

PROTEOMICS

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Plant Proteomics

Editors:
Dominique Job
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Editorial

Plant Proteomics

Plants are our “bread and butter”, the fundamental basis of human and animal nutrition. They are the most important species on our planet, controlling our food production and providing human sustenance, at least in the foreseeable future. The world population, estimated to be 6.8 billion, is projected to reach 9 billion by 2040. This rapid growth requires continuous production increases to ensure food and feed supply. Even greater increases in production are needed to alleviate the pain of the estimated 900 million people globally who are suffering from malnutrition. Besides, these higher productions will be needed in the context of a decline in arable land due to industrialization, housing and infrastructure. This is in addition to the problem of water resources that is severe in many countries, notably in the context of climate change.

Plants are also used as invaluable resources for both renewable raw material and energy, and they synthesize a great variety of essential molecules (amino acids, vitamins), lipids and secondary metabolites, including highly efficient pharmaceuticals. And yet, the full potential of plants for biosynthesis of such useful compounds has only just begun to be explored. For these reasons, it is crucial to improve the security and productivity of cultivated areas within their social, political and economic context. Achieving enhanced food and feed production in an environmentally sustainable manner will be an extremely difficult task. Nevertheless it is a vitally important enterprise.

Plants, which represent the majority of the eukaryotic biomass of the planet, are sessile organisms. Therefore, they exhibit unique physiological properties, notably in response to their biotic and abiotic environments, which cannot be deduced from studies in other organisms. Application of this knowledge for product innovation will benefit consumers and the environment, promoting sustainable agriculture and preserving biodiversity.

As is the case for other organisms, proteomics is now an important part of plant science, providing essential tools for understanding the unique functions of the many plant-specific biological processes at the molecular level. The extent of development in plant proteome research is reflected by the publication of more than 350 “plant proteomics” papers in 2010, and more than 2000 papers since 1999, as measured by a simple keyword search of the PubMed database (www.pubmed.com).

In this Special Issue, we have selected a range of articles dealing with a diverse number of fields that include both fundamental knowledge of plant physiology and major societal questions. Using both model plants and crops, these articles include analyses of plant development, the characterization of plant defense under biotic and abiotic stress, the characterization of subcellular, cellular or plant organ proteomes, the characterization of protein modifications, the characterization of protein complexes and protein networks, the development of bioinformatics tools for proteomics data, the search of biomarkers of plant product quality, the characterization of the genetic control of the accumulation of plant proteins by combining proteomic and quantitative trait loci mapping approaches and the use of MALDI-Imaging mass spectrometry for the characterization of the spatial distribution of metabolites and proteins in intact plant tissues. We introduce the Issue with a vision for the future of plant proteomics, which is discussed in the context of the launching of the International Plant Proteomics Organization.

We believe that these articles will be of interest for general readers, proteomics researchers, and plant biologists. We thank all contributors of this Special Issue for highlighting future trends and challenges. We also thank all reviewers for their many positive comments.



Dominique Job



Paul A. Haynes



Michel Zivy

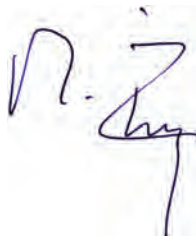
This Special Issue is dedicated to the proteomic community in Japan to which we, and the Journal, express our best wishes and support in the current difficult situation.



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SPECIAL

PLANT PROTEOMICS

**Editors: Dominique Job,
 Paul A. Haynes
 and Michel Zivy**



EDITORIAL

1557

Plant Proteomics

*Dominique Job, Paul A. Haynes
 and Michel Zivy*

1559



Time to articulate a vision for the future of plant proteomics – A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO)

*Ganesh Kumar Agrawal, Dominique Job, Michel Zivy, Vishwanath P. Agrawal,
 Ralph A. Bradshaw, Michael J. Dunn, Paul A. Haynes, Klaas J. van Wijk,
 Shoshi Kikuchi, Jenny Renaut, Wolfram Weckwerth and Randeep Rakwal*



Given the essential role of proteomics in understanding the biology of plants, we are establishing a global plant proteomics organization to properly organize, preserve and disseminate collected information on plant proteomics. We call this organization ‘International Plant Proteomics Organization (INPPO; <http://www.inppo.com>).’ Ten initiatives of INPPO are outlined along with how to address them in multiple phases. As our vision is global, we sincerely hope the scientific communities around the world will come together to support and join INPPO.

