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Escherichia coli Sequence Type 131 Is a Dominant, Antimicrobial-Resistant Clonal Group Associated with Healthcare and Elderly Hosts

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Abstract

OBJECTIVE—To determine prevalence, predictors, and outcomes of infection due to *Escherichia coli* sequence type ST131.

DESIGN—Retrospective cohort.

SETTING—All healthcare settings in Olmsted County, Minnesota (eg, community hospital, tertiary care center, long-term care facilities, and ambulatory clinics).

PATIENTS—Ambulatory and hospitalized children and adults with extraintestinal *E. coli* isolates.

METHODS—We analyzed 299 consecutive, nonduplicate extraintestinal *E. coli* isolates submitted to Olmsted County laboratories in February and March 2011. ST131 was identified using single-nucleotide polymorphism polymerase chain reaction and further evaluated through pulsed-field gel electrophoresis. Associated clinical data were abstracted through medical record review.

RESULTS—Most isolates were from urine specimens (90%), outpatients (68%), and community-associated infections (61%). ST131 accounted for 27% of isolates overall and for a larger proportion of those isolates resistant to fluoroquinolones (81%), trimethoprim-sulfamethoxazole (42%), gentamicin (79%), and ceftriaxone (50%). The prevalence of ST131 increased with age (accounting for 5% of isolates from those 11–20 years of age, 26% of isolates from those 51–60 years of age, and 50% of isolates from those 91–100 years of age). ST131 accounted for a greater proportion of healthcare-associated isolates (49%) than community-associated isolates (15%) and for fully 76% of *E. coli* isolates from long-term care facility (LTCF) residents. Multivariable predictors of ST131 carriage included older age, LTCF residence, previous urinary tract infection, high-complexity infection, and previous use of fluoroquinolones, macrolides, and extended-spectrum cephalosporins. With multivariable adjustment, ST131-associated infection outcomes included receipt of more than 1 antibiotic (odds ratio [OR], 2.54 [95% confidence interval (CI),

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1.25–5.17]) and persistent or recurrent symptoms (OR, 2.53 [95% CI, 1.08–5.96]). Two globally predominant ST131 pulsotypes accounted for 45% of ST131 isolates.

CONCLUSIONS—ST131 is a dominant, antimicrobial-resistant clonal group associated with healthcare settings, elderly hosts, and persistent or recurrent symptoms.

The rapid worldwide increase in antimicrobial resistance among *Escherichia coli* has exceeded the pace of new antimicrobial development. The increasing prevalence of antimicrobial-resistant *E. coli* has been driven largely by expansion of a single clonal group, sequence type (ST) 131. Although ST131 has been reported globally,[1–5] and its expansion is recognized as a pandemic,[6] it has received comparatively little attention in the United States.

E. coli ST131 exhibits serotype O25b:H4 and is associated with fluoroquinolone resistance, sometimes coupled with coresistance to aminoglycosides, trimethoprim-sulfamethoxazole, and extended-spectrum cephalosporins,[4,6,7] the latter usually being mediated by the CTX-M-15 extended-spectrum β-lactamase (ESBL).[8] In addition to its multidrug resistance phenotype, the ST131 clonal group is characterized by genes for multiple virulence factors[9] and a wide diversity of pulsed-field gel electrophoresis (PFGE) profiles, several of which are highly prevalent and globally distributed.[10]

It is not clear what features of the pathogen, host population, and/or environment have enabled ST131 to disseminate so broadly and to expand so rapidly. Both person-to-person[11] and foodborne[12] transmission of ST131 have been documented. Furthermore, ST131 has been found in both ambulatory and inpatient settings, but most molecular epidemiological studies to date have used convenience samples or highly selected samples.[4,9] Consequently, it is not known whether ST131 is associated with certain host characteristics (and if so, which) or whether it is primarily found in health-care-associated or community-associated infection. Because the sources, risk factors, and transmission pathways of ST131 are poorly defined, it is challenging to design preventive interventions to curb its emergence and spread or to know when to anticipate its presence.

