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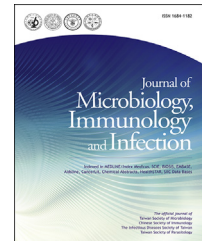
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CORRESPONDENCE

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Dear Editor,

Community-acquired pneumonia (CAP) is an important cause of morbidity and mortality in the Asia Pacific region.¹ In this region, the pathogens associated with CAP are rarely identified.¹ Nontuberculous mycobacteria (NTM), including *Mycobacterium abscessus*, are increasingly recognized as opportunistic pathogens responsible for respiratory tract infections.² Because NTM culture and identification is not routinely performed in most of the Pacific islands, NTM infections are underestimated.

To highlight the interest in identifying the etiological agents of CAP in the Pacific, we herein present the case of a French Polynesian man who fulfilled the American Thoracic Society criteria² for *M. abscessus* lung infection. Signed informed consent was obtained from the patient, and the French Polynesia Committee for Ethics approved this study.

A 77-year-old chronic obstructive pulmonary disease patient was admitted in May 2014 to our hospital with severe hypoxemia, cough, increased sputum purulence, and recurrent fever episodes since January 2014 after sequential amoxicillin–clavulanate and moxifloxacin treatments. A heavy ex-smoker, he received inhaled salmeterol/fluticasone and azithromycin long-term prophylaxis for 2 years. Computed tomography scanner showed large bullous emphysema and bilateral consolidations. Eight sputum specimens were collected from May 2014 to July 2014; all specimens were acid-fast bacilli (AFB) negative at direct examination, four yielded AFB colonies on Löwenstein–Jensen media (bioMérieux, La-Balme-les-Grottes, France) incubated at 37°C in a 5% CO₂ atmosphere. Isolates were identified as *M. abscessus* by hybridization using commercial probes (GenoType *Mycobacterium* CM/AS, Hain Lifescience, Nehren, Germany). The identification was confirmed by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) with 1.65 ± 0.31 log scores for *M. abscessus* DSM 44196^T (Bruker Mycobacteria Library version v2.0, Bruker Daltonics,

Bremen, Germany). Further 16S ribosomal RNA, partial *rpoB* gene sequencing,³ and multispacer typing⁴ characterized the four isolates as belonging to the *M. abscessus* subsp. *abscessus* group.

The four positive sputum specimens were not consecutively collected and were identified during different processes and thus an in-laboratory contamination was unlikely.

As pulmonary rehabilitation (oxygen, chest physiotherapy, and protein diet) improved the respiratory function, we decided to stop azithromycin and delay cefoxitin and amikacin therapy. The patient left the hospital by mid-August 2014 and 6 months after the diagnosis, the patient is under medical surveillance for long-term follow-up, as previously reported.⁵

This case illustrates that NTM should be considered as etiological agents of CAP in the Asia Pacific region and that *M. abscessus* is present in remote South Pacific islands where it can act as an opportunistic respiratory tract pathogen.

Culture and identification of NTM in respiratory tract specimens is strongly advised, including rapid MALDI-TOF MS identification, in order to guide medical management of patients and monitoring of NTM in these tropical islands. In addition, the identification of etiological agents of CAP may prevent or delay the emergence of antibiotic resistance in the Asia Pacific region.

Conflicts of interest

Authors declare no conflict of interest.

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