Tuberculosis transmission in the pediatric population: clinical significance of molecular-epidemiological analysis

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Objectives: The pediatric tuberculosis (TB) represents a complex challenge due to various limitations in its diagnosis and treatment. It is estimated that in 2022 there were 1.25 million children with TB, with 51% remaining undiagnosed. To eradicate this disease in pediatric population, faster diagnostics and identification of transmission chains is necessary.

Methods: Samples were collected between January 2023 and June 2024 from reference mycobacteriological laboratories in Slovakia and the Czech Republic. Culture samples were sequenced using whole-genome short-read sequencing technology and bioinformatically processed.

Results: A total of 37 patients were included. Based on the phylogenetic and cluster analyses, the Euro-American lineage was prevalent (86.5 %), and 4 clusters, including 24 patients, were identified. The Beijing lineage (characterized by the highest virulence and transmissibility) was confirmed in 5 patients. Resistance to isoniazid, as well as multi-drug-resistant and ethambutol-resistant strains, was found in 6 patients.

Conclusions: WGS is critical for detecting drug resistance and elucidating transmission chains through genetic similarity between the strains. A combination of WGS with basic epidemiological investigation can be beneficial and may lead to a better understanding of TB epidemiology and prevention of its spread.

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