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**Case Report**

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# Mixed anaerobic bacteremia involving *Gabonibacter massiliensis* following colorectal perforation: a case report

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## Abstract

***Gabonibacter massiliensis*** **is a recently described obligate anaerobic bacterium and a member of the human gut microbiota. No cases of human infection caused by this organism have been reported to date, and its pathogenicity and clinical significance remain unclear. We report a case of mixed anaerobic bacteremia involving *G. massiliensis* associated with colorectal perforation. A 75-year-old man presented with sigmoid colon perforation associated with rectal cancer and fecal peritonitis. Emergency Hartmann's procedure was performed. Anaerobic blood culture bottles became positive after 77 h, and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry identified *G. massiliensis* (score 2.39) and *Butyricimonas faecihominis* (score 2.13). The patient developed postoperative septic shock but recovered following surgical source control and antimicrobial therapy. This case suggests that *G. massiliensis* may be involved in bacteremia secondary to colorectal perforation as part of polymicrobial intra-abdominal infection.**

***Keywords*** *Gabonibacter massiliensis, Butyricimonas faecihominis,* **bacteremia, colorectal perforation, peritonitis**

## Introduction

Colorectal perforation with fecal peritonitis is a life-threatening intra-abdominal infection caused by polymicrobial contamination with intestinal microbiota. Recent advances in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) have enabled species-level identification of anaerobic bacteria that were previously difficult to identify.

*Gabonibacter massiliensis* is a recently described obligate anaerobic bacterium and a member of the human gut microbiota. No human infection caused by *G. massiliensis* has been reported. We report a case of mixed anaerobic bacteremia involving *G. massiliensis* and *Butyricimonas faecihominis* associated with colorectal perforation.

## Case report

A 75-year-old man with abdominal distension developed severe abdominal pain following bowel preparation for colonoscopy and was transferred to our hospital. His medical history was unremarkable.

On admission, his body temperature was 36.4°C, blood pressure 115/79 mmHg, heart rate 91 beats/min, respiratory rate 26 breaths/min, and oxygen saturation 97% on room air. Physical examination revealed generalized peritonitis. Laboratory tests showed a white blood cell count of 7500/$\mu$l and C-reactive protein level of 0.06 mg/dl. Arterial blood gas analysis showed a pH of 7.37 and lactate level of 3.1 mmol/l. Two sets of blood cultures were obtained before intravenous meropenem administration. Contrast-enhanced computed tomography (CT) demonstrated rectal cancer and sigmoid colon perforation (Fig. 1), and emergency surgery was performed.

Laparotomy revealed generalized fecal peritonitis, a rectal tumor, and sigmoid colon perforation. The perforation was located close to the rectal tumor, and the intervening bowel wall was markedly thinned and fragile. Therefore, we decided to resect the rectal tumor together with the perforated sigmoid colon. Hartmann's procedure with abdominal lavage and drainage was performed. Peritoneal fluid was collected after initiation of meropenem. Histopathological examination revealed rectal adenocarcinoma (pT3N0M0, pStage IIA).

The patient developed postoperative septic shock requiring noradrenaline and vasopressin, which were discontinued on postoperative day (POD) 2. He was extubated on POD 4.

Peritoneal fluid culture yielded AmpC-producing *Escherichia coli*, *Klebsiella pneumoniae*, *Bacteroides thetaiotaomicron*, anaerobic Gram-negative rods, and *Candida* spp. The three identified bacterial species were susceptible to meropenem and cefmetazole.

The anaerobic bottles from both sets of blood cultures became positive after 77 h. MALDI-TOF MS (MALDI Biotyper, Bruker Daltonics, Bremen, Germany) identified *G. massiliensis* (score 2.39) and *B. faecihominis* (score 2.13). The identification log score reflects the similarity between the measured mass spectrum and reference spectra in the database. Scores of ≥2.0 generally support species-level identification,

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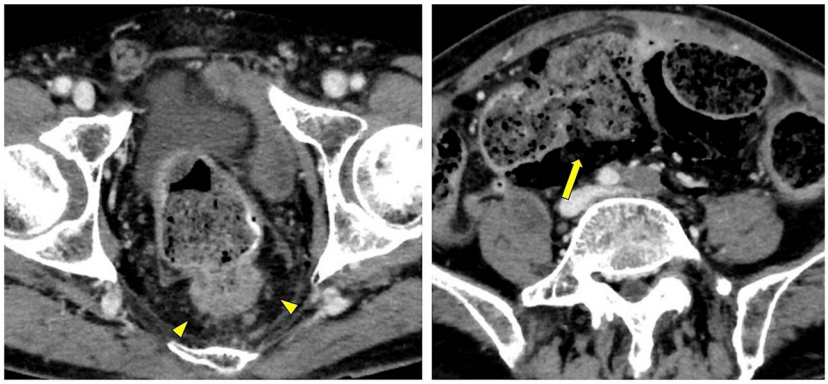


**Figure 1** Contrast-enhanced CT findings. The left image shows circumferential wall thickening of the rectum (arrowheads). The right image shows discontinuity of the colonic wall with leakage of fecal material into the peritoneal cavity (arrow).

whereas scores of 1.7–1.99 support genus-level identification. Antimicrobial susceptibility testing was not performed for either organism. Follow-up blood cultures on POD 7 were negative. Meropenem was continued until POD 13 and then de-escalated to cefmetazole based on the culture and susceptibility results of the major pathogens isolated from the peritoneal fluid. Cefmetazole was administered for an additional 5 days.

