We previously described how retail meat, particularly chicken, might be a reservoir for extraintestinal pathogenic Escherichia coli (ExPEC) causing urinary tract infections (UTIs) in humans. To rule out retail beef and pork as potential reservoirs, we tested 320 additional E. coli isolates from these meats. Isolates from beef and pork were significantly less likely than those from chicken to be genetically related to isolates from humans with UTIs. We then tested whether the reservoir for ExPEC in humans could be food animals themselves by comparing geographically and temporally matched E. coli isolates from 475 humans with UTIs and from cecal contents of 349 slaughtered animals. We found genetic similarities between E. coli from animals in abattoirs, principally chickens, and ExPEC causing UTIs in humans. ExPEC transmission from food animals could be responsible for human infections, and chickens are the most probable reservoir.

Extraintestinal pathogenic Escherichia coli (ExPEC) is the leading cause of community-acquired urinary tract infections (UTIs) in humans, accounting for >85% of UTIs (1). Each year, 6–8 million UTIs are diagnosed in the United States, and 130–175 million are diagnosed worldwide. Estimated direct health care costs related to uncomplicated UTIs in the United States are $1–$2 billion per year (1,2). UTIs also can lead to more severe illnesses, such as pyelonephritis, bacteremia, and sepsis (3). During the past decade, the emergence of drug-resistant E. coli has dramatically increased. As a consequence, the management of UTIs, which was previously straightforward, has become more complicated; the risks for treatment failure are higher, and the cost of UTI treatment is increasing (4).

In the past, extraintestinal E. coli infections have been described as sporadic infections caused by bacteria that originate from the host’s intestinal tract. However, ExPEC strains recently have been associated with possible outbreaks (5). Communitywide outbreaks have been described in south London (E. coli O15:K152:H1) (6); Copenhagen (E. coli O78:H10) (7); Calgary, Alberta, Canada (extended-spectrum β-lactamase–producing E. coli) (8); and California, USA (trimethoprim/sulfamethoxazole–resistant E. coli) (9). These outbreaks suggest that ExPEC can be spread to the intestinal tracts of persons in the community by a common source or vehicle.

We recently described the results of a study that characterized the genetic similarities between E. coli isolates recovered from retail meat, particularly chicken, and ExPEC in humans causing community-acquired UTIs (10). That study oversampled isolates from retail chicken because evidence suggested that chicken was likely to be the primary reservoir of ExPEC in humans (11–16). To exclude the possibility that isolates from other retail meat sources (beef and pork) might also be genetically related to...
UTI isolates from humans, we first aimed to characterize additional *E. coli* isolates recovered from retail beef and pork sources. These new isolates from retail meat were added to the preexisting collection of retail meat isolates and compared with the same UTI isolates from humans. Second, we aimed to determine whether transmission was primarily human to human through food or whether an animal source was involved. In the case of human-to-human transmission through food, *E. coli* strains from humans would be introduced during the meat preparation process by food handlers. In the case of an animal source, the *E. coli* would derive from the cecal content of the animal itself, and contamination would occur during the slaughtering process. On the basis of previous findings, we hypothesized that a food animal reservoir exits for ExPEC that cause UTIs in humans and that chicken is the primary source. To evaluate this hypothesis, we analyzed isolates from animals entering the food chain. *E. coli* isolates recovered from the cecal contents of slaughtered food animals (beef cattle, chickens, and pigs) were compared with the preexisting geographically and temporally matched collection of isolates from humans with UTIs.

**Methods**

**Study Design**

A total of 1,561 geographically and temporally matched *E. coli* isolates from animals and from humans with UTIs were used for the different comparisons (Table 1). The study target area was primarily the province of Quebec, Canada; however, other regions were included as described below. The study period was 2005–2007. The McGill University Institutional Review Board approved the study protocol (A01-M04-05A).

