OPEN ACCESS Freely available online

Journal of Glycomics & Lipidomics

ISSN: 2153-0637

Commentary

Printed Glycan Microarray from the Consortium Functional Glycomics (CFG)

David Salmen*

Department of Biochemistry, The Glycomics Center, Emory University School of Medicine, Georgia, USA

DESCRIPTION

Glycan microarrays have become the standard method for high-throughput analysis of protein-glycan binding events and for screening Glycan-Binding Proteins (GBPs) as a result of the development of microarray technologies. For use with GBPs, including as lectins, antibodies, bacteria, and viruses, glycan microarrays are exhibits of several glycans or glycoconjugates printed on a single slide. Glycans are typically complexes with functional groups and immobilised at similar concentrations for each glycan on the activated glass slides. The quantity and variety of glycans present on the printed surface for GBPs to access directly affect the effectiveness of a glycan microarray.

Glycan microarray has developed into a sensitive and versatile method for observing changes in glycosylation in complex biological samples. It can analyse the kinetics of glycan-protein interactions in addition to looking at glycan-GBPs binding. This application has developed quickly and effectively differentiates between interactions with glycans and proteins, viruses, bacteria, eukaryotic cells, and most significantly, responses to immobilised glycans by living cells. Determining functional glycans, analysing glycan-processing enzymes, and identifying pathogens for diagnosis all are possible using a glycan microarray. With a wide range of bioassay capabilities, it is also suitable for monitoring numerous biochemical interactions with biomolecules in which glycans are involved.

Major international consortia are increasingly coordinating efforts to accomplish huge goals like defining mammalian glycomes. The Consortium for Functional Glycomics (CFG) is the most established and influential of these. The CFG is broken up into seven scientific "cores," which offer resources, tools, reagents and databases for biologically relevant examination from the international glycobiology community. The Analytical Glycotechnology Core's (Core-C) primary goal is to collect and disseminate information about the structures of glycans, enabling the scientific community to better understand the GBP ligand structures are formed. Core-C has developed and implemented optimized methods for the glycomic characterization of glycosyltransferase knockout mouse tissues.

The Protein-Glycan Interaction Core (formerly Core H) and the Bioinformatics Core (formerly Core B) are the CFG's two scientific cores. A coordinator and a core director are in charge of each core and are in charge of the core's day-to-day operations. In order to facilitate data mining and advance glycomics analysis, the Bioinformatics Core provides the community with integrated databases and specialized analytical tools. The CFG's website, the CFG Functional Glycomics Gateway, contains information about glycans, glycan-binding proteins and glycosyltransferases is free to access.

The Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-MS) method is used by the Analytical Glycotechnology Core (AGC) to obtain profiles of glycans derived from human tissues and cells as well as those of mice (both wild-type and knock-out strains). Based on its mass, composition, biosynthesis and biological source, each annotated glycan structure in the MALDI-MS profile represents the highest level of information that was captured. Resolving isobaric structures requires more in-depth analysis, such as tandem MS-MS fragmentation of specific mass ions (these ions are highlighted in a shaded box in the MALDI-MS profile). A high-throughput snapshot of the most likely glycan structures derived from specific cells and tissues is provided by the MALDI-MS profiling data. Different search criteria, such as molecular weight, composition, biological source, linear nomenclature and citation, can be used to search and retrieve the glycan structures in the database.

Correspondence to: David Salmen, Department of Biochemistry, The Glycomics Center, Emory University School of Medicine, Georgia, USA, E-mail: davidsalmen444@gmail.com

Received: 29-Nov-2022, Manuscript No. JGL-23-21509; **Editor assigned**: 01-Dec-2022, Pre QC No. JGL-23-21509(PQ); **Reviewed**: 15-Dec-2022, QC No. JGL-23-21509; **Revised**: 22-Dec-2022, Manuscript No. JGL-23-21509 (R); **Published**: 29-Dec-2022, DOI: 10.35248/2153-0637.22.11.325.

Citation: Salmen D (2022) Printed Glycan Microarray from the Consortium Functional Glycomics (CFG). J Glycomics Lipidomics. 11:325.

Copyright: © 2022 Salmen D. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.