Rice proteomics: recent developments and analysis of nuclear proteins

Phytochemistry, 2004, **65**, 1671

Md. Monowar Karim Khan, Setsuko Komatsu

Department of Molecular Genetics, National Institute of Agrobiological Sciences, Kannondai 2-1-2, Tsukuba 305-8602, Japan

The proteome research in rice is reviewed and presented a comprehensive research on nuclear proteome. In the nucleus of rice 549 protein spots were resolved on 2-DE by CBB staining. One hundred and ninety proteins were identified and sorted into different functional categories. Proteins involved in signaling and gene regulations dominated others in the nucleus.

Rice Proteome Database
(http://gene64.dna.affrc.go.jp/RPD/main.html)

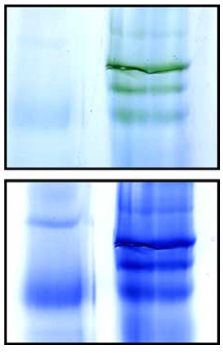
Proteomic approach to characterize the supramolecular organization of photosystems in higher plants

Phytochemistry, 2004, **65**, 1683

Jesco Heinemeyer [a], Holger Eubel [a], Dirk Wehmhöner [b], Lothar Jänsch [b], Hans-Peter Braun [a]

[a]*Institut für Angewandte Genetik, Universität Hannover, Herrenhäuser Str. 2, D-30419 Hannover, Germany*
[b]*Gesellschaft für Biotechnologische Forschung, Mascheroder Weg 1, 38124 Braunschweig, Germany*

Using Blue-native polyacrylamide gel electrophoresis of digitonin solubilized chloroplast fractions from *Arabidopsis*, nine protein supercomplexes containing either photosystem I or II were resolved in a molecular mass range between 600 and 3200 kDa. A strategy for systematic subunit identifications of supercomplexes is suggested, which employs direct trypsination of complexes and afterwards peptide identifications by mass spectrometry. Based on this approach, eight different proteins of the light harvesting complex II family are shown to form part of a 1300 kDa photosystem II supercomplex.



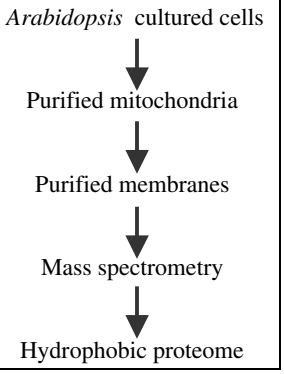
The hydrophobic proteome of mitochondrial membranes from *Arabidopsis* cell suspensions

Phytochemistry, 2004, **65**, 1693

Sabine Brugière [a], Soléne Kowalski [b], Myriam Ferro [a], Daphné Seigneurin-Berny [b], Stéphane Miras [b], Daniel Salvi [b], Stéphane Ravanel [b], Pierre d'Hérin [b], Jérôme Garin [a], Jacques Bourguignon [b], Jacques Joyard [b], Norbert Rolland [b]

[a]*Laboratoire de Chimie des Protéines, ERM-0201 INSERM/CEA, France*
[b]*Laboratoire de Physiologie Cellulaire Végétale, UMR-5168 (CNRS/Université Joseph Fourier/INRA/CEA), France*

A targeted subcellular proteomic approach was performed to get a more exhaustive array of mitochondrial membrane proteins from *Arabidopsis* cultured cells. The identification of these proteins is discussed with respect to their known or predicted subcellular localization, physicochemical and functional properties.



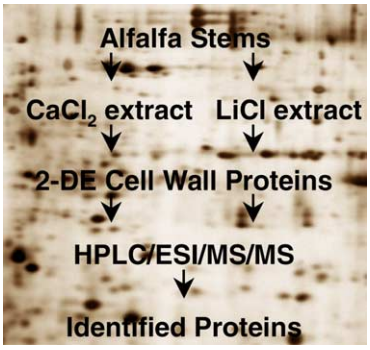
Proteomics of *Medicago sativa* cell walls

Phytochemistry, 2004, **65**, 1709

Bonnie S. Watson, Zhentian Lei, Richard A. Dixon, Lloyd W. Sumner

Plant Biology Division, The Samuel Roberts Noble Foundation, PO Box 2180, Ardmore, OK 73402, USA

An extraction method for obtaining cell wall proteins from mature alfalfa stems is outlined. Proteins were extracted, profiled by 2-DE, identified, classified, and roles in the cell wall discussed.



