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Comprehensive protein turnover analysis of a partial ¹⁵N stable isotope metabolic labelling experiment *In Planta*: Protein dynamics monitored upon drought stress recovery of *Medicago truncatula*

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Protein turnover is a well-controlled process, determined by protein synthesis and degradation rates. In order to quantify protein turnover rates, ¹⁵N stable isotope metabolic labelling of proteinogenic amino acids (AA) is one of the major approaches in MS based proteomics. For cells cultures, this can be facilitated by pulsed stable isotope labelling (SILAC). Therefore only one defined isotopically labelled AA needs to be introduced enabling further MS based protein identification. Stable isotope labelling *In Planta* (SILIP) is more challenging, since ¹⁵N partial labelling is introduced e.g. in form of isotopically labeled ammonium nitrate. Here, all AA will be labelled subsequently, making LC-MS data interpretation more complex and impeding protein identification. *In Planta* analysis is important since it reflects real time protein turnover compared to cell cultures. Novel automated software tools for the interpretation of such data have been developed. For high throughput analysis of huge data sets we have recently employed a software tool (http://promex.pph.univie.ac.at/protover).

For the presented study, protein dynamics were monitored during drought stress recovery of the model Legume *Medicago truncatula*. About 500 protein groups have been identified and relatively quantified from six time points of control and stress recovery samples. Spectral envelopes of more than 1400 partially labelled peptides (~380 proteins) were automatically extracted and turnover rates calculated. Amongst other findings, data mining revealed a significant increase in protein turnover during recovery. Proteins involved in synthesis were increased while regulation of degradation decreased already in the first 2 hours after stress. More detailed results will be discussed.

Biography

Stefanie Wienkoop has completed her PhD in 2000 at the Technical University of Darmstadt. For postdoctoral studies, she went to University of British Columbia, Risoe National Laboratories and Max-Planck Institute of Molecular Plant Physiology. She is Vice Head of the Division of Molecular Systems Biology at University of Vienna, country representative and research committee member of the International Plant Proteomic Organisation (INPPO), member of MASCP, scientific board member of the 1st INPPO World Congress on Plant Proteomics. Editorial Board: Journal of Proteomics, Frontiers in Plant Proteomics, Frontiers in Systems Biology. She has published more than 45 papers in reputed journals

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