



Outbreak of pre- and extensively drug-resistant tuberculosis in northern Italy: urgency of cross-border, multidimensional, surveillance systems

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An outbreak of (pre-)extensively drug-resistant tuberculosis was detected in Northern Italy using whole genome sequencing and epidemiological study. This experience suggests that integrated and cross-border surveillance systems should be urgently employed. <https://bit.ly/3wtQkBp>

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To the Editor:

Multidrug-resistant (MDR) and extensively drug-resistant (XDR) tuberculosis (TB) are a major public health threat because of reduced treatment options and poor patient outcomes. New antimicrobials and regimens have been developed in recent years, but their effectiveness has been hampered by the rise and spread of drug-resistant strains. Whole genome sequencing (WGS) has emerged as a tool able to revolutionise TB surveillance and the clinical management of TB. This approach is now widely used by public health agencies in detecting outbreaks and transmission chains, thus supporting the formulation of evidence-based health policies. Moreover, WGS can predict the drug-susceptibility profile of *Mycobacterium tuberculosis* complex (MTBC) strains, often in combination with phenotypic antimicrobial susceptibility testing (AST) and minimum inhibitory concentration (MIC) determination for the optimal clinical management of drug-resistant TB [1].