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Deletion of region of difference 181 in *Mycobacterium tuberculosis* Beijing strains

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ABSTRACT

Objectives/background: The region of differences (RDs) polymorphisms is a potential molecular epidemiology method to distinguish origins of *Mycobacterium tuberculosis*. To date, 68 RDs have been identified in *M. tuberculosis*. This study was designed to determine the frequency of RD deletions in *M. tuberculosis* strains that were isolated from patients with pulmonary tuberculosis who were referred to the National Research Institute of Tuberculosis and Lung Disease for diagnosis and treatment. Therefore, highly polymorphic regions (RD1, RD150, and RD181) among *M. tuberculosis* strains isolates were investigated.

Methods: A total of 250 *M. tuberculosis* isolates were identified by conventional and molecular methods. Subsequently, spoligotyping and RD typing (RD1, RD150 and RD181) were performed to genotype these strains.

Results: The most frequent spoligotype belonged to Haarlem ($n = 85$, 34.0%) followed by CAS ($n = 54$, 21.6%), T1 ($n = 27$, 10.8%), and Beijing ($n = 28$, 11.2%) lineages. Deletion in RD181 was identified only among the Beijing lineage (Fig. 1).

Conclusion: As we found a deletion in RD181 in the Beijing strains only, we propose to use this marker as an identification tool for genotyping of the Beijing strain.

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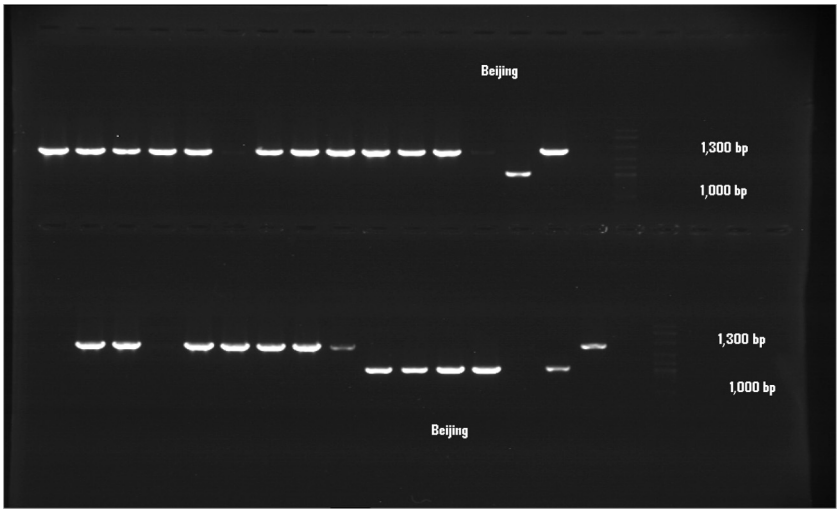

Fig. 1 – Electrophoresis fractionation of PCR products in 1% agarose gel to detect the existing deletion in RD181. The deletion can be diagnosed in the genomic region of RD181 in Beijing strains. The molecular weight of PCR products was 1000 bp. A molecular weight marker (100-bp ladder) was used. PCR = polymerase chain reaction; RD = region of difference.

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