**Draft Genome Sequence of Cloacibacterium normanense NRS-1 Isolated from Municipal Wastewater**

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**Cloacibacterium normanense** is a Gram-negative bacterium recovered from untreated human wastewater. Given its high abundance in wastewater and its apparent absence in human stool, it may contribute to biological phosphate removal. Here, we perform a whole-genome sequence of **C. normanense** NRS-1(T) and examine particular features of this draft genome.

Three strains of a novel bacterium were isolated from untreated human wastewater at a municipal water treatment plant in Norman, Oklahoma, USA (1). These strains were assigned to the novel genus *Cloacibacterium*, all within the species *Cloacibacterium normanense*. *C. normanense* NRS-1 was the designated type strain (1). *C. normanense* is a Gram-negative, nonmotile, yellow-pigmented, rod-shaped, facultatively anaerobic member of the *Flavobacteriaceae* family (1). Specifically, it belongs to a cluster within the *Bergeyella-Chryseobacterium-Riemerella* branch that is closely shared by *Riemerella columbina*, *Bergeyella zoohelcum*, and *Riemerella anatipestifer* (1).

Given the pervasiveness of *Flavobacteriaceae* members in aquatic habitats, the ability of some of these members to decompose complex organic molecules, and the high abundance of **C. normanense** in untreated wastewater (estimated counts of 1.4E4 cells/mL and 1.4E4 cells/mL at two respective water treatment plants), **C. normanense** may play a role in phosphate removal (1–4). While PCR techniques did not detect the bacterium in any of the 10 human stool samples tested (1), an undefined species belonging to the *Cloacibacterium* genus has been identified in human skin (5).

DNA was extracted from a **C. normanense** NRS-1 sample procured from ATCC, and a Nextera XT kit was used for library preparation. Whole-genome sequencing was performed by Illumina HiSeq, with a read length of 2 × 150 bp and an average insert size of 205 bp. Adapters were trimmed using Cutadapt (6), poor quality bases were removed using trimBWAstyle.pl, and reads <50 bp after trimming were removed using PRINSEQ-lite (7). Sequencing yielded 6,648,070 paired reads with a 33.03% GC content. SPAdes version 3.7.1 was used to assemble the reads with 494× mean coverage of the resulting contigs (8). QUAST reported a total scaffold length of 2,721,964 bp with a maximum scaffold length of 197,666 bp and an N50 value of 112,075 bp (9).

The IGS Annotation Engine was used for structural and functional annotation of the sequences (http://ae.igs.umaryland.edu/cgi/index.cgi, reference: 21677861). Manatee was used to view annotations (http://manatee.sourceforge.net). Manatee identified 38 tRNAs, three rRNAs, and 2,579 open reading frames, 88.5% of which are coding regions. The Comprehensive Antibiotic Resistance Database (CARD) recognized resistance genes for kanamycin and streptomycin, confirming positive *in vitro* resistance tests conducted by Allen et al. (10, 11). However, the *in vitro* tests also indicated resistance to erythromycin, which suggests that the **C. normanense** genome contains an uncharacterized erythromycin resistance gene. CARD also suggested resistance to six additional antibiotics not tested by Allen et al.: amikacin, kanamycin A, neomycin, spectinomycin, tobramycin, and viomycin. antiSMASH version 3.0 identified a terpene secondary metabolite cluster, most similar to the carotenoid biosynthetic gene cluster (28% of the genes show similarity) (12). CRISPRfinder identified three questionable clustered regularly interspaced short palindromic repeats (CRISPRs) and one confirmed CRISPR in contig 4088 (13). No intact prophage regions were detected by PHASTER (14, 15). Previously, only 16S sequence data were available for **C. normanense** (1). This draft genome provides a more comprehensive characterization of this bacterial type strain.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number MKGI00000000. The version described in this paper is the first version, MKGI01000000.

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