Case Report

Mycobacterium conceptionense infection complicating face rejuvenation with fat grafting

Ho Jik Yang,¹ Hyung Woo Yim,¹ Mi Young Lee,² Kwan Soo Ko^{2,3} and Hee Jung Yoon⁴

Correspondence

Kwan Soo Ko

ksko@skku.edu

Hee Jung Yoon

yhj822@medimail.co.kr

¹Department of Plastic and Reconstructive Surgery, College of Medicine, Eulji Medical Center, Daejeon, Republic of Korea

²Asia Pacific Foundation for Infectious Diseases (APFID), Seoul, Republic of Korea

³Department of Molecular Cell Biology, Sungkyunkwan University School of Medicine, Suwon, Republic of Korea

⁴Department of Infectious Disease, College of Medicine, Eulji Medical Center, Daejeon, Republic of Korea

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We report a third case of *Mycobacterium conceptionense* infection, which was found in a 50-year-old female following face rejuvenation surgery with fat grafting. The pathogen was identified using 16S rRNA gene and *rpoB* gene sequences. The growing diversity of non-tuberculosis mycobacterial species causing human infections emphasizes that early and precise identification is imperative for successful treatment.

Introduction

Mycobacterium conceptionense is a non-pigmented member of the rapidly growing mycobacteria (RGM) that was first described as a novel species belonging to the *Mycobacterium fortuitum* group in 2006 after isolation from the wound samples of a patient with post-traumatic osteitis (Adékambi *et al.*, 2006). The bacterium was later reported as causing a subcutaneous abscess in an immunocompetent patient (Liao *et al.*, 2009). In this report, we present another case of *M. conceptionense* infection in a patient following aesthetic surgery with fat grafting.

Case report

A previously healthy 50-year-old female arrived for an office consultation in December 2009 with multiple painful lumps on both cheeks. The patient had undergone surgery in a local clinic in November 2009, 4 weeks prior to presentation. At that time, liposuction had been performed using a tumescent technique in the abdominal regions and lipoinjection had been carried out bilaterally through the lateral canthal area of each eye to both cheeks for better reshaping of this area. The swelling accompanied by the operation did not decrease in size and gradually became associated with moderate pain. Three weeks after the operation, the patient complained of erythematous nodules and purulent discharge on both cheeks. Three days later, after no improvement was noted after being administered

500 mg cefradine orally twice a day and wound dressings being applied, the patient was taken to the operating room for incision and drainage. Despite this procedure, the erythematous nodules and purulent fluid were not resolved. At this stage, the patient was referred to a tertiary-care hospital (Eulji Medical Center, Daejeon, Republic of Korea). The patient had no systemic symptoms of infection, such as fever, chills, malaise, weight loss, respiratory or gastrointestinal manifestation; in particular, there was no significant lymphadenopathy. Physical examination showed local signs of inflammation, which included ill-defined erythematous nodules, induration, microabscesses and purulent drainage (Fig. 1). Oozing fluid was observed from several surgical incisions used previously for drainage. Laboratory examinations showed slightly elevated C-reactive protein (0.75 mg dl⁻¹) and mild leukocytosis (10 990 leukocytes µl⁻¹). Anti-streptolysin O, rheumatoid factor, human immunodeficiency virus and hepatitis B virus serology tests were negative. Liver function test, renal function tests and a chest X-ray were carried out, and all results were within normal limits.

Given the unusual delayed presentation and the absence of systemic symptoms, a sample of the purulent fluid from both the patient's cheeks (Fig. 1) was sent for bacterial and fungal culture, as well as acid-fast evaluation. Empirical antibiotic therapy with 500 mg amoxicillin/125 mg clavulanate (every 8 h) was immediately started and the wounds were irrigated with saline. The necrotic areas were debrided and a drainage tube was placed. Culture, Gram stain and acid-fast stain were all negative. After 10 days, the patient was discharged on a regimen of 300 mg oral cefcapene/

Abbreviations: CDC, Centers for Disease Control and Prevention; NTM, non-tuberculosis mycobacteria; RGM, rapidly growing mycobacteria.

