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GENOME SEQUENCES

Whole-Genome Sequencing of Two Moroccan *Mycobacterium tuberculosis* Strains

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ABSTRACT *Mycobacterium tuberculosis* is known to cause pulmonary and extrapulmonary tuberculosis. In Morocco, the spread of multidrug-resistant (MDR) tuberculosis (TB) has become a major challenge. Here, we announce the draft genome sequences of two *Mycobacterium tuberculosis* strains, MTB1 and MTB2, isolated from patients with pulmonary tuberculosis in Morocco, to describe variants associated with drug resistance.

Tuberculosis is an urgent public health problem in Morocco caused by *Mycobacterium tuberculosis* bacteria. Control of the bacteria has been recently complicated by the emergence of multidrug-resistant (MDR) strains showing resistance to the second-line treatment (rifampin, isoniazid) due to probable excessive antibiotic use (1–3). The identification of differences between MDR and sensitive *Mycobacterium tuberculosis* would improve the identification of the drug resistance site. Whole-genome sequencing using next-generation sequencing technologies is emerging as a rapid method for genetic characterization (4, 5). Thus, we provide the whole-genome sequencing data of two *Mycobacterium tuberculosis* strains, MTB1 and MTB2, with different resistance profiles.

Two *Mycobacterium tuberculosis* strains recovered from patients with pulmonary tuberculosis at the military hospital in Rabat, Morocco, and grown in Middlebrook 7H9 medium using the Bactec MGIT 320 system (Becton, Dickinson) were received for sequencing. DNA was purified using the Qiagen DNA extraction kit (QIAamp DNA mini-kit) following the kit protocol, and DNA libraries were prepared using the Nextera XT library preparation kit V3. Genomic DNA was sequenced using the Illumina MiSeq platform (San Diego, CA, USA) in paired-end (2×300-bp) format. Yields of 1,616,965 and 620,966 reads were preprocessed for quality checking using FastQC, further assembled using A5-miseq with default parameters (6) (the default settings include running Trimmomatic for read preprocessing) into 4,341,655-bp and 4,291,403-bp draft genome sequences, and divided into 242 (N_{50}, 43,730 bp) and 238 (N_{50}, 35,128 bp) contigs for MTB1 and MTB2, respectively.

The assemblies shared a GC content of 60% and 3 *arnT* operons. The genome annotation was performed using the NCBI annotation pipeline (7) and identified 4,265 and 4,422 coding DNA sequences (CDS) in MTB1 and MTB2, respectively.

Furthermore, reads were mapped to the h37rv reference genome using BWA (8). Variants were called using SAMtools (9) and annotated by SnpEff (10). The genome sequence displayed hot spot mutations in genes associated with resistance. MTB1

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harbored mutations in *katG* (Ser315Thr) and *rpoB* (Ser450Leu) responsible for resistance to isoniazid and rifampin, respectively (11). No resistance-associated mutations were identified in the genes (*gyrA*, *gyrB*, and *rrs*) linked to second-line drugs (12). However, pyrazinamide resistance was due to a mutation in *pncA* (Gly97Asp) (13), which classifies MTB1 as pre-extensively drug resistant (pre-XDR), while MTB2 did not show any mutations associated with first- or second-line drug resistance in its genotype. This study represents an initial analysis of a *Mycobacterium tuberculosis* collection to highlight the resistance profile in Morocco.

Data availability. The genome sequences of *Mycobacterium tuberculosis* MTB1 and MTB2 have been deposited in DDBJ/ENA/GenBank under the accession numbers NARM00000000.1 and NARL00000000.1, respectively. The SRA accession numbers for MTB1 and MTB2 are SRR12031346 and SRR12031345, respectively.

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