

The Lebanese LSIDCM

Genotyping of *Mycobacterium tuberculosis* in Lebanon using a novel rapid spoligotyping multiplex luminex method

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Abstract

Introduction: Incidence of Tuberculosis (TB) in Lebanon, according to the WHO, is estimated to be 35 cases per 100,000 people. However, data about the genotypes of circulating *Mycobacterium tuberculosis* isolates (MTB) in this country is lacking. This study aims to reveal the genotypes of TB isolates recovered from patients in Lebanon.

Methodology: Fifty *M. tuberculosis* isolates from patients in Lebanon were recovered and identified at the reference TB center of the Ministry of Public Health. All isolates were heat killed and subjected to DNA extraction. Spoligotyping method (TB-Spol, Beamedex, France) was used to identify the presence of 43 spacers via a multi-analyte profiling system (Luminex, Bio-Rad). Generated patterns were assigned to families using the SITVIT2 international database of the Pasteur Institute of Guadeloupe.

Results: The spoligotyping of the 50 MTB isolates revealed 13 lineages, one being novel. The most frequent shared-types (SIT) identified lineage was the Ural (34%), followed by the Central Asian lineage (10%) and a single isolate (2%) belonging to the rare Manu-Ancestor SIT523 lineage, associated with a highly virulent XDR MTB phenotype. The rest of the SIT isolates (18%) were equally distributed along 9 different lineages. The 13th non-SIT lineage is a novel one constituting 36% of the total isolates.

Conclusion: The application of Spoligotyping Multiplex Luminex method is a novel, discriminatory and rapid method to use for genotyping of MTB isolates employing the multi-spacer analysis system. Our study showed genomic diversification of MTB isolates from Lebanon.

Key words: tuberculosis; spoligotyping; luminex.

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