DIFFERENTIATION AND IDENTIFICATION OF *MYCOBACTERIUM XENOPI* AND *MYCOBACTERIUM HECKESHORNENSE*

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Infection due to *M. heckeshornense* (*Mh*) is rare. These mycobacteria are very close to *M. xenopi* (*Mx*) and thus, sometimes are misidentified. We describe a case of chronic lung infection with *M. heckeshornense* in a 30-year-old man. Histological analysis of a resected lung specimen revealed epithelioid cell granulomas and numerous acid-fast rods. A mycobacterium isolate was identified as *Mh* on the basis of its unique 16S rDNA sequencing and conventional biochemical tests. We also looked at 12 strains isolated from sputum of patients with pulmonary diseases which were identified as *Mx* using DNA-DNA hybridization kit (DDH MYCOBACTERIA KYOKUTO). Five of these turned out to be related to *Mh*.

Both mycobacterial species developed rough to smooth schotochromogenic colonies after 2 to 3 weeks on 2% Ogawa egg medium incubated at 42°C. Organisms grew on 2% Ogawa egg medium at 37, 42, and 45°C, but not at 25 and 30°C; and grew in presence of TCH(1µg/ml), but not in NaCl (5%). The mycobacteria were negative for nitrate reduction, urease, Tween 80 hydrolysis, and semi-quantitative catalase, but positive for 68°C catalase, and pyrazinamidase.

Seven of the 12 strains were consistent with 100-99.6% to *Mx* (S88, S91, DSM43995^{T}) and 94.6% to *Mh* (Wue939/99) by RIDOM analysis of 16S rDNA sequences (*E. coli* positions 18-508), and were identified as *Mx*, while the other 5 strains were consistent with 100% to *Mh* (Wue 939/99) and 94.6-94.2% to *Mx* (S88, S91, DSM43995^{T}), and were identified as *Mh*.

Three strains of *M. xenopi* so far examined were positive for arylsulfatase (3day), and resistant to PNB(500µg/ml), EB(5µg/ml) and TCH(10µg/ml), while 2 strains of *Mh* showed opposite characteristics.