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EDUCATION

University of Muenster, Germany	Diploma	1990	Biology
University of Freiburg, Germany	PhD	1994	Plant Biochemistry
University of Geneva, Switzerland	Postdoc	1998	Molecular Biology
University of Jena, Germany	Habilitation	2002	Botany

PROFESSIONAL POSITIONS

Present position: 2006-, Professor, Institute of Plant Biochemistry and Biotechnology, University of Münster, Germany

Previous positions: 2004-2005, Assistant Professor, Department of Biology, University of Pennsylvania, Philadelphia, USA; **2001- 2003**, Independent Group Leader, Department of Plant Physiology, University of Jena, Jena, Germany; **1999-2001**, C1 Assistant, Department of Plant Biochemistry, University of Freiburg, Freiburg, Germany

OTHER PROFESSIONAL ACTIVTIES

2010: Chair of a biotechnology session at the 14th International Conference on the Cell and Molecular Biology of *Chlamydomonas*, USA; **2009:** Member of DECHEMA round table for algae biotechnology; **2008**: Co-Chair of a molecular toolkit session at the 13th International Conference on the Cell and Molecular Biology of *Chlamydomonas*, France; **2007**: Member of the Editorial board of "Current Chemical Biology", Head of the examination board for Master in Biology at the University of Münster; **2006**: Invited speaker at the 13th International symposium on Iron Nutrition and Interactions in Plants, Montpellier, France; Chair of a session on new molecular toolkit resources at the 12th International Conference on the Cell and Molecular Biology of *Chlamydomonas*, Portland, USA; **2005**: Member of the Editorial board of the Journal of Biological Chemistry (2005-2010); **2004**: Chair of the Genomics and Proteomics Session at the 11th Conference on the Cell and Molecular Biology of *Chlamydomonas*, Kobe, Japan; **2003**: Associate Editor, Photosynthesis Research, special issues on *Chlamydomonas* research; Chair of the Genomics and Proteomics Session at the 3rd European Phycological Congress, Belfast, UK.

AWARDS

2000: Invitation fellowship from the Japanese Society for the Promotion of Sciences (JSPS); **1996-1998:** Long-term fellowship from the Human Frontier Science Program (HFSP); **1990:** Diploma with high honour and distinction (summa cum laude), University of Münster, Germany

PATENTS

German patent pending 103 41 595.5: Methods to identify peptides from mass spectrometric data in genomic databases. Patent application was filed September 2003.

PUBLICATIONS

1. Hippler, M., Ratajczak, R. and Haehnel, W. (1989) Identification of the plastocyanin binding subunit of photosystem I. *FEBS Lett*. **250**: 280-284.
2. Hippler, M., Riedel, A., Schroer, U., Nitschke, W. and Haehnel, W. (1996) Light-induced charge separation between plastocyanin and the iron-sulfur clusters FA and FB in the complex of plastocyanin and photosystem I. *Arch Biochem Biophys* **330**: 414-418.

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5. Hippler, M., Drepper, F., Farah, J. and Rochaix, J.D. (1997) Fast electron transfer from cytochrome c6 and plastocyanin to photosystem I of *Chlamydomonas reinhardtii* requires PsaF. *Biochemistry* **36**: 6343-6349.
6. Fischer N., Hippler, M., Setif, P., Jacquot, J.-P. and Rochaix, J.D. (1998) The PsaC subunit of Photosystem I provides an essential lysine residue for fast electron transfer to ferredoxin. *EMBO J*. **16**: 849-858.
7. Hippler, M., Drepper, F., Haehnel, W. and Rochaix, J.D. (1998) The N-terminal domain of PsaF: Precise recognition site for binding and fast electron transfer from cytochrome c6 and plastocyanin to photosystem I of *Chlamydomonas reinhardtii*. *Proc. Natl. Acad. Sci. USA* **95**: 7339-7344.
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9. Hippler, M., Drepper, F, Rochaix, J.D. and Muehlenhoff, U. (1999) Insertion of the N-terminal Part of PsaF from *Chlamydomonas reinhardtii* into photosystem I from *Synechococcus elongatus* enables efficient binding of algal plastocyanin and cytochrome c6. *J. Biol. Chem*. **274**: 4180-4188.
10. Fischer, N., Boudreau, E., Hippler, M., Drepper, F., Haehnel, W. and Rochaix, J.D. (1999) A large fraction of PsaF is nonfunctional in photosystem I complexes lacking the PsaJ subunit. *Biochemistry* **38**: 5546-5552.
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12. Rochaix, J., Fischer, N. and Hippler, M. (2000) Chloroplast site-directed mutagenesis of photosystem I in *Chlamydomonas*: electron transfer reactions and light sensitivity. *Biochimie* **82**: 635-645.
13. Hippler, M., Klein, J., Fink, T., Allinger, T. and Hoerth, P. (2001) Towards functional proteomics of membrane protein complexes: Analysis of thylakoid membranes from *Chlamydomonas reinhardtii. Plant J.* **28**: 595-606.
14. Sommer, F., Drepper, F. and Hippler, M. (2002) The luminal Helix l of PsaB is essential for recognition of plastocyanin or cytochrome c6 and fast electron transfer to photosystem I in *Chlamydomonas reinhardtii. J. Biol. Chem*. **277**: 6573-81.
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28. Stauber, E.J. and Hippler, M. (2004) *Chlamydomonas reinhardtii* proteomics. *Plant Physiol Biochem* **42**: 989-1001.
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41. Clemens, S., Naumann, B. and Hippler, M. (2009) Proteomics of metal mediated protein dynamics in plants - iron and cadmium in the focus. *Frontiers in Biosciences*, **14**, 1955-1969.
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46. Peers, G., Truong, T.B., Ostendorf, E., Busch, A., Elrad, D., Grossman, A., Hippler, M. and Niyogi, K.K. (2009) An ancient light-harvesting protein is critical for the regulation of algal photosynthesis. *Nature*, **in press**.
47. Winkler, M., Kuhlgert, S., Hippler, M. and Happe, T. (2009) Characterization of the key step for light driven hydrogen evolution in green algae. *J Biol Chem*, **in press**.

