

HRM - a new standard for comprehensive proteome profiling

Biognosys' new DIA workflow a powerful approach for high content protein quantification

March 6, 2015 – Zurich-Schlieren (CH) – Biognosys AG, a leader in next-generation proteomics, and InSphero AG, a leading supplier of in vitro 3D microtissues, teamed up for a research study that was recently published in a Molecular & Cellular Proteomics entitled “[Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen treated 3D liver microtissues](#)”. The study was co-authored by the researchers from Purdue University and ETH Zurich.

The aim was to directly compare the ability to discover differentially abundant proteins between a new data independent acquisition (DIA) workflow developed by Biognosys' called hyper reaction monitoring ([HRM](#)) and the state-of-the-art shotgun proteomics. To make a fair comparison parameters like column, gradient, mass range, and others were the same for both approaches. Results show that the HRM identified on average 60% more peptides in a single run than shotgun proteomics (28,610 and 17,547 peptides, respectively) and that the CVs of the HRM profiles were 53% lower than of the same profiles of shotgun proteomics (average CVs of 8.45 % for HRM vs 17.8 % for shotgun proteomics). The reproducibility of HRM in peptide detection was above 98 % resulting in quasi complete data sets compared to only 49 % of shotgun proteomics.

The hallmarks of the HRM workflow such as number of consistently identified peptides and precision of quantification resulted in a significantly higher sensitivity of HRM to detect differentially abundant proteins. The HRM workflow was in the second part of the study applied to discover proteome changes in acetaminophen treated InSphero's 3D InSight™ Human Liver Microtissues. The enhanced longevity and more native metabolic phenotype of 3D microtissues make them suitable for such long-term, repeat-dose toxicity studies. Importantly, the HRM approach identified and quantified for the first time human protein targets of drug-adducts in subtoxic concentrations.

[HRM-MS™](#) is a next-generation proteomics technology developed by Biognosys that is based on data-independent acquisition (DIA) performed on new generation mass spectrometric systems. With Biognosys' [Spectronaut™](#) software HRM enables reproducible and accurate quantification of 1,000s of proteins in a single instrument run. For researchers without an access to a state of the art mass spectrometer Biognosys offers [Proteome-SEQ™](#) discovery service that is based on the HRM-MS™ technology.

About Biognosys

Biognosys is the leading proteomics company offering services and products for highly multiplexed protein quantification. Founded in 2008 as spin-off from the lab of proteomics pioneer Ruedi Aebersold at ETH Zurich, Biognosys is dedicated to transform life science with superior technology and software.

Contact: info@biognosys.ch, www.biognosys.ch

About InSphero

InSphero is a leading supplier of organotypic, biological in vitro 3D microtissues for highly predictive drug testing. The company, headquartered in Zurich, Switzerland, with subsidiaries in the USA and in Germany, currently counts all of the top ten global pharmaceutical and cosmetics companies as customers. InSphero 3D Insight™ Microtissues enable more biologically relevant in vitro applications in efficacy and toxicology. The spin-off company of the Swiss Federal Institute of Technology (ETH) Zurich and the University Zurich has been recognized for its scientific and commercial achievements with a number of national and international awards, including being named the #1 Swiss Startup and ACES Award Winner for 2014. InSphero is certified to the ISO 9001:2008 standard for its Quality Management System.

Contact: randy.strube@insphero.com, www.insphero.com