IDCases 12 (2018) 133–135

Contents lists available at ScienceDirect

IDCases

journal homepage: www.elsevier.com/locate/idcases

Gemella haemolysans bacteremia in a patient with secondary peritonitis due to a duodenal ulcer perforation: A case report

Yoshiro Hadano[a,*], Yusuke Kinugasa[b], Kiyofumi Ohkusu[c], Kazushige Ishibashi[a], Miwako Isoda[a]

[a] Department of Infectious Diseases, St. Mary's Hospital, Kurume, Japan
[b] Department of Surgery, St. Mary's Hospital, Kurume, Japan
[c] Department of Microbiology, Tokyo Medical University, Tokyo, Japan

ARTICLE INFO

Keywords:
Gemella haemolysans
Bacteremia
Secondary peritonitis
MADLI-TOF MS
16S rRNA

ABSTRACT

We describe a case of *Gemella haemolysans* septic shock in a 75-year old Japanese male with a duodenal perforation and secondary peritonitis. Blood cultures on admission were positive for Gram-positive and Gram-variable cocci, and *G. haemolysans* was identified using whole cell matrix-assisted laser desorption/ionization mass spectrometry (MALDI-TOF MS), with a score value of 2.12. The 16S rRNA sequencing was difficult to use as a diagnostic test because there was more than 99% sequence homology with related bacterial strains. Based on both the biochemical profiles and whole groEL sequence, we concluded that the strain in our patient was *G. haemolysans.* The patient was successfully treated with a 16-day course of antimicrobials. His clinical condition improved, and no evidence of a relapse of the infection was noted. Although MALDI-TOF MS and 16S rRNA sequencing are useful for identification of the species, the basic biochemical profile is also important to identify a rare species.

Introduction

G. haemolyssans is a Gram-positive, catalase-negative, facultative anaerobic coccal bacterium. In general, the identification of *Gemella* species may be difficult in commercially available phenotypic systems, and is usually performed using 16S rRNA gene sequencing, a cumbersome and relatively expensive method [1,2]. Although three cases of peritoneal dialysis-related peritonitis due to *Gemella* spp. have been reported [3–5], no cases of an infection due to *G. haemolysans* in patients with duodenal perforation have been reported. We report a case of *G. haemolysans* bacteremia accompanied by peritonitis in an immunocompetent patient.

Case report

A 75-year-old Japanese man with hypertension and hyperlipidemia was admitted to our hospital because of bacterial peritonitis due to a perforated duodenal ulcer. Two days prior to admission, he developed epigastric pain and visited our emergency clinic. His symptoms transiently improved with acetaminophen. On the day of admission, he visited our emergency department due to worsening of epigastric pain. On physical examination, his blood pressure was 113/76 mm Hg, pulse rate was 78 beats per minute, temperature was 37.0 °C, respiratory rate was 28 breaths per minute, and his peripheral arterial oxygen saturation was 99% on room air. The physical examination was unremarkable, except for severe generalized rebound tenderness and muscular guarding.

Laboratory data obtained on admission revealed a white blood cell count of 5160 μL with 77% neutrophils and 20% lymphocytes. The hemoglobin level was 16.8 mg/dL, and the platelet count was 231,000 μL. A serum chemistry analysis revealed the following results: blood urea nitrogen 87.1 mg/dL, creatinine 5.2 mg dL, glucose 39 mg/dL, and C-reactive protein 37.9 mg/dL. Contrast-enhanced computed tomography showed an irregular thickening of the gastric and duodenal walls with pneumoperitoneum and ascites (Fig. 1). After an initial work-up in the emergency room, the patient was started on intravenous meropenem, 1 g administered every 12 h empirically based on the diagnosis of secondary peritonitis with an upper gastrointestinal tract ulcer perforation. Emergency surgery was performed, and his final diagnosis was duodenal ulcer perforation with secondary bacterial peritonitis. After the surgery, continuous renal replacement therapy (CRRT) was started because of severe hypotension with oliguria.