**Sampling of *E. coli* isolates from Humans with UTI, Montreal, Quebec**

The 351 *E. coli* isolates recovered from humans with UTIs were collected in Montreal during June 2005–May 2007 (17). Women 18–45 years of age who had a suspected UTI were recruited at the McGill University Student Health Services and the Centre Local de Services Communautaires Métro Guy. UTI was defined as ≥2 symptoms or signs, including dysuria, increased urinary frequency or urgency, pyuria, hematuria, and >10^5 CFU of *E. coli* per mL of clean-catch urine (18). Specimen culture and bacterial identification have been described (17). One random isolate from each urine sample was selected. In case of UTI recurrence, only the isolate from the first UTI episode was included. The collection was assembled as follows. A random set of 116 fully susceptible isolates was selected. A random set of 170 isolates resistant to ≥1 antimicrobial agents was assembled; in addition, specific groups of antimicrobial-resistant *E. coli* were included. These *E. coli* strains have been closely associated with possible outbreaks of extraintestinal infections (6–9,19–21). In particular, cephalosporin-resistant *E. coli* frequently has been observed in UTI outbreaks and in poultry products (8,13,16,19–21). Hence, all 19 cephalothin-resistant *E. coli* isolates were included. We included 46 representative members of *E. coli* clonal groups that were known to cause clusters of UTI among unrelated women on the basis of the hypothesis that they would be more likely to be related to

<table>
<thead>
<tr>
<th>Source</th>
<th>2005</th>
<th>2006</th>
<th>2007</th>
<th>2008</th>
<th>QC</th>
<th>ON</th>
<th>BC/AB</th>
<th>SK/MB</th>
<th>Maritimes</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>UTI in humans</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>All</td>
<td>102</td>
<td>174</td>
<td>137</td>
<td>62</td>
<td>379</td>
<td>37</td>
<td>23</td>
<td>24</td>
<td>12</td>
<td>475</td>
</tr>
<tr>
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<td></td>
<td></td>
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<tr>
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<td>243</td>
<td>219</td>
<td>30</td>
<td>521</td>
<td>202</td>
<td>4</td>
<td>10</td>
<td>0</td>
<td>737</td>
</tr>
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<td>84</td>
<td>72</td>
<td>86</td>
<td>12</td>
<td>210</td>
<td>32</td>
<td>4</td>
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</tr>
<tr>
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<td>84</td>
<td>70</td>
<td>98</td>
<td>12</td>
<td>170</td>
<td>71</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>242</td>
</tr>
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<td>146</td>
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<tr>
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<td>22</td>
<td>20</td>
<td>6</td>
<td>11</td>
<td>23</td>
<td>7</td>
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<td>Chicken§</td>
<td>89</td>
<td>60</td>
<td>80</td>
<td>23</td>
<td>75</td>
<td>104</td>
<td>27</td>
<td>10</td>
<td>2</td>
<td>229</td>
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<tr>
<td>Pig¶</td>
<td>26</td>
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<td>60</td>
</tr>
<tr>
<td>Total</td>
<td>510</td>
<td>518</td>
<td>471</td>
<td>30</td>
<td>62</td>
<td>4</td>
<td>1,007</td>
<td>385</td>
<td>75</td>
<td>1,561</td>
</tr>
</tbody>
</table>

*QC, Quebec; ON, Ontario; BC, British Columbia; AB, Alberta; SK, Saskatchewan; MB, Manitoba; Maritimes, New Brunswick/Nova Scotia/Prince Edward Island; UTI, urinary tract infection.
†124 *E. coli* isolates recovered from humans with UTIs in Montreal during June 2005–May 2007.
‡124 *E. coli* isolates recovered from humans with community- or hospital-acquired UTIs from sources throughout Canada during 2007–2008.
§The geographic area was unknown for 11 isolates from chicken.
¶The geographic area was unknown for 3 isolates from pigs.
food sources. This collection of 351 UTI-associated *E. coli* isolates is referred to as the Manges collection.

**Sampling of E. coli Isolates from Humans with UTIs, Canada**

We added 124 isolates from humans from sources across Canada to increase the diversity of the collection of *E. coli* isolates causing UTIs beyond those in Québec alone. These samples were collected from patients with community- and hospital-acquired UTIs during 2007–2008. This collection, provided by 1 of the authors (G.G.Z.), is referred to as the Zhanel collection.

