IDCases 37 (2024) e02008

Contents lists available at ScienceDirect

IDCases

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

Case report

Slackia exigua, an emerging anaerobic pathogen – isolation from a case of polymicrobial peritonitis and review of literature☆

Mahalakshmi Kumaresan [a], Harshita Agarwal R [a], Afzal Muhammed Fysel [b], Sangitha Jayagandan [a], Rakhi Biswas [a,*], Sudharsanan Sundaramurthi [b]

[a] Department of Microbiology, Jawaharlal Institute of Postgraduate Medical Education and Research (JIPMER), Puducherry 605006, India
[b] Department of Surgery, Jawaharlal Institute of Postgraduate Medical Education and Research (JIPMER), Puducherry 605006, India

ARTICLE INFO

Keywords:
Slackia exigua
Peritonitis
Polymicrobial
Infection

ABSTRACT

Intra-abdominal infections (IAI) are surgical emergencies ranging from appendicitis to peritonitis and intra-hepatic infections. Anaerobic bacteria including *Bacteroides* spp. and *Clostridium* spp. cause 30–50 % of these infections. *Slackia exigua* (*S.exigua*) is an obligate anaerobe part of the human oral microbiota and has been associated with periodontal problems. In this report, we describe a rare occurrence of polymicrobial infection with four anaerobes including *S. exigua* in a patient with peritonitis caused by a hidden ileal perforation.

Introduction

This case report describes a 37-year-old male diagnosed with perforation peritonitis after presenting with vomiting and abdominal pain. He underwent an emergency laparotomy. The intraoperative pus sample revealed the growth of *Escherichia coli* and four other obligate anaerobes including *S. exigua*. Although clinical infections linked to Slackia species are uncommon, they have been documented in patients with underlying immunocompromising conditions. It has been linked to periodontal disorders and is difficult to identify by conventional methods. To our knowledge, this is the first case report from India. The unexpected isolation of *S. exigua* in a peritonitis case opens new possibilities for research into the pathogenic potential of oral anaerobes in extra-oral infections and emphasizes the importance of comprehensive microbial investigation in atypical cases of peritonitis. Metabolic activities and potential implications of *S. exigua* in human health and disease represent a promising avenue for further research in microbiology and gastroenterology.

Case description

A 37-year-old male without any other known co-morbidities came with complaints of vomiting and abdominal pain of one-day duration to the emergency services. The pain was sudden in onset in the peri-umbilical region; dull aching and gradually progressed to the entire abdomen. The pain aggravated with food intake and was partially relieved after vomiting. It was associated with three episodes of bilious, non-projectile and non-blood-stained vomiting. On examination, diffuse tenderness and guarding were present and bowel sounds were sluggish. He was suspected of intestinal obstruction and admitted to the Department of Surgery.

Ultrasonography (USG) of the abdomen and pelvis revealed dilated bowel loops with to and fro peristalsis suggestive of obstruction. He was immediately posted for emergency laparotomy. Intraoperatively, there was 50 ml of frank pus collection was noted in the pelvis. About 30 cm of ileal segments near the ileocecal junction were gangrenous and had several pus pockets suggesting concealed ileal perforation. The gangrenous ileal segment was resected and a double barrel ileostomy was done. A drain was placed. The patient was empirically started on intravenous injection of ceftriaxone 1 g twice a day and metronidazole 500 mg thrice a day.

The pus sample collected intraoperatively was sent to the microbiology department for bacterial culture. The sample was inoculated into 5 % sheep blood agar and MacConkey agar and incubated aerobically at 37 °C. As a routine laboratory practice, coupled with the probability of isolation of fastidious and strict anaerobes from deep-seated pus pockets, the sample was inoculated into both Brain-Heart infusion (BHI) broth and Robertson cooked meat (RCM) broth. Aerobically incubated culture plates showed growth of flat lactose fermenting colonies which were identified as *Escherichia coli* resistant to ceftazidime, ceftriaxone,

☆ All the authors have agreed to submit the case report to ID Cases journal. None of the authors have a conflict of interest.

* Corresponding author.
E-mail address: dr.rakhibiswas@gmail.com (R. Biswas).

https://doi.org/10.1016/j.idcr.2024.e02008
Received 24 April 2024; Received in revised form 29 May 2024; Accepted 4 June 2024
Available online 5 June 2024

ciprofloxacin and piperacillin-tazobactam. The isolate was sensitive to amikacin, cefoperazone-sulbactam and meropenem. Sub-cultures were done after 48 h from RCM broth onto 5 % sheep blood agar, neomycin blood agar and phenyl ethyl alcohol agar and then incubated in anaerobic conditions using the Anaero Gas Pack™ (HiMedia laboratories Pvt. Ltd., Mumbai, India).

