Synthesis and conformational analysis of oligomers containing C-glycosyl amino acids

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With few exceptions, all organisms are limited to the 20 common amino acids for the ribosomal synthesis of proteins. However, it is clear that proteins require a higher degree of chemical complexity for many functions, as shown by the frequent use of post-translational modifications. C-glycosyl amino acids represent a group of C-glycosides in which a carbohydrate molecule is attached to the side chain or backbone of the amino acid by a C-C bond. C-glycosyl amino acids are found in nature primarily as bacterial secondary metabolites, but the addition of such amino acids to the assembly of available building blocks is likely to broaden the range of functions available to proteins and provide valuable tools for numerous areas of research.

With the aim of elucidating how the structure of C-glycosyl α-amino acids, their stereochemistry, number and distribution within the peptide sequence determine the conformation of the peptide, we prepared four types of C-glycosyl α-amino acids derived from galactose, ribose, sorbose and allose (Figure 1). Next, we developed a protocol for the solid-phase synthesis of hexamers containing one, two or three C-glycosyl α-amino acids. Finally, we used NMR spectroscopy to determine how the different types of amino acids affect the peptide conformation and which non-covalent interactions underlie the observed conformational changes.

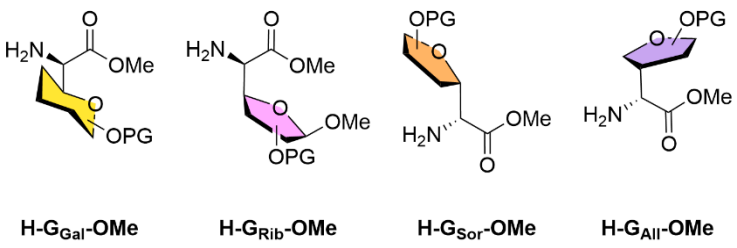

Figure 1. Structures of C-glycosyl α-amino acids used in this work.