

Next Generation Metabotyping

Neuherberg, January 14, 2015. In metabolomics there is an ever demanding growing need for more comprehensive and faster analysis methods to cope with the increasing size of biological studies. Scientists at the Helmholtz Zentrum München have shown that ultra-high resolution mass spectrometry can be used for detailed information on metabolic states. Their results have been published in the scientific journal ,Analytical and Bioanalytical Chemistry’.

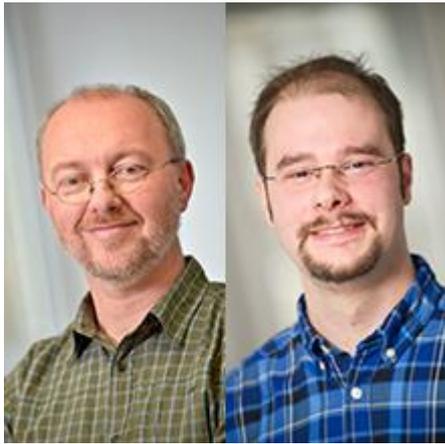


Image: Philippe Schmitt-Kopplin (left), Michael Witting (right). Source: Helmholtz Zentrum München

The team around Michael Witting and Philippe Schmitt-Kopplin used Direct Infusion Ion Cyclotron Resonance Fourier Transform Mass Spectrometry (DI-ICR-FT/MS) and a host-pathogen-model to proof that this technology is high-throughput capable and allows to obtain highly detailed snapshots of systems' metabolic states in short time. With this method several thousand known and unknown metabolites were measured.

In their study, the scientists were able to follow metabolic alterations in the model organism, *Caenorhabditis elegans* that was infected with bacterial microorganisms, *Pseudomonas aeruginosa*. The data showed that it is not only possible to separate metabolite profiles of worms infected with pathogens from those of uninfected worms, but also to decipher between the fully virulent parent strain and a highly attenuated mutant.

“better understanding of metabolic phenotypes”

“This technology enables us now to follow genetic screens in both the host and the pathogen to discover the main players of the metabolic alteration. Thereby we can better understand metabolic phenotypes“, says first author Witting.

Schmitt-Kopplin adds: “With this modern high field ICR-FT/MS technology we are faster in analysis time than with other classic metabolomic approaches and generate an information density of thousands of metabolites simultaneously from which only few hundreds are known. We currently add our obtained data to valorize this high density information into molecular/pathway/network information, to contribute to the big puzzle of metabolism.”

The technology has already been applied to various microorganisms and plant systems. Furthermore, it has been used for human samples as well to unravel effects of the meta-metabolome of altered gut microbiomes in patients suffering of metabolic diseases, such as Diabetes.

Weitere Informationen

Original publication:

Witting, M., et al. (2014). DI-ICR-FT-MS-based high-throughput deep metabotyping: a case study of the *Caenorhabditis elegans*–*Pseudomonas aeruginosa* infection model, *Analytical and Bioanalytical Chemistry*, doi: 10.1007/s00216-014-8331-5

[Link to publication](#)

As German Research Center for Environmental Health [Helmholtz Zentrum München](#) pursues the goal of developing personalized medical approaches for the prevention and therapy of major common diseases such as diabetes mellitus and lung diseases. To achieve this, it investigates the interaction of genetics, environmental factors and lifestyle. The Helmholtz Zentrum München has about 2,200 staff members and is headquartered in Neuherberg in the north of Munich. Helmholtz Zentrum München is a member of the Helmholtz Association, a community of 18 scientific-technical and medical-biological research centers with a total of about 34,000 staff members. Helmholtz Zentrum München is Partner of the German Center for Diabetes Research (DZD).

Scientific contact

Prof. Dr. Philippe Schmitt-Kopplin, Helmholtz Zentrum München - German Research Center for Environmental Health (GmbH), Analytical BioGeoChemistry Department, Ingolstädter Landstr. 1, 85764 Neuherberg, Germany - Phone: 089-3187-3246 - [Email](#)