After 48 h, multiple anaerobic organisms were isolated and were confirmed as obligate anaerobes by the aerotolerance test. Identification was done by MALDI-TOF MS (Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry, VITEK MS, Biomérieux, France) as *Bacteroides fragilis*, *Bacteroides thetaiotaomicron*, *Clostridium sporogenes* and *Slackia exigua*. The colonies of *Slackia exigua* were approximately 1 mm in diameter circular, low-convex and translucent (Fig. 1). They are biochemically inert by combining conventional tests such as catalase, indole and nitrate as described previously in the Wadsworth anaerobic bacteriology manual [1]. Gram staining of the colonies has shown discretely arranged Gram-positive bacilli (Fig. 2). The antimicrobial susceptibility profile of the isolated obligate anaerobes interpreted based on EUCAST disc diffusion breakpoints [2] is shown in Table 1. Following the culture report, the patient's antibiotic was escalated to cefoperazone-sulbactam while metronidazole was continued. The patient substantially improved. The stoma was healthy and he was discharged after 7 days without any antibiotics. On review, the patient had no complaints and the sutures were removed.

Review and discussion

Intra-abdominal infection (IAI) can range from diverticulitis and appendicitis to intra-abdominal abscess and peritonitis to intrahepatic infections. IAIs are frequent surgical emergencies that contribute globally to non-trauma mortality. Bacterial variables include virulence factors and oxygen requirement which impact the shift from contamination to infection, thus determining the pathophysiology of IAIs. Bacterial activation causes granulocyte transmigration, which results in increased permeability, edema and protein-rich peritoneal exudates [3]. Intra-abdominal infections are typically polymicrobial in nature. Amongst the anaerobes, *Bacteroides* spp. and *Clostridium* spp. are responsible for 30–50 % of these infections. Nonetheless, a large number of anaerobes remain unidentified [4]. According to Lee et al., the standard identification approach properly identifies anaerobic bacteria only up to 79.4 % at the genus level and 60.1 % at the species level [5].

Slackia exigua is an obligate anaerobic non-spore-forming Gram-positive bacillus belonging to the family Coriobacteriaceae [6–8]. This bacterium was designated as *Eubacterium exiguum* by Poco et al. in 1996

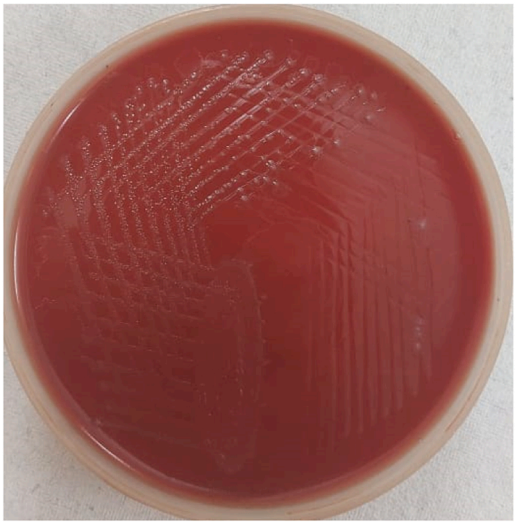

Fig. 1. Colony appearance of *Slackia exigua* on phenyl ethyl alcohol agar.

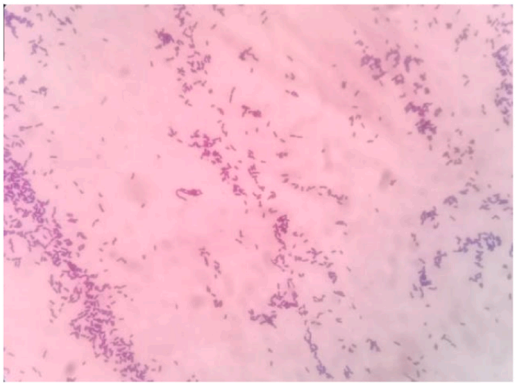

Fig. 2. Gram stain of *Slackia exigua* showing Gram-positive bacilli.

but again it was reclassified and renamed as *S. exigua* by Wade et al. in 1999 to commemorate Geoffrey Slack, a famous microbiologist and dentistry researcher. *S. exigua* is a member of the human oral microbiota and has previously been linked to periodontal disorders [8]. Other Slackia species include *S. equolifaciens*, *S. faecicanis*, *S. heliotrinireducens*, *S. piriformis* and *S. isoflavoniconvertens* [9,10].

S. exigua may be distinguished from the other species of Slackia based on phenotypic traits and specific enzymatic and physical traits. Kim et al., have used API Rapid ID 32 A and API ZYM systems for biochemical characterization. The arylamidases for alanine, glycine, histidine, leucine, phenylalanine, proline, serine, tyrosine, and valine are present in *S. exigua* and *S. heliotrinireducens*, but not in *S. faecicanis* and *S. isoflavoniconvertens*. The nitrate-positive status of *S. faecicanis* allows for the differentiation of the last two species. *S.heliotrinireducens* has a coccal form, but S. exigua has a rod-like shape.[10] The physiological and metabolic properties of *S. exigua* are thought to play a role in the gut microbiota of humans and other animals. It was suggested that it may benefit host health by promoting the production of short-chain fatty acids (SCFAs) in the gut. SCFAs are important nutrients for colonocytes and have been linked to various health benefits, including the prevention of colonic inflammation and the regulating of energy metabolism [11].

