GRAPHICAL ABSTRACTS

Phytochemistry, 2004, **65**, 1449

Plant proteome analysis by mass spectrometry: principles, problems, pitfalls and recent developments

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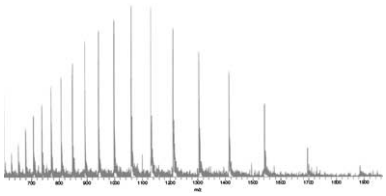
Basic strategy from extraction through fractionation and purification to mass spectrometric analysis is discussed and some plant proteomic applications are reviewed, as are imminent future developments in relevant mass spectrometric instrumentation.



Phytochemistry, 2004, **65**, 1487

Technical aspects of functional proteomics in plants

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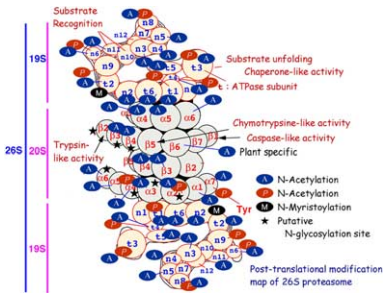
In proteome analysis, many improvements in separation and identification of proteins have rapidly been achieved, and some new techniques, which include top-down mass spectrometry and tandem affinity purification, have emerged. These techniques have provided the possibility of high-throughput analysis of function and functional network of proteins in plants. However, more sophisticated techniques and software are essential. The development and adaptation of such techniques will ease analyses of protein profiling, identification of post-transactional modifications and protein–protein interaction, which are vital for elucidation of the protein functions.



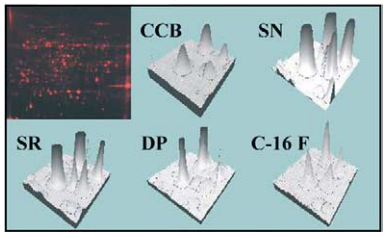
Phytochemistry, 2004, **65**, 1499

Proteomic capacity of recent fluorescent dyes for protein staining

François Chevalier, Vaérie Rofidal, Pavlina Vanova, Alexis Bergoin, Michel Rossignol

Laboratoire de Protéomique, INRA, UR 1199, 2 place Viala, 34060 Montpellier Cedex 1, France

Recent fluorophores (5-hexadecanoylamino-fluorescein, Deep Purple®, Sypro Ruby®) were compared to classical visible dyes (colloidal Coomassie blue, silver nitrate), using *Arabidopsis* total protein extract, for various parameters important in comparative proteome analysis: background, staining saturation, sensitivity, staining reproducibility.

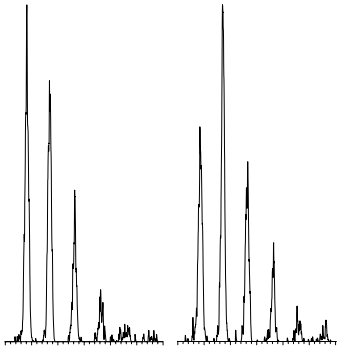


Phytochemistry, 2004, **65**, 1507

Subtle modification of isotope ratio proteomics; an integrated strategy for expression proteomics

Julian P. Whitelegge, Jonathan E. Katz, Katianna A. Pihakari, Rebecca Hale, Rodrigo Aguilera, Stephen M. Gómez, Kym F. Faull, Dmitrii Vavilin, Willem Vermaas

Modification of the $^{13}C/^{12}C$ isotope ratio of plant protein samples is being investigated as an alternative to full isotopic exchange for coding in proteomics. Provided the isotope ratio is subtly modified, protein identification experiments are not compromised and thus provide elemental composition for accurate isotope ratio decoding.



