Acute uncomplicated cystitis and pyelonephritis, most episodes of which are caused by uropathogenic strains of *Escherichia coli*, are very common infections affecting otherwise healthy women. Uropathogenic *E. coli* strains, compared with fecal strains, are more likely to possess the potential for enhanced extraintestinal virulence, which enables the organisms to overcome local host defenses and cause urinary tract infection (UTI) [1]. In general, uropathogens are thought to initially colonize the gastrointestinal tract, and their movement into the vagina and bladder with subsequent UTI is facilitated mainly by sexual intercourse [2]. It is not known, however, where uropathogens originate, when they appear, or how long they persist in the intestines or vaginas of healthy women before onset of UTI.

Given our understanding of the environmental reservoir of *E. coli*, their distribution among animals, water, and types of food, and the fact that the main vehicle for colonization and infection with these and other enteric organisms is contaminated food and water, it is not a far-fetched assumption that uropathogenic *E. coli* most likely originate from contaminated food or water. Uropathogenic *E. coli* might contaminate food or water via many routes, including sewage, wild or domesticated animals, or food handlers, but no clear linkage has been made between ingestion of contaminated food or water or direct animal contact and human UTI [3]. Colonization of the gastrointestinal tract with antibiotic-resistant *E. coli* strains has been demonstrated following travel to arenas with a high prevalence of antibiotic resistance, presumably via ingestion of contaminated food or water [4], and recent travel outside the United States has been shown to be a risk factor for UTI caused by trimethoprim-sulfamethoxazole (TMP-SMZ)–resistant *E. coli* [5]. Human-to-human transmission, presumably via the fecal-oral route, is suggested by the observations that transmission of *E. coli* among children at day care centers and from such children to household members are common [6]. There is also evidence that uropathogenic strains may occasionally be shared between sex partners, but the direction of transmission has not been determined [2].

Sporadic, nonrecurrent, community-acquired UTIs are generally considered to be unrelated events, although community outbreaks of UTIs caused by multidrug-resistant strains of *E. coli* have been reported [7]. UTI clustering is also suggested by recent investigations demonstrating that a high proportion of TMP-SMZ–resistant strains causing acute uncomplicated UTI in different geographic areas of the United States were caused by clonal group A (CgA) [5, 7]. These observations suggest that the increase in the prevalence of TMP-SMZ resistance among uropathogenic *E. coli* in the United States may in part be related to clonal spread and raise the possibility of a foodborne source for these clones. These reported clusters of UTI-causing uropathogen clones were identified by investigation of antibiotic-resistant strains, and it is possible that many community-acquired UTIs occur in epidemiologically linked clusters that are not identified, because urine cultures are often not performed for cystitis and isolates, when present, are not genotyped.

In the article by Ramchandani et al. [8] in this issue of Clinical Infectious Diseases, the authors attempt to determine whether there is an animal or environmental source of the human-associated uropathogenic CgA *E. coli* strain. Ramchandani et al. [8] compared CgA *E. coli* strains previously isolated from women with acute cystitis [7] with a large collection of animal and environmental strains to see whether there were similarities between the 2 groups. The authors used 2 main genotypic methods, enterobacterial repetitive intergenic consensus (ERIC2) PCR and PFGE, to examine their culture collection. Of 495 iso-
lates, 128 (26%) had an ERIC2 PCR electrophoretic pattern that was indistinguishable from that of the human-associated CgA E. coli isolates—14 of the 128 isolates were resistant to TMP-SMZ. Cluster analysis of PFGE patterns showed that 1 of these 14 isolates, which was obtained from a cow, was 94% similar to one of the human-associated CgA E. coli strains isolated >10 years later, and the isolate was grouped into 1 cluster comprised of 5 human-associated UTI CgA isolates with PFGE patterns that were >80% similar. Ramchandani et al. [8] conclude that these observations are evidence that human-associated drug-resistant E. coli strains potentially have an origin in animals.

Although we agree with the basic premise of the article [8], we are not convinced that the data strongly support the asserted link between the animal- and human-associated strains. None of the tested CgA E. coli isolates collected from animals and from the environment had PFGE patterns that were identical to those of the isolates collected from humans. PFGE is generally considered to be the gold standard of molecular typing methods and is more discriminating than the PCR-based typing methods [9]. The authors’ conclusion that the isolate from the cow is linked to the isolate collected from a human >10 years later is a potential overinterpretation of the PFGE data, given the lack of a clear epidemiologic linkage between the 2 strains. The criteria for similarities among PFGE patterns should only be applied to bacterial isolates that are epidemiologically linked to each other (e.g., strains isolated from food and patients in a foodborne outbreak) [10].

Moreover, it appears to us that the isolates from the cow and the human are not as similar as is suggested, given that there are differences in several PFGE bands between the 2 isolates [8, figure 2]. Further evidence that the animal-associated and environmental strains were not linked to the human-associated strains was the absence of identical matches in the antimicrobial susceptibility and virulence profiles. The findings of the study would have been much more convincing if there had been an epidemiologic link between the animals and humans and if the strains had had identical PFGE patterns.

In attempting to determine the reservoir of uropathogenic E. coli, it is prudent to use sensitive subtyping methods such as PFGE for screening specimens collected from animals, food, and the environment for culture. In the event that source isolates are found that match the uropathogenic E. coli, the next step would involve use of secondary and tertiary enzymes in PFGE and determination of the antibiotic resistance and virulence profiles of the matching isolates. It is preferable of course to study isolates that have a clear epidemiologic relationship, but study of isolates separated by time or place is reasonable and often necessary when one is investigating the origin of pathogenic strains of bacteria, as long as the subtyping methods used are highly discriminatory and several subtyping reactions are performed before a conclusion is reached.

Uropathogenic E. coli, at least in some cases, likely originate from foods of animal origin or from food or water contaminated with feces (the most common type of food and water contamination), especially because there is no other plausible explanation as to how most persons become colonized. This makes sense for young college women, given their high incidence of UTI and frequent use of common dining areas. Contaminated food products are recognized sources of community outbreaks of infections due to enteric pathogens, such as E. coli O157:H7, Salmonella species, and Campylobacter species, including episodes caused by drug-resistant strains [3]. However, it has not been clearly demonstrated that uropathogenic human-associated E. coli strains come from animals. We agree with Ramchandani et al. [8] that demonstration of a link between animal colonization with multidrug-resistant uropathogens and human UTI would have major public health implications and add fire to the debate about the use of antibiotics in animals and the subsequent impact on resistance in human disease [3]. Clearly, this is an area that warrants further research using modern tools of molecular epidemiology.

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References