Change in characteristics of community-onset ciprofloxacin-resistant *E. coli* isolates causing community-acquired acute pyelonephritis in South Korea

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Background

The aim of this study was to examine the change in characteristics of community-onset ciprofloxacin-resistant (CIP-R) E. coli isolates causing community-acquired acute pyelonephritis (CA-APN) in South Korea between 2010-2011 and 2017-2018.

Methods

- **Study design**
  - Study period: Mar 2010 – Feb 2011 & Sep 2017 – Aug 2018
  - Study hospitals: 12 hospitals during 2010-2011 & 8 hospitals during 2017-2018
- **Collection of *E. coli* isolates**
  - *E. coli* samples isolated from the blood or urine were collected from patients with CA-APN aged 19 years and more.

  **Definition of CA-APN: i) presence of fever (≥37.8℃) ii) pyuria (≥5-9 WBC/HPF)*
  - One isolate was collected from each patient.
  - If *E. coli* was cultured simultaneously in blood and urine, the strains detected in the blood were chosen.
- **Antimicrobial susceptibility testing**
  - Disk diffusion test was performed for ampicillin, amikacin, gentamicin, tobramycin, trimethoprim/sulfamethoxazole, cefepime, cefotaxime, cefoxitin, ceftazidime.
  - The breakpoints were defined in reference to the according to the Clinical and Laboratory Standards Institute (CLSI), and R or I were defined as resistance.
- **Characterization of CIP-R *E. coli* isolates**
  - Phylogenetic typing, multilocus sequence typing (MLST), and molecular characterization of β-lactamase resistance and plasmid-mediated quinolone resistance (PMQR) determinants were performed.

Results

- A total of 346 and 300 *E. coli* isolates were collected during 2017-2018 and 2010-2011, respectively.
- Among them, 76 (22.0%) and 77 (25.7%) were CIP-R.

Table 1. Change in antibiotic susceptibility of CIP-R *E. coli* isolates

	Isolates from 2010-2011	Isolates from 2017-2018	*P*-value
Ampicillin	56/74 (75.7)	77/77 (100)	<0.001
Amikacin	5/62 (8.1)	0/77 (0)	0.016
Gentamicin	40/76 (52.6)	47/77 (61.0)	0.329
Tobramicin	41/71 (57.7)	47/77 (61.0)	0.684
Trimethoprim/ sulfamethoxazole	42/76 (55.3)	48/77 (62.3)	0.414
Cefepime	18/72 (25.0)	60/77 (77.9)	<0.001
Cefotaxime	17/71 (23.9)	60/77 (77.9)	<0.001
Cefoxitin	19/57 (33.3)	7/77 (9.1)	<0.001
Ceftazidime	19/75 (25.3)	32/77 (41.6)	0.034

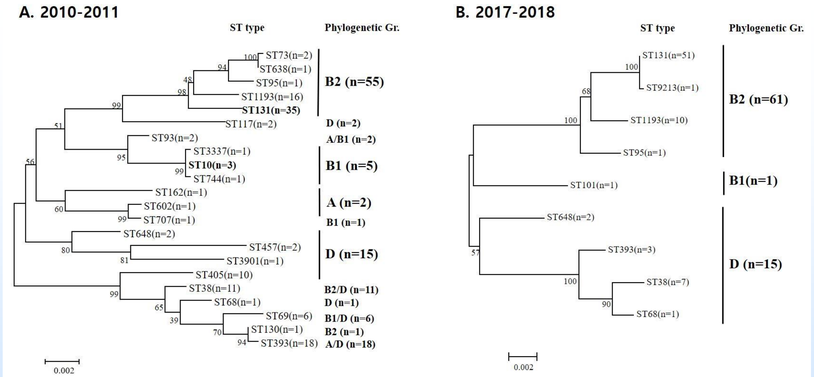

Figure 1. Phylogenetic trees for CIP-R *E. coli* isolates

Table 2. Change in molecular characteristics of CIP-R *E. coli* isolates

	Isolates from 2010-2011 (n=76)	Isolates from 2017-2018 (n=77)	*P*-value
Phylogenic groups			
A	4 (5.3)	0 (0)	<0.001
B1	4 (5.3)	1 (1.3)	-
B2	34 (44.7)	61 (79.2)	-
D	44 (44.7)	15 (19.5)	-
Major clones by MLST			
ST131	21 (27.6)	51 (66.2)	<0.001
ST393	14 (18.4)	3 (3.9)	0.004
ST1193	8 (10.5)	10 (13.0)	0.637
ST38	6 (7.9)	7 (9.1)	0.791
ESBL/PABL			
Total	18 (23.7)	61 (79.2)	<0.001
CTX-M-14	8 (10.5)	30 (39.0)	<0.001
CTX-M-15	10 (13.2)	30 (39.0)	<0.001
CMY-2	2 (2.6)	1 (1.3)	0.620
PMQR determinants			
Total	9 (11.8)	31 (40.3)	<0.001
aac(6')-1b-cr	7 (9.2)	28 (36.4)	<0.001
qnrB	1 (1.3)	0 (0)	0.497
qnrS	0 (0)	3 (3.9)	0.245

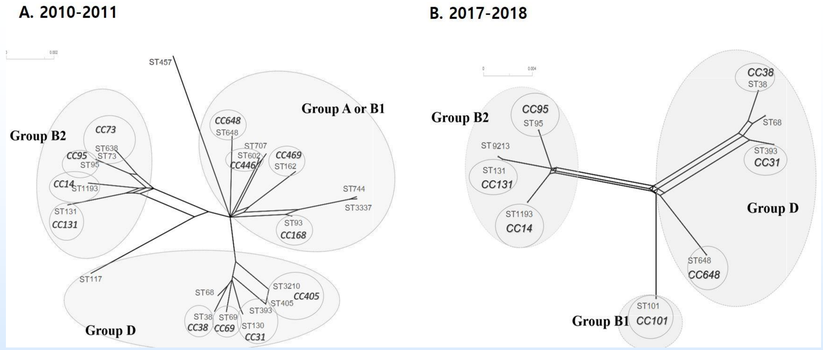

Figure 2. Clonal clusters for CIP-R *E. coli* isolates

Conclusions: Among uropathogenic CIP-R E. coli isolates in South Korea, ST131 predominance had become more prominent and the proportion of containing ESBL/PABL and/or PMQR determinants had increased.