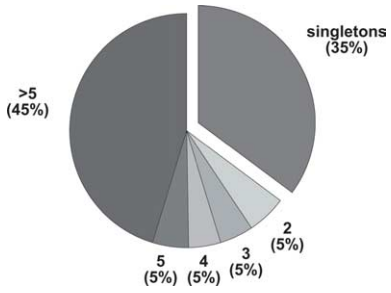
Untangling multi-gene families in plants by integrating proteomics into functional genomics

Phytochemistry, 2004, **65**, 1517

Pia G. Sappl, Joshua L. Heazlewood, A. Harvey Millar

Plant Molecular Biology Group, School of Biomedical and Chemical Sciences, The University of Western Australia, M310, Biochemistry, 35 Stirling Highway, Crawley, Perth 6009, WA, Australia

The classification and study of gene families is emerging as a constructive tool for fast tracking the elucidation of gene function. We review the growing role of proteomics in analysing gene families in model plant species by specifically identifying the products of closely related genes, determining their abundance, and coupled to affinity chromatography and subcellular fractionation studies, providing location within cells and functional assessment of specific family members.



Multivariate approaches in plant science

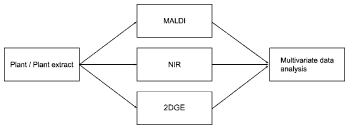
Phytochemistry, 2004, **65**, 1531

David M. Gottlieb [a], Jakob Schultz [b], Susanne W. Bruun [b], Susanne Jacobsen [b], Ib Søndergaard [b]

[a] *Plasma Product Division, Statens Serum Institut, Artillerivej 5, DK-2300 Copenhagen S, Denmark*

[b] *Biochemistry and Nutrition Group, BioCentrum-DTU, Technical University of Denmark, Søltofts Plads, building 224, DK-2800 Kgs. Lyngby, Denmark*

This paper suggests how classical proteomics can be improved by use of multivariate statistical analysis. Multivariate statistics offers a cognitive approach in handling large data sets. An introduction to the most widely used methods and three practical examples of analysing proteomic data of plant extracts are given.



Genome-scale, biochemical annotation method based on the wheat germ cell-free protein synthesis system

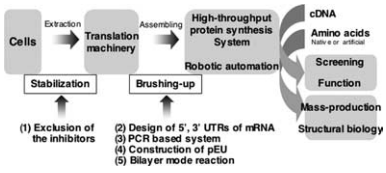
Phytochemistry, 2004, **65**, 1549

Tatsuya Sawasaki [a], Yoshinori Hasegawa [a], Ryo Morishita [a], Motoaki Seki [b], Kazuo Shinozaki [b], Yaeta Endo [a]

[a] *Cell-Free Science and Technology Research Center, The Venture Business Laboratory, Ehime University, Matsuyama 790-8577, Japan*

[b] *Plant Mutation Exploration Team, Plant Functional Genomics Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan*

This report reviews the high-throughput, genome-scale biochemical annotation method based on the cell-free system prepared from wheat embryos.



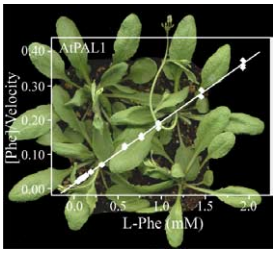
The *Arabidopsis* phenylalanine ammonia lyase gene family: kinetic characterization of the four PAL isoforms

Phytochemistry, 2004, **65**, 1557

Fiona C. Cochrane, Laurence B. Davin, Norman G. Lewis

Institute of Biological Chemistry, Washington State University, Clark Hall 467, Pullman, WA 99164-6340, USA

In *Arabidopsis thaliana*, four genes have been annotated as provisionally encoding phenylalanine ammonia lyase (PAL). In this study, recombinant native AtPAL1, 2, and 4 were demonstrated to be catalytically competent for L-phenylalanine deamination (K_m values between 64 and 71 μM), whereas AtPAL3 was of very low specific activity in its N-terminal His-tagged form.