In our geographic area, we have noted a dramatic increase since 2008 in fluoroquinolone-resistant *E. coli* that was highly suggestive of ST131 expansion.[13] To better understand the reservoirs and transmission dynamics of ST131, we collected and analyzed an unbiased population of extraintestinal clinical *E. coli* isolates to determine the prevalence, clonality, predictors, and outcomes of ST131 infection across hospital and community settings.

METHODS

Specimen Collection

We collected and analyzed all nonduplicate extraintestinal *E. coli* isolates from all specimen types submitted to Olmsted County laboratories (serving Mayo Clinic and Olmsted Medical Center, the only healthcare centers in Olmsted County, Minnesota) during February and March 2011. These 2 hospital-affiliated microbiology laboratories handle specimens from all outpatient offices in the county. We included only 1 isolate per patient from children and adults who provided general research authorization (because under the Minnesota Research Authorization Law, all patients at both medical facilities are asked permission to have their medical records used for research purposes). Isolates were not restricted to Olmsted County residents. Antimicrobial susceptibility testing was performed by the participating clinical microbiology laboratories[14] and was interpreted using breakpoints recommended by the Clinical and Laboratory Standards Institute.[15] Isolates that were resistant or intermediate to a given antimicrobial were considered nonsusceptible. The Mayo Clinic and Olmsted Medical Center Institutional Review Boards approved this study.

Clinical Data Abstraction

We abstracted the following demographic and clinical variables from inpatient and outpatient medical records for assessment as risk factors and effect modifiers: patient age and sex, specimen type, antimicrobial use within 7 months before culture specimen collection, service prescribing antibiotics, site of infection acquisition (nosocomial, healthcare associated, or community associated, as defined below), comorbidities, illness severity, recent surgical procedures, use of home healthcare services or urinary catheters, length of hospitalization at time of culture collection, and zip code of residence.

Infections were categorized by presumed site of acquisition as follows: nosocomial (collected from inpatients more than 72 hours after hospitalization), healthcare associated (collected from outpatients who had been hospitalized within 90 days before culture specimen collection; were residents of a nursing home or long-term care facility [LTCF]; and/or had received home intravenous therapy, wound care, specialized nursing, urinary catheterization, dialysis, or chemotherapy within 30 days before specimen collection), and community-associated (collected from outpatients or from inpatients hospitalized for less than 72 hours without any healthcare-associated risk factors). An infection was considered noncomplex if *E. coli* was cultured from a urine specimen, the patient was treated as an outpatient, and the host was immunocompetent and lacked genitourinary abnormalities (other than neurogenic bladder) and evidence of upper urinary tract infection. An infection was considered complex if *E. coli* was cultured from any nonurine site (blood, peritoneal or intra-abdominal abscess fluid, bone, or bronchial washings) or if the patient was immunocompromised or required hospitalization, had significant genitourinary abnormalities other than neurogenic bladder (eg, severe ureteral stricture and ureteral stent), or had upper urinary tract infection.

Assessed outcomes (as defined below) within 30 days of initial culture specimen collection were cure, persistent or recurrent symptoms, number and type of antibiotics prescribed, and hospitalization or repeated healthcare contact for any reason. Death within 6 months of initial culture was also recorded. Cure was defined as resolution of symptoms or documented clearance of *E. coli* from a sterile site within 30 days of initial culture. Colonization was defined as *E. coli* cultured from a urine specimen obtained from a patient without any signs or symptoms of clinical infection. Colonizing isolates were excluded from analyses of cure or treatment failure.

