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GENOME SEQUENCES

Draft Genome Sequence of *Blautia* sp. Strain BCRC 81119, Isolated from Human Feces

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ABSTRACT *Blautia* sp. strain BCRC 81119 was isolated from a fecal sample from a 34-year-old male in Taiwan. The genome assembly comprised 4,098,441 bp, with a 43.95% G+C content.

Culturomics technology is a powerful tool for discovering new species in the human gut, and it can be used to complement metagenomics by overcoming the depth bias issue (1). During a study aimed at isolating novel bacterial species present in the human gut, we isolated strain BCRC 81119 from a fecal sample of a 34-year-old male in Taiwan by using a culturomics approach (2, 3). Based on the sequencing of the complete 16S rRNA gene, BCRC 81119 was found to exhibit 99.51% sequence identity with *Blautia massiliensis* DSM 101187 (GenBank accession number LN913006). In addition, the average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) values between BCRC 81119 and DSM 101187 were 98.07% and 86.2%, respectively. These values were clearly higher than the generally accepted cutoff threshold of 95 to 96% and 70%, respectively, for delineation of prokaryotic species, thus confirming that strain BCRC 81119 belongs to the species *B. massiliensis*. It has been reported that *B. massiliensis* might be an important species for human health, because it has been frequently isolated and detected in the human gut (4).

Blautia sp. strain BCRC 81119 is a rod-shaped, strictly anaerobic, non-spore-forming bacterium. It grows on yeast extract, Casitone, fatty acid, and glucose (YCFAG) medium (5) within 48 h at 37°C under anaerobic conditions. Genomic DNA was extracted using an EasyPrep HY genomic DNA extraction kit (Tools, Taiwan, Republic of China) following the manufacturer's protocol. Libraries were constructed using approximately 1 μl of genomic DNA, and the draft genome was sequenced from an Illumina paired-end library with an average insert size of 350 bp by using an Illumina HiSeq 4000 instrument with a paired-end 125-bp read length at the Beijing Novogene Bioinformatics Technology Co., Ltd. (Beijing, People's Republic of China). The low-quality sequences of the paired-end and mate pair reads were analyzed using an in-house program by Novogene Bioinformatics Technology Co., Ltd. Sequencing of strain BCRC 81119 generated 1,216 Mb of data. After adapter filtering and quality trimming, *de novo* assembly of the reads was performed using SOAP*denovo* (6), which resulted in 77 scaffolds with an N_{50} value of 112,070 bp. The draft genome contains 4,098,441 bp, with a G+C content of 43.95%, and was annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) to obtain 3,922 predicted genes, 14 rRNAs, 87 tRNAs, and 4 noncoding RNAs (7). Annotation of the protein-coding genes with Rapid Annotations using Subsystems Technology (RAST) (8) predicted 4,429 protein-coding genes, 2,306 of which had functional categories of SEED subsystems, while analysis with antiSMASH version 4.1 (9) predicted one sactipeptide biosynthetic gene cluster.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number QJHD00000000 (BioProject number PRJNA473893). The version described in this paper is the first version.

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