We present here the draft genome sequences of two Mycobacterium setense strains. One of them corresponds to the M. setense type strain DSM-45070, originally isolated from a patient with a posttraumatic chronic skin abscess. The other one corresponds to the nonpathogenic strain Manresensis, isolated from the Cardener River crossing Manresa, Catalonia, Spain. A comparative genomic analysis shows a smaller genome size and fewer genes in M. setense strain Manresensis relative to those of the type strain, and it shows the genome segments unique to each strain.

In the search for nonpathogenic mycobacteria that could be used as a probiotic for tuberculosis prevention, we isolated a novel bacterial strain from the Cardener River near Manresa, Catalonia, Spain. We found its 16S rRNA sequence to be identical to that of Mycobacterium setense (1). We also observed a high similarity to M. setense in other genes commonly used in the classification of Mycobacterium species, such as rpoB, rpoC, hsp65, and sodA. Thus, we named this new strain M. setense strain Manresensis.

Virulence tests based on intravenous administration in severe immunocompromised mice (SCID) revealed that Manresensis is significantly less virulent than the immunocompromised mice (SCID) revealed that Manresensis is significantly less virulent than the immunocompromised mice (SCID) revealed that Manresensis is significantly less virulent than the

The type strain DSM-45070 was first isolated from a patient in Sète, France (1), and clinical isolates have been reported in Marseille, France (74023791) (2) and Iran (HNTM46, HNTM49, and HNTM91) (3). The biochemical characterization of the Manresensis and DSM-45070T strains revealed further differences between them regarding growth in glucose, gelatinase, urease, 5% NaCl tolerance, and mycoidic acid patterns.

To provide insight into the genetic causes of these phenotypic differences, we sequenced the genomes of M. setense strain DSM-45070T and strain Manresensis. We obtained 1,771,796 (250 nucleotides [nt] long) and 22,250,521 paired-end reads, respectively, using the Illumina SBS technology on a MiSeq sequencer. After merging the paired-end reads with FLASH (4), de novo assemblies were generated using SPAdes version 3.0 (5). The Manresensis genome size amounted to 6.06 Mb, split into 22 contigs, with an average depth of coverage of 788×. The DSM-45070T genome was 6.26 Mb long, divided into 21 contigs, with 71× coverage. The G+C contents in both strains (66.5%) were found to be expected for Mycobacterium species. The average nucleotide identity by BLAST (ANIb) calculated with JSpecies (http://www.jbigs .eds/JSpecies) was 98.5% between the two genomes, corroborating that they belong to the same species. The closest published Mycobacterium genome based on ANIb is that of M. septicum (DSM-44393) (ANIb, 87%); however, the contigs were ordered with Mauve (6) using the Mycobacterium sp. strain MCS (accession no. NC_008146) genome assembly as reference guide, since it was the closest one (ANIb, 76.5%) with a fully complete genome. In addition to the difference of 0.2 Mb in genome size, genome annotation using the RAST engine (7) also revealed differences in the gene numbers. Manresensis and DSM-45070T were predicted to have 5,716 and 5,953 protein-coding genes, respectively. We mapped sequence reads from Manresensis to the DSM-45070T genome and vice versa using the Burrows-Wheeler aligner (BWA) (8) to identify the segments unique to each genome. Using this strategy, we found Manresensis to have 3.7% of its genome without homology in Manresensis. An analysis of the gene contents of these stretches revealed 144 genes unique to Manresensis and 373 genes unique to DSM-45070T, which might explain the distinct phenotypes we observed between the strains.
Nucleotide sequence accession numbers. The whole-genome assemblies of *M. setense* DSM-45070 and *M. setense* strain Manresensis have been deposited in DDBJ/EMBL/GenBank under accession numbers JTJW00000000 and JTLZ00000000, respectively. The versions described in this paper are JTJW01000000 and JTLZ01000000, respectively.

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