Conclusions

Description

In conclusion, all the bioinformatic tools described here are pivotal support to the interpretation of experimental data and represent a key point for the description of the chemical structure and the conformation of complex glycans.

Advances in analytical methods, including Mass Spectrometry- and NMR spectroscopy-based techniques, increased the qualitative and quantitative data of glycans collected in different databases. In recent years, in addition to libraries and platforms dedicated to eukaryotic glycans, progress has been made in developing databases and tools containing information on bacterial glycans. Data sources based on annotated mass spectra of bacterial glycans derivatives provide fruitful information for the sugar compositional analysis. On the other hand, computerized approaches assist the structural and conformational analysis of complex bacterial glycoconjugates, helping in NMR spectra assignment and the elucidation of glycans conformational behaviour in solution.

Thus, glycoinformatics resources are increasingly being used in the analysis of peculiar oligo- and poly-saccharide structures isolated from bacteria, as done for example, in the case of the structural/conformational determination of the O-chain from the LPS of *Rhodopseudomonas palustris* strain CGA009, (63) or the exopolysaccharides isolated from *Zymomonas mobilis*. (64)

Further advances in the development of glyco-informatics tools, databases and software will facilitate the study of complex bacterial glycans, leading more easily to the synthesis of well-defined carbohydrate structures having a big impact in several biomedical sectors. For example, recently, the syntheses of glycans up to a 128-mer of the O-antigen from *B. vulgatus* has been carried out upon the elucidation of the unique structure of its LPS. (65)