On day 3, the admission blood cultures became positive for a small Gram-positive coccal bacterium and a gram variable coccal bacterium (Fig. 1). Daptomycin 8 mg/kg every 48 h was added to the treatment regimen. On day 6, the strain was identified as *G. morbillorum* by the BD

* Corresponding author at: Department of Infectious Diseases, St. Mary's Hospital, 422 Tsubukuhonmachi, Kurume, Fukuoka, 830-8543, Japan.
E-mail address: y-hadano@st-mary-med.or.jp (Y. Hadano).

https://doi.org/10.1016/j.idcr.2018.04.009
Received 15 April 2018; Received in revised form 26 April 2018; Accepted 26 April 2018

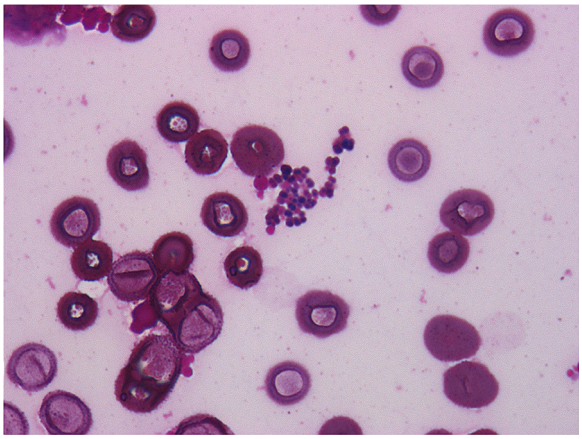

Fig. 1. Gram staining of blood cultures (×1000) showed small Gram-positive cocci and gram variable cocci.

BBL Crystal identification system (Becton Dickinson, Tokyo, Japan), although precise identification was difficult using the MicroScan WalkAway 40 plus system (Siemens Healthcare Diagnostics, Tokyo, Japan). A strain was isolated and based on whole cell matrix-assisted laser desorption/ionization mass spectrometry (MALDI-TOF MS) (MALDI-TOF Biotyper, Beckman Coulter, Tokyo, Japan), *Gemella haemolysans* was identified with a score value of 2.12. In addition, we performed molecular identification by PCR amplification and sequencing analysis of the 16S rRNA gene using DNA extracted from the isolates. The universal primers 8UA (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1485B (5′-ACGGGCGGTGTGTRC-3′ were used as described previously [6]. Sequencing and gene analysis was performed using a GenBank BLAST search and EzTaxon (http://www.ezbiocloud.net/eztaxon/).

The bacterial strain was difficult to identify because the sequence homology between *G. haemolysans*, *G. parahaemolysans*, and *G. taiwanensis* was more than 99%. Biochemical tests were performed to differentiate this strain [7]. The d-mannitol, d-sorbitol, leucine arylamidate, and Voges-Proskauer test were all negative. A whole groEL sequence analysis showed that the homology with *G. haemolysans* was the highest (94%). Based on these results, this strain was identified as *G. hemolysans*. Minimal inhibitory concentration breakpoints were defined according to the Clinical and Laboratory Standars Institute (M45) criteria. The isolates of *G. haemolysans* exhibited susceptibility to penicillin, ampicillin, ceftriaxone, meropenem, erythromycin, levofloxacin, clindamycin and vancomycin (Table 1).

On day 7, the patient began treatment with intravenous ampicillin/sulbactam, 3 g every 12 h based on the findings of the susceptibility test. The patient was successfully treated with a 16-day course of antibacterials. A follow-up endoscopy was performed, and no evidence of malignancy was found. His clinical condition improved, and no evidence of a relapse of the infection was noted.

Table 1
Susceptibility testing of the isolated *Gemella haemolysans*.

Antimicrobial agent	Minimal inhibitory concentration (μg/mL)
Penicillin	< 0.03
Ampicillin	< 0.06
Ceftriaxone	< 0.12
Meropenem	< 0.12
Erythromycin	0.25
Levofloxacin	< 0.25
Clindamycin	< 0.12
Vancomycin	0.5

Discussion

We present a case of *G. haemolysans* bacteremia in a patient with secondary peritonitis due to a duodenal perforation. *Gemella* are facultative anaerobic Gram-positive cocci, which are commensal organisms of the human oral cavity, gastrointestinal tract, upper respiratory tract, and genitourinary tract [8]. To date, the members of this genus include *G. haemolysans*, *G. morbillorum*, *G. bergeri*, *G. sanguinis*, *G. palaticanis,* and *G. cuniculi*. DNA hybridization and comparative 16 s rRNA gene sequencing is used to classify the different members of this genus [2]. Moreover, *G. parahaemolysans* and *G. taiwanensis* have been identified recently using phylogenetic analysis of groEL, rpoB, and recA sequences [7].

