

Isolation and Identification of Some Slow Growing Mycobacteria from Patient Suffering from Chronic Tuberculosis Like Disease

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Background & Objectives: Many species of slow-growing non-tuberculous Mycobacterium (NTM) like *Mycobacterium kansasii*, *M. avium* complex (MAC) and *M. simiae* been reported to cause localized or disseminated disease similar to that of caused by *M. tuberculosis*. As many of the NTM are not amenable to routine antituberculosis therapy, it is important to correctly identify the causative mycobacteria for patient management and infection control. The aim of this study was molecular identification of 17 clinical strains of SGM which recovered from patients suffering from chronic tuberculosis like disease.

Methods: The isolates were identified by amplification and sequence analysis of 440 bp of hsp65 gene.

Results: Out of 17 isolates, 11 isolates were identified as *M. kansasii*, 5 isolates were identifies as *M. simiae* and 1 isolate identified as *M. avium*.

Conclusion: From clinical point of view, pulmonary infections caused by NTM are not clearly distinguishable from tuberculosis. Isolation of causative agent and identification based on sequencing genes like hsp65 may be better diagnostic tools and have become a hot-topic public health care issue.

Keywords: Mycobacteria; Non-tuberculous Mycobacterium (NTM)

