

Immunologists present improved mass spectrometric method for proteomic analyses

March 18 2014

When it comes to analyzing cell components or body fluids or developing new medications, there is no way around mass spectrometry. Mass spectrometry is a highly sensitive method of measurement that has been used for many years for the analysis of chemical and biological materials. Scientists at the Institute of Immunology of the University Medical Center of Johannes Gutenberg University Mainz (JGU) have now significantly improved this analytical method that is widely employed within their field. They have also developed a software program for the integrated analysis of measurement data called ISOQuant. Their optimized mass spectrometric workflow allows to identify and quantify significantly more proteins than before. The development of this enhanced method of measurement and the specially designed software is described in an article recently published in the prestigious journal *Nature Methods*.

A proteome represents the entire set of proteins expressed by a cell. Through analysis of proteomes, it is thus possible to obtain a comprehensive picture of the proteins and peptides present in cells or body fluids. However, many of the traditional mass spectrometric methods used to date for proteomic analysis are relatively slow and do not always provide reproducible results. Dr. Stefan Tenzer of the Institute of Immunology and his colleagues have perfected a relatively new, data-independent technique that facilitates a very accurate and reproducible quantitative analysis. With its help, many more proteins can be identified than before. "Figuratively speaking, the equipment we use is as exact as a scale that can tell whether a two-euro coin is present in a

VW Beetle or not," explains Tenzer.

Tenzer's work group focuses in particular on developing novel techniques for quantitative proteomic analysis with the aid of so-called ion mobility [mass spectrometry](#). This technique allows not only to measure the mass of a molecule but can also to determine its cross section. This additional analytical dimension renders the technique optimally suited for the comprehensive investigation of highly complex samples. Tenzer and his colleagues have also managed to enhance the technique known as label-free quantification. This eliminates the need for samples to be labeled in the laboratory before being analyzed, an otherwise complex procedure. "We are now able to directly analyze patient samples and specific immune cells without prior cost-intensive preparation," says Tenzer. The Mainz-based scientists specifically developed their ISOQuant software program for this purpose. This provides for standardized analysis of complex data material and generally simplifies the technique of quantitative mass spectrometric analysis.

These groundbreaking innovations were developed under the aegis of the technology platforms "Quantitative Proteomic Analysis" of the JGU Research Center Immunology (FZI) and "ProTIC" of the Research Unit Translational Neurosciences (FTN) at the Mainz University Medical Center. They were now published in *Nature Methods*, one of the most respected international journals. This was already the third article published in the *Nature* journal group in 2013 by Dr. Stefan Tenzer and his colleagues.

"The years of work within the technology platform have paid off in terms of a quantum leap forward with regard to the improvement of the technique of proteomic analysis mass spectrometry," stated Professor Hansjörg Schild, Director of the Institute of Immunology and Coordinator of the Research Center Immunology (FZI) at the Mainz

University Medical Center. "The results obtained by Dr. Stefan Tenzer and his colleagues reflect the quality of achievement of this team. I think we can look forward to new and exciting collaborations in future," said Schild.

"Mass spectrometry is a technique that has now become indispensable within the field of the neurosciences. In this area, we specifically need highly sensitive analytical techniques and Dr. Tenzer has opened up new perspectives in this regard," emphasized Professor Robert Nitsch, Coordinator of the Research Unit Translational Neurosciences and of the Collaborative Research Center 1080 on "Molecular and Cellular Mechanisms of Neuronal Homeostasis" at the Mainz University Medical Center. "The collaboration between the Research Center Immunology and the Research Unit Translational Neurosciences in the field of mass spectrometry represents an excellent opportunity for us to gain new insights into the way the brain functions," claimed Nitsch.

More information: Ute Distler, Jörg Kuharev, Pedro Navarro, Yishai Levin, Hansjörg Schild & Stefan Tenzer, "Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics", *Nature Methods* 11, 167–170 (2014) 15 December 2013.
[DOI: 10.1038/nmeth.2767](https://doi.org/10.1038/nmeth.2767)

Provided by Universitaet Mainz

Citation: Immunologists present improved mass spectrometric method for proteomic analyses (2014, March 18) retrieved 25 April 2024 from <https://phys.org/news/2014-03-immunologists-mass-spectrometric-method-proteomic.html>

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