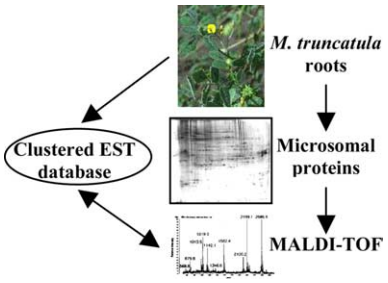
Sub-cellular proteomic analysis of a *Medicago truncatula* root microsomal fraction

Phytochemistry, 2004, **65**, 1721

Benoît Valot, Silvio Gianinazzi, Dumas-Gaudot Eliane

UMR 1088 INRA/CNRS 5184/UB Plante-Microbe-Environment, INRA/CMSE, BP 86510, 21065 Dijon cedex, France

Membrane-associated proteins of *Medicago truncatula* roots were characterized on 2-DE following sub-cellular fractionation. Ninety-six proteins were identified using *M. truncatula* clustered EST database for mass spectrometry identification by fingerprinting.



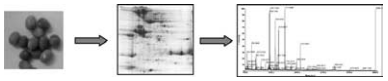
High-throughput peptide mass fingerprinting of soybean seed proteins: automated workflow and utility of UniGene expressed sequence tag databases for protein identification

Phytochemistry, 2004, **65**, 1733

Brain P. Mooney, Jay J. Thelen

Department of Biochemistry and Proteomics Center, University of Missouri-Columbia, 125 Chemistry, Columbia, MO 65211, USA

Soybean seed polypeptides resolved by 2-D electrophoresis were quantified and identified using an automated peptide mass fingerprinting workflow.



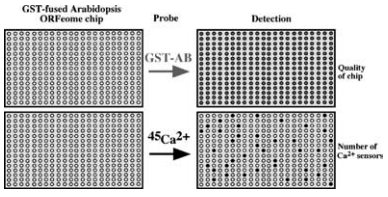
Proteomics of calcium-signaling components in plants

Phytochemistry, 2004, **65**, 1745

Vaka S. Reddy, Anireddy S.N. Reddy

Department of Biology and Program in Cell and Molecular Biology, Colorado State University, 200 West Lake Street, Fort Collins, CO 80523, USA

Calcium functions as a versatile messenger in mediating responses to hormones, biotic/abiotic stress signals and a variety of developmental cues in plants. Calcium circuitry consists of at least three major nodes. The components of each node and their functions are discussed. An overview of genome-wide approaches in unraveling Ca^{2+}-signaling circuitry is presented.



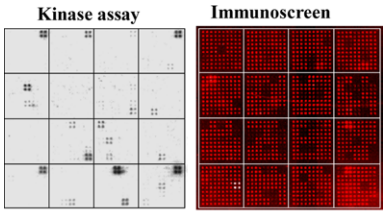
Identification of barley CK2α targets by using the protein microarray technology

Phytochemistry, 2004, **65**, 1777

Armin Kramer [a], Tanja Feilner [a], Alexandra Possling [a], Volodymyr Radchuk [b], Winfriede Weschke [b], Lukas Bürkle [a,c], Birgit Kersten [a]

[a] *Department of Lehrach, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany*
[b] *Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), D-06466 Gatersleben, Germany*
[c] *Institute of Veterinary Biochemistry and Molecular Biology, University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland*

Twenty-one potential targets of the barley protein kinase CK2α were identified out of 768 different barley proteins by means of a novel protein microarray-based kinase assay.