Molecular Characterization

Major *E. coli* phylogenetic group (A, B1, B2, and D) was determined by triplex polymerase chain reaction (PCR).[16] Three resistance-associated *E. coli* clonal groups—ST131, clonal group A (CGA), and O15:K52:H1—were identified by using both PCR-based detection of clonal group–specific single-nucleotide polymorphisms in selected housekeeping genes[17] and a newly described 2-locus clonal typing strategy based on sequencing of *fumC* and *fimH* (ie, CH typing).[18] ST131 isolates were further resolved by *Xba*I PFGE analysis.[10]

Statistical Analysis

Comparisons between ST131 and non-ST131 isolates were evaluated using Wilcoxon rank-sum, χ^2, and Fisher exact tests. These comparisons were further evaluated using univariable and multivariable logistic regression models. A multivariable model to predict an isolate's ST131 status was developed using a stepwise selection procedure, with the *P* value for a variable to enter or leave the model set at .05. Univariable and multivariable logistic regression models were also used to evaluate the association of ST131 isolates with various outcomes. All tests were 2-sided. *P* values <.05 were considered to be statistically significant.

RESULTS

ST131 Prevalence

Among the 299 study isolates, 268 (90%) were from urine specimens, 203 (68%) were from outpatients, and 180 (61%) were from community-associated infections. ST131 accounted for 80 (27%) of the isolates overall and for an even higher proportion of those isolates resistant to fluoroquinolones (FQs; 71 [81%] of 88), trimethoprim-sulfamethoxazole (TMP-SMX; 37 [42%] of 88), gentamicin (23 [79%] of 29), and ceftriaxone (8 [50%] of 16). By patient age, the prevalence of ST131 decreased from 22% among those 0–10 years old to 5% among those 11–20 years old ($P = .19$) but then increased linearly up to 50% among those 91–100 years old ($P < .001$; Figure 1). By site of acquisition, ST131 prevalence was lowest among community-associated infections (27 [15%] of 180), slightly higher among nosocomial infections (5 [26%] of 19), and highest among healthcare-associated infections (48 [49%] of 98). ST131 accounted for fully 28 (76%) of 37 isolates from LTCF residents.

PFGE of ST131 Isolates

PFGE analysis of the 80 ST131 isolates identified 38 distinct pulsotypes (Figure 2). The predominant pulsotypes were 968 and 800, which accounted for 23 (29%) and 13 (16%) of the ST131 isolates, respectively. Together, these 2 types accounted for half (36 [51%] of 71) of the FQ-resistant ST131 isolates but 0 of the 9 FQ-susceptible ST131 isolates ($P = .004$). Pulsotypes 968 and 800 also accounted for a numerically greater proportion of healthcare-associated isolates (23 [48%] of 48) than community-associated isolates (9 [33%] of 27; $P = .24$). The *fimH*30 allele (which identifies the H30 ST131 subclone)[18] was present in 70 (88%) of the 80 ST131 isolates, including 35 (97%) of 36 isolates of pulsotypes 968 or 800 and 70 (99%) of 71 of the FQ-R ST131 isolates. In contrast, *fimH*30 was absent from the 9 FQ-susceptible ST131 isolates, which instead contained *fimH* alleles 22 (4 isolates; 44%), 41 (2 isolates; 22%), or 207 (1 isolate; 11%) or novel variants (2 isolates; 22%; Figure 2).

Antimicrobial Susceptibility

Compared with non-ST131 isolates, ST131 isolates exhibited a significantly higher prevalence of resistance to ampicillin, ampicillin-sulbactam, cefazolin, ceftriaxone, gentamicin, FQs, and TMP-SMX (Table 1). Approximately 80% of ST131 isolates were resistant to FQs, ampicillin, and 3 or more drugs, and nearly half were resistant to TMP-SMX. In contrast, resistance to nitrofurantoin, extended-spectrum cephalosporins, and carbapenems was infrequent and did not differ significantly in prevalence between ST131 and non-ST131 isolates.

Risk Factors for ST131

Univariable analysis indicated that, in comparison with patients with non-ST131 isolates, those with ST131 isolates were older (per 10 years: odds ratio [OR], 1.32 [95% confidence interval (CI), 1.17–1.49]), more likely to be LTCF residents (OR, 12.50 [95% CI, 5.56–28.10]), and more likely to have hypertension (OR, 2.21 [95% CI, 1.30–3.75]), genitourinary anomalies (OR, 1.90 [95% CI, 1.14–3.20]), cancer (OR, 2.17 [95% CI, 1.20–3.90]), recent surgery (OR, 2.64 [95% CI, 1.39–5.04]), recurrent urinary tract infections (UTIs) within 30 days before culture specimen collection (OR, 3.54 [95% CI, 1.80–6.98]), and recent exposure to various antimicrobial agents (Table 2). Correspondingly, their index infection episode also was significantly more likely to be healthcare associated (OR, 5.44 [95% CI, 3.08–9.61]) and complex (OR, 2.53 [95% CI, 0.92–6.96]). In contrast, sex, specimen type, and inpatient or outpatient location at time of culture were not associated with ST131.

