Carbohydrate Modeling by Internet: New features of W3-SWEET

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The mysteries of the functions of complex glycoconjugates have enthralled scientists over decades. Theoretical considerations have ascribed an enormous capacity to store information to oligosaccharides. It is beyond doubt that the object of the sugar code, i.e. the monosaccharide units, establishes the prerequisites for the „most complex known chemical code in a short sequence among all biological oligomers“ [1]. Elegant and efficient strategies have been established to analyze glycoconjugate sequences [2] and the idea exists to establish an automatic glyco-molecule sequencing before the year 2005. If the sequence is known the next challenge is posed by the necessity for the description of the conformation and the structural flexibility of oligosaccharides. X-ray diffraction techniques give a precise structural description of an oligosaccharide in a particular crystal environment. Unfortunately, complex oligosaccharides are difficult to crystallize. Thus, for many carbohydrates of biological interest, such as complex gangliosides and highly branched glycan , only a small number or even no X-ray crystal structures are available at all. The most powerful and frequently-used tool for the investigation of the solution conformations of oligosaccharides is NMR spectroscopy in combination with several molecular modeling techniques, i.e. mainly force field-based calculations.

SWEET [3] is a software tool accessible through Internet which rapidly converts the commonly used sequence information of complex carbohydrates directly into a preliminary but reliable 3D model. Here we present the extension to highly branched and macrocyclic structures. The basic idea of SWEET is to link pre-constructed 3D molecular templates of monosaccharides in a specific way of binding as defined in the sequence information. For macrocyclic structures a new input spread sheet and a special library of internal co-ordinates to enable a quick initial construction were implemented. The geometrically constructed structures are subsequently optimized with the MM3 force as implemented in the TINKER software [4]. The standard SWEET procedure caused sometime problems for highly branched structures. Therefore a fast check for close contacts has been implemented and an optimization of the complete molecule is automatically forced in such cases. SWEET will open modeling techniques to a broader range of scientists, especially for those who do not have access to the required hard - and software equipment

[1] R.A Laine, The Information-Storing Potential of the Sugar Code, In: Glycosciences: Status and Perspectives, Gabius, H.-J. and S. Gabius (eds), London-Weinheim Chapman & Hall, (1997) pp. 1-14.
[2] R.A. Dweck, Glycobiology: Toward Understanding the Function of Sugars, Chem.Rev. 96, (1997) 683-720,
[3] A. Bohne,.E. Lang; C.-W. von der Lieth, W3-SWEET: Carbohydrate modeling by Internet. J. Mol. Model. 4/1 (1998) 33-43.
[4] Kong, Y. and Ponder, J. W. Calculation of the reaction field due to off-center point multipols. J. Chem. Phys. **107** (1997) 481-492.