BOOK ARTICLES

1. R Bock and M Hippler (2002) Extranuclear inheritance: Functional genomics in chloroplasts. In: Progress in Botany, 63, Springer-Verlag, Berlin Heidelberg, pages 106-131
2. F Sommer and M Hippler (2002) Photosystem I: Structure/Function and Assembly of a transmembrane light-driven Plastocyanin/Cytochrome c6 – Ferredoxin Oxidoreductase. Handbook of Photochemistry and Photobiology Vol. 4, Ed. H.S. Nalwa, American Scientific Publishers, Stevenson Ranch, California, USA, pages 269-294
3. M Hippler and R Bock (2004) Extranuclear inheritance: Chloroplast Proteomics. In Progress in Botany. Springer-Verlag Berlin Heidelberg, Vol. 65, pp. 90-105
4. F Drepper and M Hippler (2006) Binding and electron transfer between photosystem I and plastocyanin or cytochrome c6. In Advances in Photosynthesis and Respiration Springer-Verlag, in press
5. B. Naumann and M. Hippler (2008) Insights into chloroplast proteomics: from basic principles to new horizons. In Topics in Current Genetics Ed. R.Bock, Springer-Verlag.

CURRENT RESEARCH INTERESTS

Our research is aimed to understand plant cell responses and adaptation strategies to environmental stresses. Furthermore we aim to elucidate molecular mechanisms which are involved in assembly, function, maintenance and regulation of the photosynthetic machinery in oxygenic chloroplast photosynthesis. For this purpose, we are mainly using the green alga *Chlamydomonas reinhardtii* as a model system and combining molecular techniques like reverse genetics and proteomics to elucidate these processes. Hereby, we are engaged in different research lines.

(**i**) We are currently investigating the adaptation and remodeling of the photosynthetic apparatus as a response to iron-deficiency. We are also interested in an understanding of chloroplast iron-homeostasis

as a whole. To gain insights into chloroplast iron-homeostasis we are carrying out a comparative proteomic approach and take advantage of stable isotope labeling by amino acids in Chlamydomonas (Naumann et al., 2007; Naumann et al., 2005) The investigation of putative candidate gene products in plastid iron homeostasis is done by reverse genetics using an RNAi approach as described by Cerutti and colleagues (Rohr et al., 2004). This approach was already successfully employed in our laboratory to suppress expression levels of Lhca3 (Naumann et al., 2005) and ferritin (Busch et al., 2008). Momentarily a focus is on the analysis of PGRL1 in iron-deficiency responses. In an RNAi strain, which accumulates lower PGRL1 levels in both Fe –replete and –starved conditions, the photosynthetic electron transfer rate is decreased, respiratory capacity in Fe sufficient conditions is increased, and the efficiency of cyclic electron transfer (CEF) under iron-deprivation is diminished. Furthermore, *pgrl1-kd* cells exhibit iron-deficiency symptoms at higher Fe concentrations than does the wild-type, although the cells are not more depleted in cellular iron relative to the wild-type as measured by mass spectrometry. Thiol trapping experiments indicate iron-dependent and redox-induced conformational changes in PGRL1 that may interconnect iron metabolism and CEF and thereby partitioning between linear photosynthetic electron transfer and CEF. We propose therefore that PGRL1 in *C. reinhardtii* possesses a dual function in iron sensing as well as modulation of cyclic electron transfer (Petroutsos et al., 2009). Future experiments will be directed to elucidate protein-protein-interactions of PGRL1 and metal-binding dynamics of the protein.

