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Complete Genome Sequence of the Human Gut Symbiont *Roseburia hominis*

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We report here the complete genome sequence of the human gut symbiont *Roseburia hominis* A2-183T (≡ DSM 16839T = NCIMB 14029T), isolated from human feces. The genome is represented by a 3,592,125-bp chromosome with 3,405 coding sequences. A number of potential functions contributing to host-microbe interaction are identified.

O
e of the most proficient butyrate producers in the human gut is *Roseburia hominis* A2-183, which produces up to 20 mM of butyrate (1). In ulcerative colitis (UC) the numbers of *R. hominis* are significantly lower compared to control (2, 3). Its use for nutritional/medical applications has been proposed (D. Kelly, 13 August 2014, WO Patent App. PCT/GB2012/052,495), and it has received an orphan drug designation for UC (http://www.accessdata.fda.gov/scripts/opdlisting /oopd/OOPD_Results_2.cfm?Index_Number=439114). Flagellins from this bacterium are potent immunomodulators (D. Kelly, A. Patterson, E. Monnais, I. Mulder, 16 October 2014, WO Patent App. PCT/GB2014/051,123). We sequenced and annotated its genome to reveal beneficial properties.

The strain was grown as described before (4). Chromosomal DNA was isolated using an UltraClean Microbial DNA isolation kit (MoBio Laboratories) and a Wizard Genomic DNA purification kit (Promega). 1.5- to 3.5-kb fragments were cloned using the CloneSmart LCAmp kit (Lucigen), 4- to 8-kb fragments using the pJAZZ-OC vector (Lucigen), and 40-kb fragments using the CopyControl fosmid library production kit (Epigenetx Biotechnologies). End reads were obtained by Sanger sequencing. Genomic DNA was sequenced using 454 GS20/454 FLX sequencing. Reads were assembled using MIRA 3 (http://chevreux.org /projects_mira.html). The RAST (5) and Prokaryotic Genome (6) pipelines were used for annotation and comparative genomics.

The genome harbors a single circular genome of 3,592,125 bp, with a G+C content of 48.5%. We identified 3,285 genes, 3,143 potential protein-encoding sequences, 4 ribosomal operons with 12 tRNA genes, and 57 tRNA genes. The largest gene counts belonged to carbohydrate metabolism (17.6%), biosynthesis of amino acids and derivatives (10.8%), and protein metabolism (10.7%). Comparative genomics identified *Roseburia inulinivorans*, *Roseburia intestinalis*, and *Eubacterium rectale* as closest relatives, which is consistent with their close phylogenetic relationship (7).

*R. hominis* produces butyrate via the acetyl-CoA pathway. The pathway genes are found at four locations: (i) acetyl-CoA acetyl-

REFERENCES


