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 accurate and specific for detection of Mycobacterium tuberculosis strains and, therefore, are not useful for differentiating Mycobacterium tuberculosis from Mycobacterium bovis strains (10, 11). The mtp-40 and CYP141 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

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References