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1569

RESEARCH ARTICLE

Proteomics reveals potential biomarkers of seed vigor in sugarbeet

*Julie Catusse, Juliane Meinhard, Claudette Job, Jean-Marc Strub, Uwe Fischer,
 Elena Pestsova, Peter Westhoff, Alain Van Dorsselaer and Dominique Job*

 **Supporting information see www.proteomics-journal.com**



- 1581 **RESEARCH ARTICLE**
A PQL (protein quantity loci) analysis of mature pea seed proteins identifies loci determining seed protein composition

Michael Bourgeois, Françoise Jacquin, Florence Cassecuelle, Vincent Savoie, Maya Belghazi, Grégoire Aubert, Laurence Quillien, Myriam Huart, Pascal Marget and Judith Burstin

 **Supporting information see www.proteomics-journal.com**

- 1595 **REVIEW**
Proteomes of the barley aleurone layer: A model system for plant signalling and protein secretion

Christine Finnie, Birgit Andersen, Azar Shahpiri and Birte Svensson

 **Supporting information see www.proteomics-journal.com**

- 1606 **REVIEW**
Reboot the system thanks to protein post-translational modifications and proteome diversity: How quiescent seeds restart their metabolism to prepare seedling establishment

Erwann Arc, Marc Galland, Gwendal Cueff, Béatrice Godin, Imen Lounifi, Dominique Job and Loïc Rajjou

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- 1619 **REVIEW**
Comparative proteomics of seed maturation in oilseeds reveals differences in intermediary metabolism

Martin Hajduch, Radoslava Matusova, Norma L. Houston and Jay J. Thelen

- 1630 **REVIEW**
Rice proteomics: A move toward expanded proteome coverage to comparative and functional proteomics uncovers the mysteries of rice and plant biology

Ganesh Kumar Agrawal and Randeep Rakwal

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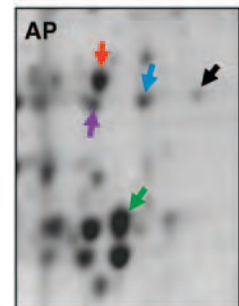
- 1650 **REVIEW**
Investigating the plant response to cadmium exposure by proteomic and metabolomic approaches

Florent Villiers, Céline Ducruix, Véronique Hugouvieux, Nolwenn Jarno, Eric Ezan, Jérôme Garin, Christophe Junot and Jacques Bourguignon

- 1664 **RESEARCH ARTICLE**
Proteomic analysis of defense response of wildtype *Arabidopsis thaliana* and plants with impaired NO-homeostasis

Christian Holzmeister, Andreas Fröhlich, Hakan Sarioglu, Norbert Bauer, Jörg Durner and Christian Lindermayr

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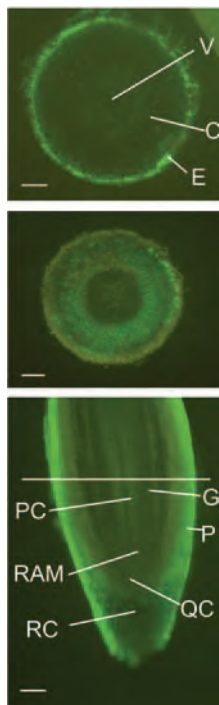
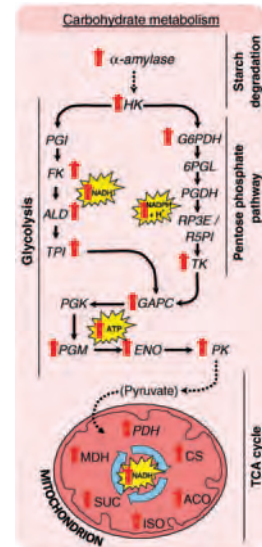





- 1684 **RESEARCH ARTICLE**
Implications of high-temperature events and water deficits on protein profiles in wheat (*Triticum aestivum* L. cv. Vinjett) grain

Fen Yang, Anders D. Jørgensen, Huawei Li, Ib Søndergaard, Christine Finnie, Birte Svensson, Dong Jiang, Bernd Wollenweber and Susanne Jacobsen

 **Supporting information see www.proteomics-journal.com**

- RESEARCH ARTICLE
 1696 **Quantitative proteomic analysis of cold-responsive proteins in rice**
Karlie A. Neilson, Michael Mariani and Paul A. Haynes
 **Supporting information see www.proteomics-journal.com**
- RESEARCH ARTICLE
 1707 **Comparative proteomic profiles of the soybean (*Glycine max*) root apex and differentiated root zone**
Ulrike Mathesius, Michael A. Djordjevic, Marie Oakes, Nicolas Goffard, Farzad Haerizadeh, Georg F. Weiller, Mohan B. Singh and Prem L. Bhalla
 **Supporting information see www.proteomics-journal.com**
- RESEARCH ARTICLE
 1720 **The *Arabidopsis thaliana* 2-D gel mitochondrial proteome: Refining the value of reference maps for assessing protein abundance, contaminants and post-translational modifications**
Nicolas L. Taylor, Joshua L. Heazlewood and A. Harvey Millar
 **Supporting information see www.proteomics-journal.com**
- RESEARCH ARTICLE
 1734 **Dynamics of post-translational modifications and protein stability in the stroma of *Chlamydomonas reinhardtii* chloroplasts**
Willy V. Bienvenut, Christelle Espagne, Aude Martinez, Wojetec Majeran, Benoît Valot, Michel Zivy, Olivier Vallon, Zach Adam, Thierry Meinnel and Carmela Giglione
 **Supporting information see www.proteomics-journal.com**



