International Journal of Research in Interdisciplinary Studies
Volume 4, Issue 4, April 2026
www.ijris.com | E-ISSN: 2584-1017

Summary Report on Proteomics, Lipidomics and Glycomics

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Abstract—This paper presents a summary report on proteomics, lipidomics and glycomics.

Index Terms— **Proteomics, lipidomics and glycomics**

1. Summary Report

Since the genomics revolution, a number of scientific efforts have also allowed the growth of our knowledge regarding the characterization, function and interaction of other key biomolecules for the cell such as DNA transcripts, proteins, and metabolites. These efforts gave birth to other omic fields known now as transcriptomics, proteomics, and metabolomics (Figure 1). Currently, subsets of metabolomics are evolving such as lipidomics, glycomics, and fluxomics with the ultimate goal of integrating the omics picture by means of the interactome of genes, transcripts, proteins, and metabolites representative of the cellular function complexity [1].

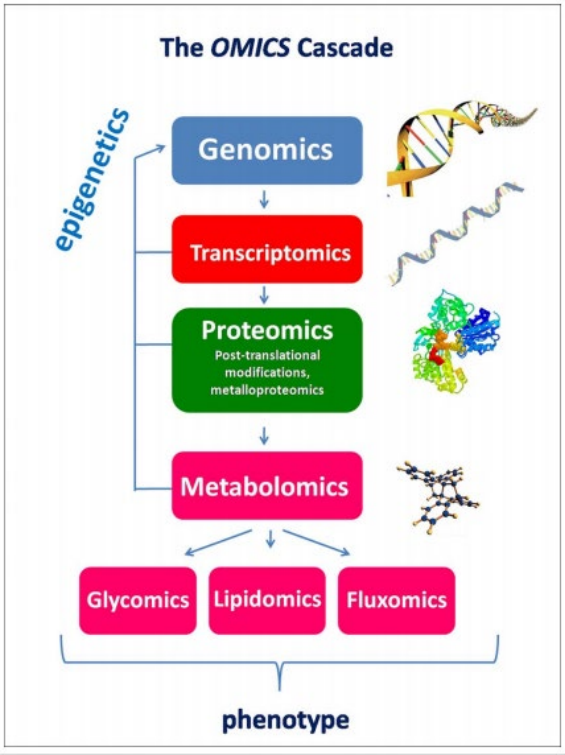

Fig. 1.

Proteomics is generally defined as the identification and quantification of all the expressed proteins of a biological sample, such as cells or embryos, with the goal of understanding their functions, their interactions, and their contribution to biological processes. Similarly, metabolomics has the goal to catalogue and quantify the entire range of metabolites. The emerging field of lipidomics focuses on the whole variety of lipid molecules.

The “omics revolution” is closely related to recent technical revolutions in mass spectrometry (MS). MS is a well-established yet still a rapidly expanding technique in both industry and academia. It is widely and routinely used for biomolecule analysis aimed at drug discovery, diagnostics, and comprehensive assessment of biological, physiological, and pathological conditions [2].

Furthermore, proteomics has steadily gained momentum over the past decade with the evolution of several approaches. Few of these are new and others build on traditional methods. Mass spectrometry-based methods and micro arrays are the most common technologies for large-scale study of proteins.

There are two mass spectrometry-based methods currently used for protein profiling. The more established and widespread method uses high resolution, two-dimensional electrophoresis to separate proteins from different samples in parallel, followed by selection and staining of differentially expressed proteins to be identified by mass spectrometry. Despite the advances in 2DE and its maturity, it has its limits as well. The central concern is the inability to resolve all the proteins within a sample, given their dramatic range in expression level and differing properties [3].

