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Preface

Translational Proteomics Special Issue

As an associate editor of the JoP in charge of the plant section (JVJN), it was my compromise trying to edit a monographic issue at around every two years; so, one year ago, I began to make plans, starting by the invitation to my friend, colleague, and from now on co-editor, Dr. Luis Valledor. Then, we asked ourselves: *which should be the focus?* It had to depend on the papers published in the last two years and it also had to be something new or at least original. According to Web of Knowledge (Thomson Reuters), the number of plant proteomics papers published in the Journal of Proteomics (JoP) during the period April 2008–August 2013 was 144, representing a 12.8% of the articles published in the journal (1127). Considering all journals the representation of plant proteomics decreases to 7.6% (2850 out of 37,237). During this period, 2008–2013, two plant proteomics special issues have been released by JoP, the first one by April 2009 (Vol. 72, Iss. 3, Plant Proteomics), and the second one by August 2011 (Vol. 74, Iss. 8; Plant Proteomics in Europe). These special and other regular issues contained a number of reviews on plant proteomics, either generalists [1,2] or with focus on plant systems [3–6], plant organs [7], biological processes [8–12], post translational modifications [13], translational [14,15] or methodological [16–18]. Considering all of these works, if we had to summarize the state of the art in the field of plant proteomics we would say that proteomics itself is progressing at much more speed than its application to plant research, following the trend stated in previous reviews [1,6]. The full potential of proteomics as an experimental approach is quite far from being fully exploited in plant biology research. It is true that apart from the model systems (mainly *Arabidopsis* and rice) the number of plant species (herbaceous, woody, gymnosperms and angiosperms, monocot and dicots) and biological processes (from growth and development to responses to the environment) to which proteomics is being applied has notably increased. Methodological advances in plant proteomics, including instrumentation, workflows and protocols (with discussion on its realities, limitations, and challenges) have been collected and accurately described in a book that appears in parallel to this special issue: “Plant proteomics. Methods and protocols. 2nd edition”, edited by Jorin-Novo, Komatsu, Weckwerth and Wienkoop. Methods in Molecular

Biology Series, 1072, Humana Press. In the introductory chapter, Prof. Dr. Jorrín Novo stated:

“We should recognize that proteomics is starting to make contributions to a proper gene annotation, identification and characterization of gene products or protein species, and to the knowledge of living (in this case plants) organisms, having also an enormous potential of application to translational research. However, and despite its great potential, and as in any other experimental approach, it is far from being a Pandora’s Box. In the case of plant research, the full potential of proteomics is quite far from being totally exploited, and second, third, and fourth generation proteomics techniques are still of very limited use. Most of the plant proteomics papers so far published belong to the descriptive, subcellular and comparative proteomics subgroup, mainly using a few experimental model systems — those whose genome has been sequenced, and being from a biological point of view quite descriptive and speculative. From now on we should put more emphasis on the study of post-translational proteomics and interactomics, and move to targeted, hypothesis driven approaches. Furthermore, and even more important, we should validate our data through other -omics or classical biochemical strategies, in an attempt to get a deeper, real and more accurate view and understanding of cell biology. In the modern Systems Biology concept, proteomics must be considered as a part of a global, multidisciplinary approach. Making biological sense of a proteomics experiment requires a proper experimental design, data validation, interpretation, and publication policy.”

The last paragraph is recognized as the new direction in the JoP publication policy as written by Prof. Calvete, JoP editor in chief, in the editorial that appeared in the December 2012 issue (Vol. 76, 1–2), also been discussed in detail by Prof. Weckwerth [19].

Coming to the focus of this issue, we had three options, keeping out one more “plant proteomics” generalist issue. The first one was methodological; it did not make sense

considering the publication of the above mentioned book. The second one was directed at basic research that can be called “proteomics in the frontier of plant biology research”. This was probably our preferred option but, and because of the different reasons, we should not expect many contributions to justify the issue, but for sure it will be the next. The last and more realistic one was our final choice: “practical or translational proteomics”, a topic very well covered and understood in biomedicine but not that well in agriculture. This topic was in our mind since 2010, and briefly discussed during the roundtable discussion session at the 4th EuPA meeting in Portugal and appeared in the paper by Cox et al. [20]. Later on, Agrawal et al. [21] published an excellent review on translational plant proteomics.