- RESEARCH ARTICLE
 1751 **Integrated proteome and metabolite analysis of the de-etiolation process in plastids from rice (*Oryza sativa* L.)**
Sonja Reiland, Jonas Grossmann, Katja Baerenfaller, Peter Gehrig, Adriano Nunes-Nesi, Alisdair R. Fernie, Wilhelm Gruissem and Sacha Baginsky
 **Supporting information see www.proteomics-journal.com**
- REVIEW
 1764 **Toward a definition of the complete proteome of plant peroxisomes: Where experimental proteomics must be complemented by bioinformatics**
Sigrun Reumann
- RESEARCH ARTICLE
 1780 **Simplified enrichment of plasma membrane proteins for proteomic analyses in *Arabidopsis thaliana***
Zhe Jenny Zhang and Scott C. Peck
 **Supporting information see www.proteomics-journal.com**
- RESEARCH ARTICLE
 1789 **Towards the profiling of the *Arabidopsis thaliana* plasma membrane transportome by targeted proteomics**
Jean-Marc Monneuse, Madeleine Sugano, Thierry Becue, Véronique Santoni, Sonia Hem and Michel Rossignol
 **Supporting information see www.proteomics-journal.com**

- 1798 RESEARCH ARTICLE
Analysis of the xylem sap proteome of *Brassica oleracea* reveals a high content in secreted proteins

Laetitia Ligat, Emmanuelle Lauber, Cécile Albenne, Hélène San Clemente, Benoît Valot, Michel Zivy, Rafael Pont-Lezica, Matthieu Arlat and Elisabeth Jamet

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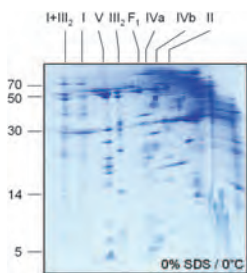
- 1814 RESEARCH ARTICLE
Concerted action of the new Genomic Peptide Finder and AUGUSTUS allows for automated proteogenomic annotation of the *Chlamydomonas reinhardtii* genome

Michael Specht, Mario Stanke, Mia Terashima, Bianca Naumann-Busch, Ingrid Janßen, Ricarda Höhner, Erik F.Y. Hom, Chun Liang and Michael Hippler

 **Supporting information see www.proteomics-journal.com**

- 1824 REVIEW
Isolation and characterization of plant protein complexes by mass spectrometry

Delphine Pflieger, Jean Bigeard and Heribert Hirt



- 1834 RESEARCH ARTICLE
Low-SDS Blue native PAGE

Jennifer Klodmann, Dagmar Lewejohann and Hans-Peter Braun

 **Supporting information see www.proteomics-journal.com**

- 1840 REVIEW
MALDI-imaging mass spectrometry – An emerging technique in plant biology

Stephanie Kaspar, Manuela Peukert, Ales Svatos, Andrea Matros and Hans-Peter Mock



Time to articulate a vision for the future of plant proteomics – A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO)

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Given the essential role of proteomics in understanding the biology of plants, we are establishing a global plant proteomics organization to properly organize, preserve and disseminate collected information on plant proteomics. We call this organization ‘International Plant Proteomics Organization (INPPO; <http://www.inppo.com>).’ Ten initiatives of INPPO are outlined along with how to address them in multiple phases. As our vision is global, we sincerely hope the scientific communities around the world will come together to support and join INPPO.

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1 Proteomics of plant biology

The credit for coining the term ‘proteomics’ goes to Marc Wilkins [1], who was able to put forward a vision of what

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Abbreviations: INPPO, International Plant Proteomics Organization; QTL, quantitative trait locus

could be done using what were, at the time, very new technologies. The groundswell of support since then has helped transform proteomics into a truly international scientific discipline in its own right (for views and reviews, [2–19]). As is the case for other organisms (especially

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microorganisms and mammals), proteomics is now an essential part of plant science.

Plants are our 'bread and butter,' the fundamental basis of human and animal nutrition. They are the most important species on our planet, controlling our food production and providing human sustenance, at least in the foreseeable future. With the predicted increase in human population in the next 50 years, there is looming uncertainty regarding the state of food production. Put simply, at current levels we will be unable to cope with this vast human and concomitant animal population. To give a few statistics, as of May 2010, the world population, estimated to be 6.8 billion, is projected to reach 9 billion by 2040 (US Census Bureau, International Data Base). The rapid growth of the world's population requires continuous production increases to ensure food and feed supply, while globally 900 million people suffer from malnutrition. Plants are also used as resources for both renewable raw material and energy, and they synthesize a great variety of essential molecules (amino acids and vitamins), lipids and secondary metabolites, including pharmaceuticals. And yet, the full potential of plants for biosynthesis of such useful compounds has only just begun to be explored. In addition, we are facing a decline in arable land due to industrialization, housing and infrastructure. Also, the problem of water resources is severe in many countries, notably in the context of climate change. For these reasons, it is crucial to improve the security and productivity of cultivated areas within their social, political and economic context. Achieving enhanced food and feed production in an environmentally sustainable manner will

be an extremely difficult task. Nevertheless, it is a vitally important enterprise [20]. Here, all plant biologists come into view, and the scientific spirit of curiosity, discovery and passion will play a crucial role in achieving the seemingly insurmountable challenges within a short time.

