GlycomeAtlas: A visualization tool of glycan structure expression in human and mouse

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1 Introduction

By virtue of many glycomics technologies such as mass spectrometry (MS), tandem MS and HPLC, we can now obtain glycan structure profiles of various biological samples. Although the Consortium for Functional Glycomics (CFG) [1-4] has provided a web resource including tools such as an interactive spectrum viewer using a Java applet for obtaining these profiling data, it is not necessarily easy to search for a particular glycan structure in a particular tissue or to compare one tissue with another in a single organism to find commonalities between them, for example. Therefore, to enable researchers who are interested in vast glycomics data to use these valuable profile data obtained from mass spectra and other advanced technologies effectively, we developed a tool called GlycomeAtlas which is preloaded with the data from the CFG and can visualize such data. This tool is available from our RINGS web site (http://www.rings.t.soka.ac.jp) [5].

GlycomeAtlas allows users to see the expressed glycans in human and mouse tissues via a user-friendly interface. Also, this tool provides users with a user-friendly glycan search and compare function through the user interface. Moreover, it can also visualize a user's personal data. Therefore, this tool can aid glycomics research by allowing easier analysis of glycomics data.

This tool is available at the following URL: http://www.rings.t.soka.ac.jp/GlycomeAtlasV2/GUI.html.

2 Materials and Methods

The user interface of GlycomeAtlas was built using Adobe Flash. ActionScript 3.0 and Adobe Flex framework were used in combination with the use of Adobe FlashBuilder 4. Also, the profiling data were obtained from the CFG website for each wild-type tissue sample in human and mouse. Then we stored these data in a MySQL database on the RINGS resource at http://www.rings.t.soka.ac.jp/. Finally, we developed server software using Java Server Pages (JSP) to communicate between the user interface and the MySQL database.

3 Results and Discussion

The most important features of GlycomeAtlas include 1) glycan profile visualization of human and mouse tissue samples, as provided by the CFG, 2) glycan structure search of profile data and 3) visualization of the results. The main interface of this tool is depicted in Figure 1. The left panel contains a list of buttons providing a variety of functionality. The 'Home' button will jump to the RINGS web resource where this tool is housed. The 'Help' button will display the Help page of RINGS and the 'Feedback' button will display the Feedback form of RINGS in a new window. Also, the 'Data source' button will display a dialog listing the tissue sample data that are stored in the database for this tool. Finally, 'Glycan search' button will display a dialog containing the glycan structure search form where the user can input a glycan structure in LinearCode[®] format [6] as a query. Recently we have added functionality to search for substructures using a partial match retrieval function.

The center panel contains two tabs of illustrations, that is, one for human and the other for mouse

samples. Also, the list of available tissues is displayed next to the illustrations with the numbers of glycan structures annotated for each tissue sample. By clicking directly on the diagram or the tissue name in the list, the glycan profile of the tissue will be loaded and each glycan of the profile will be displayed in the right-hand panel. By clicking on one of the listed glycans, the tissues expressing the clicked glycan will be highlighted in purple, as depicted in Figure 1. Note that the glycans listed have been analyzed using MALDI-TOF MS. so the glycosidic bond information is unavailable in some cases and some glycans have ambiguous linkage information. In addition, we have recently added glycan profiling data of human serum obtained by HPLC.





Fig.1. The main interface of GlycomeAtlas. In the center panel, the images of the organs of selected organism (i.e., human or mouse) are displayed. The right panel shows all glycans expressed in the selected organ. If the user clicks and selects particular glycans, the organs expressing the glycans are automatically highlighted in left panel.

Visualization of users' own profiling data is also possible by providing a text file of the data. A sample text file is available for users to use as a reference. Thus, we hope glycomics researchers find this tool useful for their analyses.

With the visualization of glycan structures in various tissues, the user can get an idea of the tissue localization of glycan structures. Also, this tool can support students interested in glycomics as an educational resource. We are planning on further developing this tool to perform higher-level analyses to compare differences between tissues and animals. Moreover, easier methods for inputting and searching glycan structures are also being considered.

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