Colonization with *Escherichia coli* Strains among Female Sex Partners of Men with Febrile Urinary Tract Infection

Peter Ulleryd, Torsten Sandberg, Flemming Scheutz, Connie Clabots, Brian D. Johnston, Paul Thuras, James R. Johnson

Department of Communicable Disease Control and Prevention, Region Västra Götaland, Sweden; Department of Infectious Diseases, Institute of Biomedicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden; WHO Collaborating Centre for Reference and Research on *Escherichia* and *Klebsiella*, Statens Serum Institute, Copenhagen, Denmark; Veterans Affairs Medical Center, Minneapolis, Minnesota, USA; Department of Medicine, University of Minnesota, Minneapolis, Minnesota, USA; Department of Psychiatry, University of Minnesota, Minneapolis, Minnesota, USA

Of 23 unique *Escherichia coli* strains from 10 men with febrile urinary tract infections (UTIs) and their female sex partners, 6 strains (all UTI causing) were shared between partners. Molecularly, the 6 shared strains appeared more virulent than the 17 nonshared strains, being associated with phylogenetic group B2, sequence types ST73 and ST127, and multiple specific virulence genes. This indicates that UTIs are sometimes sexually transmitted.

*Escherichia coli* is the leading cause of urinary tract infection (UTI), a tremendously common and costly illness (1). Although the causative *E. coli* strains usually derive from the host’s own gastrointestinal microbiota (2, 3), their more proximate reservoirs are poorly understood.

Sharing of *E. coli* strains, whether pathogenic or not, is common among closely associated hosts, including pets and sex partners (4–19). However, strain sharing between a man with an *E. coli* UTI and his healthy female sexual partner (FSP) has not been reported. We capitalized on a large cohort of men with *E. coli* febrile UTIs (FUTIs) to assess this phenomenon’s frequency and the characteristics of any shared strains.

Subjects and specimens. Ten men with community-acquired *E. coli* FUTI and an FSP who was willing to participate in the study were identified within a larger cohort study of male FUTI at Sahlgrenska University Hospital, Gothenburg, Sweden, from 1993 to 1996 (21, 22). Men had to have a temperature of ≥38.0°C, at least one urinary tract-referable symptom or sign (e.g., frequency, dysuria, flank pain, or costovertebral angle tenderness), and ≥10⁴ CFU/ml of a uropathogen on urine culture (21, 22). Consenting subjects underwent culture surveillance of urine, feces, and (for FSPs) the vagina initially and with any subsequent UTI episode in either partner.

Midstream urine samples, collected per protocol, were kept at 4°C until cultured semiquantitatively on blood and cysteine lactose electrolyte-deficient agar. Significant growth was defined as ≥10⁴ CFU/ml of *E. coli*. The last three free-lying colonies were saved.

Men self-collected rectal samples per protocol. One of the authors (P.U.) collected vaginal and rectal samples from FSPs. Swabs were streaked to modified Conradi-Drigalski agar for overnight incubation. The last three free-lying colonies on each plate, plus any morphologically distinct colonies, were picked for analysis; this provided ≥97% sensitivity for detecting the quantitatively predominant clone in rectal samples (23). Confirmed *E. coli* isolates were stored in agar stabs (24).

Isolate characterization. *E. coli* isolates underwent O typing or full O:K:H serotyping at Statens Serum Institute, Copenhagen, Denmark. One colony per O:K:H serotype per specimen, and colonies differing by O type from the index FUTI isolate, underwent molecular typing, including XbaI pulsed-field gel electrophoresis (PFGE) profiling (25). Pulsotypes (herein equated with strains) were assigned based on ≥94% profile similarity to index profiles within a large PFGE database (26).

One representative per sample per PFGE type underwent PCR-based major phylogenetic group determination (25). Extended virulence genotypes were determined by multiplex PCR (27–29). Sequence type (ST) and clonal complex (CC; cluster of closely related STs) were determined by PCR (27), *fimC-fimH* sequence analysis (30), and/or multilocus sequence typing (http://mlst.warwick.ac.uk).

Statistical methods. Comparisons of proportions and virulence score were tested using Fisher’s exact test and the Mann-Whitney U test, respectively, with significance set at a *P* value of <0.05.

