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## Editorial

# Plant proteomics in Europe — COST action FA0603

The story begins in 2006, with the scientific dissatisfaction upon returning from a “Proteomics conference” and only having spotted a few lonely posters (less than 1% of total) and only one oral presentation dedicated to plant proteomics. Although, it is clear for everyone that plants are essential for the living, for food, feed, fibre, fuel and industrial products,<sup>1</sup> and increasing food production remains the main challenge in this century, with more people dying from hunger-related causes than from disease. After discussing with colleagues, an opportunity arose to propose an action dedicated to plant proteomics in the frame of the “European Cooperation in the field of Scientific and Technical Research (COST, [www.cost.esf.org](http://www.cost.esf.org))” in the domain “Food and Agriculture”.

The main objective of this COST action was the improvement and exchange of scientific knowledge and technology in plant proteomics through the creation of a network between European proteomic scientists focusing on plants. For this, COST provided us with the requested financial and administrative support to organize workshops, training schools, conferences and to researchers’ education.

In 2007, the COST action FA0603 “Plant Proteomics in Europe or EUPP” was launched and gathered 18 countries and the very first working group (WG) meeting was held in Munich in October 2007. After that, seven other WG workshops were organized in Cordoba, Luxembourg, Viterbo, Nitra, Namur, Luxembourg and Dijon. Books of abstracts of these different meetings can be downloaded on the Action’s website ([www.costfa0603.org](http://www.costfa0603.org)). At the end of the Action, 26 European countries (Austria, Belgium, Bulgaria, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Ireland, Italy, Lithuania, Luxembourg, Netherlands, Norway, Poland, Portugal, Serbia, Slovak Republic, Slovenia, Spain, Sweden, Switzerland, Turkey, United Kingdom) were involved as well as New Zealand that also joined the group.

During the running of the Action, almost 250 researchers actively participated to the various activities organized in the frame of this action and received financial support from

the COST office, while more than 500 people were present at the different WG workshops, conferences and training schools.

The Action’s activities can be classified into two working groups: in the first one, the focus was set particularly on the technical aspects inherent to plant proteomics. The difficulties encountered have been discussed between participants and with experts. Among the subjects that have been addressed, five points were extensively presented:

- Experimental design, sampling, and protein extraction, these preliminary steps of the typical workflow being critical for the success of an experiment,
- introduction of new technical approaches such as difference in gel electrophoresis and label-free quantification,
- detection of post-translational modifications,
- analysis of membrane proteins and
- identification of proteins from ‘orphan’ plants, those whose genome is not yet sequenced and are almost absent in DNA databases.

Following the publication of the genomes of *Arabidopsis* and rice, two “model” plants, other species have been sequenced such as poplar, grape, cucumber, apple, soybean, cocoa, papaya, date palm, rice, *Brachypodium*, maize, sorghum, *Physcomitrella patens*, and other non-models plants. It appeared that most of the laboratories from the different countries involved in this Action were more attracted by those species or even by ‘orphan’ species.

The second working group was more devoted to the transfer of the techniques to applied fields. Indeed, this WG gathered COST participants from laboratories studying:

- plant stress (exposure to abiotic stress or biotic stress),
- phytoremediation/phytoextraction,
- symbiotic interactions,
- allergens,
- plant development, plant growth,
- and crop improvement and yield.

Evidently, a lot of interactions existed among the groups as, for example, the researchers involved in plant stress physiology may encounter problems linked to the extraction of their

<sup>1</sup> Food, Feed, Fibre, Fuel and Industrial Products of the Future: Challenges and Opportunities. Understanding the Strategic Potential of Plant Genetic Engineering, Kern M., Journal of Agronomy and Crop Science (2002) 188, pp. 91–305.