Multivariable models were developed using a stepwise selection procedure, with all variables in Table 2 used as candidate predictors (model 1). Because model 1 unexpectedly identified earlier use of a macrolide antibiotic as a risk factor for ST131, a separate model that excluded macrolide use was developed (model 2). Both models identified age, LTCF residence, UTI within previous 30 days, and complex infection as statistically significant predictors of ST131 (Table 3). However, as predictors of ST131, the 2 models identified different antibiotic exposures, including extended-spectrum cephalosporins (OR, 4.28 [95% CI, 1.60–11.49]) and macrolides (OR, 7.48 [95% CI, 1.97–28.43]) for model 1 and extended-spectrum cephalosporins (OR, 3.34 [95% CI, 1.24–8.97]) and FQs (OR, 2.42 [95% CI, 1.19–4.94]) for model 2.

Outcomes Associated with ST131

Compared with patients with non-ST131 isolates, those with ST131 isolates were treated, on average, with a greater number of antibiotics. That is, the mean number of antibiotics prescribed within 30 days after culture specimen collection was 1.3 for patients with non-ST131 isolates versus 1.8 for patients with ST131 isolates ($P < .001$). Additionally, compared with patients with non-ST131 isolates, those with ST131 isolates were more likely to have persistent or recurrent symptoms after therapy, were less likely to be cured, and had higher mortality (Table 4). In multivariable models of these outcomes after adjustment for age, LTCF residence, history of UTI, complex infection, and earlier fluoroquinolone use, ST131 remained an independent predictor of receiving more than 1 antibiotic within 30 days after culture specimen collection (OR, 2.54 [95% CI, 1.25–5.17]) and of having persistent or recurrent symptoms within 30 days after therapy (OR, 2.53 [95% CI, 1.0–5.96]) but was no longer significantly associated with treatment failure or mortality (Table 4).

DISCUSSION

In this retrospective cohort study involving nearly 300 consecutive patients with extraintestinal *E. coli* infection, we found ST131 to be a dominant, antimicrobial-resistant clonal group associated with healthcare, elderly hosts, and persistent or recurrent symptoms. Specifically, we found that ST131 infection was associated with older age, LTCF residence, complex infection, a history of UTI, previous antimicrobial use, receipt of more than 1 antibiotic within 30 days after diagnosis, and having recurrent or persistent symptoms after therapy. In addition, we found a high prevalence of 2 predominant PFGE types among the ST131 isolates, which suggests that our region, like others in the United States, is experiencing the global ST131 pandemic.

In our cohort, ST131 isolates were more than twice as common among healthcare-associated infections as they were among community-associated infections. This suggests that, in our area, ST131 is primarily a healthcare-associated clonal group. This conflicts with the many studies that have identified ST131, especially when harboring ESBL genes, as community-associated.[11,19,20] This discrepancy likely stems from differences in sample type and collection, because our isolates were collected consecutively, were not selected on the basis of patient or pathogen characteristics, and included few ESBL-producing strains, whereas in other studies, isolates were often selected on the basis of specific resistance phenotypes or patient characteristics. Alternatively, geographic variation may exist in the relative prevalence of ST131 between hospital and community settings.

