

BEIJING GENOTYPE IS THE MOST DOMINANT GENOTYPE AMONG CLINICAL ISOLATES OF *M. TUBERCULOSIS* IN KAZAKHSTAN

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Introduction. Methods of genotyping of *M. tuberculosis* play important role in tuberculosis (TB) infection control. These techniques are used to detect or exclude laboratory errors, control recurrent cases and determine ways of TB transmission. Today, there are more than 10 methods of genotyping, MIRU-VNTR being one of the most widely used methods in the world.

Aim. Estimation of biological diversity of clinical isolates of *M. tuberculosis* from different regions of Kazakhstan based on MIRU-VNTR analysis.

Materials and methods. MIRU-VNTR genotyping of 134 clinical isolates of *M. tuberculosis* isolated from new cases and recurrent cases of TB from different regions of Kazakhstan was carried out in this study. Amplification was done using 15 MIRU-VNTR loci. Determination of the number of tandem repeats in corresponding locus was performed via Quantity One v.4.4.0 (BioRad, USA) software. H37Rv (NC_000962) reference strain was used as a positive control.

Results. Phylogenetic tree was built using www.miru-vntr.org web-resource based on the results of MIRU-VNTR analysis. Beijing family strains associated with drug resistance to antituberculosis drugs prevail among all isolates of *M. tuberculosis* circulating in Kazakhstan. Strains of Beijing genotype prevail both in new cases and recurrent cases of tuberculosis showing 65.0% and 89.4%, respectively. The second meaningful genotype that is spread in the territory of Kazakhstan is LAM, the frequency of distribution is 7.3% and 4.5%, respectively. Other families of *M. tuberculosis* such as Ural, Haarlem, CAS, NEW-1, S were found in less than 4% cases.

Conclusions. Prevalence of Beijing family strains among all isolates of *M. tuberculosis* from different regions of Kazakhstan was shown (65.0% and 89.4%). Strains of this family prevail among young people. The genotype is responsible for ongoing TB transmission in the present time. Genotype is more virulent, that is why investigation of epidemiology of Beijing genotype plays crucial role in monitoring of tuberculosis.