It is not easy to differentiate *G. haemolysans* from viridans streptococci and from *Gemella* strains not of the species *G. haemolysans* by the standard identification procedures. First, *G. haemolysans* is easily decolorized in the Gram stain and may therefore appear as either Gram-variable or even Gram-negative. It can be misidentified as a viridians streptococcus or remain unidentified. Second, identification of *Gemella* in the laboratory has also some limitation because of the characteristics of these bacteria. When slow growing, catalase negative, gram-positive cocci are observed in samples, *Gemella* should be considered. Although infections caused by *Gemella* are rare, *G. haemolysans* has been reported in cases of infectious endocarditis [10–12], meningitis [13–15], spondylodiscitis [16], bone infection [17], infected aneurysm [18], liver abscess [19], and eye infections [20–22]. Although three cases of peritoneal dialysis-related peritonitis due to *Gemella* spp. have been reported [1–3], no cases of secondary bacterial peritonitis in patients with a duodenal perforation associated with *G. haemolysans* have yet been reported. Our patient was in septic shock. In general, *Gemella* infections have a good prognosis, but fatal cases due to *Gemella* spp. have been reported, such as septic shock syndrome and Ludwig's angina [23–25].

In our case, the results differed between the commercial biochemical tests using phenotypic identification systems and MALDI-TOS MS. Although commercial phenotypic identification systems are readily available, precise identification requires additional testing, especially in cases of uncommon strains. To date, a few studies have evaluated the accuracy and sensitivity of the test to detect *Gemella* spp. strains and even less studies have focused on differentiating the species of the genus [9]. Our identified *G. haemolysans* score was higher than that described by Chiristensen et al (median of 1.870 for six strains studied) [17]. Thus, MALDI-TOF MS seems promising for the identification of strains belonging to the genus *Gemella*. Similarity, precise identification of rare species is usually performed using 16S rRNA gene sequencing. However, MALDI-TOF MS and 16S rRNA sequencing are not perfect in cases of rare species. For example, Hikone at al. reported a case of infective endocarditis caused by *G. taiwanensis*, but they initially showed that *G. haemolysans* was identified by MALDI-TOS MS because *G. taiwanensis* was not included in the database at that time. They found that the biochemical profile was atypical. Based on the findings with the 16S rRNA sequencing, distinguishing *G. haemolysans* from *G. taiwanensis* was difficult because the sequence homology was more than 99%. Finally, *G. taiwanensis* was identified by whole groEL sequence analysis [25]. Actually, Hung at al. reported that distinguishing *G. haemolysans*, *G. parahaemolysans,* and *G. taiwanensis* is not possible using 16S rRNA gene sequencing because these strains have a sequence homology of more than 99.6% [7]. Although MALDI-TOF MS and 16S rRNA sequencing are useful for identification of the species, the basic biochemical profile is also important to identify a rare species.

Conclusion

In conclusion, we report here a case of *Gemella haemolysans* bacteremia in a patient with a duodenal perforation and secondary peritonitis. The interpretation of the finding of *Gemella* spp. must be done

carefully even when determined by either MALDI-TOF MS or 16S rRNA sequencing. Further studies are needed to clarify the accuracy of identification for rare species, including *Gemella haemolysans*.

Conflict of interest

None to declare.

