

TRANSMISSION AND ANTIMICROBIAL RESISTANCE OF TUBERCULOSIS IN RESIDENT AND DISPLACED POPULATIONS IN LEBANON BY WHOLE GENOME SEQUENCING

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The aim of the research is to study TB transmission and to detect the potential emergence and clonal expansion of MDR and XDR TB strains among the national and non-national population, including Syrian and non-Syrian refugees residing in Lebanon, by using a large-scale genomic and epidemiological approach based on the next-generation sequencing (NGS) of the *Mycobacterium tuberculosis* complex (MTBC) genome. By using most advanced whole genome-based molecular tracing and DST prediction approaches combined with state-of-the-art phenotypic DST and collection of clinico-epidemiological data, the study is expected to provide unique, new insights into the situation of TB propagation and drug resistance in the displaced and resident populations in Lebanon.

Key words : Tuberculosis, Epidemiology, refugees, clonal expansion, resistance, Lebanon