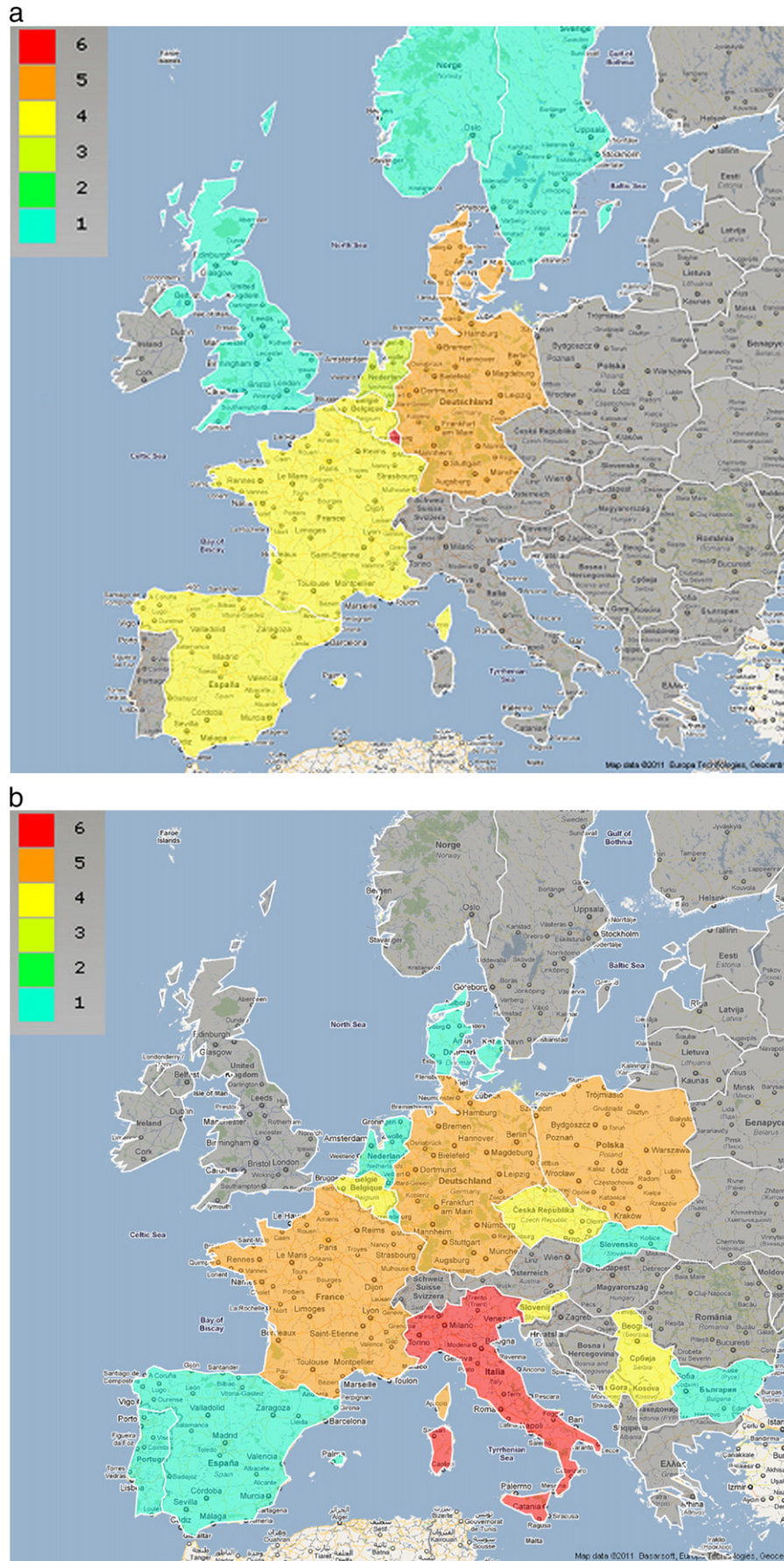


Fig. 1 – Maps representing the countries hosting STSMs (a) and those sending successful STSM applicants (b).

proteins, and the researchers having developed expertise in protein preparation want to see their work applied to concrete biological issue. It is also worthwhile to notice that beside the participants that were reimbursed by the COST office for their active participation, an important number of non-reimbursed scientists were also attending these workshops dedicated to plant proteomics, showing the need for such events in the plant community. A continuation of such gatherings is foreseen by organizing, every two years, a conference dedicated to plants and microorganisms in Luxembourg (ProteomLux).

The possibilities offered by COST allowed the network to provide training schools, typically for young researchers, and exchange of young scientists among different countries with the accomplishment of 32 short-term scientific missions (STSMs) (Fig. 1). These STSMs aimed mainly at establishing formal collaborations between laboratories and also to allow the applicants to learn new techniques or to use techniques they do not have access to in their home laboratories during their project. Major outcomes of these STSMs are co-authored research articles and establishment of long lasting collaborations between the 2 laboratories involved. In this current issue of JOP, two papers are the result of such STSMs; “The alteration of plasma membrane-bound redox systems of iron deficient pea roots by chitosan” and “The assessment of response to ionizing radiation in *Arabidopsis thaliana*” by C. Meisrimler and M. Gicquel, respectively.

Four training schools were offered to improve skills in different domains: Membrane proteomics by 2D-BN-PAGE, Forest and water stress in a changing environment: from cell to ecosystems, Comparative label-free LCMS for Quantitative Proteomics and From 2D gel to bioinformatics.