The final aim of plant translational proteomics is the development of new practices compromised with the environment, biodiversity conservation and human health, considering the life quality of not only developed but also poor populations in a World that is expected to support nearly 10 billion figures by 2050. Considering the increase in the world population and the enormous pressure that will be put to increase agricultural production, the use of biotechnology will play a relevant role. Nowadays it is not a matter of discussion, being more than obvious, that science and scientists should go beyond just the generation of knowledge: their research must have an additional value, even admitting this additional value is a consequence of that generation of knowledge. This is summarized in the new fashion key word “translational”, with the main goal being the use of research in generating innovative and productivity — technologies that are crucial to agricultural and economic growth, thus helping to fulfill future needs for food, fiber, and fuels. This concept is well understood in the biomedicine field, but not so well in the agricultural and environmental area, being necessary an increased interaction between bench and field.

Any research, scientific area, and methodology have the potential of being translated and offering solutions, and proteomics, despite being a very young one, is not an exception. This justifies the launching of this special issue by Journal of Proteomics, actually the third monographic one plant proteomics after the special issues by “Plant Proteomics” (2009, vol. 73, Iss. 3) and “Plant Proteomics in Europe” (2011, vol. 74, Iss. 8). We should realize that it will probably be a very long journey before all the promises become reality. The full potential in plant research is far from being fully exploited since a number of technical challenges implicit to working with proteins and the lack of proteogenomic data for most of the species is limiting research. However plant translational proteomics is a field of quick evolution and a number of key discoveries and methodological advances have been recently achieved.

We sent invitation letters to the authors by the end of February 2012, trying to contact with all of the research groups that have been publishing works framed under translational proteomics, covering most important research topics: food and beverage traceability, transgenic analysis, allergen identification, post-harvest technology, agronomic techniques, crop improvement, proteotyping and marker assisted breeding, biofuels, bioactive compounds and recombinant proteins, nanotechnology, and other approaches fitting in the translational

concept. It is true that only proteomics in combination with other classical and -omics approaches will get us to a deeper insights and a closer view of the cell biology and its translation in a systems biology context, and because of that the manuscripts should not only contain proteomics techniques, methods and protocols, but also include other approaches validating proteomics results. As an emerging discipline with a constant development in terms of topics and researchers, we didn't want to make this a closed issue — hence, we opened the invitation letter by making this call public in the Journal of Proteomics webpage and also by offering the possibility of being included in this special issue to the authors of fitting papers that were just accepted for publication in this journal.

We contacted 75 authors, from which 22 answered positively to this invitation, constituting the most part of this special issue (19 out 26 articles). Summarizing, this issue is conformed by 26 articles, 10 reviews and 16 original research manuscripts.

Plant productivity strongly depends on its genetic background, with noticeable differences in plant growth, yields, and organoleptic traits between varieties of the same species. Furthermore, environmental stresses during the growth period often reduce seedling growth and crop yield in terms of quality and quantity, and damages suffered during the harvest, conservation, and transport (post harvest) can affect the final quality of the yield. The determination of the changes in -omics profiles (including proteomics, transcriptomics and metabolomics) for linking plant phenotype and its behavior during productive processes to its molecular phenotype is one of the main challenges for improving agricultural production.

The importance of these topics (plant production, stress resistance, biomarkers for breeding) is reflected in the contents of this special issue, with fifteen contributions (60% of total). Six review articles and 9 original research papers reflect the state-of-the-art in related topics to this field. Vanderschuren et al. [2] and Boggess et al. [22] described in their reviews the current status and limitations of proteomics of model and crop plant species, anticipating the future direction that could turn the contributions of plant proteomics into crop improvements. Four original research manuscripts of this issue directly target the improvement of agricultural practices by using a proteomics approach. Gomez-Garay et al. [23] contributed with a proteomic perspective of *Quercus suber* somatic embryogenesis bringing up some potential targets for the improvement of plant propagation, while Li et al. [24] provided molecular insights of gravitropic response in peanut gynophores thus defining the capability of forming peanuts. Post-harvesting practices towards improving the control of ripening were studied by Zheng et al. [25], who identified the proteins implied in apple-ripening modulation by exogenous ethylene, and by Liu et al. [26], who studied the effect of exogenous cytokinins towards improved practices for amelioration of postharvest yellowing in broccoli. These four approaches followed a classic 2-DE approach, despite the different protein labeling/staining systems that were used.

The application of proteomics and metabolomics towards a comprehensive molecular phenotyping aimed to constitute the next generation toolbox for breeders is reviewed by Kumar et al. [27]. Kamal et al. [28] revisited the wheat chloroplast proteome introducing all of the basic and applied advances

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