

Draft genome sequence of a representative strain of the *Catenibacterium* genus isolated from human feces

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ABSTRACT A strain from a previously undescribed species belonging to the *Catenibacterium* genus was isolated from the stool of a healthy volunteer. The strain is strictly anaerobic, and the genome encodes a CRISPR-Cas system and genes related to trimethylamine production.

KEYWORDS Catenibacterium, gut microbiome

The *Catenibacterium* genus belongs to the Erysipelotrichaceae family, with only one known species, *Catenibacterium mitsuokai* (1). Metagenome-assembled genomes suggest an expanded predicted diversity for the *Catenibacterium* genus (2), which also comprises some taxonomically unassigned isolates.

Catenibacterium strain CMD8551 was isolated in an anaerobic chamber (95% N₂/5% H₂) from the feces of a healthy volunteer (protocol no. 2021–007 by the Ethical Committee of the University of Trento). The fresh sample was homogenized, serially diluted, and spread (10⁻⁵ dilution) onto chopped meat agar plates with 4% defibrinated sheep blood (Microbiol Diagnostics), 0.2% carbon sources (pectin, arabinoxylan, glucose, maltose, cellobiose, and resistant starch), 2.5 g/L yeast extract, 0.005% vitamin K1, and 5 mg/L hemin. After 2 days at 37°C, a single colony was inoculated in modified chopped meat broth.

Genomic DNA was isolated from liquid culture using the Wizard Genomic DNA Purification Kit (Promega) and used for library preparation with Illumina DNA Prep and Tagmentation Kit (Illumina). Libraries were sequenced (150 bp paired-end reads) on a NovaSeq6000 S4 flowcell (Illumina) at the University of Trento, following a cleaning step (0.6× Agencourt AMPure XP beads). Raw reads were filtered with Trim Galore (parameters: --stringency 5 --length 75 --quality 20 --max_n 2 --trim-n; <https://github.com/FelixKrueger/TrimGalore>). Illumina PhiX adapters and human DNA reads were removed using Bowtie2 (3) against the corresponding reference genomes. A total of 23,527,050 high-quality paired-end reads (mean Q value of 35.70) were retained (mean read length of 147.48 bp). Genome assembly was performed using SPAdes 3.15.2 (parameters: --careful -k 21,33,55,77,99,127) (4) on 40% randomly rarefied reads (<https://github.com/lh3/seqtk>, parameters: sample module). Assembly statistics, computed using QUAST v5.1.0rc1 (5), completeness, and contamination obtained with CheckM v1.1.2 (6), are reported in Table 1. Mean coverage was computed using CMseq v1.0.4 (<https://github.com/SegataLab/cmseq>). Unless specified, all the computational tools used in this work were applied with default parameters.

The Prokka (v1.14) (7) annotation of the assembly revealed a total of 2,326 genes, including CRISPR-Cas system and genes for choline metabolism (8). Fifteen glycoside hydrolases were identified by dbCAN2, suggesting high carbohydrate catabolic potential. The analysis with *Resistance Gene Identifier* (version 5.1.1) (9) showed four putative genes involved in resistance to carbapenem and glycopeptide antibiotics.

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TABLE 1 Summary of the statistics from *Catenibacterium* CMD8551 genome assembly

Parameter	Value
Total length (bp)	2,320,430
No. of scaffolds	113
GC content (%)	33.7
Mean coverage (×)	519×
Size of longest scaffold (bp)	105,579
N_{50} (bp)	44,791
L_{50}	18
No. of coding sequences	2,239
No. of RNAs	10 rRNA 76 tRNA
Estimated completeness (%)	100%
Estimated contamination (%)	0%

PhyloPhlAn version 3.0 (January 21 database version) (10) was used to perform taxonomic assignment and reconstruct the phylogenetic tree in Fig. 1 (parameters: -d phylophlan --diversity low --fast --force_nucleotides), using MAFFT (v7.508) for the multiple-sequence alignment step of the 400 universal proteins (11) and RAxML (v8.2.12) for the phylogenetic reconstruction (GTR + CAT substitution model). *C. mitsuokai* (GCA_018785505) was the closest species to the new strain, with three reference genomes showing <94% average nucleotide identity (ANI) values (Fig. 1). By comparing the strain assembly with NCBI's publicly available reference genomes assigned to *C. mitsuokai*, two subtrees were clearly identified, corresponding to *C. mitsuokai* and a previously unidentified species. We propose the species name *Catenibacterium tridentinum*, represented by the strain CMD8551, and the other genomes previously assigned to *C. mitsuokai* that show species-level similarity (intraspecies min–max ANI%: 95.85–99.77).

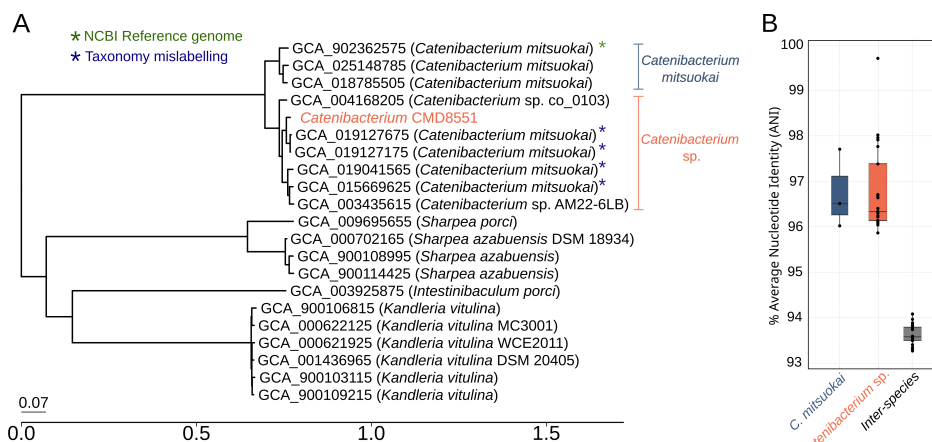


FIG 1 (A) Phylogenetic tree of the new *Catenibacterium* isolate and related taxa with available reference genomes obtained from sequencing of isolates. The marked reference genomes were taxonomical missassigned (as *C. mitsuokai*) based on average nucleotide identity (ANI, <94%) to its reference strain (GCA_902362575). These reference genomes, along with the CMD8551 strain, cluster as a different taxonomic group distant from *C. mitsuokai* compatible with a new species inside the *Catenibacterium* genus. (B) Comparison of the ANI of the available genomes from *Catenibacterium* genus inside each species genomes defined by the phylogenetic tree (*C. mitsuokai* and the proposed *C. tridentinum*) and between them (interspecies).

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DATA AVAILABILITY

This study project is available under NCBI accession ID [PRJNA939950](#). The sample used to assemble the genome and the assembly are available under accession [SAMN33794588](#) and [JARNBK000000000](#), respectively.

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