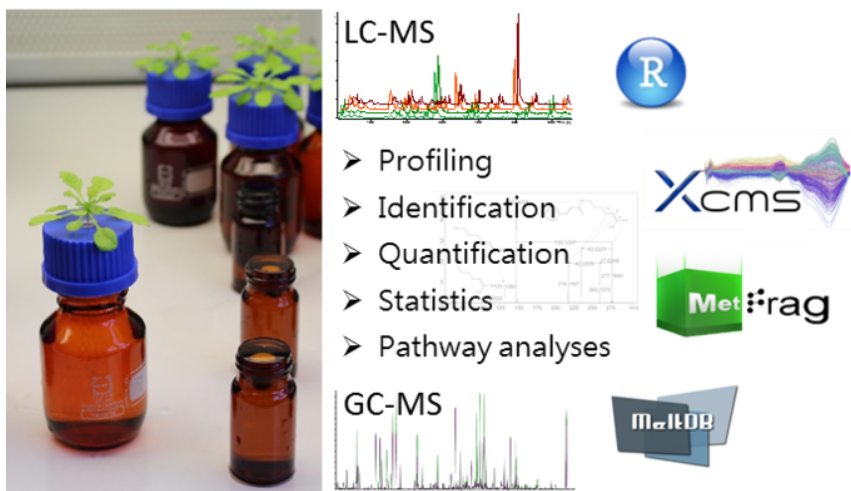




Metabolomics

Dierk Scheel

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The diagram illustrates the metabolomics workflow. On the left, a photograph shows several small brown glass vials with blue caps, some containing small green plants. To the right, a list of steps is provided: Profiling, Identification, Quantification, Statistics, and Pathway analyses. Above the list is an LC-MS chromatogram showing multiple peaks. Below the list is a GC-MS chromatogram showing a series of sharp peaks. To the right of the list are logos for R, XCMS, MetSrag, and MetDB.

During development and in response to variable environmental conditions, plants exhibit altering metabolite patterns. Among these low molecular weight compounds, the numerous and heterogeneous secondary metabolites play crucial roles in plant development, adaptation and defense. Using liquid and gas chromatography-coupled mass spectrometry, the metabolomics research group is specialized on the sensitive metabolite detection, identification and quantification as well as elucidation of turnover rates of these metabolites. Tissue-specific analyses allow a more detailed localization of metabolites. The main focus of our research is the interaction of plants with their below-ground environment: root metabolism and exudation, i.e. the controlled, highly specific release of metabolites from roots into the soil. In cooperation with the Bioinformatics and Mass Spectrometry group, versatile tools for data analysis have been developed and made publicly available.