The patient recovered without recurrence of infection and was transferred for rehabilitation on POD 36.

## Discussion

This case describes mixed anaerobic bacteremia involving *G. massiliensis* associated with colorectal perforation. No cases of human infection caused by *G. massiliensis* have been reported to date.

*Gabonibacter massiliensis* is an obligate anaerobic Gram-negative coccobacillus that was first isolated from the feces of a healthy individual by Mourembou et al. in 2016 using a culturomics approach [1]. It is considered a member of the normal human gut microbiota. The pathogenicity and clinical significance of *G. massiliensis* remain poorly understood.

In the present case, colorectal perforation resulted in fecal peritonitis, and peritoneal fluid culture yielded multiple enteric microorganisms, including *E. coli*, *K. pneumoniae*, and *B. thetaiotaomicron*. Blood cultures subsequently yielded *G. massiliensis* and *B. faecihominis*. These findings support the hypothesis that both organisms leaked into the peritoneal cavity following colorectal perforation and subsequently entered the bloodstream through the inflamed peritoneum. Anaerobic Gram-negative rods that were not identified to the species level were isolated from the peritoneal fluid. Therefore, the possibility that these isolates included *G. massiliensis* and *B. faecihominis* cannot be excluded. Because peritoneal fluid was collected after the initiation of intravenous meropenem, the possibility that antimicrobial therapy influenced the culture results cannot be excluded. In contrast, *E. coli*, *K. pneumoniae*, and *B. thetaiotaomicron* isolated from the peritoneal fluid were not recovered from the blood cultures, suggesting that *G. massiliensis* and *B. faecihominis* may have been the organisms responsible for the bacteremia.

*Butyricimonas faecihominis* is also an obligate anaerobic bacterium of the human gut microbiota, and invasive infections caused by members of the genus *Butyricimonas*, including bacteremia, peritonitis, and gastrointestinal infections, have been reported. Gastrointestinal malignancy has been recognized as a predisposing factor for these infections [2]. Prompt surgical source control and appropriate antimicrobial therapy are essential for the treatment of polymicrobial intra-abdominal infections [3]. In the present case, meropenem was selected empirically because the patient presented with generalized fecal peritonitis complicated by septic shock. Following adequate surgical source control, antimicrobial therapy was de-escalated to cefmetazole based on the culture and antimicrobial susceptibility results of the major pathogens isolated from the peritoneal fluid.

Recent advances in MALDI-TOF MS have enabled rapid and reliable species-level identification of anaerobic bacteria that were previously difficult to identify in routine clinical laboratories. However, identification of uncommon organisms remains dependent on the quality and completeness of the reference database, and misidentification of *Sanguibacteroides justesenii* as *G. massiliensis* has been reported [4]. Although MALDI-TOF MS did not directly influence antimicrobial selection in the present case, it enabled recognition of *G. massiliensis*. Identification of uncommon organisms may contribute to the accumulation of clinical evidence regarding their pathogenicity and clinical significance.

Confirmatory molecular identification by 16S rRNA gene sequencing could not be performed because the clinical isolates were not preserved after routine microbiological testing. Therefore, the possibility of misidentification cannot be completely excluded. In addition, antimicrobial susceptibility testing was not performed for either blood culture isolate. Therefore, the antimicrobial susceptibility of *G. massiliensis* and *B. faecihominis* could not be determined.

This case suggests that *G. massiliensis* may be involved in bacteremia secondary to colorectal perforation as part of polymicrobial intra-abdominal infection. Further accumulation of well-characterized cases, ideally with molecular confirmation and antimicrobial susceptibility testing, is needed to clarify the pathogenicity and clinical significance of *G. massiliensis*.

## Author contributions

M.K. contributed to the conception and design of the study, data collection, analysis, and drafting of the manuscript. N.I. critically reviewed and revised the manuscript. T.K., Y.O., and S.H. contributed to patient management and provided important clinical input. T.O. supervised the study and critically revised the manuscript. All authors read and

approved the final manuscript and agreed to be accountable for all aspects of the work.

## Conflicts of interest

The authors declare no conflicts of interest.

## Funding

None declared.

## Data availability

The data supporting the findings of this case report are included within the article.

## Ethical approval

Ethical approval is not required for the publication of a single case report at our institution.

## Patient consent

Written informed consent was obtained from the patient for publication of this case report and accompanying images.

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