In addition to the largely classical approach to study plant biology and tackle the problem of food security, the past ten years have witnessed the rapid progress of plant functional genomics, following the landmark genome sequencing events in plant science; first the *Arabidopsis thaliana* model plant [21] and second the rice (*Oryza sativa*) crop [22–24] genomes. To date, genomes of several other plants have already been decoded such as poplar [25], castor [26], sorghum [27], grape [28], soybean [29], tomato (International Tomato Genome Sequencing Project; http://solgenomics.net/about/tomato_sequencing.pl) and maize [30], and some are in the pipeline such as banana (Global Musa Genomics Consortium; http://www.musagenomics.org/latest_news/article/article/musa_genome_sequencing.html), *Medicago truncatula* (<http://www.medicago.org/genome/>), and rapeseed (http://www.press.bayercropscience.com/bcsweb/cropprotection.nsf/id/EN_20091009). Plant biology has now embraced high-throughput omics technologies to accelerate the process of discovering the gene functions in a systematic manner. Herein, we have seen progress on three main fronts: transcriptomics, proteomics and metabolomics, for system-wide profiling of genes, proteins and metabolites, respectively [31–33]. These disciplines have been loosely grouped into 'systems biology' [34–38] with the goal of modeling, prediction and design of new plants tailored to specific uses. The rapid development of genomics tools has proven indispensable to fully exploit these genomic sequences in the quest toward a fundamental understanding of the plant system. Plants, representing about 99% of the eukaryotic biomass of the planet [39, 40], are sessile organisms. Therefore, they exhibit unique physiological properties, notably in response to their biotic and abiotic environments, which cannot be deduced from studies in other organisms [41]. Application of this knowledge for product innovation will benefit consumers and

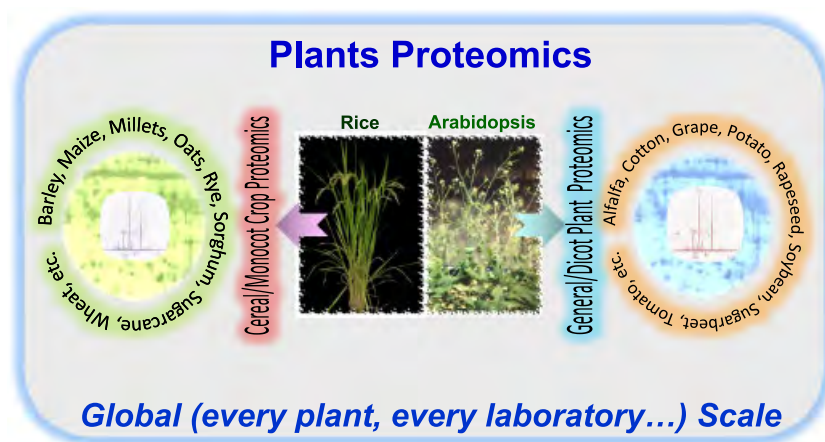


Figure 1. Plant proteomics and its globalization. Going from model plants proteomics to other plants/crops proteomics. The future of food production and human sustenance lies squarely on the hands and minds of the farmers and scientists who practice and study plant biology, wherein proteomics as a science is of paramount importance and use.

the environment, promoting sustainable agriculture and preserving biodiversity.

2 Proteomics

Proteomics is one of the potent approaches developed in the era of ‘omics,’ complementing and linking transcriptomics and metabolomics. In this context, proteomics offers unique insight into the cellular function at the level of cell, organelles, tissues, organs and whole organisms [42]. Figure 1 highlights where we are on the plant proteomics front, with model species including *Arabidopsis* [43–46] and rice [24, 47] paving the way for emerging model and non-model plants to be involved in proteomics research (for further reading on the subject, readers are referred to [8, 48, 49]). We must recognize the fact that plant proteomics lags behind yeast and human proteomics as shown by a search of the number of publications in these disciplines from the ISI Web of Science (May 2010). Yet the impact of human proteomics is proportionally smaller than that of plant proteomics. This is simply because laboratories around the world have shown a great interest in embracing proteomics at a global scale to address their biological question(s) in plants [8, 48, 50–55]. The graph presented in Fig. 2 reveals the extent of development in plant proteome research with more than 300 papers in 2009, after the publication of the first plant proteomics paper in 1999, using the single term plant proteom* to search the PubMed database (www.pubmed.com). Plant proteomics statistics clearly reveals progress in unraveling the proteomes, particularly of *Arabidopsis*, rice and maize, and other emerging model plants and crops, as well as progress in techniques and bioinformatics for plant proteomics analysis. It is worth mentioning that the proteomics subcommittee of the Multinational *Arabidopsis* Steering Committee (MASC; <http://www.masc-proteomics.org/>) has been established to assist in the coordination of research in *Arabidopsis* in the area of proteomics. The participating research groups assembled most of the available proteomics databases to the largest

proteomics resource for a single model plant *A. thaliana* [11]. Thus, this platform could be seen as a template how to translate proteomics technologies such as 2-DE, genome-wide targeted proteomics or ‘Mass Western’ [56, 57], screening methods like shotgun proteomics in abiotic and biotic stress and mass spectrometric analysis of tissue and subcellular protein localization [33, 54, 58] to other plant model systems.

