

Whole Genome Sequence of Polyresistant *Mycobacterium tuberculosis* CWCFVRF PRTB 19 Sputum Isolate from Chennai, India, Closely Clustering with East African Indian 5 Genogroup

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We announce the draft genome sequence of a polyresistant *Mycobacterium tuberculosis* strain (CWCFVRF PRTB 19) isolated from the sputum of a clinically suspected tuberculosis patient, and it closely clusters to the East African Indian 5 (EAI5) lineage.

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Drug resistance in *Mycobacterium tuberculosis* is mainly due to the mutations in relatively restricted regions of the genome (1, 2). *M. tuberculosis* resistance to antituberculosis drugs has emerged as a serious problem. The management of tuberculosis relies on strong laboratory investigations and trained and dedicated personnel for treatment oversight and supervision. Treatment should be individualized for each patient on the basis of *in vitro* susceptibility pattern to antituberculosis drugs. In general, *M. tuberculosis* that exhibits *in vitro* drug resistance to more than one antituberculosis drug (either isoniazid or rifampin) is referred to as a polyresistant strain. Though the detection of mutations in the *M. tuberculosis* target genes by PCR-based DNA technology plays an important role in the detection of drug resistance, it will not provide a holistic view of the genomic evolution leading to drug resistance. Hence, there is a need for whole-genome sequencing technology to explore the complete mechanism of drug resistance emerging in *M. tuberculosis* strains.

We announce here the draft genome sequence of a polyresistant sputum isolate of *M. tuberculosis*, strain CWCFVRF PRTB 19, isolated from a patient clinically suspected to have tuberculosis. The isolate was found to be phenotypically resistant to streptomycin, isoniazid, ethambutol, and pyrazinamide by using the Bactec microMGIT culture system. Whole-genome sequencing was performed using an Ion Torrent PGM platform, similarly to in our previous work (3).

The generated sequence reads with a Phred score cutoff of ≥ 20 were *de novo* assembled using MIRA Assembler 3.4.1.1, which resulted in 115 contigs of 4,332,844 bp sequence length, with $130.93\times$ coverage and an N_{50} of 81,962 bp. These sequences were further reordered to *M. tuberculosis* H37Rv (accession no. NC_000962.3) using Mauve (4) and in-house written scripts. The assembled sequences were annotated by NCBI

PGAAP (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which revealed 4,058 protein-coding genes and 54 RNA-coding genes. The genome was also computationally spoligotyped using the SpolPred program (5), which resulted in the spoligotype octal code 075067737003511. Further spotclust analysis revealed that the strain belongs to a novel spoligotype closely clustering to East African Indian lineage 5 (EAI5), with a spotclust (6) probability of 0.99. This genome analysis will pave the way to understanding the epidemiology and genetic variations (mutations/polymorphisms) occurring in the polyresistant *M. tuberculosis* strains circulating in Chennai, India.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JMIM00000000](https://www.ncbi.nlm.nih.gov/nuccore/JMIM00000000). The version described in this paper is version JMIM00000000.1.

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