Mycobacterium tuberculosis genotyping by MIRU-VNTR method

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Abstract

Background and Objective: MIRU-VNTR typing is currently one of the most frequently-used standardized genotyping systems in molecular epidemiology of tuberculosis in the world. This study was done to determine the Mycobacterium tuberculosis genotyping by MIRU-VNTR method.

Methods: This descriptive study was done on sputum, gastric lavage clinical specimens of 53 tuberculosis suspected patients. Fifty-three isolates were identified by 16S rRNA and Rv-typing followed by RD typing. They were then subjected to a 12-locus (ETRA, ETRB, ETRC, ETRD, ETRE and ETRF, MIRU-10, MIRU-26, MIRU-39, MIRU-30 plus QUB-11b) MIRU-VNTR typing system.

Results: In MIRU-VNTR typing, forty-four types were identified with 13 isolates classified in 4 clustered and the remaining 40 isolates representing 40 orphan patterns. In comparative analysis of MIRU-VNTR loci, MIRU-26 with 7 alleles displayed the highest diversity level (Simpson’s diversity index = 0.767. Out of the 53 isolates, only one was identified as Mycobacterium bovis. All the remaining isolates were characterized as Mycobacterium tuberculosis. None of the samples was affected to Mycobacterium complex strain. No evidence of either double or co-infection of the patients with more than one species/strain was detected.

Conclusion: While the genomic diversity observed by MIRU-VNTR typing sounds extensive, the population genomic structure on the whole however, seems to be homogenous. Recent transmission between studied patients does not appear to be a frequent event as only 13 isolates representing 4 MIRU-VNTR types, were assumingly epidemic.

Keywords: Mycobacterium tuberculosis complex, Mycobacterium bovis, RD typing, Rv-typing, MIRU-VNTR genotype

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