

Port-related *Delftia tsuruhatensis* bacteremia in a patient with breast cancer

Omur Tabak¹, Bilgul Mete², Selda Aydin², Nil Molinas Mandel³,
Baris Otlu⁴, Resat Ozaras², Fehmi Tabak²

¹Istanbul Education and Research Hospital, 1st Internal Medicine Clinic, Istanbul, Turkey;

²Istanbul University, Cerrahpasa School of Medicine, Department of Infectious Diseases and Clinical Microbiology, Istanbul, Turkey;

³Istanbul University, Cerrahpasa School of Medicine, Department of Internal Medicine, Section of Oncology, Istanbul, Turkey;

⁴Inonu University, Faculty of Medicine, Department of Microbiology, Division of Molecular Microbiology, Malatya, Turkey

SUMMARY

Delftia tsuruhatensis is a non-glucose fermenting, oxidase positive, motile, gram-negative bacillus first isolated from activated sludge collected from a domestic wastewater treatment plant in Japan. To the best of our knowledge only one case of infection with *Delftia tsuruhatensis* exists in the medical literature. This is the second case report of human infection having *Delftia tsuruhatensis* as a causative agent.

KEY WORDS: *Delftia tsuruhatensis*, Bacteremia.

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INTRODUCTION

Delftia tsuruhatensis was first described in 2003 by Shigematsu *et al.* (Shigematsu *et al.*, 2003). It was isolated from activated sludge collected from a domestic wastewater treatment plant (Shigematsu *et al.*, 2003).

It is a non-glucose fermenting, oxidase positive, motile, gram-negative slightly curved short rod and was described as a plant growth-promoting bacterium (Han *et al.*, 2005).

To the best of our knowledge, only one case of human infection with *Delftia tsuruhatensis* exists in the medical literature.

We present the second human infection case report of port-related bacteremia due to *Delftia tsuruhatensis*.

CASE

A 53-year-old woman was diagnosed with breast cancer six years ago and was recently on follow-up for metastatic disease. The patient had been receiving chemotherapy for about two years and a central venous port was implanted for access two years ago. She had been complaining of fever and chills attacks developing after chemotherapy and resolving spontaneously in one or two days for the last year.

She was admitted to our clinic since these symptoms had recently become continuous. On physical examination, there was neither tenderness nor redness on the skin over the port, and systemic examination did not reveal any infectious focus. She had mild leukocytosis (11.000/mm³) and elevated CRP (43 mg/dl; N:0-5 mg/L) level. Other laboratory findings were unremarkable. Blood cultures obtained simultaneously from the peripheral vein and port catheter revealed positive signals 24 hours after incubation in an automated system (BacT/Alert, bioMerieux). Gram-negative bacilli were seen on Gram-stained slides. The isolated bacterium was non-fermentative, motile, catalase and oxidase positive, indole, hydrogen

Corresponding author

Bilgul Mete, MD

Istanbul University

Cerrahpasa Medical Faculty

Department of Infectious Diseases

and Clinical Microbiology

Kocamustafa Paşa, 34098, Istanbul, Turkey

E-mail: bigimete@yahoo.com

sulfide and urease production were negative. The bacterium was identified as *Comamonas testosteroni* by means of an automated system (API ID 32 GN, bioMérieux). To confirm the identification 16S rDNA sequencing was done. Bacterial DNA was extracted from culture suspension by the EZ1 one automated extraction system (Qiagen, Hilden, Germany). Broad-range eubacterial primers (p8FPL 5'-AGTTTGATCCTG-GCTCAG-3' and p806R 5'-GACTACCAGGGTATCTAAT-3') were used for PCR amplification of approximately 800 base pairs (bp) of 16S rDNA. The temperature cycling profile was as follows: initial denaturation at 95°C for 4 min and 35 cycles at 95°C for 30 s, 56°C for 30 s, 72°C for 1 min with an additional extension step at 72°C for 7 minutes. The PCR products were checked by the 2% agarose gel electrophoresis before purifications of amplicon.

Amplicons by Qiaquick PCR purification kit (Qiagen, Hilden, Germany) were sequenced using the Bigdye Terminator V3.1 cycle sequencing kit with an automated DNA sequencing on ABI Prism 310 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). The sequence was submitted to the blastn program located at NCBI blast server (<http://blast.ncbi.nlm.nih.gov>). Megablast algorithm and Nucleotide Collection (nr/nt) search set was selected. A total 618 bases were sequenced. The query coverage was 99%, E-value was 0.0, and max identity 99%.

Standard antibiotic susceptibility testing was performed using the Kirby Bauer disk diffusion method as recommended by the Clinical and Laboratory Standards Institute. The microorganism was susceptible to third generation cephalosporins, cefepime, quinolones, and beta-lactamase inhibitors.

Since the patient's signs and symptoms improved after treatment with ceftriaxone 1 g/day for 14 days, the oncologists discussed keeping the port to be able to give chemotherapy. However, the core temperature increased again after cessation of antibiotherapy and the same organism was isolated from blood cultures. The patient was diagnosed with port-related bacteremia, ceftriaxone treatment was re-started and the port was removed. Growth of the same microorganism was shown in the port culture. Fever did not recur after the removal of the port and the second antibiotherapy.

DISCUSSION

Delftia infections are very rare in humans. To our knowledge only one case of infection with *D. tsuruhatensis* exists in the medical literature. Central venous catheter-related bacteremia due to *D. tsuruhatensis* developed in a patient with severe pulmonary hypertension.

The patient had recovered after removal of the catheter and intravenous ciprofloxacin therapy (Preiswerk *et al.*, 2011).

Our patient had been receiving chemotherapy for the last two years and was immunosuppressed. She had been occasionally subfebrile but a recent worsening was observed in her fever after chemotherapy.

The bacterium possibly colonized the port catheter. In addition, the long duration of port use would serve as a predisposing factor. The infection was confirmed by the growth of the same bacteria in blood cultures of samples obtained from the port and peripheral veins. Despite multiple antibiotic treatments, fever and recurrent bacteremia were persistent. Following the removal of the port, fever subsided and the same microorganism was isolated from the culture of the port. Since antibiotic resistance was not an issue, the treatment for the last attack was given for 14 days and then discontinued. During follow-up, no other attack of bacteremia was observed.

D. tsuruhatensis is closely related to *D. acidovorans* which was formerly named *Comamonas acidovorans* (Preiswerk *et al.*, 2011). An automated commercial system may fail to identify non-fermentative Gram-negative bacteria. For accurate identification gene sequencing is recommended (Zbinden *et al.*, 2007). As in our case report, the bacterium was misidentified as *Comamonas testosteroni* by means of API ID 32 GN but 16S rDNA gene sequencing revealed that the isolate was *Delftia tsuruhatensis*. Preiswerk *et al.* also first misidentified the bacterium as *D. acidovorans* with the VITEK 2 colorimetric card and the isolate was identified as *D. tsuruhatensis* by means of 16S rRNA gene sequencing (Preiswerk *et al.*, 2011).

In conclusion, *D. tsuruhatensis* is rarely isolated from clinical samples. However, in order not to overlook an infection by this organism, it should be kept in mind by both clinical microbiology lab-

oratory staff and clinicians that this particular microorganism may be a causative agent for human infections. As commercial biochemical systems may fail to identify this bacterium, gene sequencing should be addressed before identification of Gram-negative bacteria in the family of *Comamonadaceae*.

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