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Genome Sequence of *Microbacterium yannicii*, a Bacterium Isolated from a Cystic Fibrosis Patient

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***Microbacterium yannicii* is a Gram-positive, aerobic, yellow-pigmented, rod-shaped, nonmotile, oxidase-negative, and catalase-positive bacterium isolated on Columbia colistin-nalidixic acid (CNA) agar with 5% sheep blood from the sputum of a cystic fibrosis patient. The present study reports the draft genome of a *Microbacterium yannicii* strain.**

Many new, emerging, and/or multidrug-resistant bacteria have been recently reported in cystic fibrosis (CF) patients using different technologies, including new culture media and molecular methods (1, 2). We report the isolation of *Microbacterium yannicii* from a sputum sample from an adult CF patient. *Microbacterium* belongs to the family *Microbacteriaceae* (8), order *Actinomycetales*, class *Actinobacteria*, which comprises mainly aerobic Gram-positive bacteria with high G+C content and a peptidoglycan defined by a B-type cross-linkage (9). Bacteria of the genus *Microbacterium* are endophytic Gram-positive bacteria that usually live within plant hosts. From the mid-1990s, the presence of *Microbacterium* was recognized in human clinical specimens. The Gram-positive strain that was isolated on Columbia colistin-nalidixic acid (CNA) agar with 5% sheep blood (bioMérieux) grew after 24 h of culture at 37°C with 5% CO_2. Although its pathogenicity in humans is unknown, this bacterium could be an emerging pathogen in the context of CF. *Microbacterium yannicii* has also been isolated from the roots of *Arabidopsis thaliana* (3). Here, we present the genome of *Microbacterium yannicii*. To date, only one *Microbacterium* sp. genome, of *Microbacterium testaceum*, has been reported (7).

Genomic DNA from *Microbacterium yannicii* (strain PS01; CSUR reference no. P191) was fully sequenced by pyrosequencing using the genome sequencer Titanium (454 Life Sciences, Branford, CT) (8). A library of paired-end fragments was created following the manufacturer's instructions (454 Life Sciences, Branford, CT). This library was sequenced using the GS Titanium sequencer (454 Life Sciences, Branford, CT) (6).

Reads originated from each strain were assembled into contigs using Newbler 2.53 (454 Life Sciences, Branford, CT). The assembly was verified using the CLC Genomics software (CLC Bio, MA). Predicted proteins were compared against a nonredundant GenBank database using BLASTP (http://www.ncbi.nlm.nih.gov) for functional annotation. tRNAs and rRNAs were predicted using ARAGORN (5) and RNAmmer (4), respectively.

Microbacterium yannicii draft genome sequencing generated 67 contigs. The genome exhibits a total size of 3,952,501 bp and a G+C content of 69.5%. A total of 3,772 protein-coding open reading frames (ORFs) with an average size of 953 bp were identified and cover 90.97% of the genome. Among those genes we found 324 orphan ORFs (ORFans) (8.59% of the total gene content), 46 tRNAs, and 2 ribosomal operons with the 3 expected RNA genes (5S, 23S, and 16S). In conclusion, this bacterium should be added to the list of new or emerging bacteria in CF patients.

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited with EMBL under the accession numbers CAJF01000001 to CAJF01000067. The version described in this paper is the first version.

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