

ASSOCIATION OF MULTI DRUG RESISTANT TUBERCULOSIS WITH THE BEIJING FAMILY OF *M. TUBERCULOSIS* IN KAZAKHSTAN

Abilova Zh.¹, Akhmetova A.¹, Kadenova T.¹, Satvaldina N.¹, Daniyarov A.², Kairov U.², Akilzhanova A.¹, Almazan J.³, Kozhamkulov U.¹

¹National Laboratory Astana, Nazarbayev University, Laboratory of Genomic and Personalized Medicine, Astana, Kazakhstan,

² National Laboratory Astana, Nazarbayev University, Laboratory of Bioinformatics and Systems Biology, Astana, Kazakhstan,

³ School of Medicine Nazarbayev University, Astana, Kazakhstan

*Corresponding author: zhannur.nurkina@nu.edu.kz

Kazakhstan is on the list of countries with a high burden of MDR TB according to the WHO for 2021-2025. The purpose of the study is to determine the relationship of MDR with the Beijing *M. tuberculosis* family, as well as further genomic analysis of the data of whole-genome sequencing of clinical MDR *M. tuberculosis* isolates common in Kazakhstan [1].

The objective of this study was to investigate the association between multidrug resistance (MDR) and the Beijing lineage of *Mycobacterium tuberculosis*, as well as to conduct a comprehensive genomic analysis of MDR clinical isolates circulating in Kazakhstan using whole genome sequencing (WGS) [2].

A total of 76 clinical MDR *M. tuberculosis* isolates were collected from various regions of Kazakhstan. Genotyping was performed using spoligotyping, and drug susceptibility testing (DST) to first-line anti-TB drugs was conducted using the BACTEC MGIT 960 system. DNA library preparation for WGS was carried out in accordance with the Illumina DNA Prep Reference Guide (Illumina, USA), and sequencing was performed using the Illumina NovaSeq 6000 platform.

Genotyping results revealed a high prevalence of the Beijing lineage, identified in 85.5% (65/76) of MDR isolates. The remaining isolates belonged to the following lineages: LAM9 – 3 isolates (3.9%),

LAM-RUS – 3 (3.9%), T1 – 2 (2.6%), H3 – 1 (1.3%), MANU2 – 1 (1.3%), and S – 1 (1.3%).

The most frequent resistance pattern included resistance to isoniazid, rifampicin, and ethambutol, observed in 23 isolates (30.2%). Resistance to isoniazid, rifampicin, pyrazinamide, and ethambutol was detected in 21 isolates (27.6%), while resistance to isoniazid, rifampicin, and pyrazinamide was found in 17 cases (22.4%). Resistance to only isoniazid and rifampicin was identified in 15 isolates (19.7%).

Beijing family strains of *M. tuberculosis* were identified as a dominant family and associated with a high risk of MDR-TB in Kazakhstan. Genomic analysis using databases CASTB, MTBseq, Mykrobe, and TB Profiler is in process and will allow determining the genetic profile of whole drug resistance.

Grant references: This study was funded by a grant from Nazarbayev University under Collaborative Research Program №11022021CRP1511, U.K.

Keywords: tuberculosis, drug resistance, MI-RU-VNTR analysis, genotyping, *M. tuberculosis*.

Global tuberculosis report. World Health Organization; 2025. WHO Publication; 2025/

A. Daniyarov, A. Molkenov, et al. Genomic Analysis of Multidrug-Resistant *Mycobacterium tuberculosis* Strains From Patients in Kazakhstan. *Front Genet.* 2021.