Conformational Analyis of Complex Glycans

Description

The elucidation of complex glycans conformation in solution is one of the main intriguing aspects of bacterial oligo- and polysaccharides' full characterisation.

The function and the biological role of glycans are indeed strictly related not only to their structure but, above all, to their conformation. Even single furanoid or pyranoid monosaccharides can adopt possible shapes; furanose structures occur in an envelope and twist conformations which can be represented on a pseudo-rotational wheel; whereas, six-membered ring structures can occur in two chairs (C), six boats (B), six skew (S), and twelve half-chair (H) conformations. In practice, the two chair conformations exhibit the lowest energy and strongly dominate. However, cases occur where different conformations are in equilibrium. For example, the iduronic acid adopts more than one solution conformation, with an equilibrium between three low energy conformers. These are the $^{1}C_{4}$ and $^{4}C_{1}$ chair forms and an additional 2S0 skew-boat conformation. Furthermore, in monosaccharides with an exocyclic hydroxymethyl group, three staggered situations denoted as gg/ tg/ gt (? -60°/180°/60° respectively), have to be taken into account.

In oligo- or polysaccharides, the relative orientation of the composing monosaccharide units should be considered. It is usually described by the ? (H1-C1-O-CX') and ? (C1-O-CX'-HX') torsional angles around the glycosidic bonds. In the case of a 1?6 linked sugar, an extra torsion angle, namely ? (O'6?C'6?C5'?O'5), further influences the entire three-dimensional glycan structure.

Thus, if it is hard to elucidate the chemical structure of complex glycans, assigning saccharides three-dimensional architecture is even more difficult, given the great conformationally flexibility of saccharides, implying the identification and the quantification of an ensemble of conformations in chemical exchange. Different web portals that combine tools and databases related to glycomics can build 3D models of complex saccharides within this frame. (62) Among them, glycoscience.de provides access to PDB containing glycan structures, but it also offers tools for 3D structure modelling of glycans and tools and databases to analyse the adopted conformations. In particular, the GLycoMapsDB tool is handy to analyse the conformational space that a glycan can adopt; indeed, it provides the conformational maps covering several disaccharides' energy landscape. These conformational data can be used to support interpretation results such as NMR data and represent a key step for the description of the behaviour of a glycan both in its free state and when interacting with a receptor protein.

Analogously, GLYCAM-Web is a portal, including continuously updated tools, predicting glycans 3D structures.

Finally, in the field of bacterial glycans, the LPS Modeler Module of Charmm Gui is also remarkable, a tool that makes simpler the production of LPS structure files.

The web-portals and tools are useful for modelling glycans, and programs to visualise 3D structures of complex carbohydrates are listed. In the end, two databases that collect information about known

carbohydrate sequences recognised by lectins or antibodies have been mentioned.

Category

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