A young child with acute perforated appendicitis due to *Comamonas kerstersii*: a rare case report

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**Abstract**

*Comamonas* species are rarely associated with human infections. Recent reports found that *Comamonas kerstersii* was associated with severe diseases such as abdominal infection and bacteremia. However, *Comamonas kerstersii* may be confused with *Comamonas testosteroni* using the automatic bacterial identification systems currently available. An 8-year-old boy who had a right iliac fossa pain and classic migration of pain at the temperature of 38.9°C. The positive strain of aerobic and anaerobic bottles of blood cultures was identified. The patient was diagnosed as acute appendicitis.
Peritonitis and perforated appendix with abdominal abscess. The bacterium was identified by routine methods, MALDI-TOF-MS. The patient was treated with exploratory laparotomy, appendectomy, tube drainage, and prescribing antibiotic treatment. The patient was discharged with complete recovery. The organisms were confirmed as Comamonas kerstersii by MALDI-TOF MS and a combination of the other results. Our findings suggest that Comamonas kerstersii infection occurs most often in association with perforated appendix and bacteremia. We presume that Comamonas kerstersii is an opportunistic pathogen or commensal with the digestive tract and appendix bacteria.

**Introduction**

The genus Comamonas was originally created in 1985, and it included a single species, *C. terrigena*. In 1987, *C. testosterone* and *C. acidovorans* were reclassified as members of the Comamonas genus. *C. acidovorans* was subsequently reclassified as Delftia acidovorans on the basis of its 16S rRNA gene sequence in 1999. Comamonas kerstersii (*C. kerstersii*) was described as one of three genotypically separate groups of *C. terrigena* in 2003. Now, Comamonas genus contains 17 species including *C. terrigena*, *C. aquatica*, *C. kerstersii*, *C. testosterone*, *C. denitrificans*, *C. nitrativorans*, *C. koreensis* and other [1]. Comamonas species have a wide geographic distribution and are commonly found in soil, plants, animal, water saprophytes, and in humidifier reservoir water. *C. kerstersii* infection could originate from the water that the patient drank in the countryside [2].

Comamonads are Gram-negative, nonfermenting, oxidase and catalase-positive bacteria that are motile largely because of the presence of polar flagella [1]. Comamonas species have rarely been associated with infection in humans despite their ubiquitous distribution in the environment, possibly because of the difficulty in accurately distinguishing Comamonas species from Pseudomonas species in the pre MALDI-TOF era [3]. However, in recent years, several publications have incriminated *C. testosterone* and *C. kerstersii* in human diseases, including severe invasive infections, such as abdominal infection and bacteremia [4]. *C. kerstersii* may be confused with *C. testosterone* because of the difficulties in accurately identifying it using the automatic bacterial identification systems currently available. Some important biochemical tests, matrix assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF-MS) and gene sequencing by polymerase chain reaction (PCR) amplification of the 16S rRNA can confirm the specific Comamonas species [4]. We report a rare case of a young child with acute perforated appendicitis due to *C. kerstersii*.

**Patient and observation**

**Patient information:** an 8-year-old boy presented to the emergency department of our hospital with onset of right iliac fossa pain followed by nausea and vomiting at a temperature of 38.9°C with bowel obstruction.

**Clinical findings:** his white blood cell was 18.91*10³/L, and differential white blood count were: neutrophils 89.2%, lymphocytes 6.1%, monocytes 4.6%, eosinophils 0%. A follow-up visit revealed that he was diagnosed with acute peritonitis and perforated appendix with abdominal abscess. He was discharged with complete recovery after exploratory laparotomy, appendectomy, and tube drainage.

**Diagnostic assessment:** a microscopic examination of peritoneal pus showed small numbers of Gram-negative bacilli that were plated into Colombia blood agar, MacConkey, nutrition agar and chocolate agar (Figure 1). The colonies grew to a diameter of 1.5 mm on blood agar and on nutrient agar in ambient air. They were white, smooth, and nonadherent, and they had entire edges (Figure 2). Other tests showed that oxidase and catalase activities were positive. After 24 h of incubation at 36°C in ambient air, colonies on the blood agar plate were identified by MALDI-TOF as *C. kerstersii*.
and Escheria coli. An antibiogram with disc showed a multi sensitive profile (Figure 3).