In our cohort, LTCF residence was the strongest predictor of ST131 infection, with LTCF residents having 8-fold greater multivariable odds of having ST131 compared with non-LTCF residents. Although a LTCF reservoir for ST131 has been noted previously,[21–24] our data are the first, to our knowledge, to demonstrate that LTCF residence is a risk factor for ST131 in the United States. LTCFs are well-known sources for other antimicrobial-resistant

pathogens[23,25–28] and for outbreaks in acute care hospitals and other settings.[29–31] The increasing prevalence of ST131 that we observed among patients older than 65 years is consistent with the association of ST131 with LTCFs. It is likely that extensive antibiotic exposure, close contact with other antibiotic-exposed individuals, and age- and health-associated alterations in intestinal microbiota[32] all contribute to the high prevalence of ST131 among the elderly population.

Cure rates and mortality did not differ between patients with ST131 versus non-ST131 infections after adjustment for host characteristics such as age and LTCF residence, which suggests that ST131 is not more virulent, on average, than non-ST131 *E. coli*. This is supported by recent in vivo studies that found no difference in experimental virulence between ST131 and other extraintestinal *E. coli* in mice,[33] *Caenorhabitis elegans*,[34] and zebrafish.[34] Similarly, no difference in mortality associated with ST131 versus non-ST131 was seen in a recent study of patients with ESBL *E. coli* bacteremia.[19]

However, here ST131 was associated with having recurrent or persistent symptoms, which is likely attributable to receiving inappropriate empirical therapy. Among patients with ST131, of whom 40% had received a FQ in the recent past, a quarter received empirical treatment with FQs, which are largely ineffective against this clonal group, and required a change in antibiotic regimen after culture and susceptibility results became available. This phenomenon doubtless contributed to the greater number of antibiotics received by patients with ST131 infection compared with non-ST131 infection. This suggests that many prescribers are unaware of the increasing prevalence of FQ-resistant pathogens (including ST131) and that earlier FQ therapy selects for them.

Molecular typing showed that more than 80% of the ST131 isolates represented the *fimH*30 subclone, of which half were pulsotype 968 or 800. Together, these predominant pulsotypes accounted for nearly half of the ST131 isolates that were FQ resistant or caused a healthcare-associated infection and over one-third of community-associated ST131 isolates. We speculate that, although sporadic emergence and expansion of new ST131 types is occurring in hospital and community settings alike, globally dominant pulsotypes 968 and 800 are expanding primarily within healthcare facilities and LTCFs, perhaps because of suboptimal infection control practices and extensive (and often inappropriate) antimicrobial use.

Limitations of this study include that it was from a single center and analyzed primarily isolates obtained from urine specimens. Thus, our results may not be generalizable to other locales or other clinical syndromes, such as *E. coli* bacteremia or meningitis. Additionally, because the study was retrospective, we likely were unable to accurately distinguish colonization from infection in all patients and may have misclassified some of the outcomes. Finally, the study's observational nature precludes confident assessment of causality; all associations are simply that, with multiple possible explanations.

Despite these limitations, the study results have important clinical implications. We have identified significant risk factors for ST131 infection; this can assist with more timely and appropriate empirical treatment of patients with ST131 infection, which, in turn, has the potential both to minimize the spread of ST131 and to improve outcomes of ST131-associated infections. In addition, we have confirmed that, in the United States, as in Europe, healthcare settings and LTCFs likely are reservoirs and sites of ongoing transmission of ST131, including its globally predominant pulsotypes 968 and 800. Our results highlight the necessity of implementing enhanced antimicrobial stewardship and infection control interventions in these settings to reduce selection for and interrupt transmission of the highly successful antimicrobial-resistant ST131 clonal group.

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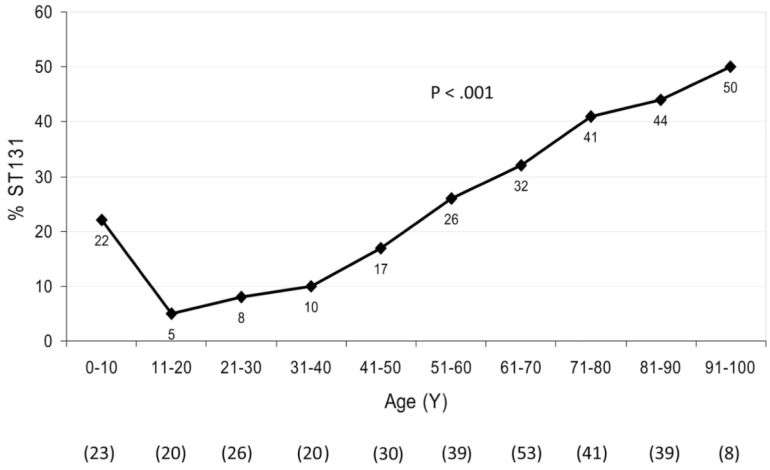

FIGURE 1.

