



## Note

# Structural and genetic characterization of the O-antigen of *Enterobacter cloacae* C5529 related to the O-antigen of *E. cloacae* G3054



Runhua Han<sup>b, c</sup>, Andrei V. Perepelov<sup>a, \*</sup>, Yuanyuan Wang<sup>b, c</sup>, Andrei V. Filatov<sup>a</sup>,  
Min Wang<sup>b, c</sup>, Alexander S. Shashkov<sup>a</sup>, Lei Wang<sup>b, c, d</sup>, Yuriy A. Knirel<sup>a</sup>

<sup>a</sup> N. D. Zelinsky Institute of Organic Chemistry, Russian Academy of Sciences, 119991, Moscow, Russian Federation

<sup>b</sup> TEDA Institute of Biological Sciences and Biotechnology, Nankai University, TEDA, Tianjin, 300457, China

<sup>c</sup> Key Laboratory of Molecular Microbiology and Technology of the Ministry of Education, College of Life Sciences, Nankai University, Tianjin, 300071, China

<sup>d</sup> Tianjin Biochip Corporation, TEDA, Tianjin, 300457, China

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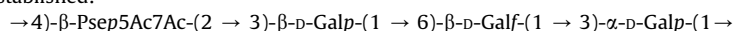
Bacterial polysaccharide structure

O-antigen gene cluster

Pseudaminic acid

## ABSTRACT

On mild acid degradation of the lipopolysaccharide of *Enterobacter cloacae* C5529, the O-polysaccharide chain was cleaved at the linkages of 5,7-diacetamido-3,5,7,9-tetradeoxy-L-glycero-L-manno-non-2-ulonic acid (di-N-acetylpsudaminic acid, Psep5Ac7Ac). The resultant oligosaccharide and an alkali-treated lipopolysaccharide were studied by sugar analysis along with <sup>1</sup>H and <sup>13</sup>C NMR spectroscopy, and the following structure of the tetrasaccharide repeating unit of the O-polysaccharide was established:



It differs from a structurally related O-polysaccharide of *E. cloacae* G3045 studied early (Perepelov, A. V.; Wang, M.; Filatov, A. V.; Guo, X.; Shashkov, A. S.; Wang, L.; Knirel, Y. A. *Carbohydr. Res.* 2015; 407:59–62) in positions of substitution of  $\beta$ -Psep5Ac7Ac (O-4 vs. O-8) and  $\beta$ -Galp (O-3 vs. O-6) and the absence of a side-chain  $\alpha$ -Galp residue. The O-antigen gene clusters of *E. cloacae* C5529 and G3045 are organized identically and include genes with the same putative functions in the O-polysaccharide synthesis. Based on these and serological data, it is suggested to combine *E. cloacae* C5529 and G3054 in one O-serogroup as two subgroups.

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*Enterobacter cloacae* has been isolated from a wide range of infections in hospitalized patients, particularly in neonatal critical care [1]. Extended-spectrum  $\beta$ -lactamases (ESBLs) and carbapenemases have been reported to be widespread in *E. cloacae* [2]. With the growing worldwide spread of *E. cloacae* strains that produce extended-spectrum  $\beta$ -lactamases (ESBLs) capable of hydrolyzing almost all  $\beta$ -lactams except carbapenems [3,4], *E. cloacae* became an emerging drug-resistant nosocomial pathogen [5].

In order to substantiate the antigenic heterogeneity and cross-reactivity on the molecular level, detailed structural studies of the O-antigens are performed, which help to improve the classification of *E. cloacae* strains. A few *E. cloacae* O-antigen-related studies have been reported, and until recently, O-polysaccharide structures have

been established for four strains from different O-serogroups [6–10]. The O-polysaccharides of two strains, C6285 and G3054, include non-2-ulonic acids, namely, di-N-acetyllegionaminic acid and di-N-acetylpsudaminic acid, respectively. In this work, we studied another pseudaminic acid-containing O-polysaccharide of a clinical isolate of *E. cloacae*, C5529, and found it to be structurally, genetically, and serologically related to that of *E. cloacae* G3054 from serogroup O1 [9].

The lipopolysaccharide (LPS) was isolated from *E. cloacae* C5529 cells by extraction with hot phenol-water. On degradation with dilute acetic acid, the LPS afforded no expected O-polysaccharide but an oligosaccharide (OS), evidently owing to cleavage of acid-labile glycosidic linkages of an O-polysaccharide component. Further studies showed that this component was 5,7-diacetamido-3,5,7,9-tetradeoxy-L-glycero-L-manno-non-2-ulonic acid (di-N-acetylpsudaminic acid, Pse5Ac7). Sugar analysis using GLC of the alditol acetates derived after full acid hydrolysis of the

\* Corresponding author.

