

Draft Genome Sequence of a Clinical Isolate of Multidrug-Resistant *Mycobacterium tuberculosis* East African Indian Strain OSDD271

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We describe the genome sequencing and analysis of a clinical isolate of *Mycobacterium tuberculosis* East African Indian (EAI) strain OSDD271 from India.

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Tuberculosis has emerged as one of the major public health issues worldwide, accounting for approximately 1.4 million deaths in 2010 alone (1). Over 40% of the global incidence in tuberculosis is accounted for by cases in India and China, with 24% of cases occurring in Africa (1). Closely related species of *Mycobacterium*, named the *Mycobacterium tuberculosis* complex (MTBC), are responsible for the pathogenesis of tuberculosis (2). Clinical isolates of the *Mycobacterium tuberculosis* complex are mainly clustered into distinct lineages based on spoligotype patterns (3). These lineages include the Indo-Oceanic (IO), East African Indian (EAI), East Asian (Beijing), Central Asian (CAS), Euro-American (Haarlem, LAM, T, and X), West African I (AFRI2), and West African lineage II (AFRI1) (4). The CAS and EAI lineages have been found to be distributed across the world. CAS and EAI genotypes, along with the Beijing genotypes, contribute to the major proportion of clinical strains in India (5–8). EAI strains have also been reported as one of the major genotypes in many countries of Southeast Asia and Africa (9). EAI strains have been shown previously to be associated with slow transmissibility in human populations/patients in some parts of the world (10) and along with CAS strains have been suggested to be involved in extrapulmonary tuberculosis in some regions of the world (11, 12). EAI strains have also been important in the study of the evolutionary history of *Mycobacterium tuberculosis*, because they are primitive strains (13).

In this report, we describe the draft genome of a multidrug-resistant clinical isolate of *Mycobacterium tuberculosis* conforming to the EAI spoligotype. The clinical isolate of OSDD271 was obtained from the strain repository maintained at the National JALMA Institute of Leprosy and Other Mycobacterial Diseases and is part of the CSIR Open Source Drug Discovery project open access repository. Spoligotyping was performed and drug sensitivity was evaluated per standard protocols (14–16). Drug sensitivity

analysis revealed the isolate to be resistant to rifampin, isoniazid, pyrazinamide, ethambutol, streptomycin, and 4-aminosalicylic acid (PAS). DNA was isolated per standard protocols. The raw sequence data were generated after library preparation on Ion Torrent PGM and Roche 454 platforms according to protocols recommended by the manufacturers. Draft genomes were assembled de novo using CLC Genomics Workbench 6. The assembly resulted in 182 contigs at N_{50} values of 37,178 bp and a total assembly of 4,169,405 bp. The scaffolds were ordered using Mauve (17). Automated gene prediction on the draft genomes was performed using the RAST server (18). Analysis revealed that the draft assembly encoded 4,186 genes, including 48 RNA genes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AQQC00000000](https://www.ncbi.nlm.nih.gov/nuccore/AQQC00000000). The version described in this report is version [AQQC01000000](https://www.ncbi.nlm.nih.gov/nuccore/AQQC01000000).

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