

## GENOMIC CHARACTERIZATION AND DRUG RESISTANCE PROFILES OF *MYCOBACTERIUM TUBERCULOSIS* LINEAGE 2 IN KAZAKHSTAN: PRELIMINARY RESULTS

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Tuberculosis remains a highly contagious infection, with an estimated annual transmission of about 10 million people globally, as reported in the latest Global Tuberculosis Report by the World Health Organization (WHO). The primary objective of this research is to determine the geographical distribution and drug resistance profiles of *Mycobacterium tuberculosis* lineage 2, which is predominant in Kazakhstan.

A total of over 200 clinical isolates of *M. tuberculosis* complex (MTBC) were collected from regional phthisiopulmonology centers across all regions of Kazakhstan between 2012 and 2024. Clinical isolates were genotyped using a PCR assay targeting the *dnaA-dnaN:IS6110* region, specific for the modern Beijing genotype. Subsequently, selected samples were sequenced using the Illumina MiSeq platform. The TB-Profiler prediction tool was utilized to identify resistance against anti-tubercular drugs and to genotype the lineages.

A total of 102 clinical isolates belonging to the L2 modern Beijing genotype were selected for whole-genome sequencing (WGS). The L2.2.1 ge-

netic cluster was identified as the only sublineage present, according to Coll et al.'s classification. More than half of the specimens were found to be multidrug-resistant (n=60, 59%). Among the analyzed samples, monoresistance to isoniazid (IHN) was detected in 17 (16%) cases, while 14 (14%) cases were drug-susceptible TB. Additionally, 7 (7%) cases were identified as Pre-XDR (resistant to rifampicin, isoniazid, and either fluoroquinolones or second-line injectable drugs), 3 (3%) cases were monoresistant to streptomycin, and 1 (1%) case exhibited resistance to rifampicin only.

Regional distribution of samples is as follows: Aktau and Kostanay are 14% (n=13/102), Kyzylorda (n=12/102), Taldykourgan (n=11/102), Pavlodar, Karaganda, and Atyrau are at 6% (6/102); Semey is 10% (n=9/102), Almaty and Taraz at 4%, and Shymkent city is 1% (n=1/102).

This ongoing research is focused on resistance patterns, genotypes, and transmission dynamics among different regions of Kazakhstan using next-generation sequencing, followed by bioinformatics analysis and interpretation of the data.