

**The whole genome sequence data analyses of a mycobacterium tuberculosis strain sbh321 isolated in Sabah, Malaysia, belongs to ural family of lineage 4**

**ABSTRACT**

In 2019, 10 million new cases of tuberculosis have been reported worldwide. Our data reports genetic analyses of a Mycobacterium tuberculosis strain SBH321 isolated from a 31-year-old female with pulmonary tuberculosis. The genomic DNA of the strain was extracted from pure culture and subjected to sequencing using Illumina platform. M. tuberculosis strain SBH321 consists of 4,374,895 bp with G + C content of 65.59%. The comparative analysis by SNP-based phylogenetic analysis using maximum-likelihood method showed that our strain belonging to sublineage of the Ural family of Europe–America–Africa lineage (Lineage 4) and clustered with M. tuberculosis strain OFXR-4 from Taiwan. The whole genome sequence is deposited at DDBJ/ENA/GenBank under the accession WCJH000000000 (SRR10230353).