First whole genome sequencing data of a Mycobacterium tuberculosis STB-T1A strain isolated from a spinal tuberculosis patient in Sabah, Malaysia

ABSTRACT

Spinal tuberculosis, also referred to as Pott's disease, presents a significant risk of severe paralysis if not promptly detected and treated, owing to complications such as spinal cord compression and deformity. This article presents the genetic analysis of a Mycobacterium tuberculosis STB-T1A strain, isolated from the spine of a 29-year-old female diagnosed with spinal tuberculosis. Genomic DNA was extracted from pure culture and subjected to sequencing using the Illumina NovaSeq 6000 sequencing system. The genome of the M. tuberculosis STB-T1A strain spans 4,367,616 base pairs with a G+C content of 65.56 % and 4174 protein-coding genes. Comparative genomic analysis, conducted via single nucleotide polymorphism (SNP)-based phylogenetic analysis using the Maximum Likelihood method, revealed that the strain falls within the Indo-Oceanic lineage (Lineage 1). It clusters with the M. tuberculosis 43-16836 strain, which was isolated from the cerebrospinal fluid of a patient with tuberculous meningitis in Thailand. The complete genome sequence has been deposited at the National Center for Biotechnology Information (NCBI) GenBank database with the accession number JBBMVZ000000000.