Prevalence of sequence type (ST) 131 according to age cohort in years (Y). Percentage of isolates within each age cohort that are ST131 is shown above the corresponding point in the graph. The number of patients per age cohort is shown in parentheses below the *X*-axis. The *P* value is from a univariable logistic regression model for the association of age with ST131 status.

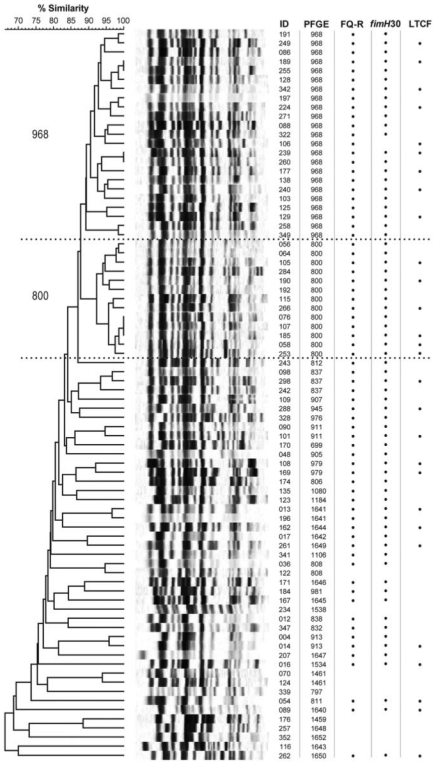

FIGURE 2.

Pulsed-field gel electrophoresis (PFGE) profile dendrogram for 80 sequence type (ST) 131 *Escherichia coli* isolates from Olmsted County, Minnesota, February–March 2011. Bullets indicate the presence of the characteristic, and blank spaces indicate the absence of the characteristic. FQ-R, fluoroquinolone resistant; LTCF, long-term care facility.

TABLE 1

Antimicrobial Resistance by ST131 Status among Patients in Olmsted County, Minnesota, February–March 2011

	No. of isolates nonsusceptible to indicated agent/no. of isolates tested (%)		
Antimicrobial	**ST131**	**Non-ST131**	***P*** [a]
Ampicillin	65/80 (81)	91/219 (42)	<.001
AMP-SLB	54/70 (77)	73/198 (37)	<.001
Cefazolin	45/79 (57)	48/218 (22)	<.001
Ceftriaxone	8/71 (11)	8/188 (4)	.046
Gent	23/80 (29)	6/219 (3)	<.001
FQ	71/80 (89)	17/219 (8)	<.001
TMP-SMX	37/80 (46)	51/219 (23)	<.001
Nitrofurantoin	3/68 (4)	5/206 (2)	.41
Carbapenem	0/71 (0)	3/187 (2)	.56
MDR			
Resistant to ≥3 drugs	63/80 (79)	60/219 (27)	<.001
Resistant to ≥5 drugs	30/80 (38)	12/219 (5)	<.001

NOTE. AMP-SLB, ampicillin-sulbactam; FQ, fluoroquinolone; Gent, gentamicin; MDR, multidrug resistant; TMP-SMX, trimethoprim-sulfamethoxazole.

[a] *P* values were determined by χ^2 or 2-tailed Fisher exact test.