For Lipidomics, a subset of metabolomics, is the large-scale study of pathways and networks of cellular lipids in biological systems [4]-[6]. The word "lipidome" is used to describe the complete lipid profile within a cell, tissue, organism, or ecosystem. Lipidomics is a relatively recent research field that has been driven by rapid advances in technologies such as mass spectrometry (MS), nuclear magnetic resonance (NMR) spectroscopy, fluorescence spectroscopy, dual polarisation interferometry and computational methods, coupled with the recognition of the role of lipids in many metabolic diseases such as obesity, atherosclerosis, stroke, hypertension and diabetes. This rapidly expanding field [7] complements the huge progress

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made in genomics and proteomics, all of which constitute the family of systems biology.

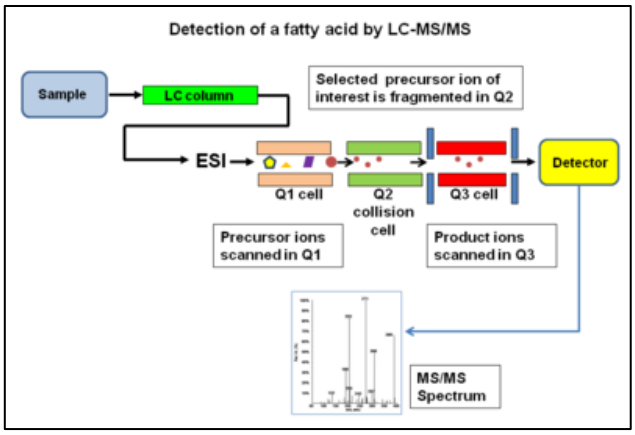

Fig. 2.

The progress of modern lipidomics has been greatly accelerated by the development of spectrometric methods in general and soft ionization techniques for mass spectrometry such as electrospray ionization (ESI) [8] and matrix-assisted laser desorption/ionization (MALDI)9 in particular.

On the other hand, Glycomics is the comprehensive study of glycomes—the entire complement of sugars, whether free or present in more complex molecules of an organism, including genetic, physiologic, pathologic, and other aspects [10], [11] Moreover, it is the systematic study of all glycan structures of a given cell type or organism" and is a subset of glycobiology [12].

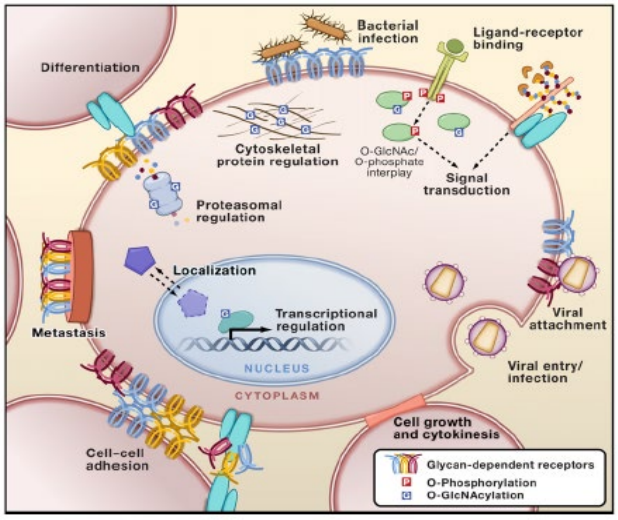

Fig. 3.

Glycan are important as glycoproteins found on the cell surface play a critical role in bacterial and viral recognition (Figure 3). Furthermore, they are involved in cellular signaling pathways and modulate cell function. They are important in innate immunity. They determine cancer development. They orchestrate the cellular fate, inhibit proliferation, and regulate circulation and invasion. They affect the stability and folding of proteins. They affect the pathway and fate of glycoproteins. There are many glycan-specific diseases, often hereditary diseases. Moreover, glycomics is particularly important in microbiology because glycans play diverse roles in bacterial physiology [13].

For glycan analysis, the most commonly applied methods are MS and HPLC, in which the glycan part is cleaved either enzymatically or chemically from the target and subjected to analysis [14]. In case of glycolipids, they can be analyzed directly without separation of the lipid component. Although MRM has been used extensively in metabolomics and proteomics, its high sensitivity and linear response over a wide dynamic range make it especially suited for glycan biomarker research and discovery [15], [16].

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