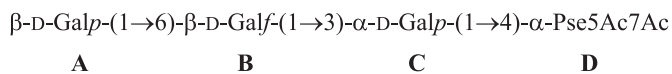
E-mail address: [perepel@ioc.ac.ru](mailto:perepel@ioc.ac.ru) (A.V. Perepelov).

OS revealed only galactose. GLC analysis of the acetylated (S)-2-octyl glycosides indicated that Gal has the  $\alpha$  configuration.

The  $^{13}\text{C}$  NMR spectrum of the OS (Fig. 1, top) showed signals for four anomeric carbons at  $\delta$  97.9, 98.0 (quaternary carbon; data of a DEPT experiment), 104.7, and 110.5, three  $\text{OCH}_2\text{—C}$  groups at  $\delta$  62.3, 62.9, and  $\delta$  72.4 (data of a DEPT experiment), one  $\text{CH}_3\text{—C}$  group at  $\delta$  16.8, one  $\text{C—CH}_2\text{—C}$  group at  $\delta$  33.3, two nitrogen-bearing carbons at  $\delta$  49.2 and 54.2, 15 oxygen-bearing sugar ring carbons in the region  $\delta$  68.4–84.3, two *N*-acetyl groups at  $\delta$  23.4, 23.5 (both Me), and  $\delta$  175.2 (2 CO). The  $^1\text{H}$  NMR spectrum of the OS contained *inter alia* signals for three anomeric protons at  $\delta$  4.44–5.13, one  $\text{CH}_3\text{—CH}$  group at  $\delta$  1.09 (d,  $J \sim 7$  Hz), one  $\text{CH—CH}_2\text{—C}$  group at  $\delta$  2.11 and  $\delta$  1.86, and two *N*-acetyl groups at  $\delta$  1.97 and 2.02.

The  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra of the OS were assigned using 2D  $^1\text{H}$ ,  $^1\text{H}$  COSY, TOCSY, and  $^1\text{H}$ ,  $^{13}\text{C}$  HSQC experiments, and spin systems for  $\beta$ -Galp (**A**),  $\beta$ -Galf (**B**),  $\alpha$ -Galp (**C**), and  $\beta$ -Psep5Ac7Ac (**D**) were identified (Table 1). The last sugar was confirmed by a comparison of  $^{13}\text{C}$  NMR chemical shifts and  $^3J_{\text{H,H}}$  coupling constants with published data [11].

Significant downfield displacements of the signals for C-3 of unit **C**, C-4 of unit **D**, and C-6 of unit **B**, as compared with their positions in the corresponding non-substituted monosaccharides [11,12], indicated the linkage position in each sugar residue. A 2D ROESY experiment revealed strong interresidue cross-peaks at  $\delta$  4.44/3.77, 5.13/3.74, and 5.05/4.23, which were assigned to **A** H-1, **B** H-6a; **B** H-1, **C** H-3; and **C** H-1, **D** H-4 correlations, respectively. These data were in agreement with the  $^{13}\text{C}$  NMR chemical shift data and defined the monosaccharide sequence in the OS, which, therefore, has the following structure:



To confirm that the OS represented a chemical repeat (O unit) of the O-polysaccharide and to determine the linkage mode between the oligosaccharide repeats, the LPS was O-deacetylated with aqueous ammonia. The resultant polymer ( $\text{LPS}_{\text{OH}}$ ) was studied by NMR spectroscopy as described above for the OS (for the  $^{13}\text{C}$  NMR

spectrum see Fig. 1, bottom; assigned  $^1\text{H}$  and  $^{13}\text{C}$  NMR chemical shifts are tabulated in Table 1). Spin systems of the same four monosaccharide residues as in the OS were identified. The  $^1\text{H}$ ,  $^{13}\text{C}$  HSQC spectrum revealed a downfield displacement of the H-3/C-3 cross-peak of unit **A** from  $\delta$  3.65/74.0 in the OS to  $\delta$  4.11/76.4 in the  $\text{LPS}_{\text{OH}}$ , and thus indicated substitution of unit **A** at position 3. A relatively large difference between the H-3ax and H-3eq chemical shifts of unit **D** (0.96 ppm) and a lower-field position of the C-6 signal at  $\delta$  74.4 in  $\text{LPS}_{\text{OH}}$ , as compared with its position at  $\delta$  71.6 in OS, demonstrated the  $\beta$  configuration of Psep5Ac7Ac [11].