TABLE 2

Univariable Analyses of Epidemiological Correlates of Having ST131 versus Non-ST131 *Escherichia coli* among Patients in Olmsted County, Minnesota, February–March 2011

Variable	No. (%) of isolates		OR (95% CI)	*P*
	ST131 (*n* = 80)	Non-ST131 (*n* = 219)		
Age (10-year increase)	…	…	1.32 (1.17–1.49)	<.001
Sex				
Female	63 (79)	175 (80)	1.0 (reference)	.83
Male	17 (21)	44 (20)	1.07 (0.57–2.01)	
Race (*n* = 266)				
White	62 (90)	181 (92)	1.0 (reference)	
Other	7 (10)	16 (8)	1.28 (0.50–3.25)	.61
Comorbidity				
Hypertension	51 (64)	97 (44)	2.21 (1.30–3.75)	.003
Diabetes	22 (28)	50 (23)	1.28 (0.72–2.30)	.40
Coronary artery disease	18 (23)	32 (15)	1.70 (0.89–3.23)	.11
Genitourinary anomalies	43 (54)	83 (38)	1.90 (1.14–3.20)	.01
Cancer	25 (31)	38 (17)	2.17 (1.20–3.90)	.01
Dialysis	3 (4)	2 (1)	4.23 (0.69–25.78)	.12
CVC	6 (8)	7 (3)	2.46 (0.80–7.54)	.12
Urinary catheter	15 (19)	24 (11)	1.88 (0.93–3.79)	.08
Surgical procedure within prior 30 days	21 (26)	26 (12)	2.64 (1.39–5.04)	.003
Hospitalization within prior 30 days	8 (10)	21 (10)	1.05 (0.44–2.47)	.91
Recurrent UTI within prior 30 days	21 (26)	20 (9)	3.54 (1.80–6.98)	<.001
LTCF residence (*n* = 298)	28 (35)	9 (4)	12.50 (5.56–28.10)	<.001
Specimen type				
Urine	68 (85)	200 (91)	1.0 (reference)	
Other	12 (15)	19 (9)	1.86 (0.86–4.03)	.12
Location (*n* = 298)				
Outpatient	56 (70)	147 (67)	1.0 (reference)	
Inpatient	17 (21)	34 (16)	1.31 (0.68–2.54)	.42
ER	7 (9)	37 (17)	0.50 (0.21–1.18)	.11
Acquisition (*n* = 297)				
CA	27 (34)	153 (71)	1.0 (reference)	
HA	48 (60)	50 (23)	5.44 (3.08–9.61)	<.001
Nosocomial	5 (6)	14 (6)	2.02 (0.67–6.08)	.21
Illness severity (n = 293)				
Colonization	7 (9)	27 (13)	1.0 (reference)	
Noncomplex	52 (67)	159 (74)	1.26 (0.52–3.07)	.61
Complex	19 (24)	29 (13)	2.53 (0.92–6.96)	.07
Antimicrobials[a]				
Aminoglycoside	6 (8)	0	23.73 (3.37 to infinity)[b]	<.001

Variable	No. (%) of isolates		OR (95% CI)	*P*
	ST131 (*n* = 80)	Non-ST131 (*n* = 219)		
Antifungal	12 (15)	13 (6)	2.80 (1.22–6.42)	.02
Antiviral	5 (6)	12 (5)	1.15 (0.39–3.37)	.80
Carbapenem	9 (11)	4 (2)	6.81 (2.04–22.80)	.002
Clindamycin	2 (3)	5 (2)	1.10 (0.21–5.77)	.91
ESC	18 (23)	9 (4)	6.77 (2.90–15.83)	<.001
NSC	18 (23)	22 (10)	2.60 (1.31–5.16)	.006
Fluoroquinolone	32 (40)	31 (14)	4.04 (2.25–7.27)	<.001
Macrolide	9 (11)	4 (2)	6.81 (2.04–22.80)	.002
Metronidazole	12 (15)	9 (4)	4.12 (1.66–10.19)	.002
Nitrofurantoin	7 (9)	15 (7)	1.30 (0.51–3.33)	.58
Penicillin	9 (11)	21 (10)	1.20 (0.52–2.73)	.67
Piperacillin-tazobactam	6 (8)	4 (2)	4.36 (1.20–15.87)	.03
Tetracyclines	5 (6)	8 (4)	1.76 (0.56–5.54)	.33
TMP-SMX	11 (14)	27 (12)	1.13 (0.53–2.41)	.74
Vancomycin	12 (15)	5 (2)	7.55 (2.57–22.20)	<.001
Miscellaneous[c]	4 (5)	3 (1)	3.79 (0.83–17.32)	.09