Fig. 1. Multiple microabscesses and erythematous nodules on both cheeks of the patient 4 weeks after lipoinjection with fat obtained from the abdominal region.

pivoxil daily in good general and local condition. However, the dressing of the wound was continued in an outpatient setting for 2 months without dramatic improvement.

In early March 2010, the patient was admitted and received combination therapy due to suspicion of non-tuberculosis mycobacteria (NTM) infection. Wound drainage fluid was collected and sent for culture and identification to the Asia Pacific Foundation for Infectious Diseases. The patient was started on an 8 week course of treatment with parenteral cefoxitin (1 g every 24 h), amikacin (500 mg every 24 h), ciprofloxacin (400 mg every 12 h), and oral sulfamethoxazole/trimethoprim (400/80 mg every 12 h) and clarithromycin (500 mg every 12 h). After the immediate use of ciprofloxacin, the patient complained of an itching sensation over her whole body, so ciprofloxacin was changed to levofloxacin (500 mg every 12 h). Wounds were left open to prevent early closure of the skin, which can result in reaccumulation of pus and the appearance of new draining fistulas. In late March, an NTM isolate, NCH-C2, was identified by partial gene sequencing of 16S rRNA and *rpoB* genes as *M. conceptionense*.

The patient had a good response to the combination antibiotic therapy and wound dressing, with resolution of the erythematous nodules, induration and microabscesses. The patient was discharged with oral levofloxacin (100 mg every 12 h), sulfamethoxazole/trimethoprim (400 mg/80 mg every 12 h) and clarithromycin (500 mg every 12 h) treatment. Her progress was followed in both the plastic and reconstructive surgery and infectious disease clinics.

Molecular identification and antimicrobial susceptibility

Conventional automated methods in the clinical microbiology laboratory, such as the VITEK 2 system (bioMérieux), failed to identify the isolate to a given species. To identify isolate NCH-C2, 16S rRNA gene and *rpoB* sequence analyses were conducted. Portions of the 16S rRNA and *rpoB* genes were amplified using the primer sets fd1/rp2 (Al Masalma

et al., 2009) and MyCO-F/MyCO-R (Adékambi *et al.*, 2003), respectively. DNA sequences were edited by EditSeq and MEGALIGN programs (DNASTAR). Determined sequences were compared with the GenBank public database using the BLASTN program (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and the EzTaxon public database (<http://www.eztaxon.org/>) (Chun *et al.*, 2007). Sequences were aligned using the CLUSTAL_X program. A phylogenetic tree was constructed by the neighbour-joining method. Bootstrap values were evaluated from 1000 replications.

The 16S rRNA gene sequence (1390 bp) of isolate NCH-C2 showed 100% similarity with those sequences of several strains of *Mycobacterium senegalense*, *M. conceptionense* and *M. fortuitum*. The 16S rRNA gene sequence analysis suggested that isolate NCH-C2 belonged to the *M. fortuitum* group. To clarify the identification of isolate NCH-C2, the *rpoB* sequence was analysed. The partial *rpoB* gene sequence (705 bp; GenBank accession no. HM366453) of NCH-C2 was closest to the sequence of *M. conceptionense* CIP 108544 (99.3% nucleotide similarity). A constructed phylogenetic tree also indicated that isolate NCH-C2 clustered with *M. conceptionense* CIP 108544 (Fig. 2). Based on the *rpoB* sequence, we identified isolate NCH-C2 as *M. conceptionense*.

In vitro antimicrobial susceptibility testing was carried out by the broth microdilution protocol according to the guidelines of the Clinical and Laboratory Standards Institute (formerly the National Committee on Clinical Laboratory Standards) (NCCLS, 2003). The results of the *in vitro* susceptibility testing are shown in Table 1. Isolate NCH-C2 was susceptible to amikacin, cefoxitin, ciprofloxacin, clarithromycin, doxycycline, imipenem and moxifloxacin, but was resistant to tobramycin and vancomycin. The MICs of amoxicillin/clavulanate and sulfamethoxazole/trimethoprim were rather high.

