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Genetic relatedness of multidrug-resistant *Escherichia coli* cultured from geographically diverse outpatient, midstream urine specimens

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Abstract

Genomic DNA from 70 demographically matched geographically diverse pairs of urinary isolates of antimicrobial-susceptible and multidrug-resistant *Escherichia coli* was restricted using *Xba*I and analyzed by pulsed-field gel electrophoresis. Antimicrobial-susceptible isolates demonstrated limited genetic relatedness, whereas 2 epidemiologic clusters containing a total of 40 isolates (57.1%) were identified among the multidrug-resistant isolates.

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Urinary tract infections (UTIs) are one of the most frequently acquired human bacterial infections. Escherichia coli is the primary pathogen causing UTIs in both outpatients and inpatients, accounting for 75% to 90% of isolates cultured from midstream urine specimens of patients with uncomplicated UTIs (Gupta et al., 2001; Nicolle, 2001). The recent emergence of multidrug-resistant isolates of E. coli cultured from midstream urine specimens has been well documented, and published studies suggest that the prevalence of multidrug-resistant isolates may be increasing in the United States and Canada (Karlowsky et al., 2006; Karlowsky et al., 2002; Sahm et al., 2001). Multidrug-resistant isolates of E. coli from urine are typically resistant to ampicillin and trimethoprim-sulfamethoxazole (SXT), less frequently resistant to fluoroquinolones (e.g., ciprofloxacin), and rarely resistant to nitrofurantoin (Karlowsky et al., 2006; Karlowsky et al., 2003; Sahm et al., 2001). When present, fluoroquinolone resistance in E. coli is identified predominantly in multidrug-resistant isolates (Karlowsky et al., 2002; Karlowsky et al., 2003; Sahm et al., 2001). Clonal expansion and

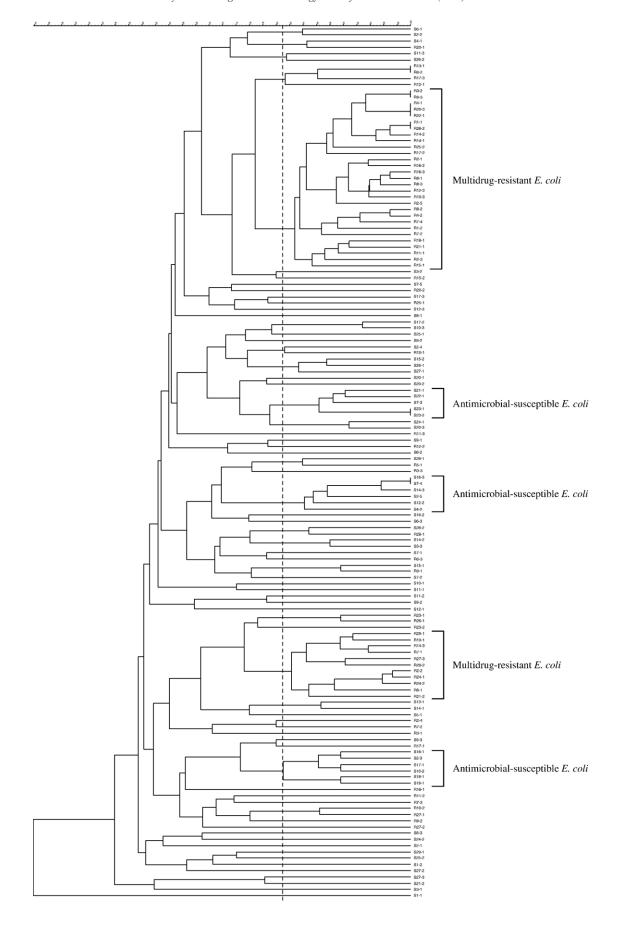
Although substantial published literature exist describing trends in in vitro antimicrobial susceptibility testing for urinary isolates of *E. coli*, only a few publications have reported on the relatedness of antimicrobial-resistant isolates of *E. coli* (Burman et al., 2003; Johnson et al., 2002; Manges et al., 2001; Manges et al., 2006; Petrof et al., 2002; Phillips et al., 1988). The intent of this study was to compare the degree of genetic relatedness of outpatient urinary isolates of geographically diverse demographically matched sets of isolates of *E. coli* with antimicrobial-susceptible (susceptible to ampicillin, SXT, and ciprofloxacin) and multidrug-resistant (resistant to ampicillin, SXT, and ciprofloxacin) phenotypes.

The isolates of *E. coli* selected for testing were chosen from frozen stock culture collections of 2 chronologically overlapping UTI antimicrobial surveillance studies; each isolate selected for the current study was originally cultured from an outpatient midstream urine specimen between January and June 2004 in 1 of 29 medical center laboratories (22 US, 7 Canadian) (Karlowsky et al., 2006;

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spread of multidrug-resistant isolates may potentially occur when patients infected or colonized with such an isolate receive any antimicrobial agent for which the isolate harbors resistance. Multidrug-resistant isolates may complicate the therapeutic management of patients with infection by increasing morbidity and treatment costs, and by limiting therapeutic options.

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