**Sampling of E. coli from Retail Meat**

We systematically selected and evaluated additional isolates from retail beef and pork. The retail meat collection totaled 737 isolates from beef (242), chicken (253), and pork (242) (10). These isolates were collected in Montréal, areas of Québec outside Montréal, parts of Ontario, and other areas of Canada during 2005–2007. All of these isolates originated from the collection of the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS). Because antimicrobial resistance has been associated with ExPEC clonal groups and outbreaks of UTIs (6–9,17,22), we oversampled antimicrobial-resistant isolates from retail meat; 60% of sampled isolates were resistant to ≥1 antimicrobial drugs, and 40% were fully susceptible. However, resistance in retail beef was fairly low; therefore the proportion of resistant *E. coli* from retail beef was only 48%.

**Sampling of E. coli from Food Animals in Abattoirs**

From the CIPARS collection, we selected 349 *E. coli* isolates from animals in abattoirs. These bacteria were isolated from the cecal contents of slaughtered food animals (23). Because the primary hypothesis concerned a chicken reservoir and we already had demonstrated that isolates from humans are less likely to be related to isolates from beef and pork, we included isolates in the following proportions: 20% beef cattle, 60% chickens, and 20% pigs. We chose 299 isolates from 2005–2007 as follows. Isolates from chickens were selected from abattoirs in Québec and Ontario because there are poultry abattoirs operating in Québec and Ontario and because *E. coli* from humans with UTIs was recovered primarily from women in Québec. In contrast, beef cattle and pig abattoirs are fewer and are located across Canada. Therefore, isolates were selected on the basis of the annual slaughter volume rather than on location. Sampling was conducted in proportion to the susceptibility levels for each animal species within the whole CIPARS collection. However, we included all 5 nalidixic acid–resistant isolates because this agent can be used as an indicator of resistance to fluoroquinolones (24). Furthermore, because the study focused on chicken, we included a random sample of 50 additional isolates from chickens in abattoirs in other Canadian provinces. They were also selected from the CIPARS collection during the same period (2005–2007).

**Antimicrobial Susceptibility Testing**

We performed antimicrobial susceptibility testing on all *E. coli* isolates, except those from the Zhanel collection. Antimicrobial susceptibility screening using a panel of 15 agents (amikacin, amoxicillin/clavulanic acid, ampicillin, cefoxitin, cefotiofur, ceftriaxone, chloramphenicol, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfisoxazole, tetracycline, and trimethoprim/ sulfamethoxazole) was conducted by the Public Health Agency of Canada, Laboratory for Foodborne Zoonoses. The protocol of the broth microdilution method used was fully described in the 2007 CIPARS report (23). Intermediate resistance for all isolates was classified as susceptible. The antimicrobial resistance patterns are provided for informational purposes only because isolates were sampled in part according to their antimicrobial resistance phenotype. Thus, the patterns observed do not reflect the prevalence of antimicrobial resistance for any of the sources.

**Clonal Group Definition and Typing**

Isolates were typed by multilocus variable number tandem repeat analysis (MLVA) (25) and enterobacterial repetitive intergenic consensus sequence 2 (ERIC2) PCR fingerprinting (26) in our laboratory and the McGill University and Genome Québec Innovation Center as described. A clonal group was defined as ≥2 *E. coli* isolates from human and animal sources that shared the same MLVA profile and ERIC2 PCR fingerprint. All clonal group members were further typed by phylotyping and multilocus sequence typing (MLST). Then, according to the results obtained, related isolates were selected for O:H serotyping and pulsed-field gel electrophoresis (PFGE).

Phylotyping (27) and MLST (28) (http://mlst.ucc.ie/mlst/dbs/Ecoli) were performed in our laboratory and in the McGill University and Genome Québec Innovation Center as described. Allelic profile and sequence type (ST) were assigned according to the scheme at this website. O (somatic) and H (flagellar) antigens were serotyped for clonal group isolates that shared the same phylogenetic group and MLST profile; serotyping was performed by the Public Health Agency of Canada, Laboratory for Foodborne Zoonoses, according to established protocols. Isolates that did not react with O antisera were classified as nontypeable. PFGE of *XbaI*-digested DNA was conducted in our laboratory by using the protocol for molecular subtyping of *E. coli* O157:H7 developed by the
Centers for Disease Control and Prevention (29). Clonal
group members that exhibited the same phylotype and
MLST profile were tested. Gel fingerprints were visually
compared, and strain relatedness was classified according
to the Tenover criteria (30).

