Case Report

Successfully treated spondylodiscitis due to a previously unreported mycobacterium

Enrico Tortoli,1,2 Antonia Mantella,3 Alessandro Mariottini,1,4 Gianna Mazzarelli,1,5 Patrizia Pecile,2 Pier G. Rogasi,6 Gaetana Sterrantino,6 Elisa Fantoni6 and Francesco Leoncini6

Correspondence

Enrico Tortoli
e.tortoli@libero.it

1,2,4,5,6Regional Reference Centre for Mycobacteria1, Microbiology and Virology Laboratory2, Cytogenetics and Genetics Unit4, Microbiological and Virological Serum-Immunology Laboratory5 and Infectious Diseases Unit6, Careggi Hospital, viale Morgagni 85, 50134 Florence, Italy

3Infectious Diseases Unit, University of Florence, Florence, Italy

A non-tuberculous mycobacterium was isolated, following a vertebral needle aspiration, from the blood of a patient with severe spondylodiscitis. The strain turned out to be different from any known mycobacterial species and was quite drug-susceptible in vitro. The patient improved markedly following treatment with meropenem, clarithromycin and amikacin.

Introduction

The rapidly growing non-tuberculous mycobacteria were considered for many years to be minor members of the genus Mycobacterium, with only a few species recognized, and those often incorrectly grouped together in the Mycobacterium fortuitum-Mycobacterium chelonae complex (Wolinsky, 1979; Wayne & Sramek, 1992). In recent years, however, a quite different scenario has emerged mainly thanks to the investigations of Wallace and co-workers (Brown-Elliott & Wallace, 2002). Not only has the number of rapidly growing species identified increased considerably, but the prevalence of clinically significant infections due to such organisms has also become clear. The present case joins the large number of mycobacterial pathologies involving joints and bone (Brown-Elliott & Wallace, 2002).

Case report

A 61 year old male suffering from cirrhosis was hospitalized because of severe backache. Radiographic and tomographic pictures revealed clear signs of infection, with massive destruction of the 3rd and 4th dorsal vertebrae (Fig. 1). A needle biopsy yielded purulent material which was cultured for common bacteria without isolation of significant pathogens (rare colonies of coagulase-negative staphylococcus). Culture for mycobacteria was not done. The day after the intervention, because of a sudden rise in the patient’s temperature, three blood cultures were made for aerobic and anaerobic bacteria. An empirical treatment with meropenem (1 g i.v. q8h), undertaken at the same time, turned out to be effective, with rapid disappearance of the fever. The isolation of an unidentified mycobacterium from all three blood cultures for aerobic bacteria led to the addition to the treatment of clarithromycin (500 mg i.v. bid) and amikacin (1 g i.v. die), to which the strain was susceptible in vitro. The patient was discharged after 56 days with prescription of protracting the treatment for 4 months. At a 15-week check-up, the patient did not report any fever relapse, while the backache had improved substantially.

Microbiological investigation

In the case described here, a previously unreported rapidly growing mycobacterium was responsible for spondylodiscitis in an elderly man. Although neither the biopsy specimen

Abbreviation: ITS, internal transcribed spacer.

The GenBank/EMBL/DDBJ accession numbers for the partial 16S rRNA gene and 16S–23S ITS sequences of strain FI-05038 are DQ067465 and DQ185131.

Fig. 1. Tomographic scan revealing massive destruction of vertebral bodies.
nor the blood of the patient were cultured for mycobacteria, the infection could be diagnosed thanks to the ability of the strain to grow in three blood-culture bottles specific for aero-
bic organisms (Bactec Plus Anaerobic/F; Becton Dickinson) taken at 30 min intervals when the patient was feverish. All bottles were scored positive by the automatic instrumenta-
tion Bactec 9240 (Becton Dickinson) within 2 to 4 days of incubation, and smooth, white colonies, which turned out

to belong to a Gram-uncertain rod (strain FI-05038), grew

on a blood agar subculture in 2 days at 37°C. Because of the

failure to obtain a confident identification with conven-
tional phenotypic methods, the sequence of the first third of

the 16S rRNA gene of the organism was determined (Cloud

et al., 2002). On the basis of this sequence (GenBank

accession no. DQ067465), the strain was shown to belong to

the genus Mycobacterium but differed from any known

species. The most closely related taxa were Mycobacterium

farcinogenes, M. fortuitum, Mycobacterium mucogenicum,

Mycobacterium porcinum and Mycobacterium senegalense, all
differing by 6 bp in a 466 bp region of the 16S rRNA gene

sequence (Fig. 2). The partial sequence of the 16S–23S

internal transcribed spacer (ITS) (GenBank accession no.