Discussion

In this report, we have documented what is believed to be the third case of *M. conceptionense* infection in humans and

Fig. 2. Phylogenetic relationships of NCH-C2 and other members of the *M. fortuitum* group based on partial *rpoB* gene sequences. This unrooted tree was constructed by the neighbour-joining method. Numbers at branching nodes are percentages of 1000 bootstrap replications. Only values >50 % are shown.

the first one following aesthetic surgery with fat grafting. Because conventional methods failed to identify the bacterium at the species level, we tried to identify it using 16S rRNA gene and *rpoB* gene sequences. Based on both gene sequences, the infectious agent was concluded to be *M. conceptionense*. *M. conceptionense* belongs to the *M. fortuitum* group of RGM. Among the RGM, the *M. fortuitum* group is one of the most common mycobacterial pathogens (Brown-Elliott & Wallace, 2002). The *M.*

fortuitum group includes *M. fortuitum*, *Mycobacterium peregrinum*, *Mycobacterium mucogenicum*, *M. senegalense* and *Mycobacterium mageritense*. In addition, several new species including *Mycobacterium septicum*, *Mycobacterium boenickei*, *Mycobacterium houstonense*, *Mycobacterium new-orleansense* and *Mycobacterium brisbanense* have been reported recently mainly based on molecular methods (Schinsky *et al.*, 2000, 2004). These organisms most commonly cause localized skin and soft tissue infections,

Table 1. Results of antimicrobial susceptibility tests

Antibiotic	MIC (mg l ⁻¹)	Susceptibility*
Amikacin	1	S
Cefoxitin	16	S
Ciprofloxacin	1	S
Clarithromycin	0.5	S
Doxycycline	0.25	S
Imipenem	4	S
Tobramycin	16	R
Amoxicillin/clavulanate	>32/16	NA
Moxifloxacin*	0.12	S
Trimethoprim/sulfamethoxazole	8/152	NA
Vancomycin*	>64	R

NA, MIC interpretative breakpoints not available; R, resistant; S, susceptible.

*MIC breakpoints of moxifloxacin and vancomycin are those recommended for aerobic organisms.

usually in previously healthy hosts. Numerous case reports have documented the *M. fortuitum* group as an important cause of infection in cosmetic surgeries, including liposuction, abdominoplasty and face-lift procedures (CDC, 2004).

We had planned to take environmental samples in the operating room of the local clinic for culture but the doctor refused permission, so we could only assume that a possible contamination of the operating room equipment was the potential aetiological factor of the infection. The hospital environment, as well as the patient's own skin, is a possible source, since bacteria of the *M. fortuitum* group may be skin commensals, albeit transiently (Heistein *et al.*, 2000).

Isolate NCH-C2 was susceptible to amikacin, cefoxitin, ciprofloxacin, clarithromycin, doxycycline, imipenem and moxifloxacin, but resistant to tobramycin and vancomycin, which is similar to the result of the first and type strain of *M. conceptionense* (Adékambi *et al.*, 2006). Although the optimal regimen for the treatment of *M. conceptionense* infection has not been established, our patient showed a good response to antimicrobial combination therapy, wound dressing and surgical intervention. It is consistent with the results reported from a case in Taiwan, in which treatment with clarithromycin and linezolid, and surgical intervention, improved the patient's condition (Liao *et al.*, 2009). However, medications should be adjusted and individualized to each patient based on their antibiogram (Behroozan *et al.*, 2000). Although the duration of treatment has not been clearly defined, our experience suggests that an antimicrobial combination treatment should be continued until the resolution of symptoms and cutaneous lesions to avoid development of drug resistance. Surgical interventions also are essential to accelerate the resolution of the infection, but can result in undesirable scars with skin deformities and disfigurement that can cause psychological problems in patients including profound depression, anxiety and anger (Dessy *et al.*, 2006). Thus, the emotional care of the patient and family should be considered during treatment.

As NTM are encountered as emerging pathogens and the number of species within the *M. fortuitum* group has recently increased, it is important to prevent mycobacterial infections. Because of the increasing diversity of NTM species causing human infections, early and precise identification of the causative pathogen, combined with an adequate antimicrobial agent and a prompt surgical approach for patients with suspicious symptoms not responding to conventional therapy, may avoid morbidity and the costs involved in a prolonged hospital stay.

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