Molecular epidemiology of tuberculosis in Mongolia: Sources and pathways of MDR Mycobacterium tuberculosis strains

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Mongolia is a country with a high burden of tuberculosis (TB). The emergence and spread of multidrug resistance (MDR) TB in Mongolia is associated with problems of early diagnosis and the possibility of cross-border spread of MDR-TB along the Trans-Siberian Railway line from Russia or China. The objective of this study was to reveal sources and pathways of Mycobacterium tuberculosis (MTB) strains in Mongolia.

A total of DNAs of MTB from Mongolia (309 strains) were studied. All tested 309 MTB isolates distributed to four lineages: Beijing (228/309 — 73.8%), LAM (33/309 — 10.7%), T (30/309 — 9.7%), H (9/309 — 2.9%), and orphan (9/309 — 2.9%). 21 clusters uniting 187 strains were identified. Out of 228 Beijing strains 165 were clustered and significantly exceeded of 228 Beijing strains. The size of subtype CC2/W148 cluster was extended to CC1 group in Irkutsk region, Primorsky Krai and Sakha (Yakutia). Buryatia and Zabaykalsky Krai had unexpectedly low level of CC1, as there were endemic Beijing and Zabaikal regions. Phylogenetic analysis established high genetic close between Mongolian and Chinese profiles of Beijing strains, but Mongolian isolates were grouped in specific cluster.

We determined that there were no significantly transmission of MDR strains from Russia to Mongolia. Our study confirms possibility of cross-border spread of Chinese strains in the past, but now Mongolia has own MDR strains source.

Molecular epidemiology of tuberculosis in Eastern Siberia and Far East

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The highest burdens of tuberculosis in Russia have Asian regions. Beside of social and health care problems this area gained specific geographic spread of Mycobacterium tuberculosis (MTB) genotypes and high level of multi drug resistance (MDR). The aim was to carry out comparative evaluation of distribution epidemic MTB strains in Eastern Siberia and Far East of Russia.

We studied 1419 clinical MTB strains collected in Irkutsk region (398), Buryatia (306), Sakha (Yakutia) (351), Zabaykalsky Krai (65) and Primorsk Krai (99). All tested 309 MTB isolates distributed to four lineages: Beijing (228/309 — 73.8%), LAM (33/309 — 10.7%), T (30/309 — 9.7%), H (9/309 — 2.9%), and orphan (9/309 — 2.9%). 21 clusters uniting 187 strains were identified. Out of 228 Beijing strains 165 were clustered and significantly associated with MDR-TB cases from Ulaanbaatar and big railway stations settlements (p < 0.001), but MIRU-VNTR profiles of Beijing strains were found among Russian isolates (58 isolates), 3819-32 (33 isolates) and 1773-32 (33 isolates). Specific deletion in the kdpD gene. Mongolian MIRU-VNTR patterns of MTB were compared with evaluable published Chinese and Russian profiles.

Genotypic structure of the MTB population in the Asian Russia mainly reflects the epidemic expansion feature of tuberculosis: luminescent microscopy, cultivation on solid media (Finn and Levenstein–Jensen), use of the liquid medium of the BAKTEK 320/960 analyzer, molecular genetic methods in various formats: real-time PCR, GenXpert TB-Rif, Hain test, biochips. The emergence of new technologies does not lead to the rejection of ineffective classical methods. So, in my opinion, the presence of molecular genetic methods in the algorithm of a clinical doctors allows to abandon the microscopy of a clinical material due to low sensitivity and specificity and thereby