Statistical Analyses
Differences in proportions were assessed by use of
the $\chi^2$ test. Statistical significance was defined as a p value
<0.05. All analyses were conducted using Stata version 9.0
(StataCorp LP, College Station, TX, USA).

Results

Isolates from Retail Meat

We identified 15 clonal groups, comprising 63 isolates.
The 15 groups contained 22 isolates from humans with UTIs
and 41 isolates from retail meat. Of the 41 isolates from
retail meat, 6 (15%) were from retail beef, 29 (71%) from
retail chicken, and 6 (15%) from retail pork. Considering
the sampling proportions (66% beef and pork [484/737]
and 34% chicken [253/737]), the fraction of isolates from
beef and pork related to isolates from humans with UTIs
was significantly lower than expected on the basis of
the sampling fraction (29% observed vs. 66% expected;
p=<0.001, $\chi^2$ test). Isolates from chicken were represented
in greater numbers among clonal groups. All clonal group
members had the same phylotype. According to MLST, 2
of these clonal groups (groups 1 and 3) contained isolates from
newly sampled retail beef and pork (EC01DT07-0827-01
and EC01DT06-1559-01) and isolates from humans with
UTIs that shared the same STs. These isolates were further
typed (Table 2): XbaI PFGE patterns differed by $\geq$7 bands
within the clonal groups associated with retail meat.

Isolates Collected from Abattoirs

We identified 8 clonal groups containing 46 isolates
from humans and from food animals at abattoirs. These
clonal groups comprised 17 isolates from humans with
UTIs and 29 from abattoir animals (1 [3%] beef cattle, 23
[79%] chickens, 5 [17%] pigs). The proportion of chicken
was higher than expected with 79% observed versus 60%
expected, in accordance with the 60% sampling fraction (p
= 0.034, $\chi^2$ test). The 3 clonal groups including isolates that
were further characterized, and thus more closely related,
are described below (Table 2). According to the Tenover
criteria (30), PFGE patterns of all animal strains differed
from those of the human strains.

Abattoir clonal group 1 contained 11 isolates (2 from
humans, 8 from chickens, 1 from a pig). All belonged to
the same phylogenetic group (D) and showed the same
sequence type (ST117). Two isolates from chickens
(EC01AB07-0105-01 and EC01AB07-0425-01) had the
same serotype (O180:H4), and the rest of the isolates had
unique serotypes.

Abattoir clonal group 2 included 6 isolates (3 from
humans, 1 from a chicken, 2 from pigs). They all belonged
to phylogenetic group A but showed 4 different MLST
profiles. Among them, ST746 was shared by 3 isolates (1
each from a human, chicken, and pig). However, they did
not show the same O:H serotype.

Abattoir clonal group 3 contained 13 isolates (5
from humans, 6 from chickens, 2 from pigs), which all
belonged to phylogenetic group A. The MLST profile
ST10 was shared by 7 isolates (4 from humans, 3 from
chickens). The 6 other isolates displayed different MLST
profiles. Among the isolates exhibiting ST10, 3 from
chickens (EC01AB05-0765-01, EC01AB07-0005-01, and
EC01AB07-1330-01) showed the same serotype (O16:H48).

Discussion

Our first goal was to exclude retail beef and pork
as a probable food source of E. coli causing UTIs. Our
previous study (10), in which the sampling proportions for
beef, chicken, and pork were not the same, clonal groups
identified included 17% isolates from beef and pork and
83% from chicken (p = 0.03). In the current investigation,
where the sampling proportions from retail meat were the
same, 12 (29%) of isolates belonging to clonal groups
were from beef and pork and 29 (71%) were isolated from
chicken (p<0.001). Retail beef and pork isolates are much
less likely than retail chicken isolates to be clonally related
to isolates from humans with UTIs.

