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Discovery of the New Target for Identification of *Mycobacterium tuberculosis*

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Dear Editor,

Tuberculosis has been one of the most important infectious diseases in human history, which causes deaths of 2 million people around the world annually (1). Inhalation of 1 - 3 bacillus *Mycobacterium tuberculosis* is sufficient for infection with this bacterium. According to the existing reports, almost one-third of the world's population is infected with M. tuberculosis, although they may not show any symptoms of this disease (2, 3). Due to the spread of HIV epidemics in the world, and emergence of the drug-resistant strains of *Mycobacterium tuberculosis* (DR-TB), eradication of tuberculosis is impossible (1).

One of the most important strategies of TB control is to identify those patients with active TB and to prevent transmission of infection from these patients to healthy people. In addition, patients with latent tuberculosis, who are infected with HIV are in fact the source of infection and should be identified and treated quickly (4, 5). Conventional methods for diagnosis of tuberculosis such as acid-fast staining, biochemical tests, and drug susceptibility testing are time-consuming, confusing, and require trained technicians. In addition, these methods are of poor accuracy and specificity in cases of extra-pulmonary tuberculosis (6, 7). Molecular methods, including hybridization techniques, DNA probes, and sequencing are more rapid and cheaper in comparison to culture and phenotypic tests. In addition, they can determine the antimicrobial susceptibility results before culture and traditional tests (6, 7). However, molecular tests on samples with low numbers of TB bacilli are usually false negative; this method could not distinguish between live microorganisms and dead bacteria. Consequently, these tests could not be used to evaluate the response to treatment. Moreover, in many of the developing countries, molecular techniques are not utilized due to high costs and the need for equipment. Therefore, the conventional method is known as the gold standard and the molecular techniques could be applied as complementary methods (8).

For molecular identification of *Mycobacterium tuberculosis* complex, some genes including *IS6110*, *IS986*, *IS990*, *IS1081*, *mtb-40*,*dnaJ*, *groEl*, and also those genes that code 32 KDa, 38 *Kda*, and 65 KDa proteins, *devR* response regulator gene, *hupB*, *pncA*, *CYP141*, and *oxyR* could be used (9, 10). IS elements such as *IS6110* are the most important ones for detection of *Mycobacterium tuberculosis* strains, however, today it has become clear that *IS6110* in Beijing strains (one of the most common strains of *Mycobacterium tuberculosis* in the world) lacks this gene. *Mycobacterium bovis* strains contain few copies of this gene that leads to limitations for detection of these strains. Additionally, the methods based on this IS element require a large amount of pure DNA and analysis of the results of these methods is time-consuming and requires trained personnel (10, 11). The *mtp-40* and *CYP 141* genes are not present in all members of the *Mycobacterium tuberculosis* strains and, therefore, are not useful for differentiating *Mycobacterium tuberculosis* from Mycobacterium *bovis* (10, 11). The gene for histone-like protein *hupB* of *Mycobacterium tuberculosis* has been identified as a target for differentiation of MTB complex and also polymorphisms in *pncA* and *oxyR* are good options for rapidly differentiate *M. bovis* from *M. tuberculosis*; thus, for rapid and reliable detection of *Mycobacterium tuberculosis* complex from clinical specimens, it is needed to study genes that are simply analyzed and are conserved (9-12).

In summary, in order to control tuberculosis, we require the rapid diagnosis of TB patients, who act as the source of disease. If remain untreated, these patients can spread the disease throughout the population. Therefore, we need to introduce and discover the new targets for quick and accurate identification of *Mycobacterium tuberculosis* strains, while it seems *IS6110-RFLP* and MIRU-VNTR typing are best methods for accurate identification, epidemiological study and genetic relationships between strains of Mycobacterium tuberculosis complex.

Footnotes

Authors' Contribution: Masoud Keikha designed and wrote the manuscript.

Conflict of Interest: There is no conflict of interest.

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