

**P1619 Dissemination of extended-spectrum beta-lactamase genes and resistance to oral antibiotics among *Escherichia coli* urine isolates from outpatient departments in Germany, 2010-2016**

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**Background:** *Escherichia coli* (ECO) is the leading pathogen of community-acquired UTI. Resistance to oral antibiotics in ECO and the emergence of ESBLs have complicated the management of UTIs. The objectives of this study were i) to evaluate the development of resistance to oral antibiotics and occurrence of multidrug-resistant strains among uropathogenic ECO from outpatients, ii) to identify the ESBL genes in these isolates, and iii) to investigate the presence of high risk clone ST131 among ESBL-producing isolates.

**Materials/methods:** Isolates from patients in outpatient departments were collected prospectively at 22 laboratories in Germany, in each case over a three-month-period of three surveillance studies conducted in 2010, 2013 and 2016. Verification of species identification and susceptibility testing were performed in one reference laboratory. MICs were determined by broth microdilution according to the ISO-standard, and interpreted by German NAK (amoxicillin ± clavulanic acid) or EUCAST criteria (v.8.1; cefuroxime, cefpodoxime, ciprofloxacin, trimethoprim/sulfamethoxazole (T/S), fosfomycin, nitrofurantoin). Isolates with a confirmed ESBL phenotype were characterized by PCR amplification and sequencing of *bla* genes. Furthermore, the prevalence of ST131 among ESBL-producing isolates was investigated by a PCR-based assay (*rfbO25b/16* gene presence) or whole genome sequencing (Illumina, MiSeq).

**Results:** 1.313 isolates were collected, of which 36 (8.2%), 17 (3.9%) and 32 (7.3%) showed an ESBL phenotype in 2010 (n=439), 2013 (n=434) and 2016 (n=440), respectively. For each study year, about half of the isolates were fully susceptible, while 6.2%, 3.2% and 7.2% showed combined resistance to amoxicillin, cefuroxime, ciprofloxacin and T/S. Individual resistance rates are given in the Table. Genes encoding CTX-M-ESBL were confirmed for 35, 16, and 31 isolates, respectively. The *bla*<sub>CTX-M-15</sub> gene was identified in 23 isolates in 2010, 7 isolates in 2013, and 20 isolates in 2016. *bla*<sub>CTX-M-15</sub> was associated with ST131 in 16/23 (70%), 2/7 (29%) and 12/20 (60%) cases, respectively.

**Conclusions:** Overall, the level of resistance to oral antibiotics in urinary ECO from outpatient departments remained stable between 2010 and 2016. *bla*<sub>CTX-M-15</sub>-producing isolates of high-risk clone ST131 were responsible for about 1-3% of the UTIs in the community setting.

**Table: Resistance rates (%) of *E. coli* isolates by year of collection**

Antibacterial agent	Year			Chi-squared-test for linear trend; p value
	2010 (n=439)	2013 (n=434)	2016 (n=440)	
Amoxicillin	44.4	42.9	41.6	0.397
Amox./Clav.	33.9	34.8	15.2	<0.0001
Amox./Clav. <sup>a</sup>	10.5	9.0	4.5	0.0012
Cefuroxime <sup>a</sup>	10.5	5.7	9.8	0.7116
Cefpodoxime <sup>a</sup>	8.7	5.1	9.3	0.7114
Ciprofloxacin	21.2	15.0	18.0	0.2136
Cotrimoxazole	32.6	24.0	26.6	0.0477
Fosfomycin <sup>a, b</sup>	1.4	0.2	2.3	0.2342
Nitrofurantoin <sup>a</sup>	0.7	0.5	1.1	0.4395

<sup>a</sup> Uncomplicated UTI only; <sup>b</sup> Note, that we used broth microdilution which is not the reference method of susceptibility testing for fosfomycin.