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Short Communication

Methods Involved in the Analysis of Glycomes

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DESCRIPTION

Glycomics, a branch of glycobiology, is the systematic study of all glycan structures of a cell type or organism, genomics and proteomics. Carbohydrate, glycan, saccharide, and sugar are all molecules that include monosaccharides, oligosaccharides, polysaccharides, and their derivatives. Hydrated carbon makes up carbohydrates [1]. The building blocks of oligosaccharides and polysaccharides are monosaccharides, which are a type of carbohydrate that cannot be digested into a simpler carbohydrate. The linear or branched chains of monosaccharides known as oligosaccharides are joined together by glycosidic connections and the quantity of monosaccharide units varies [2].

Glycans made up of monosaccharides are often longer than 10 monosaccharide units known as polysaccharides. The glycome is more complex than the proteome due to higher diversity of the carbohydrates that comprise the glycome and the sheer number of combinations, modes in which the carbohydrates can interact with one another with proteins. The glycome has an enormous range of glycan structures [3]. The amount of proteins encoded by the human genome, which accounts for 1% of all proteins and Glycan-related proteins include those that produce bind sugar chains, and their size is referred to as glycanogenesis.

The external surface of a cell is made up of a sea of lipids and a fleet of sugar molecules, many of which are joined to proteins, fats, or both. These sugar molecules interact with molecules outside the cell and are essential for cell-to-cell communication as well as for a cell's stickiness. Glycans typically do not activate or deactivate physiological processes; rather, they change the behaviour of the cell in response to environment [4].

Methods

High-Performance Liquid Chromatography (HPLC) and Mass Spectrometry (MS): The two most widely used methods are MS and HPLC, which split the target's glycan portion either chemically or enzymatically before subjecting it to analysis. Glycolipids can be examined directly without the lipid component getting separated [5]. After identifying the reducing end of the sugars with a fluorescent molecule, N-glycans from glycoproteins are commonly evaluated by High-Performance Liquid Chromatography (reversed phase, normal phase, and ion exchange HPLC). Anthranilic Acid (AA), 2-Aminobenzamide (AB), 2-Aminopyridin (PA), 2-Aminoacridone (AMAC), and 3-(Acetylamino)-6-Aminoacridine (AA-Ac) only contain a several labels that have been created in recent years. O-glycans are often analysed without any tags since the chemical release factors make it difficult to identify them.

MALDI-TOF-MS (Matrix Assisted Laser Desorption/Ionization-Time of Flight-Mass Sectroscopy) can be used to conduct additional analysis on fractionated glycans from High-Performance Liquid Chromatography (HPLC) devices to learn more about their structure and purity. However, it is more difficult or often impossible to distinguish between isobaric glycan structures when glycosyl pools are examined directly by mass spectrometry without prefractionation. The glycan pool may be quickly and simply illustrated by direct MALDI-TOF-MS (Matrix Assisted Laser Desorption/Ionization-Time Of Flight-Mass Sectroscopy) analysis. However high performance liquid chromatography corresponding to mass spectrometry has made a significant change recently. Even non-derivatized glycans can be examined using porous graphitic carbon as a stationary phase for liquid chromatography.

Mass spectrometry is used for detection; however, Electrospray Ionisation (ESI) is more typically employed than MALDI-MS (Matrix Assisted Laser Desorption/Ionization).

Multiple Reaction Monitoring (MRM): A triple quadrupole instrument is used for MRM (Multiple Reaction Monitoring), and it is programmed to look for a specific precursor ion in the first quadrupole, a fragmented ion in the collision quadrupole, and a specific fragment ion in the third quadrupole. It is a non-scanning method in which each transition is independently recognised and several transitions are simultaneously detected. The immunological glycome is being characterised using this method [6].

Glycans can be metabolically labelled in order to identify glycan structures. The use of azide-labeled sugars that can undergo the Staudinger ligation reaction is a well-known tactic. Glycan imaging has been done using this technique both *in vitro* and *in vivo*. It is a challenging and complicated subject to fully analyze

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the structure of complex glycans using X-ray crystallography and Nuclear Magnetic Resonance (NMR) spectroscopy [7].

However, a wide range of the structural under pinnings of glycome activity has been disclosed by the structure of the binding site of several lectins, enzymes, and other carbohydrate-binding proteins. Analytical electrophoresis, such as PAGE (Polyacrylamide Electrophoresis), capillary electrophoresis, affinity electrophoresis, and chromatography have been used to determine the purity of test samples.

CONCLUSION

Glycomics is the systematic study of all glycan structures of a given cell type or organism, akin to genomics and proteomics. The external surface of a cell is made up of lipids and a fleet of sugar molecules, many of which are joined to proteins, fats, or both. O-glycans are often analysed without any tags since the chemical release factors make it difficult to identify them. MALDI-TOF-MS (Matrix Assisted Laser Desorption/Ionization-Time of Flight-Mass Spectroscopy) can be used to conduct additional analysis on fractionated glycans from high-performance liquid chromatography.

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