Therefore, the O-polysaccharide of *E. cloacae* C5529 has the structure shown in Chart 1. It is structurally related to the O-polysaccharide of *E. cloacae* G3054 studied by us earlier [9] (Chart 1).

The O-antigen gene cluster of *E. cloacae* C5529 was found between the housekeeping genes *galF* and *gnd*. 12 open reading frames (Orfs) excluding *galF* and *gnd* were identified in the gene cluster, all of which have the same transcriptional direction from *galF* to *gnd*. The cluster was organized in the same manner as that of *E. cloacae* G3054 [9] and the corresponding genes showed high-level homology (Fig. 2). Therefore, they were assigned the same functions in the O-polysaccharide synthesis: i) *pseBCFGH* genes for synthesis of CMP-Psep5Ac7Ac from UPP-GlcNAc, ii) *glf* gene for mutase that converts UDP-D-Galp into UDP-D-Galf, iii) *wbaP* gene for D-Gal-1-P-transferase, which initiates the O-unit synthesis by transferring D-Gal-1-P from UDP-D-Gal to undecaprenyl phosphate [13], iv) three glycosyltransferase genes *orf7*, *orf9*, and *orf10*, and v) O-antigen processing genes: *wzx* for O-unit flippase and *wzy* for O-antigen polymerase.

Glycosyltransferases are specific for sugar donors, sugar acceptors, and the linkage between them. Orf9 shares 47% similarity with WcaN, a glycosyltransferase involved in the synthesis of the O9 antigen of *Klebsiella pneumoniae*, which shares the  $\beta$ -D-Galf-(1  $\rightarrow$  3)- $\alpha$ -D-Galp linkage with *E. cloacae* C5529. Therefore, Orf9 was suggested to be responsible for formation of this linkage in C5529. The protein sequences of Orf7 in *E. cloacae* G3054 and C5529 are identical, and there are minor differences in the protein sequences of Orf10 in the two strains. We proposed that Orf7 is responsible for formation of the  $\beta$ -D-Gal-(1  $\rightarrow$  6)- $\beta$ -D-Gal linkage that is common

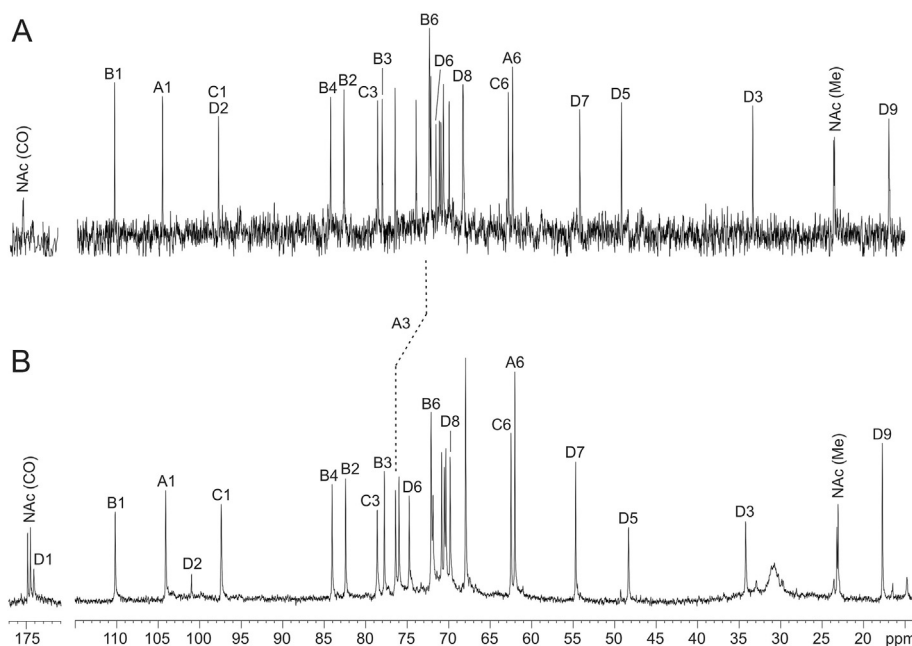


Fig. 1.  $^{13}\text{C}$  NMR spectra of the OS (top) and  $\text{LPS}_{\text{OH}}$  (bottom) from *E. cloacae* C5529. Arabic numerals refer to carbons in sugar residues denoted by letters as shown in Table 1.

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