S. exigua can thrive on various complex substrates including peptone, yeast extract and casamino acids. It has been demonstrated that fermentation of diverse substrates produces short-chain fatty acids (SCFAs) mainly acetate and propionate [11]. Since they are asaccharolytic, amino acids are crucial metabolic substrates for nutrition. Especially, arginine and lysine which are created by the enzymatic breakdown of peptides by proteinases that resemble trypsin [12]. *S. exigua* is catalase-negative, galactosidase-positive and esculin hydrolysis-positive [13].

Based on its distinct protein profile, *S. exigua* was identified using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS). Using the direct transfer approach by MALDI-TOF MS, we were able to identify *S. exigua* in our patient. Compared to 16S rRNA sequencing, MALDI-TOF MS offers a quick, affordable, and precise evaluation of microorganisms down to the species level and the turnaround time for final identification was significantly reduced, going from one to two days to minutes. MALDI-TOF MS is essential and useful for detecting bacteria that are challenging to cultivate Accurate identification of *S. exigua* by MALDI-TOF-MS has been mentioned in studies and is valuable for research and therapeutic applications [14–16].

S. exigua is a relatively newly discovered bacterium and certain case reports indicate that it may have a role in various illnesses, particularly in immunocompromised people [13]. Clinical salivary samples from adults and children were examined in a study by Shen C., et al. to determine if *S. exigua* could be detected by real-time PCR. They had amply shown that *S. exigua* was more prevalent amongst pediatric

Table 1
Antibiotic susceptibility profile of the obligate anaerobes isolated from the case of Polymicrobial anaerobic peritonitis.

Organisms Antibiotics	S (mm)	R (mm)	*Bacteroides fragilis*	*Bacteroides thetaiotaomicron*	*Clostridium sporogenes*	*Slackia exigua*
Clindamycin (2 μg)	≥ 10	< 10	S	S	-	-
Meropenem (10 μg)	≥ 28	< 28	S	S	-	-
Metronidazole (5 μg)	≥ 25	< 25	S	S	-	-

S – Susceptible breakpoint; R- Resistant breakpoint; '-' → No Kirby-Bauer's disc diffusion breakpoints available in the EUCAST for the corresponding organisms.

patients than adults. Additionally, they demonstrated a significant correlation between the prevalence of this organism and orthodontic brackets. They are most closely associated with children who receive orthodontic care [17].

S. exigua has been isolated from the blood of bacteremic patients with neutropenia, diabetes, cancer and hematopoietic stem cell transplantation. It has also been discovered in various infections such as lung, pilonidal, abdominal and breast abscesses and meningitis following mastoiditis [6,7,10,16]. It is known to cause polymicrobial infections with other obligate anaerobes.[10,16] The most recently published case report of subdural empyema with *S. exigua* and *Campylobacter rectus*, a microaerophilic pathogen was found during autopsy [18].

Though *S. exigua* infections are rare, they can be severe and difficult to treat. The antibiotic susceptibility of *S. exigua* is not well established, but the organism is generally thought to be susceptible to penicillin, cephalosporin and metronidazole [12]The antibiotic susceptibility profile of rare anaerobic bacteria interpreted based on EUCAST guidelines by Wolf et al. has shown 75 % susceptibility to penicillin and 100 % susceptibility to ampicillin-sulbactam, piperacillin-tazobactam, imipenem, meropenem, moxifloxacin, metronidazole, clindamycin and tigecycline [19].

Conclusion

This case highlights the emergence of polymicrobial anaerobic peritonitis including anaerobes like *Slackia exigua* in a patient with concealed ileal perforation. The identification of *S. exigua* emphasizes the importance of using advanced microbiological techniques in characterizing uncommon microbial organisms. Further research in this area to elucidate the clinical significance of this infection is warranted. The antibiotic susceptibility patterns of *S. exigua* can be explored considering its potential role in severe infections especially in immunocompromised patients. Practicing clinicians should maintain vigilance for infection with such rare anaerobic organisms to guide appropriate strategies in patient management. This case report signifies the importance of a multidisciplinary approach in addressing complex intra-abdominal infections ensuring optimal patient outcomes.

Ethics approval

Consent is guaranteed from all involved in this case report.

Source of funding

No funding was received concerning this case report.

CRediT authorship contribution statement

Mahalakshmi Kumaresan: Writing – original draft, Visualization, Validation, Software, Resources, Methodology, Investigation, Data curation, Conceptualization. **Harshita Agarwal R:** Writing – review & editing, Resources, Investigation, Data curation. **Afzal Muhammed Fysel:** Writing – review & editing, Resources, Investigation. **Sangitha Jayagandan:** Writing – review & editing, Visualization, Validation. **Rakhi Biswas:** Supervision, Software, Resources, Methodology, Investigation, Data curation. **Sudharsanan Sundaramurthi:** Writing – review & editing, Visualization, Validation, Supervision, Resources, Investigation.

Disclosure/Conflict of Interest Statement

- None of the authors of this paper has a financial or personal relationship with other people or organizations that could inappropriately influence or bias the content of the paper.
- It is to specifically state that "No Competing interests are at stake and there is No Conflict of Interest" with other people or organizations that could inappropriately influence or bias the content of the paper.

Acknowledgement

None.

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