Cystitis Caused by *Aeromonas caviae*▼

Khalifa Al-Benwan,1 Sharon Abbott,2 J. Michael Janda,2 Geert Huys,3 and M. John Albert4*

Department of Microbiology, Al-Amiri Hospital, Kuwait City, Kuwait; Microbial Diseases Laboratory, California Department of Health Services, Richmond, California; Laboratory of Microbiology, Faculty of Sciences, Ghent University, Ghent, Belgium; and Department of Microbiology, Faculty of Medicine, Kuwait University, Kuwait City, Kuwait

Received 4 March 2007/Returned for modification 22 March 2007/Accepted 14 May 2007

*Aeromonas* sp. organisms rarely cause urinary tract infection. We report for the first time a case of urinary tract infection caused by *A. caviae* in an adult patient with a history of increased frequency of urination, dysuria, hematuria, and weight loss.

CASE REPORT

A 39-year-old Bangladeshi male presented to the emergency department of Al-Amiri Hospital, Kuwait, with a 2-month history of increased frequency of urination, dysuria, hematuria, and weight loss of 7 kg. Seven weeks earlier, he was treated with amoxicillin for 5 days by his general practitioner. But despite the therapy, his symptoms deteriorated.

On examination, the patient was afebrile (37°C) with normal vital signs for his age. His suprapubic area was tender. Ultrasonography of the abdomen and pelvis revealed generalized and irregular thickening (4 to 5 mm) of the wall of the urinary bladder suggestive of cystitis. A chest X-ray was normal. Hematological examination revealed a hemoglobin level of 153 g/liter, a white-cell count of 7.7 × 10^9/liter, and an erythrocyte sedimentation rate of 3 mm/h (all values were within the normal range). The biochemical profile revealed an alane aminotransferase level of 57 mg/liter, alkaline phosphatase level of 76 IU/liter, creatinine level of 80 μmol/liter, and blood urea level of 2.6 mmol/liter (all were within the normal ranges). Stool culture was negative for *Aeromonas* spp., *Salmonella* spp., *Shigella* spp., and *Campylobacter* spp.

The urine analysis showed an erythrocyte level of 30/hpf and a leukocyte level of 4/hpf. The urine sample was plated on cystine-lactose-electrolyte-deficient agar, MacConkey agar, and incubated at 37°C. After 24 h, pure growth of smooth, gram-negative, motile bacillus and was catalase and oxidase positive. The API-20E identification strip (bioMérieux, Marcy l’Etoile, France) profile obtained (3006126) identified LMG 24107 as either *Vibrio flavidus* or *Aeromonas caviae* with differential tests of growth in KCN and growth without salt for *A. caviae*. Results of further biochemical characterization as described previously (1) are shown in Table 1. The extensive biochemical characterization of the isolate indicated that the isolate was not *V. flavidus* (growth without salt supplementation and growth in KCN broth) and was, in fact, *A. caviae*. Next, we performed molecular identification of the isolate by sequencing of the 16S rRNA and gyrB genes. Bacterial DNA was extracted by the cetyltrimethylammonium bromide method (10) for 16S rRNA sequencing and by the method of Pitcher and colleagues (9) for gyrB sequencing. The entire 16S rRNA gene was amplified by the primer pair S-D-Bact-0008-a-S-20 F (‘5’AGAGTTTGATCCTGGCTCAG3’) and S-Univ-1492-b-A-21R (‘5’ACGCTACCTTGTTACGACTT3’) as described previously (11). A gyrB fragment of approximately 1,100 bp was amplified using the primers gyrB3F and gyrB14R and sequenced using the same primers and additional primers gyrB7F, gyrB9R, and gyrB9Rs as described previously (12), using the following temperature program: initial denaturation at 95°C for 4 min, 30 cycles of denaturation at 94°C for 30 s, annealing at 55°C for 30 s, and elongation at 72°C for 60 s, and a final extension at 72°C for 7 min. The 16S rRNA and gyrB amplicons were sequenced in both directions using the BigDye v3.0 Ready Reaction cycle sequencing kit (Applied Biosystems, Foster City, CA) in an ABI PRISM 3100 Avant genetic analyzer (Applied Biosystems). Sequences were compared with the GenBank database using the BLAST program of the National Center for Biotechnology Information. Based on its 16S rRNA gene sequence, isolate LMG 24107 was confirmed as an *Aeromonas* member, but it could not be reliably assigned to a known species in this genus (data not shown). In contrast, partial gyrB sequence analysis indicated that LMG 24107 belonged to *A. caviae* DNA hybridization group 4 (HG4) as the first-choice identification based on highest gyrB sequence similarities with *A. caviae* HG4 strains LMG 3755 (GenBank accession no. AY 101794; 99.0% sequence similarity) and LMG 3775T (GenBank accession no. AY 101783; 97.6% sequence similarity).