(ii) Light is a necessary substrate for photosynthesis, but its absorption by pigment molecules such as chlorophyll can cause severe oxidative damage and result in cell death. The excess absorption of light energy by photosynthetic pigments has led to the evolution of protective mechanisms that operate on the time scale of seconds to minutes and involve feedback regulated de-excitation of chlorophyll molecules in photosystem II (qE). Despite the significant contribution of eukaryotic algae to global primary production, little is known about their qE mechanism, in stark contrast to flowering plants. Data that have been obtained in cooperation the group of Prof. K. Niyogi show that *Chlamydomonas reinhardtii* mutants diminished or -deficient in qE have an impact in the expression of *lhcsr* genes, either due to RNAi-technology or due to knock-down of two of the three genes encoding LHCSR (formerly called LI818) (Peers et al., 2009). This protein is an ancient member of the light-harvesting complex superfamily, and orthologs are found throughout photosynthetic eukaryote taxa, except red algae and vascular plants. The qE capacity of *Chlamydomonas* is dependent on environmental conditions and is inducible by growth in high light. LHCSR-RNAi or knock-out mutants have a reduced fitness in a shifting light environment compared to wild-type cells, demonstrating that LHCSR is required for survival in a dynamic light environment. Therefore the data indicate that plants and algae employ different proteins to dissipate harmful excess energy and protect the photosynthetic apparatus from damage. In the future more insight into the NPQ mechanism and its regulation in algae has to be gathered to understand the evolution of light management in algae and vascular plants.

(iii) At present we are also studying the remodeling of Chlamydomonas metabolism after transition to anaerobic growth conditions. The versatile metabolism of the green alga *Chlamydomonas reinhardtii* is reflected in its ability to acclimate to anaerobic conditions. The complex anaerobic response is also remarkable in the context of renewable energy since *C. reinhardtii* is able to produce hydrogen under anaerobic conditions. To identify proteins involved during anaerobic acclimation as well as to localize proteins and pathways to the powerhouses of the cell, chloroplasts and mitochondria from *C. reinhardtii* in aerobic and anaerobic (induced by 8 hours of argon bubbling) conditions were isolated and analyzed using comparative proteomics. A total of 2315 proteins were identified. Further analysis based on spectral counting localized 895 of these proteins to the chloroplast, including many proteins of the fermentative metabolism. Comparative quantitative analyses were performed with the chloroplast-localized proteins using stable isotopic labeling of amino acids ($^{13}C_6$ Arginine/$^{12}C_6$ Arginine in an Arginine-auxotrophic strain). The quantitative data confirmed proteins previously characterized as induced at the transcript level as well as identifying several new proteins of unknown function induced under anaerobic conditions. These proteins of unknown function provide new candidates for further investigations taking advantage of reverse genetics. An important aim hereby is to understand the anaerobic response in the green alga. Another important aim will be to engineer

Chlamydomonas strains that produce hydrogen in amounts allowing commercial exploration of the process.

(iv) In plant cells, the increase in cytoplasmic calcium $[Ca^{2+}]_{cyt}$ represents a frequent response to various abiotic and biotic stresses. After changes in cytosolic Ca^{2+} signatures have been sensed, phoshorylation cascades appear to represent general downstream responses in Ca-dependent signal transduction. To elucidate $[Ca^{2+}]_{cyt}$ dependent protein phosphorylation, identify $[Ca^{2+}]_{cyt}$ dependent phosphoproteins, map phosphorylation sites and quantify phosphorylation, we are applying a phosphoproteomics approach, in which *Arabidopsis thaliana* and *Chlamydomonas reinhardtii* are taken as model systems.

(**v**) In another research line we are aiming to explore electron transfer and binding mechanisms between the soluble electron transfer proteins plastocyanin or cytochrome c6 and photosystem I (PSI) (Finazzi et al., 2005; Sommer et al., 2004; Sommer et al., 2006; Sommer et al., 2002). Additionally we aim to investigate the molecular recognition between PSI and its light-harvesting protein complex (LHCI), allowing the formation of the PSI/LHCI complex, subunit remodeling as well as efficient excitation energy transfer (Naumann et al., 2005; Nield et al., 2004; Storf et al., 2004; Takahashi et al., 2004). Hereby we are also taking advantage of absolute quantitation by using proteotypic peptide probes to enumerate the stochiometry of LHCI subunits per PSI core complex (Stauber et al., 2009).

(**vi**) We are establishing bioinformatics tools that are aimed to facilitate mass spectrometric analyses of eukaryotic organisms with complex gene structures. Here we are aiming to use mass spectrometric data for genomic data mining and annotation of protein-coding genes. We devised an algorithm, the GenomicPeptideFinder (GPF), which takes advantage of *de novo* amino acid predictions of MS/MS data enabling detection of intron-split and/or alternatively spliced peptides when deduced from genomic DNA (Allmer et al., 2004). We generated a platform where high throughput *de novo* sequencing of MS/MS spectra is combined with GPF performance operating on a computer cluster to analyze Chlamydomonas protein data (Allmer et al., 2006). We further developed a database for storage, analysis, presentation, and retrieval of information from mass spectrometric experiments (Allmer et al., 2008). Furthermore we devised an algorithm for evaluating quantitative mass spectrometric data stemming from SILAC or ^{15}N-labeling (Specht et al., unpublished) experiments.

For proteomic analyses the laboratory is equipped with a hybrid linear ion-trap mass spectrometer (LTQ-Orbitrap, Thermo Finnigan) that is coupled to an UltiMate Nano liquid chromatography system (Dionex).

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