Ruminococcus gnavus bacteremia associated with fecal peritonitis secondary to small bowel perforation

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To the Editor,

Ruminococcus gnavus is a common and abundant member of the human gut microbiota. Infections due to *R. gnavus* have been reported only rarely. In this letter, we illustrate the importance of a comprehensive and up-to-date database for rapid and accurate identification of anaerobic bacteria by matrix-assisted laser desorption ionization-time of flight mass spectrometry.

We report a case of bacteremia with *R. gnavus* associated with fecal peritonitis secondary to a small bowel strangulated hernia and perforation (Fig. 1a,b). Surgical resection of a gangrenous small bowel segment and abdominal lavage was performed. Anaerobic blood cultures on day +5 revealed catalase negative Gram-positive diplococcic. Species identification was performed using partial 16S rRNA gene sequencing (MicroSeq 500 kit, Life Technologies, Foster City, CA) and MALDI BioTyper (software version 3.1; library version 4.0.0.1) MALDI-TOF MS system (Bruker Daltonics, Germany). Species identification of the isolate as R. gnavus was confirmed. Patient was treated with antibiotics and discharged 12 weeks after admittance.

Although the gut microbiota plays an important role in human symbiosis, these commensals can contribute to disease pathogenesis and cause infections in the susceptible host (1). *R. gnavus* is a Gram-positive, anaerobic, non-sporulating bacterium, belonging to the Firmicutes phylum, Clostridia class. *R. gnavus* is found in over 90% of individuals. Colonization is established early in life and the species is well adapted to the intestinal habitat, where it resides within the mucus layer covering the intestinal epithelium. Changes in the gut microbiota, dysbiosis, have been described in association with disease, especially in inflammatory bowel disease (2). *R. gnavus* species are increased in these conditions (2,3).

Human infections involving *R. gnavus* have only rarely been described in literature. One case reported *R. gnavus* as the causative agent of septic arthritis in an immunocompromised patient (4). In another case, *R. gnavus* was identified in a total hip arthroplasty infection in a patient with ulcerative colitis (5). Two cases described *R. gnavus* bacteremia associated with

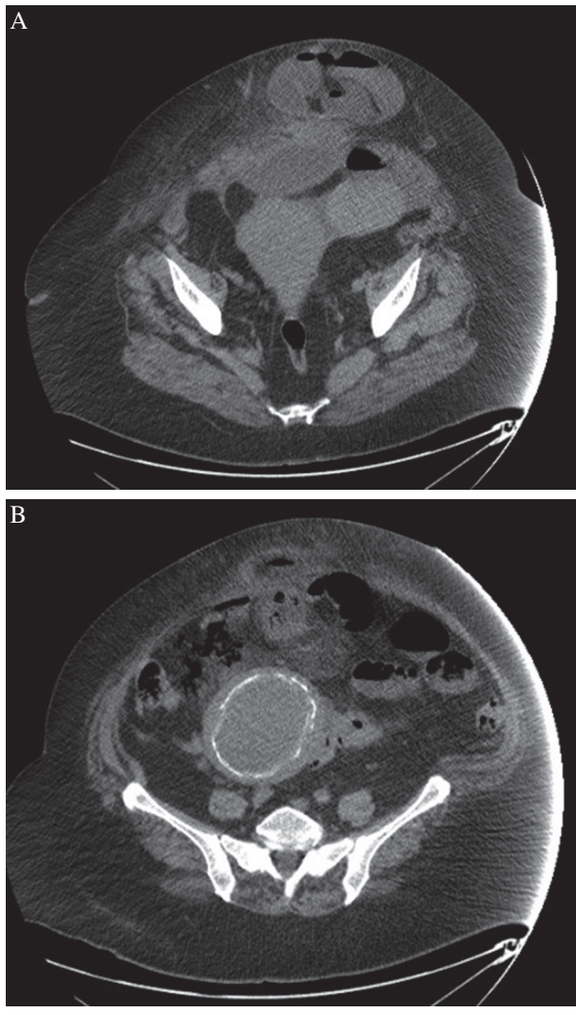

Fig. 1. a, b. — Abdominal computed tomography scan demonstrates a strangulated hernia of the small intestines through the anterior abdominal wall.

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Submission date : 27/11/2017
Acceptance date : 10/05/2018

Table 1. — **Antimicrobial susceptibility testing results**

Antimicrobial agent	*MIC (mg/liter)*	*Interpretation*[1,2]
Benzylpenicillin	*0.094*	*S*
Amoxicillin-clavulanic acid	*0.016*	*S*
Piperacillin-tazobactam	*0.5*	*S*
Cefoxitin	*8*	*S*
Cefotaxime	*0.125*	*S*
Meropenem	*0.094*	*S*
Levofloxacin	*≥32*	*-*[3]
Moxifloxacin	*4*	*I*
Clindamycin	*0.016*	*S*
Metronidazole	*0.094*	*S*
Vancomycin	*0.25*	*-*[3]
Tetracycline	*0.032*	*S*

[1] *interpretation according to CLSI M100-S24 guidelines*
[2] *R= resistant, S= sensitive, I=intermediate,*
[3] *no breakpoints defined in CLSI M100-S24*

diverticulitis (6). In our case, translocation of *R. gnavus* from the gut as consequence of fecal peritonitis due to a strangulated internal hernia was the likely source of the bacteremia.

Conventional methods for the identification of anaerobic bacteria rely on a phenotypic assay with Gram-staining, biochemical reactions and growth characteristics. They cause long turnaround times and many anaerobic species are biochemically inert, therefore, phenotypic assays do not always provide a reliable species identification. Genetic sequence-based identification methods, MALDI-TOF MS, are used in microbiology laboratories as primary microbial identification method providing rapid and accurate identification. Sequence-based methods are used in our laboratory as a secondary identification method in cases where MALDI-TOF MS fails to identify the isolate. Partial 16S rRNA gene sequencing did indeed confirm the identification of our isolate. Nevertheless, the shortcoming in the MALDI-TOF MS database resulted in a delay in the identification.

Data regarding the antimicrobial susceptibility of *R. gnavus* are scarce. All examined strains were susceptible to metronidazole and resistant to fluoroquinolones, but showed variable susceptibility to beta-lactam antibiotics and clindamycin (5,6). We started levofloxacin and ornidazole on day 0 but switched to meropenem due to no improvement. Our strain showed a similar profile (Table 1).

In summary, this case illustrates a rare occurrence of *R. gnavus* bacteremia associated with fecal peritonitis. The broad implementation in clinical laboratories of MALDI-TOF MS as a rapid and accurate identification method of anaerobic bacteria could lead to a better understanding of the potential pathogenicity of members of the human gut microbiota, like *R. gnavus*. A comprehensive and up-to-date database is a prerequisite for identification. For anaerobic species that are absent in these databases, 16S rRNA gene sequencing remains an alternative.

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