The antimicrobial susceptibility of LMG 24107 was studied using Mueller-Hinton agar (Oxoid) by the disk diffusion method according to NCCLS recommendations (8). The isolate was susceptible to ciprofloxacin, cefotaxime, and gentamicin and resistant to amoxicillin, cotrimoxazole, ampicillin, ceftaroline, and cephalothin.

▼Published ahead of print on 23 May 2007.
HEp-2 cell adherence (6) and agglutination of human group O erythrocytes (3) of the isolate were studied as described previously. The isolate showed weak adherence to the HEp-2 cells but strong agglutination of erythrocytes.

The patient was given oral ciprofloxacin, 500 mg every 12 h, for 2 weeks. This resulted in improvement of hematuria, dysuria, and frequency. A repeat urine culture after completion of the antibiotic therapy did not grow any bacteria. The patient remained well during the 3-month follow-up.

This is a clear case of urinary tract infection due to *A. caviae*.

Even though the API 20E profile identified LMG 24107 as *V. fluvialis/A. caviae*, detailed biochemical reactions identified it as *A. caviae*. Whereas 16S rRNA gene sequencing failed to place LMG 24107 in a specific *Aeromonas* species, *gyrB* sequencing confirmed the biochemical identification result and placed the isolate in HG4 of *A. caviae*. Collectively, these results thus reinforce the need for a polyphasic approach towards the accurate identification of clinical aeromonads at the hybridization group level. In addition, this case study further documents the usefulness of *gyrB* as an alternative molecular marker for the 16S rRNA gene (12), which does not allow unambiguous identification of all *Aeromonas* species due to its intragenomic heterogeneity (7).

*Aeromonas* sp. organisms rarely cause urinary tract infections. To our knowledge, there are three cases reported in the English-language articles, caused by *A. hydrophila* (2), *A. veronii* biotype sobria (4), and *A. popoffii* (5). The present report is the first case of urinary tract infection due to *A. caviae*. Our patient was otherwise apparently healthy. In other cases, there were underlying abnormalities. For example, one patient had congenital spine bifida, and therefore, urination was helped with an indwelling urethral catheter (5); another was a newborn baby with bladder and bilateral renal dilation suggestive of urethral valve involvement (2); and the third was a 69-year-old diabetic patient (4). The common feature in all these cases was leukocyturia and bacteruria, and the urine pathology resolved with proper antimicrobial therapy in all cases.

*Aeromonas* sp. organisms produce a number of putative virulence factors. In the case of *Escherichia coli*, which is a bona fide urinary pathogen, the two known virulence factors are fimbriae and hemolysin. We found our isolate to be hemolysin negative, since the colonies were nonhemolytic on blood agar, but positive for hemagglutination and adherence to HEp-2 cells. The last two properties are suggestive of possession of fimbriae by the isolate and would have contributed to the virulence of the isolate.

**Nucleotide sequence accession number.** The nucleotide sequence of the *gyrB* gene determined in this study has been submitted to the EMBL/GenBank sequence databases and assigned the accession no. AM710394.

G. Huys is a postdoctoral fellow of the Fund for Scientific Research-Flanders, Flanders, Belgium (F.W.O.-Vlaanderen). We thank S. Haridas, M. Cnockaert, and R. Coopman for assistance with the sequencing work.

**REFERENCES**


