NMR Spectroscopy Tools

Description

The combination of mass spectrometry and NMR spectroscopy represents a powerful tool for the full characterisation of glycans. NMR spectroscopy is indeed a non-destructive method that provides key information useful not only in the elucidation of the chemical structure but also in the conformational analysis of complex glycans, including, for example, the number of the sugar residues, the monosaccharide composition and sequence, the anomeric configuration, the nature and the position of appended groups.

During the years, several tools and databases have been developed to assist NMR structural and conformational studies. Anthologies of chemical shift values belonging to monosaccharide residues, an important source of information about the topology and configuration of biomolecules, have been reported for decades on different websites. (55-57)

Moreover, the Widmalm group has developed a computerised approach, named CASPER, the acronym for computer-assisted spectrum evaluation of regular polysaccharides. This tool is available to the scientific community via the Internet. It permits calculating NMR chemical shifts of oligo- and polysaccharides; it can also be used to determine unknown glycans' primary structures based on experimental NMR data. The structure determination is performed by calculating chemical shifts of possible structures and comparing them with the supplied experimental data to find the best match. The process requires experimental NMR data, coupled with results from sugar and methylation analyses if available. Different research groups have developed other software and algorithms to simulate NMR spectra and predict an unknown oligosaccharide's composing sugars. (58-60)

A lot of NMR structural information is also collected in the Glyco3D database. This is a portal for structural glycobiology of several interlinked databases covering the 3D features of mono, di, oligo and polysaccharides, and glycosyltransferases lectins, monoclonal antibodies and glycosaminoglycan binding proteins. A collection of annotated NMR data of more than 150 bioactive oligosaccharides is also available in the GLycoNMR section.

The carbohydrate structural database (CSDB) provides two NMR services, (61) which are available under the extras section of the main menu: the NMR simulation tool and the NMR-based structure ranking tool. The first predicts ^{13}C and ^{1}H NMR chemical shifts for a specified compound. The CSDB NMR predictor's key point is the ability to process almost all structural features occurring in natural glycans, including atypical and noncarbohydrate moieties. The second tool instead, given some constraints, generates all possible structures and matches them against an experimental ^{13}C NMR spectrum by using the GRASS (Generation, Ranking and Assignment of Saccharide Structures algorithm).

Above the chemical shift, other NMR parameters, including J couplings, can be useful to study glycan stereochemistry, helping define the monosaccharide ring's conformation, the exocyclic hydroxymethyl group and O-glycoside linkage (see next paragraph). In this regard, MestRe-J is a freely accessible

tool that includes several generalised Karplus equations for calculating J couplings starting from torsional angles and vice versa, allowing to obtain valuable stereochemical information.

A summary of the bioinformatic tools and databases that can help determine the glycan structure from NMR data is given below.

CASPER: Online tool to predict chemical shift and assignments for glycan structures build directly on the web. It is also possible to make a component analysis to determine the composition and a sequence determination. (http://www.casper.organ.su.se/casper/)

BCSD: Bacterial carbohydrate structure database provides information about structures and composition of bacterial carbohydrate-based compounds. Moreover, as extra tools, it is possible to obtain related NMR data. (http://csdb.glycoscience.ru/bacterial/)

Home page of Stenutz: a list of chemical shifts of different aldoses is reported as well as several coupling constant values. (http://stenutz.eu/)

MestreJ: Free software for the prediction of vicinal proton 3J (HH) coupling constants inside MestreLab research suit. (https://mestrelab.com/software/freeware/)

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