



Case report

Bacteremia due to *Streptococcus tigurinus*: A case report and literature review

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ARTICLE INFO

Article history:

Received 16 March 2016

Received in revised form

14 April 2016

Accepted 29 April 2016

Available online 25 July 2016

Keywords:

Streptococcus tigurinus

Bacteremia

16S rRNA

ABSTRACT

Gene sequence analysis methods, including 16S rRNA identification, allows accurate identification of *Streptococcus* species, which include phenotypically closely related species that are difficult to differentiate using conventional chemical methods. We report a case of bacteremia due to *Streptococcus tigurinus*, identified by 16S rRNA, in a 72-year-old woman with gastrointestinal cancer and ascites. She was hospitalized to undergo elective tumor-related surgery. Five days prior to undergoing surgery, she developed a fever with no obvious source of infection. Blood cultures identified gram-positive cocci. The patient's bacteremia was initially thought to be caused by an *Enterococcus* species, given her underlying gastrointestinal disease. However, alpha-hemolytic, mucoid, circular colonies were observed on sheep blood agar the following day. Although matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and biochemical testing suggested *Streptococcus pneumoniae*, we conducted further investigation to identify the bacterium, as the patient had no symptoms of infections usually related with *S. pneumoniae* such as pneumonia, meningitis, or sinusitis, and the bacteremia occurred 30 days after hospitalization. Finally, the gram-positive cocci were identified as *S. tigurinus*, assigned to the *Streptococcus mitis* group in 2012. Although the origin of infection was unclear, it was suspected that peritonitis or bacterial translocation from the gastrointestinal tract caused the bacteremia. This novel species was recently reported as being extremely pathogenic and different from other *Streptococcus* species. It has been reported to occur in cases of infectious endocarditis and bacteremia. In this article, we reviewed previous reports of *S. tigurinus* infection and summarized the clinical and pathogenetic features.

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1. Introduction

Streptococcus tigurinus (*S. tigurinus*), a novel species, was originally identified by Zbinden et al., in 2012 [1]. It was discovered in blood samples of patients with infective endocarditis (IE), meningitis, and spondylodiscitis, and was found to cause serious invasive infections in both immunocompetent and immunodeficient people [2]. This organism is a Gram-stain-positive, non-motile, non-spore-forming, catalase-negative coccus. On sheep blood agar culture, the

typical surface colonies are alpha-hemolytic, circular, smooth, convex, and white to grayish, with a diameter of 0.5–1 mm after 24 h of incubation at 37 °C in an anaerobic CO₂ atmosphere [1]. This species was not recognized previously because of the limitations of conventional phenotypic methods and limitations of commercially available tests. However, accurate identification of *S. tigurinus* has been facilitated by the introduction of housekeeping gene sequencing methods, such as 16S ribosomal RNA (16S rRNA). *S. tigurinus* is a new member of the *Streptococcus mitis* group and is closely related to *Streptococcus pneumoniae* (*S. pneumoniae*), *Streptococcus pseudopneumoniae*, *S. mitis*, *Streptococcus oralis*, and *Streptococcus infantis* based on phenotypic and molecular analyses [2].

We report herein on a case of bacteremia caused by *S. tigurinus*, originally identified as *S. pneumoniae* by conventional methods and

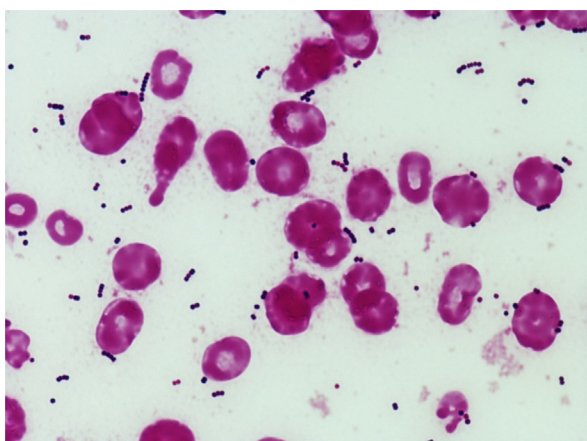
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matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), in a 72-year-old woman with gastrointestinal cancer. In addition, we summarize the clinical and pathogenetic features of this pathogen and review previous case reports.

