Actinobaculum schaalii can cause urinary tract infections and septicemia but is difficult to identify by cultivation. To obtain a fast diagnosis and identify A. schaalii, we developed a TaqMan real-time quantitative PCR. Routine urine samples were obtained from 177 hospitalized patients and 75 outpatients in Viborg County, Denmark, in 2008–2009. The PCR detected A. schaalii in 22% of samples from patients >60 years of age. This assay showed that A. schaalii is more common than implied by routine cultivation. In 90% of PCR-positive urine samples, other common uropathogens were identified. This finding suggests that A. schaalii is a common, undetected, bacterial pathogen. Our results suggest that A. schaalii may be a more common pathogen than previously thought, especially in patients with unexplained chronic urinary tract infections, who are often treated with trimethoprim or ciprofloxacin, to which A. schaalii is resistant.

Actinobaculum schaalii was first described in 1997 and named after Klaus P. Schaalii, a German microbiologist specializing in actinomycete microbiology. The genus Actinobaculum includes A. schaalii, A. suis, A. massiliae, and A. urinale and is closely related to the genera Actinomyces and Arcanobacterium (1).

These bacteria are small, gram-positive, facultative anaerobic, CO2-requiring coccolid rods. They grow as dimorphic gray colonies <1 mm in diameter, are nonmotile and non–spore forming, and show weak β-hemolysis on agar plates containing 5% horse or sheep blood after 3–5 days of growth. They are catalase, oxidase, and urease negative and resistant to trimethoprim and ciprofloxacin (2). Their habitat is probably the human genital or urinary tract (1).

Because of its slow growth and resemblance to the normal bacterial flora on skin and mucosa, A. schaalii is often overlooked or considered a contaminant. Furthermore, it is often overgrown by faster-growing commensal and pathogen bacteria. Most laboratories incubate urine samples only overnight in ambient air, which further impedes isolation of A. schaalii (2).

Difficulties identifying A. schaalii by using traditional phenotypic tests have obscured its pathologic role for many years. However, A. schaalii can cause urinary tract infections (UTIs), some of which lead to serious illnesses such as urosepsis, osteomyelitis, and septicemia, mainly among the elderly and patients predisposed to UTIs (1–6). We developed a TaqMan real-time quantitative PCR (qPCR) specific for the gyrase B (gyrB) gene for fast and sensitive detection of A. schaalii from urine and blood samples.

Materials and Methods

Patient and Control Groups

From October 2008 through January 2009, a total of 252 routine urine samples were randomly selected from patients of all ages from 3 hospitals and 150 medical practitioners in Viborg County, Denmark (population ≈230,000 persons). Seventy percent of patients were from hospitals. Urine collection was midstream, from bedpans, from catheters, or unspecified in 41%, 19%, 18%, and 21% of cases, respectively. A total of 38 control urine samples were obtained from patients before they underwent elective surgery of hips or knees. These patients were 63–81 years of age and had negative results for leukocyte esterase and nitrate by a urine dipstick test (Roche Diagnostics Ltd., Burgess Hill, UK).
Cultures and Wet Smear Microscopy of Urine Samples

Samples tested by using PCR were simultaneously analyzed by using standard laboratory tests. These tests were wet smear microscopy and incubation on 5% Columbia sheep blood agar (Becton Dickinson, Heidelberg, Germany) in an atmosphere of 5% CO2 at 35°C for 1 or 2 days.

Extraction of DNA

Bacteria were incubated anaerobically on 5% Columbia sheep blood agar in an atmosphere of CO2 at 35°C for 2 days before harvesting. DNA was purified by taking a swab of bacteria from the agar plate and transferring it to 1 mL of saline. The DNA from bacteria was extracted from 800 µL of saline by using the Kingfisher mL magnetic particle processor (Thermo Electron Corporation, Waltham, MA, USA) according to the manufacturer’s instructions, eluted in 100 µL elution buffer, and stored at 4°C until use. DNA was also obtained from 800-µL urine samples as described above.

Sequencing

Fourteen A. schaalii strains, including reference strain CCUG 27420, were used for sequencing. Universal primer pair UP-1 and UP-2r was used to amplify the gyrB gene from A. schaalii (Table 1). PCR was performed as described by Yamamoto and Harayama. (7). The PCR product was then gel purified by using the QIAquick Gel Extraction Kit (QIAGEN, Hilden Germany) and sequenced in an ABI 3130 XL genetic analyzer (Applied Biosystems, Foster City, CA, USA) according to the manufacturer’s instructions. Sequencing primers UP-1S and UP-2Sr (Table 1) were used to sequence the purified PCR product in both directions. Primers were synthesized by DNA Technology (Aarhus, Denmark).

