Draft Genome Sequence of *Paraclostridium bifermentans* subsp. *muricolitidis* Strain PAGU 1678T, Which Exacerbates Pathosis in a Mouse Model of Ulcerative Colitis

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ABSTRACT *Paraclostridium bifermentans* subsp. *muricolitidis* strain PAGU 1678T was isolated from rat feces and has the ability to exacerbate pathosis in a mouse model of ulcerative colitis. Here, we report the draft genome sequence of the 3,471,060-bp chromosome of strain PAGU 1678T.

Ulcerative colitis (UC) is classified as an inflammatory bowel disease, together with Crohn's disease. The main symptoms of UC are bloody diarrhea and abdominal pain (1). The number of UC patients has been increasing yearly worldwide, but the specific cause of UC is unknown (2). Currently, UC is considered to be caused by multiple factors, such as genetic susceptibility, environmental factors, immune dysregulation, and microbial flora (3). Using a mouse model of UC (4, 5), we found that strain PAGU 1678T was significantly increased in the feces and had the ability to exacerbate colitis by experimental infection (6). Later taxonomic studies revealed that strain PAGU 1678T was a novel subspecies of *Paraclostridium bifermentans* (7). Here, we report the draft genome sequence of *Paraclostridium bifermentans* subsp. *muricolitidis* strain PAGU 1678T.

Strain PAGU 1678T was incubated at 37°C for 24 h under anaerobic conditions (10% CO_2, 10% H_2, 80% N_2) on GAM agar plates (Nissui) (6). Genomic DNA was extracted and purified from a single colony using a Wizard genomic DNA purification kit (Promega). DNA libraries were prepared using a Nextera XT library preparation kit (Illumina) according to the manufacturer's instructions. The genome sequence was determined using 2×150-bp paired-end reads (14,989,552 reads) obtained with an Illumina HiSeq X Ten sequencer. The final coverage of the genome was $1,061\times$. These reads were trimmed on the basis of base quality (quality score limit of 0.05) and removed if the reads had more than two ambiguous nucleotides or they were less than 15 bp in length, using CLC Genomics Workbench v9.5.2 (CLC bio). The software was operated using default settings and parameters unless otherwise specified. Automated annotation was carried out with the DDBJ Fast Annotation and Submission Tool (https://dfast.nig.ac.jp) with default parameters.

Strain PAGU 1678T was assembled into 126 contigs (N_{50} = 82,995 bp) and had a genome length of 3,471,060 bp (G+C content of 28.1%). The chromosome contained 3,398 predicted protein-coding sequences, 7 rRNAs, and 70 tRNAs. BLAST calculations were performed using GENETYX NGS v15 to calculate the average nucleotide identity (ANI) between strain PAGU 1678T and *Paraclostridium bifermentans* JCM 1386T.

The ANI homology value of 96% suggested that strain PAGU 1678T is the same species as *P. bifermentans*. The genomic sequence information for this strain provides important data that may lead to elucidation of the mechanism underlying the development of UC.

Data availability. The whole-genome sequence of *P. bifermentans* subsp. *muricolitidis* PAGU 1678[T] and the raw sequence data have been deposited in DDBJ/EMBL/GenBank under the accession numbers BOQA01000001 to BOQA01000126 and DRA007030, respectively.

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