Molecular characterization of mycobacterium species isolates from patients with pulmonary tuberculosis in Sabah, Malaysia

ABSTRACT

Tuberculosis (TB) is one of the deadliest diseases worldwide, caused by members of Mycobacterium tuberculosis complex (MTBC), commonly by Mycobacterium tuberculosis (Mtb) and Mycobacterium bovis. In Malaysia, Sabah is one of the states of public health concern with the highest TB cases. Clinical presentations of TB and non-tuberculous mycobacteria (NTM) lung disease are similar, and mycobacteria appear to be identical under standard diagnosis with sputum smear microscopy, causing difficulty to diagnose TB. Identification of Mycobacterium species is essential for effective management of mycobacterial diseases treatment and their control strategy. Thus, this study aimed to identify the Mycobacterium species from suspected TB patients in Sabah using molecular methods. Sputum samples (n=595) were screened with GeneXpert MTB/RIF (Xpert), and positive TB samples (n=67) were processed and cultured in BACTEC MGIT. Forty-five isolates were successfully recovered in MGIT and characterisation of the mycobacterial isolates using PCR and/or sequencing with rpoB, RD9, hsp65, and 16S rRNA genes confirmed the presence of Mtb in 41 samples, and four non-mycobacteria, i.e. Microbacterium laevaniformans, Streptomyces sp., Streptomyces misionensis and Gordonia sp. These non-mycobacteria isolates showed negative results when tested directly with Xpert. In conclusion, Mtb is the predominant species of MTBC circulating in Sabah. The presence of non-mycobacteria in this study was due to bacterial contamination in MGIT, not bacterial cross-reactivity in Xpert, implying the high sensitivity and specificity of Xpert for diagnosis of TB.