EC Proteomics and Bioinformatics Special Issue - 2017

Towards a Basic Understanding of Proteomics

Dr. Ingrid Gandra[1] and Dr. Gefei He[2]*

[1]*Florida International University, Miami, FL, United States*

[2]*East China Normal University, Putuo District, Shanghai, China*

***Corresponding Author:** Dr. Gefei He, East China Normal University, Putuo District, Shanghai, China.

Received: November 15, 2017; **Published:** November 30, 2017

The term 'proteome' came about in 1994, when Marc R. Wilkins, then a doctoral student, defined and coined the word [1]. Much like genome, which is the collection of genetic material in an organism, proteome is described as the totality of "proteins that occur within a cell, tissue, or organism" [2,3]. Proteomics then, became a new field dedicated to the study of the structure and function of all the proteins encoded by the genome of an organism. The importance of this field becomes clear when realizing that proteins are the translation of the genes themselves. For example, amyloid fibrillation can lead to different neurological disorders, and antibody can help recognize antibody with regard to biomarker detection [4-6]. Without proteins, a DNA molecule would simply be a long chain of coiled nucleotides floating on the inside of cells, serving no particular purpose. The size of the proteome of an organism varies according to its complexity. Notably in eukaryotes, where alternative splicing takes place, various proteins may be encoded from a single gene. However, it is important to mention that not all genes encode for proteins, as a RNA molecule can be another final product obtained from it.

An organism carries only one genome, but many proteomes. This is true due to the specificity of certain cells. Specialized cells produce proteins whose functions are related to its own needs, as for example those responsible for the retinal pigment of an eye. Nonetheless nearly all cells produce proteins that are responsible for basic cellular functions. Thus, the complete proteome is the collection of all proteins produced by each individual cell which can represent certain functions in responds to input energies such as force or light [7-13]. That explains why the proteome of an organism can be much larger and much more complex than the genome of the same. This complexity is also due to the modifications a protein can go through, the so called posttranslational modifications, which may affect its structure and function.

The develop of techniques to correctly separate and identify peptides and proteins became a crucial topic of research during the past few years. Among the many challenges of protein classification are the costs related to data acquisition, the time invested into data processing and analysis, and the methodology to express it on surfaces [11,14]. The human genome contains about 26000 to 31000 genes that encode for proteins, while the total number of protein products accounted for alternative splicing and posttranslational modifications is estimated to be close to a million [15]. Such astonishing numbers offer great obstacles in the advance of the proteomics field. Nonetheless, many techniques have been implemented in the analysis and processing of proteins: LC/MS, one-dimensional and two-dimensional polyacrylamide gel electrophoresis, multidimensional protein identification technology, isotope-coded affinity tag ICAT, SILAC, isobaric tagging for relative and absolute quantitation (iTRAQ), shotgun proteomics, 2DE DIGE, protein microarrays, large-scale blot assays, multiple reaction monitoring assay (MRM) and label-free quantification of high mass resolution LC-MS data, among others [15]. The details of each technique are beyond the scope of this article.

Although the proteomics field is relatively new, its discoveries have shown to be of great importance to the advancement of humanity. Researchers are now combining the technics of both genomics and proteomics (proteogenomics) to present a more complete picture of the molecular level of a patient who has cancer, for instance [16]. The bioinformatics field is one of great relevance for further investigation of the proteome, since the large quantity of raw data obtained from the above-mentioned techniques requires a team effort

from computer scientists and mathematicians to process, analyze and store the data [17]. With combined efforts, we will soon be able to identify and classify the entire proteome of a human being.

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Citation: Dr. Ingrid Gandra and Dr. Gefei He. "Towards a Basic Understanding of Proteomics". EC Proteomics and Bioinformatics SI.01 (2017): 18-19.