

GENOTYPING OF MYCOBACTERIUM TUBERCULOSIS BY SIX LOCI

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Summary

The aim of the study was to obtain a genetic profiles of Mycobacterium tuberculosis through detection of six VNTR-loci (MIRU10, MIRU26, MIRU31, MIRU39, MIRU40, ETR-A) and to determine the peculiarity of the genotype of drug-resistant M. tuberculosis strains in tuberculosis patients.

Loci MIRU10, MIRU26, MIRU40 i ETR-A have exhibited high polymorphism in non-Beijing group, while loci MIRU26 and MIRU31 — in Beijing family. It was highly effective to detect the combination of six loci - MIRU10, MIRU26, MIRU31, MIRU39, MIRU40 i ETR-A — of Beijing and non-Beijing strains for their genotyping. That's why the genotyping of M. tuberculosis by 6 loci can be proposed as more simple alternative for detection of 24 loci.

Among Beijing family isolates there were such dominant clusters as 355335, 355344, 355345, 356335, 356344, 375334, 375344, 385345, 385334. Clusters 355335, 375334 and 385334 had high level of multi-resistance and mutations in katG and rpoB genes. The most spreading cluster among non-Beijing isolates was 452242 which along with cluster 712234 had high level of multi-resistance and mutations in katG and rpoB genes. Among HIV-infected patients the most prevalent cluster from Beijing family was 375344 and from non-Beijing group — cluster 553213.