HelmholtzZentrum münchen
German Research Center for Environmental Health

Scientific Highlight April 2015

☒ co-ordinated with the Director of the Institute / Research Unit

Analytical BioGeoChemistry

PSP-Element:
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Title of the highlight:
DI-ICR-FT/MS-based high throughput deep metabotyping: A case study of the Caenorhabditis. elegans – Pseudomonas aeruginosa infection model.

Keywords:
ICR-FT–MS; High-throughput mass spectrometry; deep metabotyping; Infection models; Metabolomics; Caenorhabditis elegans

Central statement of the highlight in one sentence:
This study fullfilled two goals. The first was a detailed metabolomics study of Caenorhabditis. elegans – Pseudomonas aeruginosa infection model to understand interorganismic interactions on a molecular level. The second was a proof of principle that the technology of ICR-FT/MS is throughput compatible and delivered hundreds of organism specific compounds in limited time.

Text of the highlight:
In metabolomics there is an ever-growing need for faster and more comprehensive analysis methods to cope with the increasing size of biological studies. Direct-infusion ion cyclotron-resonance Fourier-transform spectrometry (DIICR-FT-MS) is used in non-targeted metabolomics to obtain high-resolution snapshots of the metabolic state of a system. We applied this technology to a Caenorhabditis elegans–Pseudomonas aeruginosa infection model and optimized times needed for cultivation and mass-spectrometric analysis. Our results reveal that DI-ICR-FT-MS is a promising tool for high-throughput in-depth non-targeted metabolomics. We performed whole-worm metabolomics and recovered markers of the induced metabolic changes in C. elegans brought about by interaction with pathogens. In this investigation, we reveal complex metabolic phenotypes enabling clustering based upon challenge. Specifically, we observed a marked decrease in amino-acid metabolism with infection by P. aeruginosa and a marked

increase in sugar metabolism with infection by Salmonella enterica. We were also able to discriminate between infection with a virulent wild-type Pseudomonas and with an attenuated mutant, making it possible to use this method in larger genetic screens to identify host and pathogen effectors affecting the metabolic phenotype of infection.

Publication:
Witting, M., M. Lucio, D. Tziotis, B. Wägele, K. Suhre, R. Voulhoux, S. Garvis, **Ph. Schmitt-Kopplin**, DI-ICR-FT/MS-based high throughput deep metabotyping: A case study of the Caenorhabditis. elegans – Pseudomonas aeruginosa infection model. *Analytical Bioanalytical Chemsitry*, 2015, forfront paper, 407, 4, 1059-1073

Taking account of the HMGU mission:
The present study shows the state of the art in high resolution non targeted Metabolomics analysis of interorganism interactions with the example of a pathogen of high relevance in infectious diseases.

The internal HMGU co-operation partners with whom the highlight was compiled, if appropriate:
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