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Epidemiology and clinical significance of non-tuberculous mycobacterial isolates in a university hospital in a ten-year period

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Background: Non-tuberculous mycobacteria (NTM) are considered emerging pathogens implicated in lung, lymph node, skin/soft tissue or disseminated infection. This retrospective study assessed the microbiological characteristics, clinical relevance and risk factors of NTM isolates recovered from patients in Attikon University Hospital, Athens Greece over the decade 12/2006 – 11/2016.

Material/methods: Clinical specimens were processed by standard methodology and inoculated into L–J slants, and in MGIT960 tubes (Becton Dickinson). NTM were identified with Genotype Mycobacterium CM and AS (Hain-Lifescience), while 16S rRNA and *hsp65* gene sequencing were applied when necessary. For diagnosis, the criteria from the American Thoracic Society/Infectious Disease Society of America (ATS/IDSA) 2007 were applied to determine the clinical relevance of recovered isolates.

Results: During the study period, one or more NTM isolates, recovered from 190 patients were analyzed; 186 (97.9%) of them yielded a single species and 4 (2.1%) had two. NTM isolates belonged to 24 species. The most frequent NTM isolates were *M. lentiflavum* (recovered from 46 patients), *M. avium* (37), *M. fortuitum* (19), *M. intracellulare* (20) and *M. gordonae* (16). For 165 (86.8%) patients, NTM were recovered from respiratory and for 25 (13.2%) from extra-pulmonary specimens, while for 69 (36.3 %) patients the recovered NTM were considered as clinically significant. For 48 of 165 patients (29.1%), NTM isolates (11 species) recovered from pulmonary specimens were considered as clinically significant while for 27 (56.3%) of them, smears were positive for acid-fast bacilli. The most frequent clinically significant NTM species recovered from respiratory specimens were *M. avium* (18) and *M. intracellulare* (12). For 21 of 25 patients (84%), the NTM isolates (8 species) recovered from extra-pulmonary specimens were considered as clinically significant while for 6 of them smears were positive for acid-fast bacilli. The most frequent species was *M. avium* (10). Six

patients suffered from skin and soft tissue infection and 15 immunocompromised patients (8 with AIDS) from disseminated disease. Risk factors in patients with NTM disease were underlying lung disease, mainly chronic obstructive pulmonary disease and asthma, smoking, AIDS, and malignancies. For the remaining 121 patients the recovered NTM were not considered as clinically significant, with the most prevalent species being *M. lentiflavum* (45) *M. fortuitum* (17) and *M. gordonae* (14), probably representing contamination.

Conclusions: Only 36.3% of patients yielded NTM isolates (belonging to 15/24 of the species) that were linked to human disease. The most common clinically significant isolates were *M. avium* and *M. intracellulare*, which were responsible for 58% of NTM disease. Only the 29% of patients with pulmonary NTM isolates met the ATS criteria, mainly because of inadequate sampling of a large number of individuals.