Primers and Probe

Sequence alignment editor BioEdit (www.mbio.ncsu.edu/BioEdit/BioEdit.html) and Primer3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi) programs were used to design a primer and probe specific for A. schaalii by multiple alignment of gyrB sequences from 14 A. schaalii strains, including reference strain CCUG 27420. Potential primers and probe were analyzed for the requirements imposed by real-time PCR by using PrimeQuest (http://eu.idtdna.com/analyzer/Applications/OligoAnalyzer/) and mfold (www.bioinfo.rpi.edu/applications/mfold/cgi-bin/dna-form1.cgi) programs. Selected primers and probe were analyzed for specificity against GenBank sequences by using the BLAST program (http://blast.ncbi.nlm.nih.gov/Blast.cgi).

The primer pair A.s-forward 5′-GGCCATGCAG TGGACCTC-3′ and A.s-reverse 5′-GCACATCATCA CCGGAAGA-3′ amplified a 185-bp fragment. The probe 5′-TCCGAATCGGTCAATACCTTCGC-3′ was labeled at the 5′ end with 6-carboxyfluorescein and at the 3′ end with Black Hole Quencher 1. Primers and probe were synthesized by Sigma-Aldrich (St. Louis, MO, USA).

TaqMan qPCR

PCR amplification was performed by using a Mx3000P Real Time PCR System (Stratagene, La Jolla, CA, USA) in a 25-µL reaction volume. The PCR mixture contained 12 µL of 2× Brilliant QPCR Master Mixture (Stratagene), 2.5 µL of 100 nmol/L (final concentration) TaqMan probe, 2 µL of 200 nmol/L (final concentration) forward and reverse primers, and 5 µL of template DNA. An internal control containing 1.25 µL of internal PCR control primer/probe mixture and 0.25 µL of internal PCR control DNA (Applied Biosystems) was also used. Samples were incubated for 1 cycle at 95°C for 2 min and 50 cycles at 95°C for 30 s and 60°C for 60 s. All samples were run in duplicate. DNA from A. schaalii CCUG 27420 was used as a positive control and was included in each PCR. Sterile water was used as a negative control. Results were analyzed by using the Mx3000P software package (Stratagene).

Detection Limit and Quantification

The detection limit of the A. schaalii gyrB assay was determined by using a 10-fold serial dilution of known concentrations (1.5 × 101 to 1.5 × 108 CFU/mL) of A. schaalii CCUG 27420. Quantification of A. schaalii in urine samples was performed by using the same dilution series.

Analytical Specificity

To determine the analytical specificity of the assay, we tested 36 clinical strains of A. schaalii and strain CCUG 27420. Phylogenetically related (1) and clinically relevant bacterial strains, including several Actinomyces spp., Ar-
canobacterium spp., and reference strains A. suis CCUG 19026, A. urinale CCUG 46093, and A. massiliae CCUG 47753, were also tested (Table 2).

Verification of TaqMan qPCR Assay Results

To verify results of this assay, 6 PCR products were sequenced. The first 15 PCR-positive urine samples were cultivated, and isolates were identified as described by Reinhardt et al. (2). Identity of isolated A. schaalii strains was confirmed by using a qPCR.

Purification of DNA from Blood Cultures

Ten milliliters of blood and 1 mL of culture containing $2 \times 10^4$, $2 \times 10^5$, $2 \times 10^6$, and $2 \times 10^7$ CFU/mL of A. schaalii reference strain CCUG 27420 were added to aerobic and anaerobic BACTEC culture vials (Becton Dickinson). DNA from bacteria-positive blood cultures was extracted from 800 μL of aerobic or anaerobic media and purified by using the Kingfisher processor as described above.

Because BACTEC culture vials contain sodium polyanetholesulfonate (SPS), a known PCR inhibitor, either DNA must be purified from BACTEC culture vials by using specific purification methods or purified DNA must be diluted to prevent the SPS from inhibiting the PCR (8). Ten-fold serial dilutions of purified DNA from positive BACTEC culture vials were made and tested by using the qPCR as described above. DNA was extracted from an anaerobic BACTEC culture vial from a patient sample from which A. schaalii had been isolated by cultivation.

Statistical Analysis

The $\chi^2$ test was used to analyze differences in detection of A. schaalii. Statistical analyses were performed by using SPSS for Windows version 16.0 (SPSS Inc., Chicago, IL, USA).

Results

Cultivation of PCR-Positive Samples

Isolates were obtained from 7 of the 15 urine samples cultured. The 7 isolates were confirmed positive by our real-time PCR.