Proteomics, like other ‘omics,’ also refers to the parallel analysis of numerous molecules. Current proteomic tools have dramatically improved over the last decade, mostly due to the rapid and significant improvement in the sensitivity, throughput and mass accuracy of modern mass spectrometers. However, the coverage of proteomes is still not as comprehensive as transcriptomes. This high number of parallel analyses can be, and has been, exploited with different aims. On the one hand, proteomics has become a tool of annotation of individual proteins, by supplying information that is complementary to genomic and transcriptomics information such as: identification of the methionine of translation initiation; intron/exon boundaries; splicing variants; experimental proof of protein accumulation in different organ or tissues or in response to various stimuli; subcellular location; the presence and nature of post-translational modifications (PTMs); [59–62]; and association with other proteins in functional complexes [63–65]. These additional data provide information that can be exploited in databases where genomic and proteomics data are gathered (e.g. PPDB at <http://ppdb.tc.cornell.edu/> [66]; AtProteome at <http://fgcz-atproteome.unizh.ch/> [9]; PROMEX at <http://promex.pph.univie.ac.at/promex/> [11]; PhosPhAt at <http://phosphat.mpimp-golm.mpg.de/> [67]). On the other hand, other proteomics studies do not aim at characterizing the proteins themselves but rather to understand the cellular responses to a given biological phenomenon, such as response to environmental changes, or developmental and phenotypic variations, by identification and quantification of the proteins involved. The interpretation of these types of studies are integrative and necessitate the use of databases that link genes and proteins to

Plant Proteomics Papers

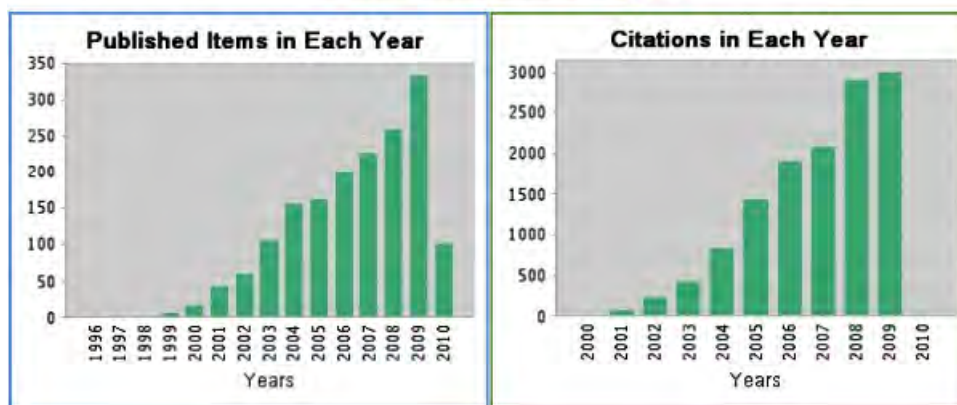


Figure 2. Growth index of plant proteomics. The literature survey (May 2010) was carried out using the key word plant proteom* and the search engine PubMed.

functions and pathways (e.g. databases based on Gene ontologies, MAPMAN and PPDB) [68–70], and would benefit from links with transcriptome and metabolome data. It is worthwhile noting that proteomics can be instrumental in linking quantitative genetics and physiology, in particular by mapping PQLs (protein QTLs (quantitative trait loci), [71–73]). While eQTLs (expression QTLs) have been detected by using transcriptome microarrays, the link with metabolism is relatively loose, partly because of PTMs, including those involved in protein turn over. Metabolomics profiling provides very interesting phenotypic data and metabolite QTLs can be mapped [74]. The integration of metabolomics with transcriptomics and proteomics is another innovative way to assign gene functions within a genome and analyze plant responses at a systems level [33, 75].

As proteins are the final products of genes, they potentially account better than transcripts for activity variations simply because: (i) their accumulation level is the result of a combination of transcription, translation and protein turn-over, and (ii) proteomics studies can also analyze PTMs that modulate their activity. All causes of these variations can potentially be studied, from genes regulating transcription to enzymes responsible for PTMs. PTMs affect enzyme activity and subcellular localization, participate in signaling (e.g. phosphorylation) and play important roles in the maturation of storage proteins. Most of these phenomena cannot be predicted from genome or transcriptome data. A feature of most plants living in temperate climates is their reliance on dehydrated stages including seeds [76] and pollen grains [77, 78], where the regulation of mRNA and protein abundances are particularly disconnected and where PTMs play an important role.

