GENOTYPING OF MYCOBACTERIUM TUBERCULOSIS ISOLATES AMONG RECURRENT CASES OF TUBERCULOSIS IN KAZAKHSTAN

A. Akhmetova[1,2], A. Akilzhanova[1,2], B. Toksanbaeva[3], V. Bismilda[3], L. Chingissova[3], U. Kozhamkulov[1]

[1]*National Laboratory Astana, Nazarbayev University, Nur-Sultan, Kazakhstan*
[2]*Department of General Biology and Genomics, L.N.Gumilyov Eurasian National University, Nur-Sultan, Kazakhstan*
[3]*National Scientific Center of Phthisiopulmonology, Almaty, Kazakhstan*

ainur.akhmetova2@nu.edu.kz

Keywords: genetics, tuberculosis, M.tuberculosis

Introduction: Tuberculosis still remains one of the major health problems in Kazakhstan. According to the World Health Organization data (2018), Kazakhstan is on the list of 30 countries with high rates of multidrug resistant tuberculosis in the world. MIRU-VNTR analysis is widely used genotyping method of M. tuberculosis. The aimof this work is to characterize biological diversity of M. tuberculosis clinical isolates among recurrent cases of tuberculosis in Kazakhstan.

Materials and methods: 95 clinical isolates of M. tuberculosis were collected from different regions of Kazakhstan among recurrent cases of tuberculosis. Genotyping of all isolates was performed by 15 MIRU-VNTR approach. PCR products were visualized on 2% agarose gel stained with ethidium bromide. Quantity 1(BioRad) program was used to determine the PCR fragment size and calculate the number of tandem repeats in each MIRU-VNTR locus. 15-digit allelic profiles of all clinical isolates were uploaded to MIRU-VNTRplus web application to identify M. tuberculosis families. Phylogenetic tree was built using UPGMA (Unweighted pair group method with arithmetic mean) algorithm.

Results: 40 genotypes were detected based on15 MIRU-VNTR genotyping results. 31(32,6%) genotypes were unique and found only in one isolate in the collection. The rest 64 (67,4%) M. tuberculosis clinical isolates were clustered into 9 clusters which included from 2to 34 isolates in one cluster. 87,4% of all clinical isolates were belonged to Beijing family. The second meaningful family that is found among the isolates was LAM family (10,5%). URAL and CAS families were identified in the rest 2,1% cases.

Conclusion: Thus, 15 MIRU-VNTR typing of 95 clinical isolates of *M. tuberculosis*showed that Beijing family strains that are associated with drug resistance prevail among recurrent cases of tuberculosis in Kazakhstan (87,4%).