Detection Limit and Analytical Specificity

Assay results were linear at bacterial concentrations from $1.5 \times 10^4$ to $1.5 \times 10^6$ CFU/mL with an $R^2$ value of 1.000 ($Y = -3.296 \times \log(X) + 25.96$). The detection limit of the assay was between $1.5 \times 10^4$ and $1.5 \times 10^5$ CFU/mL, which corresponds to 7.5–75 CFU/reaction. The assay amplified DNA from all 37 isolates of A. schaalii tested. No PCR amplification signal was detected when other species were tested (Table 2).

DNA Sequencing Analysis

The 6 PCR products amplified from bacteria-positive urine samples had the expected size. Sequence alignment of the 6 PCR products showed homology to the sequenced gyrB gene from A. schaalii strains.

Identification of A. schaalii from Blood Cultures

The 2 anaerobic BACTEC culture vials to which 1 mL of $2 \times 10^7$ CFU/mL and $2 \times 10^8$ CFU/mL had been added and 1 aerobic BACTEC culture vial to which 1 mL of $2 \times 10^7$ CFU/mL had been added showed
positive results in the BACTEC 9240 blood culture system. There was no growth recorded with lower inoculum concentrations.

PCR with undiluted and 10-fold diluted DNA was inhibited, probably by SPS. However, the 100-fold dilution of purified DNA from the 2 anaerobic and 1 aerobic BACTEC culture vials was PCR positive. The 100-fold dilution of purified DNA from a positive anaerobic BACTEC culture vial (patient specimen) was also PCR positive.

**Analysis of Urine Samples**

Of 252 urine samples, 41 (16%) were PCR positive with bacterial concentrations \(>10^4\) CFU/mL. Of 155 urine samples from patients >60 years of age, 34 (22%) were with bacterial concentrations \(>10^4\) CFU/mL. Of 155 urine samples obtained by practitioners, 30% of samples from 51 patients >60 years of age and none from 104 patients >60 years of age had Actinobaculum schaalii and that these patients had a broad spectrum of UTIs. However, the 100-fold dilution of samples from patients >60 years of age were PCR positive, probably by SPS. However, the 100-fold dilution of samples from patients >60 years of age were PCR positive (Table 3), of which 31 (91%) harbored other common uropathogenic bacteria in addition to Actinobaculum schaalii (Table 4). Species distribution of these common uropathogenic bacteria was comparable to that found in our microbiology department throughout the year. Treatment with antimicrobial drugs before specimens were obtained was reported by 19% of the patients.

The 41 PCR-positive urine samples were collected midstream from 37% of patients, from bedpans for 27%, from catheters for 12%, and by an unspecified method for 24%. Among 177 hospitalized patients, 18% of samples from 104 patients >60 years of age and 10% of samples from 73 patients \(\leq 60\) years of age were PCR positive (\(p = 0.133\)). Among 75 urine samples obtained by practitioners, 30% of samples from 51 patients >60 years of age and none of the samples from 24 patients \(\leq 60\) years of age were PCR positive (\(p = 0.002\)). There was no significant difference in the presence of Actinobaculum schaalii by sex of the patients (\(p = 0.485\)). When the control group (patients who had had hip or knee surgery) was compared with patients >60 years of age, no significant difference in the presence of Actinobaculum schaalii was found (\(p = 0.227\)). In addition, we did not find any detectable differences between PCR-positive and PCR-negative results for hospitalized patients concerning underlying urinary tract pathologic changes and concurrent conditions such as hypertension and diabetes.

**Discussion**

The real-time PCR assay confirmed that infection with Actinobaculum schaalii increases with age (2). More than 1 of 5 urine samples from patients >60 years of age were PCR positive, and Actinobaculum schaalii was most common in patients who visited medical practitioners and who had an infection with ordinary urinary pathogens. In comparison, culture findings in a study in our laboratory showed that 0.4% of cultured urine samples from patients >60 years of age had Actinobaculum schaalii and that these patients had a broad spectrum of UTIs (2).

The present study shows that bacteria species, especially anaerobic or slow-growing species, are more common than what culture results indicate. Most likely, other pathogen bacteria exist that are even more difficult to identify by cultivation than is Actinobaculum schaalii. Molecular biologic techniques such as real-time PCR can be valuable tools for identification of these organisms. Pathogenic bacteria that are difficult to cultivate or identify by cultivation should not be underestimated.

