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Paper Poster Session III

Nontuberculous mycobacteria

Pulmonary *Mycobacterium parascrofulaceum* infection in two immunocompromised patients

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Objectives: The introduction of molecular techniques facilitated the detection and identification of nontuberculous mycobacteria (NTM) species, the clinical significance of which is under constant evaluation. *Mycobacterium parascrofulaceum* is a rare, slowly growing, scotochromogenic NTM, related to *M. simiae*, first reported in 2004 (Turenne et al., 2004. Int. J. Syst. Evol. Microbiol. 54:1543-1551). This species is an opportunistic pathogen, like many nontuberculous mycobacterial species. We report, for the first time in Greece, two cases of pulmonary infection caused by *M. parascrofulaceum*, in two immunocompromised patients.

Methods: Case 1. A male, 47 years old, with a history of chronic obstructive lung disease, (COPD), type II respiratory distress syndrome and diabetes, proceeded to the hospital with fever, haemoptysis and dyspnea. The chest radiograph revealed COPD, peribronchial infiltrations and consolidations in the upper middle and lower lung zones.

Case 2. A male, 73 years old, with a history of pulmonary cancer, proceed to the hospital with fever, productive cough, dyspnea and weakness. Chest computed tomography (CT) scan revealed a nodular lesion in the right upper lobe and enlarged hilar lymph nodes.

Ziehl-Neelsen stain was negative for all sputum specimens received. Acid-fast bacilli were isolated from two sputum samples for each patient (strain GK-55 from patient 1 and GK-233 from patient 2) after ten days incubation in the Bact-Alert 3D system, followed by a positive solid culture (Lowenstein-Jensen; bioMerieux, Marcy l'Etoile, France) three weeks later.

Results: The recovered mycobacteria identified initially as *M. scrofulaceum* by the use of the commercial kit Genotype Mycobacterium CM (Hain, Lifescience, Nehren, Germany). Moreover, sequences for 16S rDNA gene (GeneBank accession: HM450379 for GK-55 and HQ167736 for GK-233) were 100% similar with the corresponding sequences of the type strain *M. parascrofulaceum* ATCC BAA-614T. According to the American Thoracic Society criteria for NTM lung disease (Am. J. Respir. Crit. Care Med. 1997, 156: S1-S25), the recovered strains were considered as clinically relevant.

Conclusion: Our findings suggest that the introduction of more advanced molecular diagnostic methods as sequencing analysis of the 16S rRNA gene improved the ability to identify less common mycobacterial species as *M. parascrofulaceum* while commercial probes could not provide correct identification of this species. From clinical point of view, *M. parascrofulaceum* seems to behave like the majority of NTM; its preferred target appears to be the lung, in particular in elderly patients with predisposing conditions.