OPEN ACCESS Freely available online

Journal of Glycomics & Lipidomics

ISSN: 2153-0637

Commentary

Comprehensive Study and Goals of Glycomics

Stephen Michel*

Department of Biotechnology, Mother Teresa Women's University, Kodaikanal, Tamil Nadu, India

DESCRIPTION

Glycomics is the comprehensive study of proteins containing carbohydrate Post Translational Modifications (PTMs), and during the past ten years, it has become an increasingly important method for finding new biomarkers. One of the most prevalent PTMs, glycosylation, commonly known as the attachment of carbohydrates to developing proteins, is biologically involved in protein folding, stability, localization, and cell communication. Glycosylation is thought to be altered or differentially controlled in malignant states as a result of its significant participation in cellular functions. Proteins are consequently abnormally glycosylated, and it is possible to identify the presence of disease using these abnormal glycoforms. Although there are still difficulties with Glycomic analysis of biological specimens, significant improvements in preanalytical separation techniques and MS have made it possible to characterize glycome and cancer-specific glycoproteins in ever-more-detailed ways. The bulk of glycomic-based biomarker studies for ovarian cancer have used Matrix-Assisted Laser Desorption/Ionization (MALDI) MS in conjunction with thorough preanalytical enrichment techniques for glycan's (such as peptide-N-glycosidase digestion, chromatographic separation, and solid-phase per methylation). The bulk of glycomic-based biomarker studies for ovarian cancer have used Matrix-Assisted Laser Desorption/Ionization (MALDI) MS in conjunction with thorough preanalytical enrichment techniques for glycan's (such as peptide-N-glycosidase digestion, chromatographic separation, and solid-phase per methylation).

Despite the wealth of information amassed, glycomic-based ovarian cancer biomarkers have not yet been clinically confirmed. Technical and biological restrictions continue to obstruct the worldwide exploration of glycosylation and the subsequent identification of potential biomarkers. It is uncertain whether these changes are actually caused by ovarian cancer or are merely the product of the metabolic phenomena that follow malignancy and inflammation, despite the fact that multiple writers have reported distinct glycomic profiles for ovarian cancer. Therefore, more research that demonstrates unequivocally that such glycomic alterations are unique to ovarian cancer is needed.

The poor ability of existing MS platforms to discriminate glycome isomers has been acknowledged as a significant technical restriction of Glycomics due to the variability and complexity of glycosylation. Finally, the lack of validated methodologies is a significant drawback of glycomic approaches to biomarker development. An enzyme-linked immunosorbent assay, which is based on antibody-antigen interactions to produce a detectable (and quantifiable) signal, is the gold-standard quantitative method for verifying potential serum biomarkers. Sadly, the repeatability of similar experiments for glycan-based epitopes is weak. There have been attempts to create lectin- or antibody-based tests, however these capture techniques frequently have limited sensitivity and poor specificity for the desired glycan epitope. As a result, it is critically necessary to create a reliable, quantitative approach for glycan-based biomarkers to confirm potential compounds found through discovery studies. Glycomics entails a thorough examination of the structural and functional properties of carbohydrates, which are crucial for the transmission and storage of biological information related to a wide range of physiological and pathological processes. It is also regarded as a subfield of metabolomics and frequently called glycobiology. Glycan's are oligo- or polysaccharides that can be found either free-floating or bound to other biomolecules. Glycans lack a proofreading mechanism and are not encoded through the template biosynthetic pathway like DNA, RNA, and proteins. While epimerase, sulfotransferase, etc. are glycan-modifying enzymes, glycosyltransferases is engaged in glycan production. To create glycoproteins, proteoglycans, and glycolipids, these enzymes must bind to proteins and lipids at particular sites. Glycans that are bound to proteins are in charge of folding, stability, and controlling the structure and function of proteins. Each cell possesses a unique type of glycolipids, glycoproteins, and proteoglycans. According to the data, glycoproteins make about 70% of therapeutic proteins that have been approved by European and American regulatory organisations. A wide range of glycans found on cell surfaces are involved in critical processes and have an impact on immune response, pathogenic events, cell-cell adhesion, differentiation, and cellular changes that result in cancer.

Correspondence to: Dr. Stephen Michel, Department of Biotechnology, Mother Teresa Women's University, Kodaikanal, Tamil Nadu, India, E-mail: stephenmichel@gmail.com

Received: 05-Sep-2022, Manuscript No. JGL-22-18610; **Editor assigned:** 07-Sep-2022, Pre QC No. JGL-22-18610 (PQ); **Reviewed:** 22-Sep-2022, QC No. JGL-22-18610; **Revised:** 29-Sep-2022, Manuscript No. JGL-22-18610 (R); **Published:** 06-Oct-2022, DOI: 10.35248/2153-0637.22.11.317

Citation: Michel S (2022) Comprehensive Study and Goals of Glycomics. J Glycomics Lipidomics. 11: 317

Goals of the glycomics

1. Analysis of glycan expression.

2. Explicitly defining the range of glycan structure.

3. Explicitly defining the physiological and pathological functions of surface-located glycan's.

4. Assessing the glycan's complexity in relation to its composition, branching, connections, and anomericity.

5. Understanding how glycan's can be used as diagnostics for disorders that include cellular changes.

6. Clarifying the N- or O-linked glycoconjugates, which are significant cell surface compounds, produced from glycoproteins, proteoglycans, and glycosphinolipidsHigh-resolution MS is one of the fundamental methods for studying glycan's, allowing even minute amounts of glycan's to be identified and characterized.

While the glycolipids can be directly sequenced without separating the lipid component, the N-glycan's of the glycoproteins can be isolated and sequenced separately. Because of its size, the glycosaminoglycan is a different glycan that is challenging for MS analysis. Multiple glycan's of any subtype can be profiled using MS. However, complex samples including several glycan's of various subtypes cannot be analyzed using a mass spectrophotometer. The manner of protein-glycan binding in glycoproteins can also be investigated with the aid of MS. Despite the fact that MS offers comprehensive glycan information, a large number of samples cannot be screened at once using this method. There are lectin and antibody arrays available for high-throughput research. Lectins (or glycan-specific antibodies) are affixed to the array chips in place of DNA spots, comparable to a DNA microarray. Lectins and glycan-specific antibodies can be used to systematically evaluate the distribution of glycan's in various cells and tissues. These serve as probes to profile the pattern of expression of various glycans.With the use of imaging reagents; the glycan's can also be metabolically tagged such that they can be seen under a fluorescent microscope. The complete glycome content of any cell or tissue can be visualized in real time with its assistance.