Other common uropathogens were identified by cultivation in 9 of 10 PCR-positive urine samples (Table 4). This finding indicates that Actinobaculum schaalii is probably a common, undetected bacterial copathogen in many UTIs. Because most PCR-positive samples were from persons with multiple infections, determining which microorganism caused the UTI is difficult. However, results from our study support findings in case reports (2,3,6) in which Actinobaculum schaalii was often found in monoculture for patients who had UTIs and therefore considered the causative agent. Furthermore, PCR showed that Actinobaculum schaalii is a more common pathogen than previously thought. However, it will be difficult to fulfill the last of Koch’s criteria and prove with animal experiments that Actinobaculum schaalii is a uropathogen.

Clinical microbiologists, clinicians, and medical practitioners should be aware of Actinobaculum schaalii in patients predis-

---

**Table 3. Distribution of Actinobaculum schaalii in 252 urine samples, Denmark, 2008–2009**

<table>
<thead>
<tr>
<th>Age of sample donors, y</th>
<th>No. (%) samples</th>
<th>95% CI</th>
<th>CFU/mL of Actinobaculum schaalii in PCR-positive samples</th>
</tr>
</thead>
<tbody>
<tr>
<td>0–10</td>
<td>12 (0)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>11–20</td>
<td>16 (6)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>21–30</td>
<td>21 (5)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>31–40</td>
<td>15 (0)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>41–50</td>
<td>11 (9)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>51–60</td>
<td>22 (18)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>61–70</td>
<td>52 (15)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>71–80</td>
<td>54 (20)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>&gt;80</td>
<td>49 (31)</td>
<td></td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>(\leq 60)</td>
<td>97 (7)</td>
<td>3–14</td>
<td>(10^4–10^5)</td>
</tr>
<tr>
<td>(&gt;60)</td>
<td>155 (22)</td>
<td>16–29</td>
<td>(10^4–10^5)</td>
</tr>
</tbody>
</table>

Healthy controls: 38 (13) 4–28

\(\ast CI, confidence interval.\)
posed for UTIs or unexplained chronic UTIs, especially if initial findings of wet smear microscopy for bacterial rods and leukocytes differ from negative growth under commonly used aerobic cultivation methods. For patients with suspected infections, urine should be sent to a department of clinical microbiology and incubated in an atmosphere of 5% CO₂ for 2 to 3 days.

For patients with clinically verified UTIs who do not respond to treatment with ciprofloxacin or trimethoprim, infection with *A. schaalii* should be suspected. If *A. schaalii* is the cause of the infection, treatment with β-lactams, such as ampicillin or cephalosporins, should be given. The optimal duration of antimicrobial drug treatment with β-lactams is not clearly defined but several weeks of treatment may be required in severe cases.

Because *A. schaalii* can be difficult to identify even when cultured in an atmosphere of 5% CO₂, the real-time PCR described in this report can be used for identification in urine and blood cultures. Alternatively, if the bacteria can be isolated by cultivation, the API Coryne and Rapid ID32A test systems (bioMérieux, Marcy l’Etoile, France) can be used for identification, as described by Reinhard et. al. (2). In conclusion, *A. schaalii* is an underestimated opportunistic copathogen that probably causes UTIs and urosepsis, particularly in elderly patients or patients predisposed for UTIs.

**Acknowledgment**

We thank J.E. Kristiansen for critically reviewing the manuscript.

Dr Bank is a physician in the Department of Clinical Microbiology at Viborg Hospital, Viborg, Denmark. His primary research interests are real-time PCR and urinary tract infections.

**References**


Address for correspondence: Steffen Bank, Department of Clinical Microbiology, Viborg Hospital, Heibergs Allé 4, DK-8800 Viborg, Denmark; email: stb@mb.au.dk

---

**Table 4. Uropathogens identified by cultivation of 155 urine samples from patients >60 y of age, Denmark, 2008–2009**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th><em>Actinobaculum schaalii</em></th>
<th>PCR positive</th>
<th>PCR negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total no. samples</td>
<td>34</td>
<td>121</td>
<td></td>
</tr>
<tr>
<td>No growth</td>
<td>3</td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>Uropathogens* ≥10⁴ CFU</td>
<td>31</td>
<td>76</td>
<td></td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>13</td>
<td>38</td>
<td></td>
</tr>
<tr>
<td>Other <em>Enterobacteriaceae</em></td>
<td>13</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td>Other organisms</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gram-negative aerobic rods</td>
<td>2</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td><em>Enterococcus faecalis</em></td>
<td>0</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>Coagulase-negative staphylococci</td>
<td>0</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td><em>Aerococcus</em> spp.</td>
<td>1</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td><em>Streptococcus</em> spp.</td>
<td>2</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>Yeast</td>
<td>0</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>&gt;3 species</td>
<td>4</td>
<td>8</td>
<td></td>
</tr>
</tbody>
</table>

*Two species were identified in 4 of 34 PCR-positive samples and in 8 of 121 PCR-negative samples.*