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Short communication

Clinical and Medical of Glycomics and Lipidomics

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INTRODUCTION

Glycomics

Glycomics is a scientific discipline focused on defining the structures and functional roles of glycans in biological systems. The staggering complexity of the glycome, minimally defined as the repertoire of glycans expressed in a cell or organism, has resulted in many challenges that must be overcome; these are being addressed by new advances in mass spectrometry as well as by the expansion of genetic and cell biology studies. Conversely, identifying the specific glycan recognition determinants of glycan-binding proteins by employing the new technology of glycan microarrays is providing insights into how glycans function in recognition and signaling within an organism and with microbes and pathogens. The promises of a more complete knowledge of glycomes are immense in that glycan modifications of intracellular and extracellular proteins have critical functions in almost all biological pathways [1].

The human glycome certainly represents a challenge in terms of defining all its structures, the metaglycomes of cells and tissues may be amenable to total analysis. We use the term "metaglycome" to denote a constituent glycome of a specific cell or tissue as well as a type or family of glycoconjugates summing up all of the human metaglycomes would then define the human glycome. In fact, targeting specific metaglycomes and providing their repertoire of glycans would likely constitute a milestone toward the direction of eventually defining the human glycome [2].

The complexity of glycomes parallels the technical difficulties in analyses as well as the number of glycan determinants that might exist . Thus, one could imagine that GAGs, with their multitude of potential disaccharide repeating units, would represent the most complex set of glycans in the human glycome, whereas GPI-anchors and human milk oligosaccharides may represent the relatively least complex set. Thus, future studies in glycomics should focus to some degree on the metaglycomes that are most definable, and functional glycomics can then define the recognition of those glycans by GBPs or the specific roles of those glycans in human physiology and disease. Such a strategy could lead to the identification of the protein-glycan interactome for that particular metaglycome [3].

In the absence of either knowing all the structures in the human glycome or having all glycan determinants available as synthetic compounds, it is possible to use a "shotgun glycomics" approach, prior to definitive structural characterization, to obtain all the cellular glycans and use fractionated glycan species for functional studies on glycan microarrays and other surfaces. Such a shotgun approach has been successful in many cases for preparing total GSL-derived glycan libraries and other types of natural glycans.

Glycan Recognition Molecules

Over a hundred different plant lectins and a few from invertebrates have been identified, and many, such as Concanavalin A (Jack bean) and Helix pomatia agglutinin (snail), have been utilized successfully to study glycan expression and function. The use of glycan microarrays has allowed the binding determinants of a large number of lectins to be explored, thereby greatly facilitating their utility in testing hypotheses regarding glycan function [4].

General Glycomic Strategies

The general strategies for glycomic analyses typically involve isolating or generating free glycans from glycoproteins/proteoglycans and glycolipids. The obtained mixture of glycans can then be derivatized and directly analyzed by MS or derivatized, separated by HPLC and other approaches, and further analyzed by MS or NMR. In shotgun glycomics for functional studies, the released glycans after separation can be printed to generate glycan microarrays. For site-specific glycosylation and identification of protein carriers, glycopeptides can be generated by proteolysis and then analyzed directly before or after glycan removal [5].

lipids play an integral part in human physiology and exhibit a high degree of specialization in specific cellular compartments, functioning as structural components of membranes, as a medium for energy storage, as an anchor for proteins, as intra- and inter-cellular signaling molecules or as cofactors in

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modulating protein activity. A multitude of nutritionally and metabolically regulated processes maintain lipid homeostasis in healthy conditions. Defects or alterations in the enzymatic metabolism of lipids may contribute to the pathogenesis of common diseases [6].

- Alzheimer's disease
- atherosclerosis
- insulin-resistant diabetes
- cancer or schizophrenia

CONCLUSION

Thus, lipid biomarkers have potential applications in the understanding of mechanisms underlying disease pathogenesis, in the prediction of future disease risk and in monitoring the responses to therapies

ipidomics approach that focuses on a limited number of predefined lipid-specific signals to establish precisely and accurately their relative abundances [7].

Untargeted lipid analysis, in contrast, aims to detect every lipid species present in a sample simultaneously and results in a huge number of compounds to interrogate. It must be coupled with chemometric methods to extract valuable information of relevant signals which are subsequently identified by database searching. It often requires very specialized and expensive software to illustrate the data, and it is usually semiquantitative, due to the impossibility to use internal standards for quantification. The advantage of the untargeted approach is that it has the potential to unravel interesting novel molecules, only limited by the sample preparation method and the analytical techniques [8].

However, specific targeted methods are required for lipid classes present at low concentrations in biological samples or characterized by instability or other physicochemical features that limit the analytical procedure (e.g., bile acids, steroid lipids, specific signaling lipids, and lipids involved in immune system regulation). The main drawbacks of untargeted lipidomics are the complexity of data processing and the necessity to identify the molecules discovered. In contrast, targeted lipidomics benefits of less complexity in data manipulation but prior knowledge of the lipids present in the sample is mandatory [9-11].

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