References

[1] La Scola B, Raoult D. Molecular identification of Gemella species from three patients with endocarditis. J Clin Microbiol 1998;36:866–71.
[2] Woo PC, Lau SK, Fung AM, Chiu SK, Yung RW, Yuen KY. Gemella bacteraemia characterised by 16S ribosomal RNA gene sequencing. J Clin Pathol 2003;56:690–3.
[3] Guney I, Isik A, Altintepe L, Er C, Kurdoglu MG. Gemella morbillorum peritonitis in a CAPD patient. Perit Dial Int 2009;29:674–5.
[4] Unal A, Sipahioglu MH, Kavuncuoglu F, Tokgoz B, Oymak O, Utas C. A rare cause of peritoneal dialysis-related peritonitis: Gemella haemolysans. Perit Dial Int 2009;29:482.
[5] Azap OK, Yapar G, Timurkaynak F, Arslan H, Sezer S, Ozdemir N. Gemella morbillorum peritonitis in a patient being treated with continuous ambulatory peritoneal dialysis. Nephrol Dial Transplant 2005;20:853–4.
[6] Masaki T, Ohkusu K, Ezaki T, Miyamoto H. Nocardia elegans infection involving purulent arthritis in humans. J Infect Chemother 2012;18:386–9.
[7] Hung WC, Chen HJ, Tsai JC, Tseng SP, Lee TF, Hsueh PR, et al. Gemella parahaemolysans sp. nov. and Gemella taiwanensis sp. nov., isolated from human clinical specimens. Int J Syst Evol Microbiol 2014;64:2060–5.
[8] Khan R, Urban C, Rubin D, Segal-Maurer S. Subacute endocarditis caused by Gemella haemolysans and a review of the literature. Scand J Infect Dis 2004;36:885–8.
[9] Schulthess B, Brodner K, Bloemberg GV, Zbinden R, Böttger EC, Hombach M. Identification of Gram-positive cocci by use of matrix-assisted laser desorption ionization-time of flight mass spectrometry: comparison of different preparation methods and implementation of a practical algorithm for routine diagnostics. J Clin Microbiol 2013;51:1834–40.
[10] Avgoustidis N, Bourantas CV, Anastasiadis GP, Sipsas N, Pikazis D. Endocarditis due to Gemella haemolysans in a patient with systemic lupus erythematosus. J Heart Valve Dis 2011;20:107–9.
[11] Khan R, Urban C, Rubin D, Segal-Maurer S. Subacute endocarditis caused by Gemella haemolysans and a review of the literature. Scand J Infect Dis 2004;36:885–8.
[12] La Scola B, Raoult D. Molecular identification of Gemella species from three patients with endocarditis. J Clin Microbiol 1998;36:866–71.
[13] Anil M, Ozkalay N, Helvaci M, Agus N, Guler O, Dikerler A, et al. Meningitis due to Gemella haemolysans in a pediatric case. J Clin Microbiol 2007;45:2337–9.
[14] Galen BT, Banach DB, Gitman MR, Trow TK. Meningoencephalitis due to Gemella haemolysans. J Med Microbiol 2014;63:138–9.
[15] Lo WB, Patel M, Solanki GA, Walsh AR. Cerebrospinal fluid shunt infection due to Gemella haemolysans. J Neurosurg Pediatr 2013;11:205–9.
[16] Rajagopal TS, Walia M, Wilson HA, Marshall RW, Andrade AJ, Iyer S. Gemella haemolysans spondylodiscitis: a report of two cases. J Bone Jt Surg Br 2012;94:825–8.
[17] Fangous MS, Hémon F, Graf P, Samier-Guérin A, Alavi Z, Le Bars H, et al. Bone infections caused by Gemella haemolysans. Med Mal Infect 2016;46:449–52.
[18] Gatibelza ME, Laroye B, Lombard J, Mameli A, Thomas E. Management of a ruptured infected abdominal aortic aneurysm and a spondylodiscitis due to Gemella haemolysans. Ann Vasc Surg 2009;23(536):e13–7.
[19] Malik I, Ghosh S, Nutt C, Macdonald A, Bal AM, Collier A. Gemella haemolysans bacteraemia in a patient with solitary liver abscess. J Microbiol Immunol Infect 2010;43:438–41.
[20] Nalamada S, Jalali S, Reddy AK. Acute postoperative endophthalmitis by Gemella haemolysans. Indian J Ophthalmol 2010;58:252–3.
[21] Kailasanathan A, Anderson DF. Infectious crystalline keratopathy caused by Gemella haemolysans. Cornea 2007;26:643–4.
[22] Elmallah MK, Munir WM, Janda WM, Tu EY. Gemella haemolysans infectious crystalline keratopathy. Cornea 2006;25:1245–7.
[23] Vasishtha S, Isenberg HD, Sood SK. Gemella morbillorum as a cause of septic shock. Clin Infect Dis 1996;22:1084–6.
[24] Sofianou D, Peftoulidou M, Manolis EN, Sofianos E, Tsakris A. A fatal case of Ludwig's angina and mediastinitis caused by an unusual microorganism, Gemella morbillorum. Scand J Infect Dis 2005;37:367–9.
[25] Hikone M, Sakamoto N, Ota M, Washino T, Kobayashi K, Iwabuchi S, et al. The first case report of infective endocarditis caused by Gemella taiwanensis. J Infect Chemother 2017;23:567–71.