In this special issue, dedicated to COST action FA0603, review papers have been written by major players in plant proteomics field. These reviews focus on N-glycoproteomics, membrane proteomics, redox proteomics, pretreatment of complex mixtures with hexapeptides, fruit development and plant response to stress. Also an important number of original research articles are published in this issue, some of them resulting from STSMs as described above.

During the action, informal and formal collaborations arose and different projects established among participants have been funded by national and international agencies such as FP7 projects or projects approved in the frame of the EUROCORES.

Gel-based plant proteomics is now well established and during the course of this Action significant progress has been made regarding gel-free proteomics, improvement of protocols for membrane proteomics or for non-model plants, together with mass spectrometry.

To cover the different approaches tackled in this action, the current issue is divided into 3 different parts: a first one on methods, a second one on plant's development and genetic variability and a third one on abiotic stress. For the sake of clarity, we will present the articles ranked by the name of their first author.

A certain number of reviews and research papers of the current issue are targeting the recent methodological developments in plant proteomics, as illustrated by the reviews of Annelies Vertommen on the identification of membrane proteins in non-model plants and Andreas Fröhlich on the pretreatment of complex mixtures with combinatorial hexapeptides ligand libraries. Additionally, this chapter contains research articles by Irene Granlund on bioinformatics



Fig. 2 – Group picture of the meeting in Dijon.

development for the clustering of MS spectra from MALDI-MS/MS, Noor Remmerie on the use of BN PAGE/LC-MS/MS and clustering methods, and A. Vertommen on peptide-based proteomics for membrane proteome analysis of banana.

The second chapter is dedicated to plant's development and its genetic variability, introduced by a review of José Palma on fruit development and ripening, followed by articles of José Valero Galvan on the variability between protein profiles of acorns, Matthias Plöschner on the membrane of etioplasts and chloroplasts, Candido Ricardo on the formation of cork in oak, and two articles on plant allergens by Colette Larré (allergens in different wheat cultivars) and Martijn Schenk (studying the allergen Bet v 1 in 15 birch species).

The third part of this issue is dedicated to plant stress physiology, opening with 2 reviews, the first by Klara Kosova on abiotic stress in general and a second one from Hamid Sobhanian on salt stress and crops. The content of this chapter represents without any doubt the interest of many research groups involved in the action on the response of plant to abiotic stress: heavy metals (e.g. arsenic by Elisa Bona, boron by Marta Alves), radiations (e.g. in *Arabidopsis* by Morgane Gicquel, and in flax seeds from Chernobyl area by Katarina Klubicova), drought (in Oak by Kjell Sergeant and poplar by Thomas Durand), wounding (in potato by Nelson Soares) and response to elicitors (in grapevine by Maria Martínez-Esteso and in the membranes of iron deficient pea roots by Claudia Meisrimler).

This special issue will be concluded by 3 reviews on a topic that is receiving a fast increasing interest by plant proteomists: the study of PTMs and their implication in plant's life cycle. This starts with Nicolas Navrot on plant redox proteomics, then Sander van der Krol on N-glycoproteomics and Philippe Grappin on protein isomerization, showing how new interests and technical improvements will help to elucidate the functioning of plants.

Other initiatives on plant proteomics have run in parallel with the COST Action, including The Multinational Arabidopsis Steering Subcommittee for Proteomics (<http://www.arabidopsis.org/portals/masc/Subcommittees.jsp#prot>). Recently, HUPO has settled the initiative on Model Organism Proteomes (<http://www.hupo.org/research/imop/>); however, this project does not include the whole plant proteomics community. It is worthwhile also to mention the international plant proteomics organization or INPPO<sup>2</sup> ([www.inppo.com](http://www.inppo.com)), in which the COST participants also play key roles.

This special issue reflects the current situation of plant proteomics, at least in Europe. We should recognize that the full potential of proteomics is far from being fully exploited in plant biology research, and we should go one step ahead, as there are a lot of exciting challenges waiting for us. We are in the way, and the COST Action played a protagonist role within the plant proteomics history in the last five years.

We would like to conclude this foreword by thanking all the participants of COST Action FA0603 for their active contribution to all events that were organized (Fig. 2). These four years showed that high quality science can take place in a very friendly and open atmosphere. Moreover all the contributors of this issue are thanked for their excellent papers. Finally we would like to acknowledge the COST office for the opportunity that they have given us to put European plant proteomics on the world map.

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<sup>2</sup> Time to articulate a vision for the future of plant proteomics — A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO), Agrawal GK, Job D, Zivy M, Agrawal VP, Bradshaw RA, Dunn MJ, Haynes PA, van Wijk KJ, Kikuchi S, Renaut J, Weckwerth W, Rakwal R. *Proteomics* (2011) 11, pp. 1559–1568.