First report of *Comamonas kerstersii* causing urinary tract infection

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**Abstract**

The association of *Comamonas kerstersii* with peritonitis resulting from perforated appendix and its isolation from a psoas abscess and pelvic peritonitis have previously been described by us. We present the first case of *C. kerstersii* urinary tract infection, broadening the spectrum of infections caused by this species.

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**Keywords:** *Comamonas kerstersii*, emerging pathogen, psoas abscess, secondary peritonitis, urinary tract infection

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*Comamonas* spp. are nonfermenting Gram-negative bacilli of the *Comamanadaceae* family. The genus includes 22 species. Mainly *Comamonas testosteroni* and *Delftia (Comamonas) acidovorans* have been implicated in human infections [1]. However, an increase in the number of reports of human infections by another species, *Comamonas kerstersii*, described in 2003 by Wauters et al. [2], has recently been observed [3,4]. In this sense, the use of new and revolutionary methodologies for bacterial identification in routine laboratory practice, such as matrix-assisted desorption ionization—time of flight mass spectrometry (MALDI-TOF MS) [5,6], could explain the increase in the frequency of isolation of this species reported in the literature in recent years [3,4,7,8].

A previously healthy 5-year-old girl with no history of urinary tract infection but with abdominal and low back pain, fever and vomiting was hospitalized to rule out an acute surgical abdomen. The physical examination and the abdominal ultrasound revealed nothing abnormal, but the patient had persistent fever, abdominal pain and positive fist percussion. Therefore, pyelonephritis was diagnosed. A peripheral venous blood sample collected at admission showed white blood cell count 24,900/mm³ (with 83% neutrophils), haematocrit 38%, haemoglobin count 12.4 g/dL, platelet count 286,000/mm³, erythrocyte sedimentation rate 86 mm, blood urea nitrogen level 2.1 mg/dL and creatinine level 0.5 mg/dL. In addition, a kidney ultrasound revealed both kidneys had preserved shape, size and structure, although an 8.1 mm left pyelocalyceal dilatation was observed.

Microscopic analysis of urine revealed 20 leukocytes per high-power field, four erythrocytes per high-power field and two epithelial cells per high-power field. The microorganism was identified as *Comamonas kerstersii* by MALDI-TOF MS using a Microflex LT instrument with Bioterpy 3.1 software (Bruker Daltonics, Bremen, Germany), with a spectral score of 2.134. Phenotypic identification was confirmed by molecular identification (amplification and subsequent sequencing of the gyrB gene) using the primers described by Tayeb et al. [9]. gyrB gene sequence analysis revealed 99% identity with the gyrB sequence of *Comamonas kerstersii* (GenBank accession no. KC714047).
| Case No. | Age/Year | Sex | Site of infection | Clinical presentation | Underlying disease | Predisposing conditions | Identified pathogens | Antibiotic treatment | Reference |
|---------|----------|-----|------------------|----------------------|-------------------|-------------------------|----------------------|---------------------|-----------|
| 1       | 43       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam followed by piperacillin/tazobactam and then meropenem | [7]       |
| 2       | 48       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 3       | 10       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam followed by piperacillin/tazobactam and then meropenem | [7]       |
| 4       | 21       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam followed by piperacillin/tazobactam and then meropenem | [7]       |
| 5       | 65       | M   | Blood            | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 6       | 12       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 7       | 10       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 8       | 9        | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 9       | 54       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 10      | 15       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 11      | 36       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 12      | 61       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 13      | 40       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 14      | 38       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 15      | 18       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 16      | 21       | F   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 17      | 84       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 18      | 18       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 19      | 19       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 20      | 35       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 21      | 67       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 22      | 63       | M   | Peritoneal fluid | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
| 23      | 5        | F   | Urine            | Septic shock, diarrhea | No underlying disease | Purulent peritonitis, sepsis | Escherichia coli, Bacteroides fragilis, Comamonas kerstersii | Ampicillin/sulbactam, ciprofloxacin and then amoxicillin/clavulanic acid | [7]       |
The minimal inhibitory concentration (μg/mL) using the VITEK 2 System (AST-082 panel; bioMérieux, Marcy l’Etoile, France) was as follows: ampicillin 16; Amoxicillin/sulbactam (AMS) ≤ 2; cephalothin ≤ 2; piperacillin-tazobactam ≤ 4; cefotaxime 2; cefazidime 2; cefepime 8; imipenem ≤ 0.25; meropenem ≤ 0.25; amikacin 16; gentamicin 8; ciprofloxacin ≤ 0.25; Trimethoprim/sulfamethoxazole (TMS) ≤ 2; colistin ≤ 0.5. The minimal inhibitory concentration results were interpreted using Clinical and Laboratory Standards Institute categories [10].

With the report of growth of a nonfermenting Gram-negative bacillus, antibiotic therapy was changed to piperacillin-tazobactam 200 mg/kg per day provided intravenously every 8 hours for a 10-day period. The patient had a favourable progress and was therefore discharged, completing a 14-day treatment with oral amoxicillin/clavulanic 50 mg/kg per day.

The association of Comamonas kerstersii with peritonitis resulting from the presence of perforated appendix has previously been described by us [7]. Recently, other authors have also reported new cases of intra-abdominal infections due to perforated appendix [3], as well as the first case of bacteraemia by C. kerstersii in a 65-year-old patient with signs of diverticulosis [4]. In addition, we have recently pointed out the isolation of this microorganism, not previously described in the literature, from two forms of unusual infection presentations: psoas abscess and pelvic peritonitis [8]. The increase in C. kerstersii isolation frequency from human infections in the literature points at it as an emerging pathogen (Table 1). These findings suggest that infections caused by C. kerstersii could be underestimated because identification of isolates using only conventional phenotypic methods does not allow accurate determination of the genus. In the pre-MALDI-TOF MS era, the identification of Comamonas isolates was only achieved by phenotypic methods, which do not allow differentiation among species of genus [7].

The use of mass spectrometry in routine bacterial identification has revolutionized microbiology. The potential for identification at the species level within minutes makes MALDI-TOF MS an ongoing revolution in the clinical microbiology laboratory [5]. MALDI-TOF MS is a powerful tool not only for routine bacterial identification but also for identification of rare bacterial species implicated in human infectious diseases [6]. In this regard, we have recently demonstrated the ability of MALDI-TOF MS to identify 29 genera of nonfermenting Gram-negative bacilli, including uncommon species. Specifically, C. kerstersii isolates (n = 10) included in our study were correctly identified at the species level [11]. In agreement with Opota et al. [4], we consider that the use of this revolutionary methodology could help establish the epidemiology and clinical impact of this species.

Here we describe the first case of urinary tract infection due to C. kerstersii. In view of the finding of this unusual pathogen as a potential cause of urinary tract infection, we 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. Comamonas kerstersii growth in pure culture of more than 10^5 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 aetiologic agent of this infection; the ascending path was the most likely route of infection.

Comamonas kerstersii isolation from the stool of patients with gastroenteritis has recently been reported by us [8] and by other authors [3], indicating a potential intestinal carriage resulting from environmental exposure.

We highlight 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.

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Conflict of interest

None declared.

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