

Univ.-Prof. Dr. Wolfram Weckwerth

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Present position:

Head of the Department for Molecular Systems Biology, University of Vienna, Austria

Place and Date of Birth: Berlin, 14.4.1969

Education:

1994 – Diploma in Chemistry, Institute of Molecular Biology and Biochemistry, Technical University Berlin, Germany

1998 - PhD in Biochemistry, Institute of Molecular Biology and Biochemistry, Technical University Berlin, Germany

2007 – Habilitation in Systems biology, Lecturer Systems Biology, University of Potsdam, Germany

2007 - Head of Central Infrastructure Systems Biology Lab, GoForSys, University Potsdam, Germany

2007 – Offerships for Associate Professor at the Department of Plant Biology, Michigan State University, USA and Full Professor at the University of Vienna, Austria

Since 2008 – Full professor and founding chair of the Department for Molecular Systems Biology at the University of Vienna, Austria

Professional duties and functions:

- Member of the advisory board of the Austrian Society of Analytical Chemistry (ASAC <http://www.asac.at/Index.aspx?site=1&main=85&sub=0&content=314>)
- Editorial Board of Frontiers in Plant Proteomics, Frontiers in Plant Physiology, Journal of Personalized Medicine, Proteomics Insights, Cell Biology Insights and Open Spectroscopy Journal
- Chairman of the Proteomics Committee MASC (Multi-National Arabidopsis Steering Committee)
- Cochair of the Metabolomics Committee MASC
- Austrian representative of the European Plant Proteomics COST action Member of the Steering
- AIST-Fellow (Advanced Industrial Science and Technology, Tsukuba, Japan)
- Advisory boards: NATO Science Series I: Life and Behavioural Sciences 2004 “Genomics for Biosafety in Plant Biotechnology, Sofia 2004; European Systems Biology (EUSYSBIO) Foresight Workshop, Heidelberg, 2005; Dynamics of Aquatic Chemical Ecology, Wilhelmshaven, 2006; Experimentelle und theoretische Metabolomforschung - metabolische Netze, Köln, 2006; Steering Committee of the systems biology programme GoFORSYS; BMBF call “New technologies in Systems Biology”, Berlin 2008
- Editor of the first edition “Metabolomics: Methods and Protocols”, in the series “Methods in Molecular Biology”, Humana Press 2007

Research interests and specific expertise:

The Weckwerth lab is a pioneering research group in method development and data integration approaches for mass spectrometric molecular high throughput profiling (HTP), metabolomics, metabolic flux analysis, proteomics and systems biology [1-6]. They have specific expertise in data handling and the integration of experimental data with modeling of dynamic metabolic networks [7]. They provided for the first time a fundamental relationship between experiment and stochastic metabolic modeling for the biological interpretation of metabolomics HTP data in a systems biology context [1]. For data management and data mining, e.g., the first mass spectral reference database for plant proteomics (PROMEX) was established and recently crossreferenced to Uniprot (<http://www.expasy.uniprot.org/>). ProMEX is further crosslinked to the GMD metabolome database, and extended to whole pathway networks based on KEGG and Mapman genome annotation [8]. The Weckwerth lab developed a so called mass western approach for the targeted analysis of low abundance proteins or whole pathway enzymes in complex proteome samples [9]. Those data are combined with modeling approaches such as flux balance analysis (FBA) or other metabolic modeling approaches. Recently, the group pioneered the application of metabolomics, proteomics and metabolic modeling to improve genome annotation [10]. The Weckwerth group combines genome-wide metabolite, protein and phosphoprotein profiling approaches with consequent development of databases, statistics and cross linkage and biological interpretation of physiological and HTP data. In 2012 Wolfram Weckwerth is one of the organizers of the International Conference in Arabidopsis Research (ICAR) in Vienna. He also organized the first international Metabolomics conference in Austria called InMetA (International Metabolomics Austria). Due to this activity, Austria is now an acknowledged member of the international Metabolomics society with regular activities and participations

worldwide. The author has published more than 70 publications in international journals and books. According to Thomson Web of Science he is one of the leading authors in "Plant Systems Biology".

Relevant publications (for a full list of publications see PubMed and Web of Science)

- [1] Weckwerth, W., Metabolomics in systems biology. *Annu Rev Plant Biol* 2003, 54, 669-689.
- [2] Kempa, S., Hummel, J., Schwemmer, T., Pietzke, M., *et al.*, An automated GCxGC-TOF-MS protocol for batch-wise extraction and alignment of mass isotopomer matrixes from differential C-13-labelling experiments: a case study for photoautotrophic-mixotrophic grown *Chlamydomonas reinhardtii* cells. *Journal of Basic Microbiology* 2009, 49, 82-91.
- [3] Weckwerth, W., Loureiro, M. E., Wenzel, K., Fiehn, O., Differential metabolic networks unravel the effects of silent plant phenotypes. *Proc Natl Acad Sci U S A* 2004, 101, 7809-7814.
- [4] Wienkoop, S., Morgenthal, K., Wolschin, F., Scholz, M., *et al.*, Integration of metabolomic and proteomic phenotypes - Analysis of data-covariance dissects starch and RFO metabolism from low and high temperature compensation response in *Arabidopsis thaliana*. *Mol Cell Proteomics* 2008.
- [5] Weckwerth, W., Wenzel, K., Fiehn, O., Process for the integrated extraction identification, and quantification of metabolites, proteins and RNA to reveal their co-regulation in biochemical networks. *Proteomics* 2004, 4, 78-83.
- [6] Kopka, J., Schauer, N., Krueger, S., Birkemeyer, C., *et al.*, GMD@CSB.DB: the Golm Metabolome Database. *Bioinformatics* 2005, 21, 1635-1638.
- [7] Morgenthal, K., Weckwerth, W., Steuer, R., Metabolomic networks in plants: Transitions from pattern recognition to biological interpretation. *Biosystems* 2006, 83, 108-117.
- [8] Hummel, J., Niemann, M., Wienkoop, S., Schulze, W., *et al.*, ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. *BMC Bioinformatics* 2007, 8, 216.
- [9] Lehmann, U., Wienkoop, S., Weckwerth, W., If the antibody fails - a Mass Western approach. *Plant J* 2008.
- [10] May, P., Wienkoop, S., Kempa, S., Usadel, B., *et al.*, Metabolomics- and proteomics-assisted genome annotation and analysis of the draft metabolic network of *Chlamydomonas reinhardtii*. *Genetics* 2008, 179, 157-166.