

Original Paper

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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Received 7 May 2013

Revised 16 Aug 2014

Accepted 17 Aug 2014

Cite this article as: Ahmadi M, Tadayon K, Mosavari N, Farazi AA, Arjomandzadegan M, Keshavarz R, Banihashemi R, Sekhavati M, Hamed D, Eramabadi M, Jabbari M, Ghaderi R, Hoseini D, Dashtipour Sh. [*Mycobacterium tuberculosis* genotyping by MIRU-VNTR method]. J Gorgan Uni Med Sci. 2015; 17(1): 97-107. [Article in Persian]