Therapeutic intervention: the patient received 3 days of intravenous amoxicillin-clavulanic acid, gentamicin, and metronidazole and was discharged on oral amoxicillin-clavulanic acid.

Follow-up and outcomes: he made a full recovery.

Discussion

Since 1987 [5-9], 34 patients infected with C. testosterone around the world have been reported: 16 with bloodstream infections, 10 with abdominal cavity infections, 8 with other kinds of infections. Among these, Gul et al. were the first to report C. testosterone from the blood cultures of a 22-year-old man with a perforated appendix in Turkey, and the organism was identified by Mini API to be sensitive to all antibiotics tested [9]. Tsui et al. presented 2 strains from bacteremia identified by the Phoenix 100 system in 2011: a 54-year-old alcoholic patient with left leg cellulitis and a 73-year-old male with chronic hepatitis B infection, liver cirrhosis, and hepatocellular carcinoma after transarterial embolization. The 2 strains were sensitive to a broad range of antibiotics, including all tested cephalosporins and quinolones [10]. Opota et al. also commented that there were 32 Comamonas sp. Strains and 38 D. acidovorans strains isolated from 1997 to 2013 in his hospital, which were isolated primarily from respiratory tract samples (33%), urogenital tract samples (23%), and digestive tract samples (21%), while bacteremia represented 5% (3 patients) of the cases [11]. In the four cases reported by Almuzara and colleagues, the C. kerstersii strains were isolated from intraabdominal infections [12]. In 12 other patients in the 2010-2015 period, C. kerstersii was isolated from the abdominal fluid of patients with diagnosed acute peritonitis. In most of them, it was the result of a gangrenous appendix or perforated appendicitis. In all cases, C. kerstersii was isolated with accompanying flora in patients between 18 and 84 years old. The clinical progress of all patients was favorable. In this work, they highlighted the isolation of this species from a localized intra-abdominal infection: a psoas abscess of potential renal origin in a diabetic patient [13]. In a series of 42 cases of psoas abscesses studied by Wong et al. [14], the most common causative organism for a primary psoas abscess was methicillin-susceptible Staphylococcus aureus, while for abscesses originating in the gastrointestinal or urinary tract it might be polymicrobial [15]. In another case, the peritonitis infection might have ascended from the vagina through the fallopian tubes because this patient had salpingitis [16]. This source of infection has been described in a previously healthy 31-year-old woman.

Salpingitis involves inflammation of the fallopian tube. It usually presents as acute abdomen, and because appendicitis usually includes the same symptoms, salpingitis diagnosis may be delayed until the appendix is surgically explored [16]. Salpingitis, mainly reported in sexually active women, is usually caused by sexually transmitted microorganisms, such as Neisseria gonorrhoeae and chlamydia trachomatis [17], although other microorganisms that colonize the lower genital tract can ascend to the endometrium, producing endometritis, salpingitis and peritonitis. The polymicrobial etiology of acute salpingitis has been well documented [17], showing that anaerobes (Peptostreptococcus and Bacteroides spp.), Enterobacteriaceae (E. coli) and aerobic streptococci are the most frequently isolated microorganisms [17]. Moreover, infrequent microorganisms like Edwardsiella tarda and Plesiomonas shigelloides [18] have also been implicated in salpingitis. However, to our knowledge, the isolation of C. kerstersii has not previously been reported in this type of infection. To date, there are only few cases of C. kerstersii reported in the literature [11]. All of the C. kerstersii isolates were identified by MALDI-TOF-MS, which is a rapid and accurate method to differentiate between Comamonas species. Some tests can also differentiate C. kerstersii from other Comamonas species according to schemes proposed by Wauters et al. [19] such as sensitivity to colistin and
deferoxamine, nonuse of testosterone, a negative pyrrolidone arylamidase test, growth at 42°C, and a positive tyrosine hydrolysis. Drug sensitivity tests showed that the isolates were sensitive to a broad range of antibiotics. Among the 9 cases reported by Smith MD et al. 2 were identified in bacteremia patients with diverticulosis and perforated appendixes and the predominant source of infection were in the peritoneal fluid of the abdominal cavity [2]. The main clinical diagnosis of these patients is perforated appendix, followed by sigmoid perforation and diverticulosis, which demonstrates the association of C. kerstersii with severe diseases.