The throughput of proteomics studies is still lower than that of transcriptomics studies regarding the number of genes and proteins analyzed. The number of proteins that can be identified and quantified in a single shotgun MS/MS-based proteomics experiment using current technology is typically from 500 to several thousands at maximum. In contrast, tens of thousands of predicted transcripts of an organism can be analyzed in one experiment (microarrays, SAGE or new generation RNA sequencing), including quantification of transcript expression levels. However, because cellular reactions directly depend on their amount and state, the analysis of protein variation is potentially more informative than the analysis of transcript abundances for the analysis of the determinism of quantitative traits. Experimental designs for this type of analysis comprise numerous genotypes (e.g. populations of recombinant inbred lines). Although up to 200–300 2-D gels can in principle be analyzed in the same experiment (e.g. [71, 79]), this is not practical for most laboratories due to the high costs of materials and labor, and complex tracking and image analysis. Advances in MS [2], and particularly in label-free quantification, have made possible the analysis of very large data sets in complex multi-variate experimental designs [33, 80]. These approaches will allow the detection of

protein QTLs and the quantification of candidate proteins in large panels for association genetics, enabling new ‘association proteomics’ programs in plants. Last but not least, continuous progress in sub-cellular identification of proteins allows pushing the limits toward a detailed understanding of plant proteomes at the sub-organelle, organelle, cell, tissue and organ levels [58, 81].

3 The rationale and birth of International Plant Proteomics Organization (INPPO)

Nevertheless, there is something lacking in our quest toward the ambitious goal of achieving complete understanding of proteomes of plant species. There are many reasons that can be proposed to explain this gap in our knowledge. To suggest a few, there is lack of access to proteomics in most plant laboratories around the world, lack of information, lack of close cooperation among proteomics researchers and most importantly lack of a suitable platform to globally discuss plant proteomics from both fundamental and applied perspectives. In addition, there is a more pressing concern that remains to be addressed, which is the incredibly large diversity of plants and crops on our planet, which means different things to different people and societies.

Only a very few plants are the subject of intensive research efforts, the vast majority are not. For example, *Arabidopsis* [82, 83] is studied as a model plant largely because it was the first plant to be sequenced, has well-established gene manipulation techniques [84], a quick life cycle and is very easy to handle. Rice, on the other hand, has a relatively long life cycle, and is difficult to handle, but is being investigated as a model for cereal monocot crops (such as wheat, rye, barley and maize), largely because it is the primary food source of half the world’s population. Oilseeds, other than providing a rich source of energy in our food, are being economically exploited as bio-fuel producers. The same holds true for sugarcane and sugarbeet for the sugar they provide us, grapes for wine production and cotton in textile industries. Poplar has been used as the model plant for woody species [85], for economic and eco-physiological reasons, as e.g. it has a wide distribution in the northern hemisphere, and hence can be transformed and easily in vitro propagated. The poplar model has been used in many studies to provide data on the effects of environmental stressors in woody plants, and to investigate features specific to woody species, i.e. formation of secondary tissues, overwintering, etc. [86]. Figure 3 highlights some of the major plants/crops in the world along with their geographical distribution. Looking globally, one thing stands out – ‘global impact of global plant proteomics.’ In other words, the importance of proteomics in the biological context, plant diversity and the essential contribution of that biodiversity to the socio-economic fabric of humankind is beyond any doubt. Although we would like to claim that proteomics of

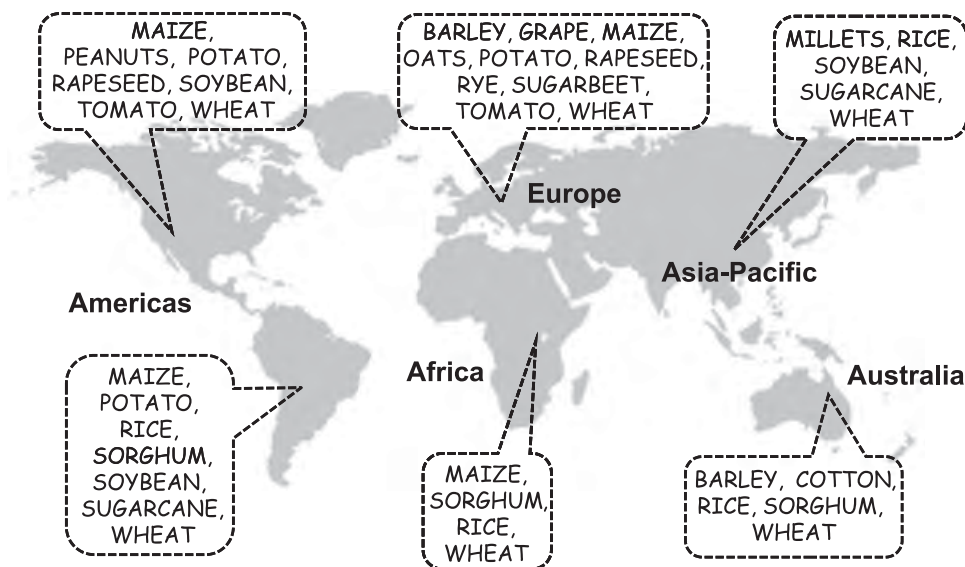


Figure 3. Major crop plants around the world. Representative crop plants in the five continents are highlighted.

plants is the next frontier for crop science research and global food security, it is more realistic to say that an ‘amalgamation of the omics trinity’ holds the key to plant biology. Therefore, if we have to move beyond the genome to provide a link between genes and metabolites [87], it is crucial that we invest in proteomics. The mood among plant proteome researchers is to fully exploit the potential of proteomics, which nonetheless is highly challenging and global in scale.