Proteome analysis differentiates between two highly homologues germin-like proteins in *Arabidopsis thaliana* ecotypes Col-0 and Ws-2

Phytochemistry, 2004, **65**, 1565

Bernhard Schlesier [a], Anne Berna [b], François Bernier [b], Hans-Peter Mock [a]

[a] *Molecular Cell Biology, Institute of Plant Genetics and Crop Plant Research, Corrensstrasse 3, D-06466 Gatersleben, Germany*
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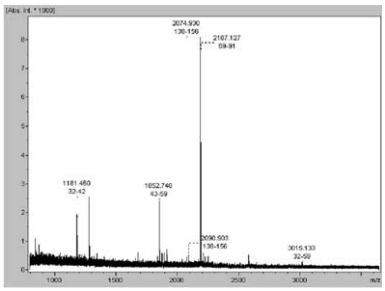


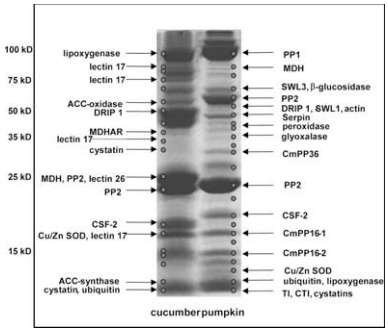
Two highly related germin-like proteins differing in only one amino acid residue were detected by proteome analysis based on 2-D gel separation of extracts and identification by mass spectrometry. Results were confirmed by 2-D Western blotting which also allowed to detect AtGER3 protein for the first time in root extracts.

Investigation of cationic peanut peroxidase glycans by electrospray ionization mass spectrometry

Phytochemistry, 2004, **65**, 1575

Cunjie Zhang [a], Amanda Doherty-Kirby [a], Robert van Huystee [a], Gilles Lajoie [a]

[a] *Department of Biochemistry, The University of Western Ontario, London, Ont., Canada N6A 5C1*
[b] *Department of Biology, The University of Western Ontario, London, Ont., Canada N6A 5B7*



The structure of the complex glycans from cationic peanut peroxidase were characterized using off-line HPLC and electrospray ionization mass spectrometry.

Mapping of the *Physcomitrella patens* proteome

Phytochemistry, 2004, **65**, 1589

Eric Sarnighausen [a], Virginie Wurtz [b], Dimitri Heintz [a], Alain Van Dorsselaer [d], Ralf Reski [a]

[a] *Plant Biotechnology, University of Freiburg, Schaenzlestr. 1, 79104 Freiburg, Germany*
[b] *Laboratoire de spectrométrie de masse Bio-Organique, CNRS-UMR 7509/ULP, 25 rue Becquerel, 67087 Strasbourg cedex 2, France*

The potential of the moss *Physcomitrella patens* to serve as a model organism for plant functional genomics is further widened by the feasibility of proteomic approaches.

A two-dimensional proteome map of maize endosperm

Phytochemistry, 2004, **65**, 1609

Valérie Méchin, Thierry Balliau, Sophie Château-Joubert, Marléne Davanture, Olivier Langella, Luc Négroni, Jean-Louis Prioul, Claudine Thévenot, Michel Zivy, Catherine Damerval

A two-dimensional reference map of maize endosperm proteins was established, with the identification of 496 spots sorted in 15 functional categories. The three most abundant categories were metabolism, protein destination and protein synthesis. This map is the first step for investigating maize endosperm development.

Zea mays
Endosperm
proteins
↓
2D PAGE
LC-MS/MS
↓
78% identified
protein spots

Environmental and transgene expression effects on the barley seed proteome

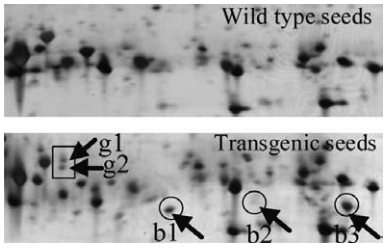
Phytochemistry, 2004, **65**, 1619

Christine Finnie [a], Torben Steenholdt [a], Oriol Roda Noguera [a,b], Søren Knudsen [c], Jørgen Larsen [c], Henrik Brinch-Pedersen [c], Preben Bach Holm [c], Ole Olsen [c], Birte Svensson [a]

