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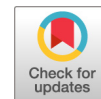
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Draft Genome Sequence of *Streptococcus anginosus* Strain CALM001, Isolated from the Gut of an Elderly Dane

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ABSTRACT Here, we present a 1.89-Mbp draft genome sequence of *Streptococcus anginosus* strain CALM001, a Gram-positive bacterium that was isolated from a fecal sample donated by a 70-year-old Dane enrolled in the Counteracting Age-Related Loss of Skeletal Muscle Mass (CALM) intervention study.

Streptococcus anginosus is a member of the “*Streptococcus milleri*” group (SMG), together with 2 other distinct species, *Streptococcus intermedius* and *Streptococcus constellatus* (1). Oral cavity, urogenital, and gastrointestinal specimens are the most common samples from which these streptococcal species have been recovered (2). Identification of the species from this group is difficult, as they share similar phenotypic characteristics (3).

S. anginosus strain CALM001 was isolated from the slurry of a homogenized fecal sample collected from the cohort of Counteracting Age-Related Loss of Skeletal Muscle Mass (CALM) intervention study (4) by overnight cultivation on Gifu anaerobic medium (GAM broth; HyServe GmbH & Co. KG). The genomic DNA of the strain was extracted using the GenElute bacterial genomic DNA kit (Sigma-Aldrich Co., St. Louis, MO). A sequencing library was prepared using the Nextera XT kit (Illumina, San Diego, CA). Genome sequencing was performed using the MiSeq platform (Illumina) with a paired-end 2 MiSeq reagent kit v2. The resulting ca. 1.97 million read pairs (≈ 0.88 Gbp) were inspected using FastQC v0.11.4 (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). Adapters and low-quality regions were trimmed using Trimmomatic v0.33 (5), with the following parameters: CROP:225 HEADCROP:20 SLIDINGWINDOW:4:20 ILLUMINA-CLIP:adapters.fasta:2:40:15 MINLEN:100. Trimmed reads were assembled using SPAdes v3.6.1 (6), with the following parameters: $-k$ 21,33,55,77,99,127 $-careful$. Contigs that most likely originated from contamination were removed based on G+C content and coverage using MetaWatt v3.5 (7), reducing the assembly to contigs classified as originating from the genus *Streptococcus*. Trimmed reads mapping to the retained *Streptococcus* contigs (ca. 1.28 million read pairs, ≈ 0.48 Gbp) were extracted using BMap v34.94 (<https://sourceforge.net/projects/bbmap/>) using the “minid=0.98” option.

The extracted reads were assembled using SPAdes, as described before, which resulted in eight contigs with ca. 254-fold coverage. The draft genome sequence of CALM001 has a total length of 1,888,139 bp, an average G+C content of 38.75%, and an N_{50} length of 1,134,963 bp. Using a marker gene set for the genus *Streptococcus*, CheckM v1.0.3 (8) estimates the genome to be 100% complete.

Data availability. The draft genome sequence of *Streptococcus anginosus* strain CALM001 is available in the GenBank database under accession number [QWDL00000000](https://www.ncbi.nlm.nih.gov/nuclink/QWDL00000000).

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Raw sequencing data have been deposited in the SRA database under accession number [SRX5707091](https://www.ncbi.nlm.nih.gov/sra/SRX5707091), with BioSample and BioProject accession numbers [SAMN09908147](https://www.ncbi.nlm.nih.gov/bioproject/SAMN09908147) and [PRJNA487690](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA487690), respectively.

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