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

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**A R T I C L E   I N F O**

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**A B S T R A C T**

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. haemolysans* 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...
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. haemolysans. Minimal inhibitory concentration breakpoints were defined according to the Clinical and Laboratory Standards 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

| 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                                     |

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

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. palatianus, and G. cuniculi. DNA hybridization and comparative 16s 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 viridans 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 Christensen 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-TOF 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.

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