To do so, we need to think globally. However, we lack a suitable globally recognized platform along with user-friendly and centralized database, and we are also deficient in media coverage and dissemination of information in the plant proteomics field. To address this situation, we established an initiative, International Plant Proteomics Organization (abbreviated INPPO) (Fig. 4). As debated above, INPPO will be an immense challenge. Though it may not be an ideal comparison, if HUPO (<http://www.hupo.org/>) was established for a single species (*Homo sapiens*), and even then it is a very challenging task, then why should we not do something similar for plants? In plants, where there are so many variations among individuals (genus and species), it may seem a ‘mission impossible.’ It should be noted that plants have ‘benefits’ over mammalian systems that help researchers unravel the biological function of a gene. Two aspects stand out, the availability and generation of mutants (in laboratory, notably TILLING (Targeting Induced Local Lesions in Genomes) and the natural variants, e.g. EcoTILLING; [88, 89]), and the technology of transformation for functional genomics and reverse genetics.

When all is said and done, INPPO, with its global appeal and need, will be necessary if the continually growing ranks of plant proteome researchers around the world are to understand each other, and thus, in turn, help promote and advance plant proteomics.

4 Plant diversity, the planet and its people

Plants are not only the few representative species depicted in Fig. 3 but are also more than that. But in this diversity and variation lies the key for understanding plant biology, and consequently translating that knowledge for the betterment of human life. Considering just one example, the humble weed *A. thaliana*, it has been stated that ‘many discoveries with direct relevance to human health and disease have been elaborated, and several processes important to human biology are more easily studied in this versatile model plant’ [45]. Safer and better food is related to human health and vice versa, which is why the impetus for research into food crops is crucial for human health and medicine, and is precisely why these are the focus of the HUPO initiative. Another front that has been recently opened is the ‘changing climate,’ which may drastically affect the quality of food and its production. Therefore, a long-term investment to secure food for all and to bring a ‘Green Environment’ to protect human and social diversity is the call of this age. And finally, ‘doing nothing is not an option.’

In the context of all we have discussed, the first task of this organization will be to articulate a permanent and ever expanding vision for the role of plant proteomics research worldwide. *The broad goals of INPPO are: to achieve the establishment of complete proteomes from plants; to exploit them to address critical biological questions (such as plant, seed and crop improvement); to achieve better basic understanding of plant systems in interaction with their biotic and abiotic environments; and to develop applications aimed toward sustainable agriculture, environmental biotechnologies, healthier and safer plants, new plant materials, nutraceuticals and more.*

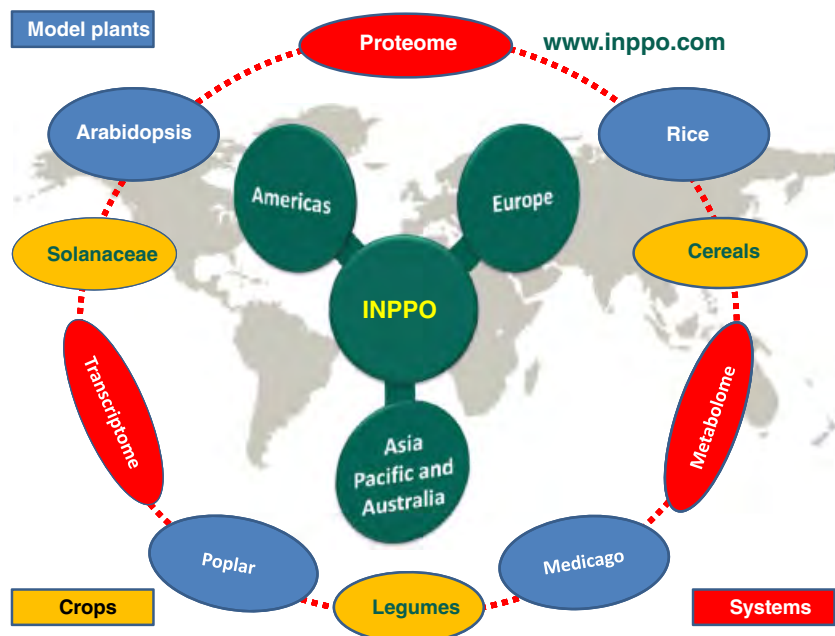


Figure 4. The INPPO initiative. INPPO is proposed to be initially based on three pillars of database organization, annotation and dissemination along with other initiatives as detailed in the text for better plant, seed quality and plant/crop yields.