Aside from the previously reported cases of C. testosterone infections, Opota et al. [11] reported the first C. kerstersii bloodstream infection in a patient with diverticulosis. C. kerstersii bacteremian is usually associated with patients with acute perforated appendixitis. Comamonas species infection has been associated with exposure to contaminated fish tank water or exploration of the abdominal cavity [2]. Thus, we presume that C. kerstersii is an opportunistic pathogen or commensal with the digestive tract and appendix bacteria. Almuzara et al. were the first to describe the urinary tract infection due to C. kerstersii [13]. In view of the finding of this unusual pathogen as a potential cause of urinary tract infection, they looked for this microorganism in the patient’s faeces, but only a few colonies of C. kerstersii were found in a culture mainly containing Escherichia coli. C. kerstersii growth in pure culture of more than 105 CFU/mL in urine culture, the presence of leukocyturia and the intestinal colonization associated with clear clinical and radiologic signs of pyelonephritis in this patient pointed to C. kerstersii as the etiologic agent of this infection; the ascending path was the most likely route of infection. They highlighted the possibility of C. kerstersii isolation from extraintestinal sites. Therefore, the isolation of C. kerstersii from urinary tract infections broadens the spectrum of infections caused by this microorganism. C. kerstersii has long been considered nonpathogenic on the basis of a lack of association with severe infections. This could be explained in part by the recent description of this species and the difficulties in accurately identifying it. The first report of polymicrobial bacteremia involving C. kerstersii reveals that this organism can be involved in severe diseases. C. kerstersii pathogenicity could be due to the versatility of this organism, which enables it to grow under various conditions. This report highlights the usefulness of MALDI-TOF for the rapid and accurate identification of nonfermenting Gram-negative bacteria that were difficult to identify in the pre-MALDI-TOF era. This could help to redefine the epidemiology and clinical syndromes due to these organisms.

Conclusion

Comamonas is a group of ubiquitous bacteria present in various natural and engineered environments. Some of them are also involved in a number of clinical cases. It has been suggested that Comamonas strains may share specific genomic features at the genus level and play certain ecological roles to different habitats. The pan-genomic analysis shows the diverse genomic features that contribute to the wide adaptation of the genus to various environments. The core genome reveals central metabolic pathways that enable Comamonas to utilize various nutrient sources and store excess resources. The conserved dissimilatory and assimilatory nitrate reductases in Comamonas explain their presence in nitrate reducing environments and suggest an important role in the nitrogen biogeochemical cycle. They also encode sophisticated redox sensory systems and effective c-di-GMP controlling systems, allowing them to adjust their biofilm lifestyle under dynamic conditions. The virulence factors in Comamonas are found to be highly species-specific. The conserved mechanisms for potentially pathogenic Comamonas are related to surface adherence, motility control, nutrient acquisition and stress tolerance. In summary, C. kerstersii, infection occurs most often in association with severe diseases, such as perforated appendix and bacteremia. This strain is always sensitive to a
broad range of antibiotics. *C. kerstersii*, which has undergone extensive reclassification, was isolated from our patient as part of a polymicrobial growth from peritoneal fluid. MALDI-TOF appeared to be a reliable tool for identifying these organisms. We emphasize that the isolation of *C. kerstersii* from free fluid in the abdominal cavity and a perforated appendix are indications of intra-abdominal infection. However, *C. kerstersii* is easily confused with *C. testosterone* by automatic bacterial identification systems currently available on the market. Overall, MALDI-TOF-MS and gene sequencing are a more accurate approach to identify the species than others. Further research is required to clarify the origins of this organism.

**Competing interests**

The authors declare no competing interests.

**Authors' contributions**

Assia El Ouaradi, Nabila Soraa and Asmaa Lamrani Hanchi contributed to conception and design, acquisition of data, analysis and interpretation of data, drafting the article and revising it critically for important intellectual content and final approval of the version to be published. All authors read and agreed to the final manuscript.

**Figures**

**Figure 1**: a microscopic examination of peritoneal pus showing small numbers of *Gram-negative bacilli*

**Figure 2**: the colonies grew to a diameter of 1.5mm on blood agar and on nutrient agar in ambient air; they were white, smooth, and nonadherent, and they had entire edges

**Figure 3**: an antibiogram with disc showing a multi sensitive profile

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