

Ulrika Olsson ^a, Kristina Lycknert ^a, Roland Stenutz ^a, Andrej Weintraub ^b and Göran Widmalm ^a

^a Department of Organic Chemistry, Arrhenius Laboratory, Stockholm University, SE-106 91 Stockholm, Sweden.

^b Karolinska Institute, Department of Laboratory Medicine, Division of Clinical Bacteriology, Huddinge University Hospital, SE-141 86 Huddinge, Sweden.

ulrika@organ.su.se

Introduction

The structure of the repeating unit of the O-antigen polysaccharide (PS) from *Escherichia coli* O152 has been solved, using component analysis and nuclear magnetic resonance (NMR) spectroscopy.

E. coli O152 is an enteroinvasive *E. coli* bacterium (EIEC) [1] that causes severe diarrhea [2,3]. In order to make conclusions about resemblance to other bacteria it is important to perform serology and cross-reactivity studies. Consequently, knowledge about the structure of the bacterial O-antigen is essential.

Results

Component analysis and NMR (figure 1) showed that the PS is built up of five different sugar residues, α -D-GlcpNAc(A), α -D-Glcp(B), β -L-Rhap(C), β -D-GlcpNAc(D) and β -D-Glcp(E).

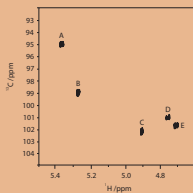


Figure 1. Part of the ¹H, ¹³C-HSQC spectrum showing the anomeric region.

The anomeric proton from residue A has an extra splitting (7 Hz) in the ¹H-NMR spectrum, indicating the presence of a phosphodiester, which was confirmed by 1D ³¹P and ¹H, ³¹P-COSY experiments (figure 2).

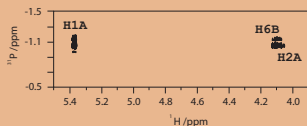


Figure 2. The cross-peaks in the ¹H, ³¹P-COSY spectrum.

Residue C is concluded to be terminal because the chemical shift do not diverge significantly from unsubstituted β -L-Rhap.

The chemical shifts were assigned using a combination of 1D and 2D homonuclear and heteronuclear NMR experiments. The linkage pattern was determined by ¹H, ¹³C-HMBC and confirmed by ¹H, ¹H-NOESY experiments. The proposed structure of the repeating unit is depicted in figure 3 (below).

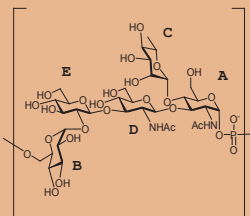


Figure 3. The proposed structure of the O-antigen PS of *E. coli* O152.

NMR

NMR spectra for the PS were recorded using Varian 400 and 600 MHz and Bruker 400 MHz instruments. NMR experiments performed were ³¹P (1D), ¹³C (1D), ¹³C-DEPT (1D), ¹H (1D), ¹H, ¹H-DQF-COSY, ¹H, ¹H-TOCSY (mixing times of 30, 60 and 90 ms), ¹H, ¹³C-gHSQC, ¹H, ¹³C-gHMBC, ¹H, ¹³C-gHSQC-TOCSY (mixing times of 20 and 50 ms) and ¹H, ³¹P-COSY.

Acknowledgement

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