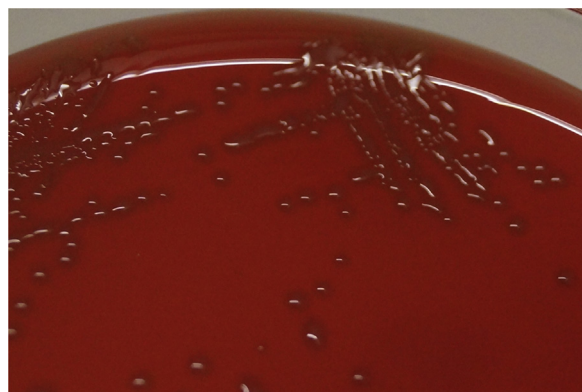
2. Case report

A 72-year-old Japanese woman with gastric and colon cancer with metastatic peritoneal dissemination and ascites, was admitted to our hospital for preoperative chemotherapy and surgery for treatment of the tumors. She had no past medical history except for her tumor. Preoperative chemotherapy was discontinued because of gastrointestinal side effects, such as nausea, vomiting, and diarrhea, therefore, surgery was planned for as soon as possible. Five days before undergoing surgery, she suddenly developed a fever and rigors. At that time she had no respiratory distress, no symptoms associated with meningitis, and her vital signs were as follows: blood pressure 118/62 mmHg, heart rate 75 beats/min, body temperature 37.9 °C, respiratory rate 16 breaths/min, and SpO₂ 99% in room air. Physical examination revealed no crackles on auscultation of her chest, no abdominal pain, and no signs of meningeal irritation. Laboratory investigation revealed a leukocyte count of 9500 cells/mm³ (neutrophils 87%, lymphocytes 6%, and monocytes 5%) and a C-reactive protein level of 8.86 mg/dL. A urine test detected no white blood cells or microorganisms. A chest radiograph showed no infiltrative shadows in either lung field. Her central venous catheter was removed, and two sets of blood cultures were immediately taken (the patient had not received any antibiotics during this episode of hospitalization). The following day, gram-positive cocci were confirmed on all four blood cultures (two sets of two bottles taken) (Fig. 1). The patient's initial diagnosis was translocational bacteremia caused by *Enterococcus* spp. given her underlying gastrointestinal disease. Hence, treatment with teicoplanin (TEIC) was started empirically. However, alpha-hemolytic, mucoid, circular colonies were detected on blood sheep agar the following day (Fig. 2). MALDI-TOF MS identified this microorganism as *S. pneumoniae*. Subsequently, abdominocentesis was performed to determine whether the patient had spontaneous bacterial peritonitis caused by *S. pneumoniae*, but we were unable to aspirate peritoneal fluid. The patient had no symptoms of infections usually related with *S. pneumoniae* (such as pneumonia, sinusitis, or meningitis), and, in general, *S. pneumoniae* causes community-



Gram-positive cocci were confirmed on blood culture

Fig. 1. Gram-stain of the blood cultures in the present case.



Alpha-hemolytic, mucoid, circular colonies were detected on sheep blood agar.

Fig. 2. Colonies on sheep blood agar.

acquired infections. The identity of this pathogen was reconfirmed by additional tests. A commercially available urine antigen test for detecting *S. pneumoniae* was negative, the bile solubility test was negative, and the optochin test showed this organism to be resistant. These results decreased the likelihood that this pathogen was *S. pneumoniae* (Fig. 3). In addition, the isolate was identified as *S. mitis* or *oralis* using VITEK[®] 2 (bioMérieux™, Marcy l'Étoile, France). We then conducted genetic investigation by 16S rRNA, which primers and sequence methods are summarized in Table 1. The results identified this gram-positive coccus as being *S. tigurinus* with 99.2% homology (1463 of 1475 bases) with the EZ taxon database (<http://www.ezbiocloud.net/eztaxon>; [3]) and 98% homology (1459 of 1475 bases) with NCBI Blast¹ database (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Although these two databases showed that the best match for the bacterium was *S. tigurinus*, the LeBIBI² database (<http://umr5558-bibiserv.univlyon1.fr/lebibi/lebibi.cgi>) suggested a possibility of both *S. tigurinus* and *Streptococcus oligofermentans*. Thus, we performed additional biochemical tests including β-D-galactosidase and raffinose to distinguish between *S. tigurinus* and *S. oligofermentans* (*S. oligofermentans*). The results of both tests were positive, meaning that this pathogen was *S. tigurinus* (*S. oligofermentans* is negative for β-D-Galactosidase). Viridans *Streptococcus* genus, which is commensal in the oral cavity and usually causes infective endocarditis, was incubated from all the patient's blood cultures. Thus, during the patient's clinical course, her oral cavity was thoroughly examined and transthoracic echocardiography was performed twice, to determine whether dental disease and/or valve vegetations were present. However, we could identify no oral source of bacterial entry, no cardiac vegetations, and no valvular disease. Based on the results of drug sensitivity testing (Table 2) and considering the possible involvement of anaerobic bacteria (because the origin of the causative organism was suspected to be the intestinal tract), TEIC was switched to sulbactam/ampicillin. The antibiotics were continued for 16 days, and were very effective. The patient recovered promptly, without recurrence, and underwent surgery after recovering from the bacteremia.

¹ NCBI-Blast, National Center for Biotechnology Information Basic Local Alignment Search Tool.

² LeBIBI/QBPP: A set of databases and a webtool for automatic phylogenetic analysis of prokaryotic sequences. Jean-Pierre Flandrois, Guy Perrière, Manolo Gouy. 2014. BMC Bioinformatics. 2015, 16:251 <http://dx.doi.org/10.1186/s12859-015-0692-z>.

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