5 The INPPO initiatives

The INPPO initiative will be to:

- (i) *Further intensify successful ongoing cooperation in the field of plant proteomics for both model and crop plants:* This will involve collaborative research with fellow plant proteome researchers at both national and international levels. It is emphasized that with the availability of genomes of many plants, which will keep increasing, people will be motivated to make a move toward global plant proteomics.
- (ii) *Promote the establishment of national plant proteomics organizations:* To encourage proteomics research in each and every country as far as possible, with more emphasis in developing countries. In this way more and more people will be interested to know about plant proteomics and its benefit. An example of that is the French Green Proteome Network, which is willing to support or defend the launching of proteomics projects under the banner of INPPO, both at the national and European levels. At the European level, the COST program 'Plant Proteomics in Europe' is also a good example of a structure allowing fruitful exchanges (<http://www.cost-fa0603.org/>). At the multinational level, the working group (of proteomics subcommittee of MASC; <http://www.masc-proteomics.org/>) devoted to *Arabidopsis* proteomics aims to combine the efforts of different research groups to develop programs that will consolidate databases, technique standards and experimentally validated candidate genes and functions.
- (iii) *Develop an open partnership around the globe:* A fruitful outcome of the organization will be in the gains made by individual researchers around the world by having open presentations and discussions aimed at not only improving their own proteomics research but gaining information, expertise and skills therein. In addition, partnerships with other organizations, such as publishing groups and news channels, are to be encouraged. For example, authors can follow the journal guidelines and find information where to submit proteomics and/or large-scale MS data sets using well-defined criteria. The HUPO Proteomics Standards Initiative (PSI) defines community standards for data representation in proteomics to facilitate data comparison, exchange and verification. The PRIDE (PRoteomics IDentifications database; <http://www.ebi.ac.uk/pride/>) is a centralized, standards compliant, public data repository for proteomics data.
- (iv) *Bridge the gap between academy and industry:* Mutually beneficial efforts to mine the proteomes of different plant species, economic or otherwise, will provide immense benefits to the industry and incentives to academia to keep working on plants.
- (v) *Establish centralized databases at several locations (Americas, Europe, Asia-Pacific and Australia) with their real-time integration:* Initiate an easily accessible and readable interlinked database for 2-D gel reference maps, large-scale protein qualitative and quantitative data sets for species, organs and organelles, as well as protein–protein interactions and PTMs. These databases will be continuously updated and maintained where deposited data will be effectively organized, annotated and disseminated. It is emphasized that

once these centers are up and running, efforts will be made to include Africa and Middle-Eastern regions into the fold. Further extension will depend on their necessity. Provide and distribute a newsletter and published articles to each and every member of INPPO and also to those interested non-members to keep them abreast of the latest developments in plant proteomics, because with knowledge comes the option of doing something fruitful, and every student, post-doc or researcher, can contribute something.

- (vi) *Organize workshops at national and international levels to train manpower and exchange information:* This will be a global venue for plant proteome researchers to present, hear and discuss their individual plants and their proteomes. We will need support from universities, industries and governments at this founding stage to help with training a new generation of young scientists, especially from developing countries in pursuing professional careers in plant proteomics.
- (vii) *Integrate proteomics-related activities and disseminate them to partners through the INPPO website:* As the information is the key of success, one such activity this initiative will involve is to enrich the scientific community by providing access to information and published articles in the field of plant proteomics. This will lead to an acceleration in plant proteomics research.
- (viii) *Bring proteomics to every laboratory working on plants around the globe:* This is critical as each country and laboratory has something to give. For example, developing countries may lag behind in facilities to conduct research on a global scale, but they may be able to help with talented manpower in bioinformatics

and computer science to help speed up the process of handling, analyzing and extracting biologically meaningful data.

- (ix) *Aim to outreach to the younger generation students at the school, college and university levels:* Engagement of students is essential in order to assure the future of plants and their proteomes, and with them, our planet.
- (x) *Help translate the proteomics knowledge into biology and vice versa:* Think ‘out of the box.’

On the way to achieving these initiatives, INPPO will actively work to be self-sustainable. To do so, and achieve our common goals, we need all interested parties to join us at INPPO (Fig. 5) in this endeavor. Nothing is impossible, if we work together, and history is evidence for that.

6 Addressing INPPO – An outline

The initiatives discussed will be addressed in multiple phases. The initial phase of INPPO will be to:

- (i) Circulate this message through websites (including INPPO and plant/proteomics-related journals) to all people (researchers and students) involved in proteomics in plants, globally. At this step the importance of INPPO, its goals and initiatives will be introduced and discussed, in order to get feedback (ideas/reactions/comments via INPPO website). This will lead to recruitment of members of INPPO in all areas.
- (ii) Install at least two representatives from each participating country.
- (iii) Launch INPPO.
- (iv) Organize a meeting of the founding members to further discuss and chalk out the next phases of INPPO, such as to organize an international meeting on INPPO with the initiators, founding members, representative and supporting members from around the globe for discussing a governing body, initiatives, and most importantly funding from governments and private sectors.



Figure 5. Join us at INPPO (<http://www.inppo.com>). Each piece of the puzzle represents a major plant/crop proteome in each continent/region/country. INPPO will function globally to link them together.

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