DQ185131) was also different from that of any other

organism, with the closest one (M. mucogenicum) differing

by 34 bp out of 360 bp investigated.

A Ziehl–Neelsen smear confirmed that the organism was

acid-fast. Phenotypic investigations revealed that the strain

was non-photochromogenic and produced smooth colonies

in 2 days at 25–37°C; it was furthermore able to grow on

MacConkey agar without crystal violet but was inhibited by

cephalothin (Wallace et al., 1993) and on Lowenstein–

Jensen agar with 5 % NaCl. Among biochemical tests, Tween

80 hydrolysis, 3-day arylsulfatase and urease were positive,

while nitrate reduction was negative. Catalase activity was

low (less than 45 mm foam). HPLC analysis revealed a

pattern of cell-wall mycolic acids roughly compatible with

that of M. mucogenicum but clearly different from those of

the other species most closely related at the genetic level

(Fig. 3).

Susceptibility testing performed using the agar elution

method (Brown et al., 1992) revealed effectiveness of

aminoglycosides (≤6 μg ml⁻¹), cefotaxime (≤30 μg ml⁻¹), cipro-

floxacin (≤2 μg ml⁻¹), clarithromycin (≤2 μg ml⁻¹), doxycycline

(≤6 μg ml⁻¹), imipenem (≤8 μg ml⁻¹) and tobramycin

(≤8 μg ml⁻¹), with the strain being resistant to trimethoprim/sulfamethoxazole (≥30 μg ml⁻¹) only. Imipenem is usually the only carbapenem tested against rapidly growing mycobacteria; at clinicians’ request, we also added meropenem and ertapenem, and both turned out to be active (≤8 μg ml⁻¹).

Fig. 2. Alignment of regions of the 16S rRNA gene sequence able to differentiate strain FI-05038 from M. farcinogenes, M. fortuitum (three different sequevars), M. mucogenicum (all sequevars available in GenBank) and M. senegalense. Base pair positions are indicated according to the Escherichia coli sequence. a, Sequences taken from Hall et al. (2003); b, from unpublished GenBank accession number AY627003.

Fig. 3. Representative HPLC pattern of cell-wall mycolic acids of strain FI-05038 in comparison with those of M. mucogenicum, M. fortuitum and M. farcinogenes. LMMIS, Low-molecular-mass internal standard; HMMIS, high-molecular-mass internal standard. The patterns of M. porcinum and M. senegalense have not been reported as overlapping substantially with that of M. fortuitum.
Discussion

We think, in this case, that the presence of the strain in the blood was accidental, having been very likely released from the vertebral lesion as a consequence of the trauma of the needle aspiration. The present isolation, obtained from a sterile site, unquestionably fulfills the American Thoracic Society criteria for clinical significance (American Thoracic Society, 1997).

The growth of several mycobacteria in non-dedicated blood-culture bottles (Jacomo et al., 1998) or on blood agar plates (Drancourt et al., 2003) has already been reported. In this case, this less known feature, along with a number of lucky coincidences, allowed a severe bone infection to be diagnosed and cured. Once again, the too-often disregarded usefulness of extending the microbiological investigation of biopsy samples to mycobacteria has been confirmed.

Once we had excluded the possibility that the test strain belonged to the species M. farcinogenes, M. fortuitum, M. porcinum and M. senegalense on the basis of the phenotypic and genotypic differences, the possibility remains that it is a previously unreported variant of M. mucogenicum. The agreement of most phenotypic features (Springer et al., 1995; Wallace et al., 1993) supports such a hypothesis. On the other hand, 1-3 and 10-1% mismatches in the investigated regions of the 16S rRNA gene and 16S–23S ITS, respectively, and the conflicting results of cephalothin tests (susceptibility to this antibiotic is very consistent in M. mucogenicum; Springer et al., 1995) favour the suggestion that it belongs to an as-yet unrecognized species. We feel that our current knowledge is not sufficient to make such a decision; furthermore, according to our convictions (Tortoli, 2003), the description of a novel species should not be based on a single strain. At the same time, we are confident that this report will stimulate others to characterize similar strains, increasing our knowledge of this organism.

The case reported here supports a large literature base (Brown-Elliott & Wallace, 2002) that contradicts the widespread conviction that rapidly growing non-tuberculous mycobacteria almost always play the role of a contaminant in clinical specimens.

References