Our second goal was to determine whether the reservoir
for ExPEC in humans causing community-acquired UTI was
food animals, particularly chickens. The initial screening
methods (MLVA and ERIC2) demonstrated that human
samples and cecal samples from food animals in abattoirs
can belong to the same clonal groups. Moreover, within
certain abattoir clonal groups, isolates showed the same
phylogenetic group and MLST sequence types, indicating
that they may have originated from a recent common
ancestor. The 3 major clonal groups with the highest level of
similarity (groups 1, 2, and 3) included isolates from abattoir
and retail meat (10), which suggests that food animals may
serve as a reservoir for ExPEC in humans.

The 2 most common STs (ST10 and ST117),
belonging to phylogenetic groups A and D, respectively,
have already been reported from human and animal sources
(11,31–33). Although phylogenetic group A is typically
associated with commensal E. coli (3), most human and
animal isolates from the abattoir clonal groups belonged
to this phylotype. Moreno et al. (34) and Ewers et al. (35)
reported data suggesting that isolates from phylogenetic
group A could be responsible for extraintestinal infections.
Phylogenetic group D, which has frequently been
associated with ExPEC in humans (3), was observed in 31% of the isolates from abattoir clonal group B2. The lack of isolates from phylogenetic group B2 was unexpected because extraintestinal pathogenic strains often belong to this group (3). Studies from Jakobsen et al. have identified phylogroup B2 isolates from meat and animal sources, which demonstrates that B2 exists in the food animal reservoir (36,37). Our results may be explained by the fact

Table 2. Composition of closely related clonal groups containing extraintestinal pathogenic _Escherichia coli_ from humans and retail meat or abattoir source isolates, Canada, 2005–2007

<table>
<thead>
<tr>
<th>Clonal group/strain</th>
<th>Type of sample</th>
<th>Isolate source</th>
<th>Year</th>
<th>Location</th>
<th>Phylotype ST</th>
<th>Serotype</th>
<th>Antimicrobial drug susceptibility or resistance†</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSHS 101A</td>
<td>Clinical</td>
<td>CA-UTI</td>
<td>2007</td>
<td>QC</td>
<td>D 117</td>
<td>O114:H4</td>
<td>Susceptible</td>
</tr>
<tr>
<td>EC01DT05-0789-01</td>
<td>Retail meat</td>
<td>Chicken</td>
<td>2005</td>
<td>ON</td>
<td>D 117</td>
<td>O114:H4</td>
<td>Susceptible</td>
</tr>
<tr>
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<td>Chicken</td>
<td>2006</td>
<td>QC</td>
<td>D 117</td>
<td>O2:H4</td>
<td>GEN, SIX, TET</td>
</tr>
<tr>
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<td>2005</td>
<td>QC</td>
<td>D 117</td>
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<td>TET</td>
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<td>Chicken</td>
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<td>QC</td>
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<td>O24:H4</td>
<td>GEN, SIX, TET</td>
</tr>
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<td>2007</td>
<td>SK</td>
<td>D 117</td>
<td>O53:H4</td>
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<td>2007</td>
<td>ON</td>
<td>D 117</td>
<td>O53:NM</td>
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</tr>
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<td>Chicken</td>
<td>2007</td>
<td>ON</td>
<td>D 117</td>
<td>O102:H4</td>
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<td>Chicken</td>
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<td>D 117</td>
<td>O103:H4</td>
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<td>2006</td>
<td>QC</td>
<td>D 117</td>
<td>O143:HA</td>
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<td>O149:H4</td>
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<td>Chicken</td>
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<td>D 117</td>
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<td>BC</td>
<td>D 117</td>
<td>O180:H4</td>
<td>KAN, STR, SIX, TET</td>
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<td>Pork</td>
<td>2007</td>
<td>ON</td>
<td>D 117</td>
<td>ONT:H4</td>
<td>STR, SIX</td>
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<td>Chicken</td>
<td>2005</td>
<td>ON</td>
<td>D 117</td>
<td>ONT:H4</td>
<td>GEN, SIX</td>
</tr>
<tr>
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<td>Chicken</td>
<td>2005</td>
<td>ON</td>
<td>D 117</td>
<td>OX182:NM</td>
<td>Susceptible</td>
</tr>
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<td>MSHS 624</td>
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<td>2006</td>
<td>QC</td>
<td>A 746</td>
<td>O20:H4</td>
<td>Susceptible</td>
</tr>
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<td>Abattoir</td>
<td>Pig</td>
<td>2007</td>
<td>ON</td>
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*ST, sequence type; MSHS, McGill University Student Health Services; CA-UTI, community-acquired urinary tract infection; QC, Québec; ON, Ontario; AB, Alberta; GEN, gentamicin; SIX, sulfisoxazole; TET, tetracycline; NM, novomotil; SK, Saskatchewan; AMP, ampicillin; NAL, nalidixic acid; TMP/SXT, trimethoprim/sulfamethoxazole; AMC, amoxicillin/clavulanic acid; FOX, cefoxitin; TIO cefotiofur; STR, streptomycin; CEF, cephalothin; Maritimes, New Brunswick/Nova Scotia/Prince Edward Island; BC, British Columbia; ONT, did not react with O antisera; KAN, kanamycin; CHL, chloramphenicol; CIP, ciprofloxacin; HA-UTI, hospital-acquired urinary tract infection; MB, Manitoba; blank cells indicate isolate not tested.
†Resistance to specific antimicrobials as indicated.
that the isolates collected from abattoirs are more likely to be generic or commensal *E. coli* rather than typical ExPEC because they were collected from the cecal contents of healthy animals. The lack of phylogenetic group B2 isolates also could be explained by sampling variability or our selection method (based on MLVA and ERIC2 PCR genotyping first, followed by phylotyping). Phylogenetic group A and D were predominant among the isolates collected from abattoirs, which is consistent with results obtained by Jakobsen et al. (38) and Cortés et al. (11).

