

## DOMINANCE OF AN XDR TUBERCULOSIS CLONE IN ESTONIA

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**Purpose of the study:** This study explores the nature and consequences of genetic variability in *M. tuberculosis* by analyzing and comparing the population structure of *M. tuberculosis* isolates collected in 1994 and 2004 in Estonia from newly diagnosed pulmonary TB cases.

**Methods:** Two molecular typing methods, spoligotyping and RFLP IS6110, were used to monitor the population trend in the proportion of patients infected by different TB genotype families and dominant clones with clinical and demographic information (age, gender, ethnicity, homelessness, employment, previous imprisonment, HIV positivity etc). To assess the importance of long-lived clones in Estonia, additional typing information from 2003-2005 was also employed.

**Results:** In this study we were able to detect the outcome of a natural competition between TB clones in Estonia. A remarkable countrywide expansion of one Beijing clone (BIX) which caused up to 16% of all TB cases in a single year and 68% of all MDR cases annually. Over the period 2003-2005 170 cases of TB were caused by this clone: 28% cases were MDR, 45% MDR*Plus* and 19% were XDR.

**Conclusions:** Our study confirms the Beijing genotype MDR/XDR-TB as an emerging pathogen in Estonia. This work suggests that measures used to fight the TB epidemic may have helped to select and disseminate this successful MDR/XDR clone.

We also show that in addition to host and environmental factors the lineages/genetic background of the *M. tuberculosis* strain can influence the transmission dynamics of drug-resistant bacteria.