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Title: Efficiency of molecular methods for epidemiological investigation in tuberculosis (TB)

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Body: Introduction. High prevalence of tuberculosis in Poland may related to active transmission. Objectives. The assessment of the transmission of TB in the city of Krakow with genetic methods and with standardized epidemiological interview and the comparison of these methods. Methods. In years 2007-2011 genomic DNA samples isolated from Mycobacterium tuberculosis complex strains coming from 274 patients were analysed by spoligotyping and IS6110-Mtb1-Mtb2 PCR method. The strains were assessed as identical if their DNA patterns were the same in both methods. In IS6110-Mtb1-Mtb2 PCR method DNA profile obtained in both PCR reactions should be identical. Results. Among 274 strains, 122 genetic patterns (spoligotypes) were identified. Unique spoligotypes occurred in 91 strains; remaining 183 strains belonged to 31 clusters stemming from the same spoligotypes. The application of the IS6110-Mtb1-Mtb2 PCR in next stage of the analysis, allowed reducing the number of clusters to 18 with 91 strains. The clusters included 2-14 patients and covered one third of analysed samples. The clusters were dominated by men below 50 years old, smokers, AFB(+), with strains sensitive to first-choice antituberculosis agents. The standard epidemiological interviews did not reveal neither direct close nor periodic contacts between the patients included in clusters (only three clusters comprised prisoners from the same penitentiary and three homeless persons with periodic contacts). Conclusion. The assessment of transmission of TB should be based on scrupulous epidemiological interview and on molecular genetic methods. Active transmission in Krakow in years 2007-2011 was responsible for 30% of diagnosed TB cases.