Although we oversampled isolates from abattoir chickens (60%), a significantly higher proportion of the isolates collected from abattoirs (79%; p = 0.034) included in the clonal groups were from chickens than from beef cattle or pigs; this proportion was higher than expected. This study confirms our hypothesis that chickens are a likely reservoir for ExPEC in humans. However, epidemiologic data, such as diet or other exposures, were not available for the humans with UTIs. This information could have been used to search for other potential routes of transmission (e.g., travel, water sources) and to strengthen the connection between poultry consumption and UTI.

We observed more heterogeneity in the PFGE results than in results from the other typing methods. PFGE is the standard for genotyping *E. coli* in the context of outbreaks, but it is generally not useful for establishing relationships between isolates from greater distances and over longer periods (12). MLST results may be a more relevant as housekeeping genes evolve more slowly and are more appropriate for examining questions related to global or regional epidemiology (39,40).

This study was strengthened by use of an ecologic design in which all isolates were systematically and purposively selected over the same period of time and geographic area (17,23), rather than sampling haphazardly by using existing clinical laboratory collections. The results suggest that potential ExPEC transmission from food animal sources is likely to be implicated in human infections and that chicken is a major reservoir. The possibility that ExPEC causing UTIs and other extraintestinal infections in humans could originate from a food animal reservoir raises public health concern. New interventions may be needed to reduce the level of food contamination and risk for transmission.

**Acknowledgments**

This manuscript is dedicated to Lucie Dutil, a wonderful person and outstanding colleague. Dr. Dutil died suddenly in August 2011 and is sadly missed by all who worked with her.

We thank members of the surveillance team of the Canadian Integrated Program for Antimicrobial Resistance Surveillance (Brent Avery and the Public Health Agency of Canada laboratory technicians).

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Ms Racicot Bergeron is a graduate student in the Department of Microbiology and Immunology at McGill University in Montréal, Québec. Her research interests include bacteriology and molecular epidemiology of ExPEC causing human diseases.

**References**

Chicken as Reservoir for ExPEC in Humans


Address for correspondence: Amee R Manges, Department of Epidemiology, Biostatistics and Occupational Health, McGill University, 1020 Pine Ave West, 36B, Montréal, QC H3A 1A2, Canada; email: amee.manges@mcmill.ca.