NOTE. The denominator for each characteristic excludes missing or unknown values. CA, community associated; CI, confidence interval; CVC, central venous catheter; ESC, extended-spectrum cephalosporin; HA, healthcare associated; LTCF, long-term care facility; NSC, narrow-spectrum cephalosporin; OR, odds ratio; TMP-SMX, trimethoprim-sulfamethoxazole; UTI, urinary tract infection.

[a] Within 7 months before the specimen collection date.

[b] Obtained using exact logistic regression.

[c] Includes aztreonam, dapsone, daptomycin, linezolid, pentamidine, and praziquantel.

TABLE 3

Multivariable Analysis of Risk Factors for ST131 *Escherichia coli* among Patients in Olmsted County, Minnesota, February–March 2011

Model, variable	Odds ratio (95% confidence interval)	*P*
Model 1		
Age (per 10-year increase)	1.16 (1.00–1.35)	.04
LTCF residence	10.00 (3.75–26.68)	<.001
UTI in prior 30 days	4.11 (1.85–9.13)	<.001
Complex infection[a]	2.53 (1.17–5.47)	.19
Extended-spectrum cephalosporin	4.28 (1.60–11.49)	.004
Macrolides	7.48 (1.97–28.43)	.003
Model 2		
Age (per 10-year increase)	1.18 (1.01–1.36)	.03
LTCF residence	8.37 (3.11–22.50)	<.001
UTI 30 days prior	3.93 (1.77–8.71)	<.001
Complex infection[a]	2.43 (1.13–5.21)	.02
Extended-spectrum cephalosporin	3.34 (1.24–8.97)	.02
Fluoroquinolone	2.42 (1.19–4.94)	.02

NOTE. LTCF, long-term care facility; UTI, urinary tract infection.

[a]Colonization and noncomplex infection were combined to serve as the reference group. Candidate predictors included all variables shown in Table 2, with macrolides included (model 1) or excluded (model 2). Six patients without available data were excluded from this analysis.

TABLE 4

Univariable and Multivariable Analyses of Outcomes Associated with ST131 *Escherichia coli* among Patients in Olmsted County, Minnesota, February–March 2011

	No. of isolates associated with outcome/no. of isolates with available data (%)		OR (95% CI)		
Outcome	**ST131 (*n* = 80)**	**Non-ST131 (*n* = 219)**	**Unadjusted**	**Adjusted[a]**	**Adjusted *P***
More than 1 antibiotic[b]	38/80 (48)	57/219 (26)	2.57 (1.51–4.38)	2.54 (1.25–5.17)	.01
Healthcare contact[b] (*n* = 288)	32/77 (42)	63/211 (30)	1.67 (0.97–2.87)	0.79 (0.40–1.61)	.53
Cure[b] (*n* = 254)	51/70 (73)	163/184 (89)	0.35 (0.17–0.69)	0.52 (0.23–1.20)	.13
Persistent or recurrent symptoms[b] (*n* = 251)	20/69 (29)	20/182 (11)	3.31 (1.65–6.64)	2.53 (1.08–5.96)	.03
Mortality[c] (*n* = 292)	10/80 (13)	9/212 (4)	3.22 (1.26–8.26)	1.39 (0.43–4.52)	.59

NOTE. CI, confidence interval; OR, odds ratio.

[a] Separate multivariable models were constructed for each outcome. Each model included age, long-term care facility residence, urinary tract infection within the previous 30 days, complex infection, and previous fluoroquinolone use. Patients with missing data or colonization were excluded from analysis of cure or persistent symptoms.

[b] Within 30 days after index culture.

[c] Within 6 months after index culture.