In an effort to explore the microbial diversity from hot springs located in Manikaran, India, we isolated a thermophilic strain, *Thermus* sp. strain RL, inhabiting water with a surface temperature of $>95^\circ$C (1). In continuation of this survey, we recently isolated a bacterial strain of the genus *Cellulosimicrobium* from microbial mats ($>45^\circ$C). The genus *Cellulosimicrobium* is characterized by Gram-positive, rod-shaped, nonmotile chemooorganotrophs (2) and mainly comprises three species: *C. cellulans* (3), *C. funkei* (4), and *C. terreum* (5). Among these, *C. cellulans* and *C. funkei* are reported to be pathogenic (6, 7). The availability of only two genomes of *C. cellulans* J36 and *C. cellulans* LMG 16121 led us to sequence the genome of this strain.

The total genomic DNA of strain MM was isolated using the cetyltrimethylammonium bromide (CTAB) method (8) and was further sequenced using Illumina HiSeq 2000 (2-kb paired-end library) and 454 GS FLX Titanium platforms (2-kb single reads). The sequenced raw data ($n = 26,536,628$) were assembled *de novo* using Velvet 1.2.10 (9), PRICE (10), and minimus2 assembler (11). The assembly produced 299 contigs, for a final assembly size of 3.85 Mbp, with an $N_{50}$ of 19,682 bp and a 74.4% G+C content. The NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and Rapid Annotation using Subsystems Technology (RAST) (12) version 4.0 were used for gene annotation. RAST annotation predicted 3,718 coding sequences and 273 subsystems. ARAGORN (13) predicted 49 genes encoding tRNAs. One copy each of 23S rRNA and 16S rRNA and two copies of 5S rRNA in the draft genome were revealed by RNAmmer (14). Twenty-eight out of 31 protein-coding bacterial genes and two copies of 5S rRNA in the draft genome were revealed by ARAGORN (13). Among these, *C. cellulans* and *C. funkei* are reported to be pathogenic (6, 7). The availability of only two genomes of *C. cellulans* J36 and *C. cellulans* LMG 16121 led us to sequence the genome of this strain.

The draft genome sequence of *Cellulosimicrobium* sp. strain MM, isolated from arsenic-rich microbial mats of a Himalayan hot spring, consists of 3,718 coding sequences, with an average % G+C of 74.4%.

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