[a] *Department of Chemistry, Carlsberg Laboratory, Gamle Carlsberg Vej 10, DK-2500 Valby, Denmark*

[b] *Departament de Ciències Experimentales i de la Salut, Facultat de Ciències de la Salut i de la Vida, Universitat Pompeu Fabra, 08003 Barcelona, Spain*

[c] *Carlsberg Research Laboratory, Gamle Carlsberg Vej 10, DK-2500 Valby, Denmark*



The water-soluble seed proteins of *Hordeum vulgare* cv. Barke and Golden Promise were compared. Protein spots that differed between greenhouse and field-grown or wild type and transgenic seeds were identified.

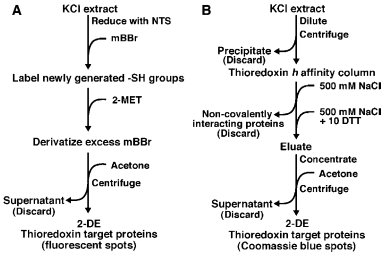
Thioredoxin targets of developing wheat seeds identified by complementary proteomic approaches

Phytochemistry, 2004, **65**, 1629

Joshua H. Wong [a], Nick Cai [a], Yves Balmer [a], Charlene K. Tanaka [b], William H. Vensel [b], William J. Hurkman [b], Bob B. Buchanan [a]

[a] *Department of Plant and Microbial Biology, University of California, 111 Koshland Hall, Berkeley, CA 94720, USA*

[b] *USDA, Agricultural Research Service, Western Regional Research Center, Albany, CA 94710, USA*



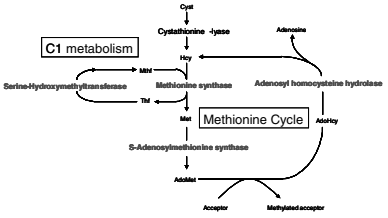
Proteomics in combination with fluorescence (A) and affinity chromatography (B) isolation procedures led to the identification of 68 thioredoxin target proteins in wheat endosperm and flour, 40 not described in seeds, that changed during development. The isolation procedures were complementary: of the total targets, 1/3 were found with both procedures and 1/3 were unique to each.

Cell-specific protein profiling in *Arabidopsis thaliana* trichomes: identification of trichome-located proteins involved in sulfur metabolism and detoxification

Phytochemistry, 2004, **65**, 1641

Stefanie Wienkoop, Daniela Zoeller, Berit Ebert, Ulrike Simon-Rosin, Joachim Fisahn, Mirko Glinski, Wolfram Weckwerth

Max Planck Institute of Molecular Plant Physiology, Metabolic Networks, 14424 Potsdam, Germany



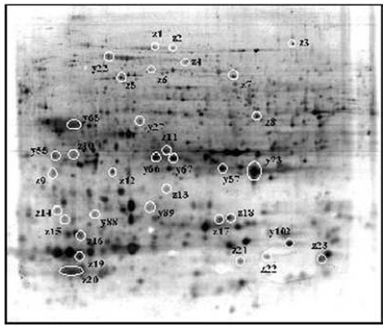
A complete *S*-adenosylmethionine pathway cluster and other proteins involved in sulfur metabolism and detoxification are shown to be present in trichome cells.

Impact of sewage sludges on *Medicago truncatula* symbiotic proteome

Phytochemistry, 2004, **65**, 1651

Gwénaëlle Bestel-Corre, Silvio Gianinazzi, Eliane Dumas-Gaudot

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



Two-dimensional electrophoresis, matrix-assisted laser desorption ionization mass spectrometry and image analysis were used to study the effects of sewage sludges on the proteome of *Medicago truncatula* roots in symbiosis with the arbuscular mycorrhizal fungus *Glomus mosseae* or the rhizobial bacterium *Sinorhizobium meliloti*.