Study population. The 10 index men with FUTI had a median age of 55 years (range, 37 to 69 years) and a median temperature of 39.3°C (range, 39.0°C to 40.5°C) (see Table S1 in the supplemental material). None affirmed anal intercourse during the preceding 6 months. Two patients had voiding problems suggestive of prostatitis. Only 3 had possible UTI-predisposing conditions, including postoperative urethral catheterization 3 days pre-FUTI episode, diabetes mellitus, and a small bladder adenoma. The median age of the 10 FSPs was 48.5 years (range, 32 to 62 years). All of the FSPs denied UTI symptoms and antibiotic treatment in the preceding 3 months.

Culture results. Culture surveillance was done once for 7 cou-
FIG 1 Pulsed-field gel electrophoresis (PFGE) profiles of *Escherichia coli* isolates from 10 men with febrile urinary tract infection and their female sex partners. Dendrogram is based on pairwise similarity relationships among XbaI PFGE profiles, as reflected in Dice similarity coefficients. Colored rectangles enclose profiles of the same pulsotype. Labels to right of dendrogram show the couple number. PFGE column lists pulsotype designation, which is also shown to the right of each rectangle for shared strains. Red circle identifies the sole instance of putative strain sharing across couples (couple 29 versus couple 95), which likely was spurious (based on differences in virulence genotype).
TABLE 1 Colonization and clinical characteristics of 23 Escherichia coli strains from 10 men with FUTI and their female sexual partners in relation to strain sharing

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Prevalence of characteristic (no. [column %])</th>
<th>$P$ value, nonshared vs shared$^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male, any site</td>
<td>Total (n = 23)</td>
<td>Nons shared strains (n = 17)</td>
</tr>
<tr>
<td>Rectum</td>
<td>18 (78)</td>
<td>12 (71)</td>
</tr>
<tr>
<td>FUTI$^b$</td>
<td>11 (48)</td>
<td>10 (59)</td>
</tr>
<tr>
<td>ABU$^c$ during follow-up</td>
<td>2 (9)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Female, any site</td>
<td>Total (n = 23)</td>
<td>Nons shared strains (n = 17)</td>
</tr>
<tr>
<td>Rectum</td>
<td>11 (48)</td>
<td>5 (29)</td>
</tr>
<tr>
<td>Vagina</td>
<td>10 (44)</td>
<td>5 (29)</td>
</tr>
<tr>
<td>Acute cystitis during follow-up</td>
<td>4 (17)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>ABU during follow-up</td>
<td>2 (9)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

$^a$ $P$ values (by Fisher’s exact test) are shown when they are <0.10.
$^b$ FUTI, febrile urinary tract infection.
$^c$ ABU, asymptomatic bacteriuria.

The potential clinical implications of cocolonization include risks of (i) acute UTI in an FSP due to the male partner’s UTI strain and (ii) reintroduction of the strain into the index subject from a cocolonized partner. The first scenario occurred here (couple 10). Whether decolonization of cocolonized sex partners is warranted deserves study.

As in previous studies (6, 7, 12, 31), shared strains were distributed more broadly, caused more infections, and exhibited more uropathogenic traits than did nonshared strains. This indicates that certain E. coli traits and lineages promote both UTI pathogenesis and intestinal coclonization (32). Conceivably, interventions directed toward these traits and/or lineages may prevent UTI by blocking both processes.

Since we investigated middle-aged male FUTI patients without serious medical or urological compromise and their middle-aged FSPs, our results cannot be extrapolated to other forms of UTI or host populations. Additionally, since our rectal sampling method detected mainly dominant fecal E. coli clones (23), we likely underestimated the true frequency of cocolonization (33).

Summary. We demonstrated frequent sharing of the causative E. coli strain between men with FUTI and their FSPs, which indicates that male UTI is sometimes sexually transmitted. Strain sharing was more common and extensive for classic urovirulent strains, suggesting that urovirulence traits may also promote colonization and transmission.

ACKNOWLEDGMENTS

This material is based upon work supported by The Medical Society of Gothenburg, Sweden (P.U.), and the Office of Research and Development, Medical Research Service, Department of Veterans Affairs, USA (J.R.J.).

The technical assistance of Susanne Jespersen, Statens Serum Institute, Copenhagen, Denmark, is greatly appreciated.

REFERENCES