Protein microarrays with 384 barley proteins

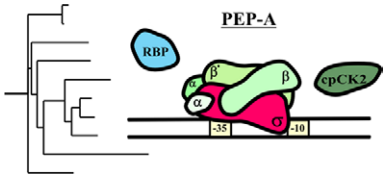
Proteomics-based sequence analysis of plant gene expression – the chloroplast transcription apparatus

Phytochemistry, 2004, **65**, 1785

Heike Loschelder, Anke Homann, Karsten Ogrzewalla, Gerhard Link

Plant Cell Physiology and Molecular Biology, University of Bochum, Building ND 2-72, Universitaetsstr. 150, D44780 Bochum, Germany

Database screening helped to identify regulatory proteins of chloroplast RNA polymerase, including a novel putative RNA-binding protein (RBP). The previously identified transcription kinase (cpCK2) is likely to play a common role in number of plant species.



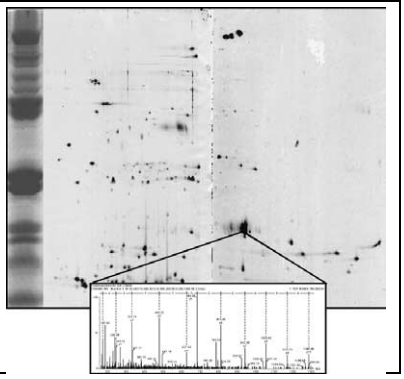
Proteomics of curcurbit phloem exudate reveals a network of defence proteins

Phytochemistry, 2004, **65**, 1795

Christina Walz [a], Patrick Giavalisco [a], Martina Schad [a], Melanie Juenger [b], Joachim Klose [c], Julia Kehr [a]

[a]*Department L. Willmitzer, Max-Planck-Institute of Molecular Plant Physiology, Am Muehlenberg 1, 14424 Potsdam, Germany*
[b]*Faculty of Biology, Ruhr-University Bochum, 44801 Bochum, Germany*
[c]*Institute for Human Genetics, Humboldt University Berlin, Charité, Augustenburger Platz 1, 13353 Berlin, Germany*

Analysis of cucumber and pumpkin phloem sap proteins by one- and two-dimensional gel electrophoresis identified a range of proteins involved in plant defence reactions against different environmental or pathogen stresses.



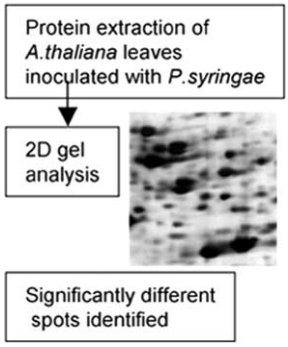
Specific changes in the *Arabidopsis* proteome in response to bacterial challenge: differentiating basal and *R*-gene mediated resistance

Phytochemistry, 2004, **65**, 1805

Alexandra M.E. Jones [a], Vincent Thomas [b], Bill Truman [a], Kathryn Lilley [c], John Mansfield [a], Murray Grant [a]

[a]*Department of Agricultural Science, Imperial College London, Wye Campus, High Street, Wye TN25 5AH, UK*
[b]*School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, UK*
[c]*Cambridge Centre for Proteomics, Department of Biochemistry, University of Cambridge, Building O, Downing Site, Cambridge CB2 1QW, UK*

We present changes to proteins from two antioxidant enzyme families through the use of two-dimensional gel electrophoresis and compare proteomic and transcriptomic data from the same inoculation system.



A proteomic approach to studying plant response to crenate broomrape (*Orobanche crenata*) in pea (*Pisum sativum*)

Phytochemistry, 2004, **65**, 1817

M. Ángeles Castillejo [a], Nardjis Amiour [b], Eliane Dumas-Gaudot [a], Diego Rubiales [c], Jesús V. Jorrín [a]

[a]*Agricultural and Plant Biochemistry Research Group, Department of Biochemistry and Molecular Biology, University of Córdoba, Campus de Rabanales, Edificio Severo Ochoa (C6), 14071 Córdoba, Spain*
[b]*UMR 1088 INRA/CNRS 5184/UB, (Plante-Microbe-Environnement) INRA-CMSE, BP 86510, 21065 DIJON Cedex, France*
[c]*Instituto de Agricultura Sostenible-CSIC, Apdo 4084, 14080 Córdoba, Spain*

By using a proteomic approach, including two-dimensional gel electrophoresis and MALDI-TOF mass spectrometry, a number of proteins differently expressed in broomrape-infected susceptible and partially resistant pea roots have been identified.