

MOLECULAR GENOTYPING AS A TOOL FOR DETERMINATION OF TUBERCULOSIS RELAPSES AND TRANSMISSION

A.Nodieva**, I.Jansone*, G.Skenders**, M.Bauskenieks*, V.Baumanis*

*- Latvian Biomedical Research and Study Centre, Ratsupites 1, Riga LV 1067, Latvia

** - State Agency of Tuberculosis and Lung Diseases, Stopini , Riga District, Latvia, LV 2118

Tuberculosis (TB) incidence is decreasing gradually in Latvia during last eight years – from 74 in 1998 to 53.5 per 100.000 population in 2005. However a high drug resistance – about 10% of primary MDR and 28% retreatment MDR of which 19% meet the XDR-TB criteria forces to improve prophylactic measures. Therefore, distinguishing of relative impact of tuberculosis transmission or reinfection in new epidemiologically linked and/or retreatment cases is of great epidemiological and therapeutic significance.

Purpose of this study was to evaluate reinfection, transmission and relapsed cases by molecular genotyping of *M.tuberculosis* isolates.

97 cultured clinical isolates in total have been analysed by molecular genotyping using spoligotyping and classical *PvuII* restricted *IS 6110* fragment length polymorphism analysis (RFLP). 66 of them were patients suffering from recurrent TB and cultures were obtained in both cases. 31 was with well established TB contacts (mainly children). The drug resistance determining mutations were localised as additional marker of isolate similarity.

Molecular genotyping and similarity of point mutations in drug resistant cases showed , that in 48.4% of contact cases genetic similarity of RFLP patterns was observed, clearly indicating on recent transmission.

In 66 recurrent cases only 16% of isolates were found to be identical, 84% were different , the latter mainly belonging to Beijing genotype group. Sociological analysis of patients and molecular genotyping confirmed predominant transmission of infection in unfavourable social groups of patients. Here mainly Beijing genotype with a high drug resistance was transmitted. However in favourable social groups –distinctive genotype in comparison with isolates from their previous TB process as well distinct genotypes obtained from the contact persons indicated on immunological problems in this patient group.

Molecular genotyping in above mentioned patient groups clearly demonstrates practical value of it in elaborating of adequate prophylactic and therapeutic measures.