

Mycobacterium seoulense Variants from Patients having Nontuberculous *Mycobacterium* Infections

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DESCRIPTION

Tuberculosis (TB) is an infectious illness caused by *Tubercle bacilli*, which are *Mycobacterium tuberculosis* complex organisms. In the lungs, the *bacillus* spreads slowly and extensively, forming hard nodules (tubercles) or cheese-like lumps that cause cavities. It is a communicable disease that mostly affects the lungs but may infect any organ in the body. TB has been around for millennia and is still a serious worldwide health issue. It affects around 10 million people each year and is one of the top ten causes of mortality globally. In 2020, the global prevalence of Multidrug-Resistant/Rifampicin-Resistant Tuberculosis (MDR/RR-TB) is expected to reach 3.3% in new cases and 18% in previously treated patients. Overall, an estimated 465,000 incident cases of MDR/RR-TB were recorded, with MDR-TB accounting for 78% of all RR-TB cases.

The emergence and spread of MDR-TB has emerged as a serious TB control challenge that cannot be addressed with current anti-TB drugs. Multidrug-resistant TB treatment entails time-consuming and costly chemotherapy with toxic and inefficient second-line drugs. Drug resistance is mostly a man-made problem caused by prescription usage and mismanagement, either alone or in combination. Rapid detection and diagnosis of *Mycobacterium Tuberculosis* (MTB) in infected patients is crucial for timely disease management. WHO-approved rapid molecular assays, such as Xpert, are used as the initial diagnostic test for tuberculosis and rifampicin resistance in adults and children. In less than 2 hours, the test identifies *Mycobacterium Tuberculosis* Complex (MTBC) and Rifampicin Resistance (RIF). Xpert MTB/RIF can identify and report mutations in the *rpoB* gene. The Xpert MTB/RIF test is extremely sensitive, specific, and fast in the diagnosis of PTB and EPTB.

Rifampicin resistance can be identified immediately, allowing tuberculosis patients to start treatment sooner rather than waiting for findings from other traditional techniques of drug susceptibility testing. Rapid identification, continuous surveillance, and frequent monitoring of drug-resistant tuberculosis are crucial for disease management and earlier treatment start in TB-endemic countries. However, only a few

studies have been conducted in Ethiopia to investigate the incidence of tuberculosis and rifampicin resistance in presumptive TB patients. As a result, the purpose of this study was to find out how common *Mycobacterium tuberculosis* and rifampicin-resistant tuberculosis were among presumptive tuberculosis patients. Nontuberculous *Mycobacterium* (NTM) refers to all *mycobacterium* species other than *Mycobacterium TB* complex and *Mycobacterium leprae*. NTM has about 200 species. Previous research has suggested that NTMs are opportunistic human infections that cause illness only when the immune system is impaired. However, the number of NTMs causing infectious illnesses in immunocompetent people has grown. NTMs usually infiltrate the lungs, although they can also invade other anatomic locations. NTM lung illness is characterised mostly by cough and expectoration, which are non-specific and readily mistaken with other lung conditions. Furthermore, its radiological manifestations, such as nodules, cavities, and lung consolidation, are shared by other disorders.

To identify NTM species, several methods have been developed, including high performance liquid chromatography based on mycolic acid, Matrix-Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry based on the protein spectrum, and molecular detection based on species-specific sequences. Whole-genome sequencing has been used to discover NTM, but clinical uses are restricted because of the high cost and the need for highly qualified specialists. Several gene sequences that differ across species, including as 16S rRNA, *rpoB*, *hsp65*, and the 16S-23S inter-region (ITS), have been used in species identification. However, the discriminating abilities of these genes differ. For example, while being the most often utilised gene, the 16S rRNA has a limited ability to identify unusual species and subspecies.

Notably, the *hsp65* gene has already been utilised for species identification, demonstrating that the dominating NTM in this location is the *Mycobacterium avium* complex. The *hsp65* gene was used in this investigation to identify *Mycobacterium seoulense* (*M. seoulense*). *M. seoulense* is a slow-growing NTM that was discovered in a patient suffering from nonspecific lung symptoms in Korea. Because there is little information about its clinical

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importance and molecular properties, we evaluated clinical records, including clinical signs and laboratory investigations, to determine its capacity to induce infection. The other regularly

used genes for species identification were investigated in order to discover the gene with the best specificity in identifying *M. seoulense*.