

Analysis of Co-Resistance Among *Escherichia coli* Urine Isolates From Female Outpatients in the United States

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Introduction

- The Centers for Disease Control and Prevention Antimicrobial Resistance (AMR) Threats Report (2019) lists extended-spectrum β-lactamase-producing (ESBL+) Enterobacteriales as a serious health threat¹
- In the past 10 years, there has been a substantial increase in AMR and multi-drug resistance (MDR) among uropathogens from community-acquired uncomplicated urinary tract infections (uUTIs), including ESBL+ Enterobacteriales²⁻⁴
- This study was designed to assess *Escherichia coli* (*E. coli*) urine culture isolates from female outpatients in the United States (US) for co-resistance, including AMR to 2, 3, and 4 drug classes

Methods

- This was a retrospective, cross-sectional study of 30-day non-duplicate *E. coli* urine culture isolates from female outpatients with presumed uUTI (≥ 12 years of age) at 304 US facilities
- Eligible patients had ≥ 3 months of data from 2011–2019, recorded in the BD (Becton, Dickinson and Company) Insights Research Database (Franklin Lakes, NJ USA)
- Index non-susceptible (NS) *E. coli* isolates from urine cultures were defined as follows:
 - ESBL+ by a commercial panel or NS (intermediate/resistant) to ceftriaxone, cefotaxime, ceftazidime, or cefepime
 - NS to any of: fluoroquinolones (FQs), trimethoprim/sulfamethoxazole (SXT), or nitrofurantoin (NFT)⁶
- Microbiological co-resistance phenotypes were characterized in isolates NS to 2, 3, and 4 of the resistance phenotypes assessed
- Results are presented for all combinations of co-resistance evaluated, when starting with one resistance phenotype

Results

- In total, 1,513,882 non-duplicate (30-day) *E. coli* isolates were evaluated, of which 6.4% were ESBL+, and 21.1%, were NS to FQ, 25.4% were NS to SXT, and 3.7% were NS to NFT
 - 856,918 of isolates had at least 1 resistance phenotype

References

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- Among the ESBL+ non-duplicate outpatient (30-day) *E. coli* urine culture isolates evaluated (Table):
 - 72.4% of isolates demonstrated co-resistance to FQ NS
 - 56.7% of isolates demonstrated co-resistance to SXT NS
 - 46.6% of isolates demonstrated co-resistance to FQ NS+SXT NS

Table. Co-Resistance Phenotype Combinations Observed Among *E. coli* Isolates From Urine (2011–2019)

Starting resistance phenotype, n (%)	ESBL+	FQ NS	SXT NS	NFT NS	FQ NS + SXT NS	FQ NS + NFT NS	SXT NS + NFT NS	NS to all 4 phenotypes
ESBL+	96,306 (100)	69,687 (72.4)	54,626 (56.7)	11,433 (11.9)	44,879 (46.6)	9053 (9.4)	7676 (8.0)	6528 (6.8)
FQ NS	319,354 (100)	69,687 (21.8)	164,853 (51.6)	25,471 (8.0)			15,648 (4.9)	6528 (2.0)
SXT NS	384,304 (100)	54,626 (14.2)	164,853 (42.9)	26,179 (6.8)		15,756 (4.1)		6528 (1.7)
NFT NS	56,954 (100)	11,433 (20.1)	25,471 (44.7)	26,179 (46.0)	15,605 (27.4)			6528 (11.5)

Note: 856,918 non-duplicate (30-day) *E. coli* isolates (with at least 1 resistance phenotype) were evaluated. Some isolates had overlapping susceptibilities/antimicrobial resistance types, hence individual phenotype totals do not reflect total number of isolates evaluated. The categories are not mutually exclusive as the isolates are grouped based on the phenotype observed.

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Results (continued)

- Of ESBL+ isolates (96,306), 72.4% were co-resistant to FQ, 56.7% to SXT, and 11.9% to NFT
 - Of the ESBL+ isolates, 46.6% were co-resistant to FQ+SXT, 9.4% to FQ+NFT, and 8.0% to SXT+NFT
 - 6.8% of ESBL+ isolates (with resistance to > 1 phenotype) demonstrated co-resistance to all 4 phenotypes
- For FQ NS isolates (319,354), 21.8% were also ESBL+, 51.6% were co-resistant to SXT, and 8.0% to NFT
 - Of the FQ NS isolates, 4.9% were co-resistant to SXT+NFT
 - 2.0% of FQ NS isolates (with resistance to > 1 phenotype) demonstrated co-resistance to all 4 phenotypes
- For SXT NS isolates (384,304), 14.2% were also ESBL+, 42.9% were co-resistant to FQ, and 6.8% to NFT
 - Of the SXT NS isolates, 4.1% were co-resistant to FQ+NFT
 - 1.7% of SXT NS isolates (with resistance to > 1 phenotype) demonstrated co-resistance to all 4 phenotypes
- For NFT NS isolates (56,954), 20.1% were also ESBL+, 44.7% were co-resistant to FQ, and 46.0% to SXT
 - Of the NFT NS isolates, 27.4% were co-resistant to FQ+SXT
 - 11.5% of NFT NS isolates (with resistance to > 1 phenotype) demonstrated co-resistance to all 4 phenotypes

Conclusions

- The data from this study demonstrate the high rates of co-resistance in isolates that are already resistant to one antibiotic, and indicate that the availability of effective oral treatments for uUTI are limited by antibiotic resistance
- These findings can be used to help inform appropriate empiric prescribing practices to optimize the treatment of uUTI, and highlight a key need for appropriate treatment of patients with uUTI in the future
- It is crucial to raise awareness among clinicians of current patterns of AMR to appropriately inform their treatment decisions and effectively serve their patients

Disclosures

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