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Editorial

Peptidomics state-of-the-art [2014]



As fresh Open Access journal of the European Proteomics Association, *EuPa Open Proteomics* (EUPROT) expands and complements the society affiliate *Journal of Proteomics*. EUPROT covers the complete spectrum of proteome sciences including subdisciplines like lipidomics, glycomics, pathway analysis, MS imaging, novel method developments, as well as bioinformatics, data processing, etc. These are all highly exciting and very productive fields within proteome research, but, well, one has to start somewhere and as guest editors we are especially enthusiastic about the decision of EUPROT to dedicate a first special issue to the theme of 'Peptidomics'.

In the last decade, the increasing performance of LC-MS platforms boosted sequence information of endogenous peptides throughout biology, which facilitated functional studies including characterization of cognate receptors and further elucidation of signaling pathways. As the focus and workflows of peptidomics differ conceptually from general proteomics, we considered a special issue on 'Peptidomics' justified and timely and a perfect means to disseminate and highlight current research and trends in natural (i.e., non-tryptic) peptides.

Our aim was to assemble expert contributions covering a broad range and diversity of current peptidomics research, providing a look into the past of this young and astonishingly fast developing discipline, and -more importantly- into its future, which seems brighter than ever. Looking now at this special issue, we dare to state that our goal has been accomplished, and we are very proud of the eminent job delivered by all authors. Our greatest and sincere thanks accordingly go to all contributors for their insightful reviews and their accounts of outstanding original peptidomics research.

Schrader and co-authors reflect on the >15 year history of peptidomics, highlighting the fundamental differences with conventional proteomics, together with the experimental challenges and technical advances in peptidome analysis. As LC tandem MS data analysis is an important tool in peptidomics (as it is in proteomics), a comparison of the performance of current de novo sequencing softwares as presented by Lin et al. fits well in this volume. Quite a few papers in this special issue deal with (neuro)peptide hormones of phylogenetically very diverse species. Particularly the invertebrate research beautifully illustrates the fundamental biological importance of peptide signalling across

metazoan animals, which despite the often minute sizes of their 'brains', have been traditional targets of peptidomics investigations, either with an evolutionary interest or for analytical technology development, still very challenging in the absence of complete genome sequences. McCoy and co-authors describe their newest approach to study the intriguing neuropeptide biology of parasitic flatworms. Husson and colleagues review the latest tools to functionally analyze peptide signalling in the somewhat less primitive nematode worms (including the model organism *Caenorhabditis elegans*), which despite the availability of excellent genetic tools remained inaccessible in the pre-peptidomics era. Pauls and co-workers show that emergent technologies of today also make quantitative peptidomics studies possible in the other illustrious invertebrate model species *Drosophila melanogaster*. Neupert and co-authors as well investigate insects, reporting recent insights in the genomic organization of CAPA peptides discovered in cockroaches. Nachman takes such insect peptidomic data to another level, exemplifying how these could be exploited to develop new specific and environmentally safe pesticides. Two more contributions complete the arthropod section of this special EUPROT issue. Yu et al. discuss the challenging mass spectrometric characterization of neuropeptides from (non-model) crustacean species, whereas a report by Schaffrath and Predel looks into a completely different but equally rich source of bioactive peptides, i.e. the arachnid (i.c. scorpion) venom. Pinkse and co-authors describe an elegant suite of mass spec based approaches to discover potentially bioactive venom peptides on the basis of distinctive post-translational modifications, by using the amphibian defensive secretion as study object. Zhang and collaborators show that using today's advanced technologies, even in mammals still novel 'traditional' neuropeptides can be discovered, and they discuss how peptidomics as such could be implemented to address neurological diseases.

This leads us seamlessly to the review by Uhlig and co-authors who compiled literature data indicating that peptides (and a fortiori peptidomics) may well become very vital in tomorrow's drug discovery.

Finally, Ferro and colleagues comprehensively review our still very limited knowledge on the biology of the many

intracellular peptides which the novel analytical repertoire presently detects. Initially considered to be 'mere' protein degradation products with little function, it now appears that several of these cytoplasmic peptides are likely to be involved in regulating many intracellular processes. This has given rise to a whole new concept in biology: functional micropeptides translated from small open reading frames lacking signal sequences, and hence intracellularly released, may be much more ubiquitous than expected. Crappé et al. review the increasing evidence for these micropeptide encoding small open reading frames, and describe the yet available functional characterisation of this hitherto overlooked segment of the proteome. To illustrate the 'red-hotness' of this field, we here remark that during production of this special issue, a similar review was published in Nature Review Genetics (Andrews and Rothnagel, *Emerging evidence for functional peptides encoded by short open reading frames*, Nat. Rev. Genet. (2014) February 11, E-pub ahead of print).

Again we want to express our sincere indebtedness to all contributors who helped to spawn this special issue. In a time of mushrooming Open Access journals, we take their eager contributions as a sign of credit to *EuPA Open Proteomics*, and of their appreciation of the continuing importance of the growing peptidomic field. We hope that this special issue will

quickly find its way to both the expert and the non-specialist, spreading the word of peptidomics and its enthusing novel developments to new areas of research.

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