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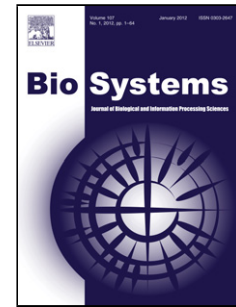
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## The Sugar Code: Why glycans are so important

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### Abstract

The cell surface is the platform for presentation of biochemical signals that are required for intercellular communication. Their profile necessarily needs to be responsive to internal and external factors in a highly dynamic manner. The structural features of the signals must meet the criterion of high-density information coding in a minimum of space. Thus, only biomolecules that can generate many different oligomers ('words') from few building blocks ('letters') qualify to meet this challenge. Examining the respective properties of common biocompounds that form natural oligo- and polymers comparatively, starting with nucleotides and amino acids (the first and second alphabets of life), comes up with sugars as clear frontrunner. The enzymatic machinery for the biosynthesis of sugar chains can indeed link monosaccharides, the letters of the third alphabet of life, in a manner to reach an unsurpassed number of oligomers (complex carbohydrates or glycans). Fittingly, the resulting glycome of a cell can be likened to a fingerprint. Conjugates of glycans with proteins and sphingolipids (glycoproteins and glycolipids) are ubiquitous in Nature. This implies a broad (patho)physiologic significance. By looking at the signals, at the writers and the erasers of this information as well as its readers and ensuing consequences, this review intends to introduce a broad readership to the principles of the concept of the sugar code.

**Keywords:** agglutinin; glycosylation; glycolipid; glycoprotein; glycosyltransferase; lectin; sugar code

### 1 Introduction

Coding of information in biomolecules and its translation into effects on the level of cells are central to life but up to now not yet fully explored and understood. In fact, a large diversity of coding modes and effector means originates from nucleic acids and proteins, the products of the first and second alphabets of life (nucleotides and amino acids used as letters) (Barbieri, 2008). When following the flow of biological information, proteins act as the three main classes of players to turn genetically encoded information into cellular processes, i.e. as i) the writers of coded signals, ii) the erasers that remove signals or sections thereof to allow dynamic and reversible changes and iii) the readers. Intriguingly, already the study of nucleic acids and proteins themselves provided paradigm-shaping insights into the cooperation of members of these three groups. For example, molecular mechanisms of epigenetics via cytosine (and adenine) methylation and further oxidation of the 5'-methyl group to the hydroxymethyl (Pelizzola and Ecker, 2011; Nabel et al., 2012; Pfeifer et al., 2014; Plongthongkum et al., 2014; Heyn and Esteller, 2015) or amino acid (Arg, Lys) substitutions in histones (Oliver and Denu, 2011; Simó-Riudalbas and Esteller, 2015) teach salient lessons on how the interplay of writers, erasers and readers lets implementing such biochemical changes realize their full physiological potential, as protein phosphorylation does.

Applying the work scheme of these role models for storing biological information to the production of oligo- and polymers, the writers generate molecular 'words' from 'letters' (monomers) and are also able to introduce position-specific changes into 'words' (the equivalent of Umlaut formation) by post-synthetic processing. Erasers then ensure dynamic flexibility by deleting sections of signal structures. Readers are

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