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PROKARYOTES

Whole-Genome Sequence of a *Mycobacterium goodii* Isolate from a Pediatric Patient in South Africa

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ABSTRACT We describe here the draft genome sequence of a *Mycobacterium goodii* isolate from a pediatric patient in Western Cape, South Africa. To our knowledge, this is the second reported genome of this rapidly growing nontuberculous mycobacterial species.

Nine specimens from a pediatric patient were submitted for culture, including specimens obtained from bronchoalveolar lavage fluid, tissue, gastric washing fluid, and a pus swab for tuberculosis investigation. No acid-fast bacilli were observed on direct auramine staining and microscopy. Cultivation of mycobacteria was successful for the gastric washing fluid, pus swab, and brochoalveolar lavage fluid specimens within a median time of 4 days (range, 2 to 14 days) using the MGIT 960 instrument (BD, Sparks, MD, USA). The presence of noncorded acid-fast bacilli was observed when we performed Ziehl-Neelsen staining on these cultures. The tuberculosis antigen MPT64 rapid test (SD Bioline) for detection of the presence of *Mycobacterium tuberculosis* complex was negative. Thereafter, species identification was performed using the Genotype Mycobacterium CM version 2.0 (Hain Lifescience GH, Nehren, Germany) on an isolate obtained from a gastric washing fluid specimen which was identified as a *Mycobacterium* species. The isolate, which was designated strain ST0139456, was then subjected to 16S rRNA sequencing using the forward primer 5′-AGTTTGATCMTGGCTCAG-3′ and reverse primer 5′-GGACTACHAGGGTATCTAAT-3′, and the resulting BLAST search (https://blast.ncbi.nlm.nih.gov) confirmed 99% homology to *Mycobacterium goodii*, a nontuberculous mycobacterium species of the *Mycobacterium smegmatis* group. The species identification as *Mycobacterium goodii* was further confirmed using the GenoType Mycobacterium AS version 1.0 kit (Hain Lifescience GH) and whole-genome sequencing.

Paired-end libraries were prepared using the Nextera XT DNA library kit, followed by 2- × 300-bp sequencing on a MiSeq instrument (Illumina, San Diego, CA, USA). The sequenced reads were quality trimmed using Sickle version 1.33 (https://github.com/najoshi/sickle) and *de novo* assembled using SPAdes genome assembler version 3.5 (1). The assembly contains 156 contig sequences of longer than 200 bp and covers 6,621,508 bp, with a G+C content of 67.07% and an N_{50} of 116,855 bp. Genome annotation was performed via the NCBI Prokaryotic Genome Annotation Pipeline

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(PGAP) (2). The total number of 6,514 genes predicted by PGAP includes 6,281 protein-coding genes, 175 pseudogenes, and 58 RNA genes.

Accession number(s). The draft genome sequence has been deposited at NCBI under the BioProject number PRJNA415539, BioSample number SAMN07828250, and GenBank accession number PEBB00000000.

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