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Abstract (poster session)

Isolation of the novel species Mycobacterium kumamotonense from a patient with lung disease and latent tuberculosis

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Objectives: The introduction of molecular techniques facilitated the detection and identification of novel non tuberculous mycobacterial (NTM) species, the clinical significance of which is under constant evaluation. M. kumamotonense is a novel, slowly growing NTM, most similar to M. terrae complex. We describe the isolation of a clinically relevant M. kumamotonense strain from the sputum specimens of a patient with latent TB. Methods: A 32-year old immunocompetent English woman, working summertime in Crete, proceeded to the hospital for positive Mantaux test (40mm). Chest computed tomography (CT) scan revealed a nodular lesion in the right upper lobe and enlarged hilar lymph nodes. Acid-fast bacilli smear was positive for one sputum sample. Acid-fast bacilli were isolated from two sputum samples after two weeks incubation in the Bact-Alert 3D system, followed by a positive solid culture (Lowenstein-Jensen; bioMeriex, Marcy l'Etoile, France) twenty days later. Further examinations like hemodiagram, blood count, biochemical tests were in normal range with the only exception of LDH, which was elevated. No other risk factor for particular NTM lung disease was found. Results: The recovered mycobacterium was identified as M.celatum by the use of the commercial kits Genotype Mycobacterium CM and AS (Hain, Lifescience, Nehren, Germany). The banding patterns obtained for GenoType AS [1,2,3,6,12,14] was specific for M. celatum while those obtained for GenoType CM [1,2,3] was only genus-specific. Moreover, the sequences for 16S rRNA gene (GeneBank accession: HQ442524) and for the 65-kDa heat shock protein (hsp65) gene were 99.9% (838/839) and 99.4% (358/360) similar with the corresponding sequences of the type strain M.kumamotonense CST7247. According the criteria for NTM lung disease by the American Thoracic Society the recovered M.kumamotonense strain was considered as clinically relevant. Conclusions: This report should increase the awareness for the ubiquity to this species and raise the index of suspicion for the detection of the pathogen, particularly in a patient with latent TB. The introduction of more advanced molecular diagnostic methods as sequencing analysis of the 16S rRNA and hsp65 gene improved the ability to identify less common mycobacterial species as M.kumamotonense while commercial probes could not provide correct identification of this species.