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Inductive proteomics and large dataset collections

Andrea Urbani,*[ab] Paola Roncada,[c] Alessandra Modesti,[d] Anna Maria Timperio,[e] Luca Bini,[f] Mauro Fasano[g] and Massimo Castagnola*[hi]

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In 1620 Francis Bacon published the Novum Organum, opening a new era in the experimental research of natural phenomena based on the principle of induction. When describing this principle, he anticipated the effects of advances in science, engineering, and technology. Such a principle opposed to the *a priori* deductive knowledge has been the corner stone for proteomics investigations based on the unsupervised observation of protein modulation in a given biological background. This approach has led to contrasting evidence in the scientific literature from the last 20 years, primarily based on the discoveries of unexpected molecular association, to the complexity of protein modulation and often to the strong will of the investigators to potentially extend the application of their experimental observation beyond the given experimental framework. A well-known example of this experience is available in the quest for protein biomarker discovery in clinical proteomics campaigns. Unfortunately inductive methods may only provide a probability for a given argument in a well-defined framework and their wide extension has been proved by a number of philosophers, *e.g.* Karl Popper and Bertrand Russell, to potentially lead to false conclusions. Although the introduction of *a priori* based proteomics investigations by applying targeted SRM (Selective Reaction Monitoring) design on proteotypic transition brought a new impulse, many researchers still prefer inductive experimental methods in order to obtain novel evidences. Inductive proteomics still provides a passage through the Pillars of Hercules, which for the ancients, symbolized the limits of possible human explorations. Beyond the pillars lay the edge of current knowledge. Thus, their crossing represents our aim toward new uncharted biological molecular mechanisms. These open-platform investigations are presently achieving a higher experimental confidence, providing large dataset collections for a more rigorous description of the experimental framework for the application of the reported results.

In this themed issue dedicated to proteomics we have a clear example of such an extended description. The paper from Claudia Desiderio *et al.*, dedicated to 'Integrated proteomic platforms for the comparative characterization of medulloblastoma and pilocytic astrocytoma pediatric brain tumors' (DOI: 10.1039/C5MB00076A), provides a good example of such a definition. Following the research on medulloblastoma, Maurizio Ronci *et al.* (DOI: 10.1039/C5MB00034C) addressed the protein determinants associated with the stemness phenotype in hedgehog models. Glioblastoma response to nitric oxide releasing compounds is addressed in the paper by Roberta Leone *et al.* (DOI: 10.1039/C4MB00725E) by applying 2DE-DIGE approaches. Redox modifications of proteins are further addressed in a well-defined model for microglia exposure to beta amyloid peptide in the work of Virginia Correani *et al.* (DOI: 10.1039/C4MB00703D) and in the paper by Claudia D'Anna *et al.* (DOI: 10.1039/C5MB00188A) on the impact of cigarette smoke on fibroblasts. While clinical proteomics investigations based on bottom-up approaches have been proving their limits, top-down proteomics investigations represent a fundamental approach to achieve the high specificity required. The current FDA 510k and CE-IVD approved proteomics-based platforms for clinical microbiology (MALDI Biotyper and Vitek MS) are in fact both based on a top-down experimental set-up. In this light, the work from Monica Sanna *et al.* (DOI: 10.1039/C4MB00719K) may

[a] *Department of Experimental Medicine and Surgery, University of Rome "Tor Vergata", Via Montpellier 1, Rome, Italy. E-mail: andrea.urbani@uniroma2.it*
[b] *IRCCS-Fondazione S. Lucia, Rome, Italy*
[c] *Section of Proteomics, Istituto Sperimentale Italiano L. Spallanzani, University of Milano, Milano, Italy*
[d] *Department of Biomedical, Experimental and Clinical Sciences, University of Florence, Italy*
[e] *Dipartimento di Scienze Ambientali, Università della Tuscia, Viterbo, Italy*
[f] *Department of Life Sciences, University of Siena, Italy*
[g] *Department of Theoretical and Applied Sciences, and Center of Neuroscience, University of Insubria, Busto Arsizio, Italy*
[h] *Institute of Biochemistry and Clinical Biochemistry, Faculty of Medicine, Catholic University, Piazza A. Gemelli, Rome, Italy. E-mail: massimo.castagnola@icrm.cnr.it*
[i] *Istituto di Chimica del Riconoscimento Molecolare, CNR, Rome, Italy*

represent an initial step toward the definition of SAPHO syndrome molecular markers in saliva. Integration of top-down and bottom-up approaches is still in its infancy. Nevertheless, the high potentiality of such a strategy is provided in the original paper of Domenico Milardi *et al.* (DOI: 10.1039/C5MB00071H). Metabolite profiling is becoming more and more popular as an integrative strategy in proteomics investigations. The paper from Anna Maria Timperio *et al.* (DOI: 10.1039/C4MB00660G) provides an example in a yeast model. Overall, the marriage of metabonomics investigations in the field of proteomics is a common leitmotif, as demonstrated by the contributions from the groups of Margherita Ruoppolo (DOI: 10.1039/C4MB00729H), Piero Del Boccio (DOI: 10.1039/C4MB00700J) and the review paper from Stefania Orrù's group (DOI: 10.1039/C5MB00030K). Moreover, following the activity of the Mitochondrial Human Proteome Project initiative of the Italian community, Antonio Lucacchini's group produced an interesting evaluation of the metabolic reprogramming of the mitochondrial proteome in a rat model of pancreatic beta cells (DOI: 10.1039/C5MB00022J).

As guest-editors, we would like to warmly thank all contributors to this collection for making it such a success. We hope the readers will enjoy the selection of papers in this year's Proteomics themed issue.