Features of the resistance profile in patients with multidrug-resistant tuberculosis based on complete genome sequencing of Mycobacterium tuberculosis in Kharkiv region, Ukraine

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The **aim** of our study was to study the features of the resistance profile in patients with multidrug-resistant tuberculosis based on complete genome sequencing of Mycobacterium tuberculosis in Kharkiv region, Ukraine.

Methods. Bacterial DNA was isolated from 223 patient samples. Following the complete genome sequencing, we analyzed reads using the TB Profiler (version 3.0.6) software to compile detailed information about drug resistance variants. Patients were categorized as MDR or XDR based on standard microbiological DSTs.

Results. Most of the patients were predicted to be highly resistant to anti-TB drugs (XDR:62,Pre-XDR:63,MDR:63,Pre-MDR:4,Sensitive:16,Other:15). Most of the samples are from the Beijing sub-lineage 2.2.1 (183).Other lineages include:4.1.2 (9),4.2.1(10),4.3.3(14),4.8 (3),*M.bovis*(4).Of the 223 patient samples,17 were identified as having 10 or more drug resistance variants. Resistance SNPs were found for most anti-TB drugs: rifampicin (17/17), isoniazid (17/17), pyrazinamide (17/17)**,** ethambutol (17/17), streptomycin(17/17), fluoroquinolones(16/17), kanamycin(16/17), ethionamide (16/17),capreomycin(6/17), aminoglycosides (5/17),para-aminosalicylic_acid (4/17),linezolid (2/17), bedaquiline(2/17),clofazimine(2/17).

Conclusions. Our results confirm the importance of full genome sequencing to provide a detailed view of the growing threat of drug-resistant tuberculosis. Tracking TB lineages allows for monitoring epidemiological routes of tuberculosis and pinpointing the sources of outbreaks. Clinical data collected together with corresponding genomic and radiological information help to optimize treatment practices and proactively identify difficult-to-treat cases.