

EVALUATION OF MYCOBACTERIAL INTERSPERSED REPETITIVE UNIT-VARIABLE NUMBER TANDEM REPEAT TYPING TO DISCRIMINATE *MYCOBACTERIUM TUBERCULOSIS* STRAINS FROM MYANMAR

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Abstract. Mycobacterial interspersed repetitive unit-variable number tandem repeat (MIRU-VNTR) typing is a fast and promising method to discriminate *Mycobacterium tuberculosis* (MTB) strains. The present study was carried out to evaluate the applicability of MIRU-VNTR method for genotyping of clinical MTB strains from new pulmonary TB patients in Myanmar, and to compare the discriminatory ability between 15 loci and 24 loci MIRU-VNTR typing. One hundred and seven clinical MTB isolates which were collected during 2012-2013 were examined for anti-TB drug susceptibility using both proportion method and commercial line-probe assay. The results of internationally standardized 15 loci and 24 loci MIRU-VNTR typing methods were analyzed by a MIRU-VNTR *plus* web application together with Hunter-Gaston discriminatory index (HGDI) as numerical index to describe the discriminatory power. All tested MTB isolates showed unique patterns, which did not cluster and were distributed among 14 lineages. EAI genotype (30%) was the most prevalent genotype, followed by Beijing genotype (29%) that is significantly associated with multidrug-resistant TB ($p < 0.0004$). Both 15 and 24 loci MIRU-VNTR were highly discriminatory (HGDI= 0.9833 and 0.9874, respectively). This study indicates that MIRU-VNTR could be used as a genotyping tool for Myanmar MTB strains.

Keywords: *Mycobacterium tuberculosis*, genotyping, MIRU-VNTR, Myanmar

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