

## Prevalence of phylogroups and O25/ST131 in susceptible and extended-spectrum $\beta$ -lactamase-producing *Escherichia coli* isolates, the Netherlands

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### Abstract

To assess the distribution of phylogroups and O25/ST131 in the Netherlands, we performed a real-time polymerase chain reaction (PCR) on a collection of 108 wild-type *Escherichia coli* (WT-EC) and 134 extended-spectrum  $\beta$ -lactamase-producing *E. coli* (ESBL-EC). Phylogroup B2 was predominant, but ESBL-EC were less likely to belong to this phylogroup (48.5%) than were WT-EC (66.7%;  $p = 0.005$ ). In WT-EC, phylogroups B2 and D seem to be more virulent, having a higher prevalence among midstream urine isolates and blood culture isolates, than in catheter-related urine isolates (83.3% and 87.9% vs. 61.9%;  $p = 0.048$ ). O25/ST131 is associated with ESBL production, being almost absent among phylogroup B2 WT-EC (61.5% vs. 5.6%;  $p < 0.001$ ).

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### Introduction

*Escherichia coli* is an important cause of urinary tract infections and systemic infections in humans [1]. The primary reservoir for infections due to *E. coli* is the patient's own intestinal tract [2]. Factors associated with increased risk of infection are patient- and pathogen dependent. Patient-dependent factors include underlying illnesses, female sex, the use of indwelling catheters, and previous antimicrobial use [3]. Pathogen-dependent factors include differences in virulence between phylogenetic group A, B1, B2 and D [4] *E. coli*. Isolates belonging to phylogroup B2 or D are often extraintestinal pathogenic *E. coli* (ExPEC), causing urinary tract infections and systemic infections [5,6].

Antimicrobial resistance due to production of extended-spectrum  $\beta$ -lactamases in *E. coli* (ESBL-EC) is increasing [7,8]. One subgroup within the ESBL-EC B2 phylogroup, O25/ST131 *E. coli*, has successfully spread worldwide [9] and in the community [10].

### Materials and methods

In this study we determined the distribution of phylogroups A, B1, B2, and D, and the prevalence of O25/ST131 in the Netherlands, within a collection of ESBL-EC obtained from rectal colonisation samples, and ESBL-EC and wild-type *E. coli* (WT-EC) obtained from urine and blood cultures. All isolates were collected in our laboratory for medical microbiology, situated in a large teaching hospital in the southern part of the Netherlands. The rectal colonisation samples were obtained from hospitalized patients during routine cross-sectional surveys in November 2012 and 2013. ESBL-EC obtained from urine samples are routinely stored at  $-80^{\circ}\text{C}$ , and retrospectively collected between January 2010 and March 2013. A comparable number of WT-EC isolates were collected prospectively between February and August 2013. Isolates obtained from blood cultures are routinely stored at  $-80^{\circ}\text{C}$ , and all available ESBL-EC obtained from unique patients were retrospectively collected between January 2010 and March 2013. For every ESBL-EC, the next available WT-EC isolate was included.

Phylogenetic typing was performed on all *E. coli* isolates using real-time polymerase chain reaction (PCR) [11], and an O25/ST131 specific real-time PCR was performed on all phylogroup B2 *E. coli* isolates [12]. Sequence analysis was performed on isolates with inconclusive results in the O25/ST131-specific

real-time PCR to detect the pathognomonic A and T single nucleotide polymorphism in the *pabB* gene.

Differences in the prevalence of phylogroups and O25/ST131 were analysed with  $\chi^2$  analysis using the Statistical Package for Social Sciences software (SPSS, version 17). Statistical significance was accepted if the chance for coincidence was <5%.

## Results

A total of 242 *E. coli* isolates were included in the study. All blood culture isolates, all rectal swab isolates, and all but one of the catheter-related urine isolates (95.2% of WT-EC and 100% of ESBL-EC) were obtained from hospitalised patients, whereas the majority of midstream urine isolates was obtained from general practitioners' patients (40 WT-EC; 74.1% and 34 ESBL-EC; 79.1%). Table 1 shows the age and sex distribution of patients with *E. coli* from the different origins, with patients for whom a midstream isolate was included being more often female and significantly younger than the other patients.

The majority of isolates belonged to phylogroup B2 (56.6%; Fig. 1), and this was the predominant phylogroup in all sub-categories. ESBL-EC isolates were less likely to belong to this phylogroup (48.5%) compared with WT-EC (66.7%,  $p$  0.005; 49.0% vs. 66.7% and  $p$  0.010 when excluding the rectal swab isolates from the analysis). The majority of the B2 phylogroup ESBL-EC isolates belonged to clonal complex O25/ST131 (61.5%) vs. a small minority of the B2 phylogroup WT-EC (5.6%;  $p$  < 0.001). The prevalence of O25/ST131 in ESBL-EC was lowest in the rectal colonization isolates (18.4%) vs. 37.2%, 36.8% and 29.4% for midstream urine isolates, catheter related urine isolates and blood culture isolates, respectively. However, these differences were not statistically different ( $p$  0.27).

Significant differences in occurrence of phylogroup A, B1 and D between ESBL-EC and WT-EC were only present for phylogroup A, with this phylogroup being more present in ESBL-EC than in WT-EC obtained from blood cultures (26.5% vs 6.1%;  $p$  0.024).

For WT-EC, phylogroups B2 and D were more prevalent in midstream urine isolates and in blood culture isolates than in catheter-related urine culture isolates (83.3% and 87.9% vs. 61.9%;  $p$  0.048). The prevalence of other phylogroups was comparable between the groups of isolates.

## Discussion

In the present study, remarkable differences were found between the prevalence of phylogroups and O25/ST131 in ESBL-EC and WT-EC from different origins. Most striking is the difference in prevalence of O25/ST131, being the most prevalent clone in ESBL-EC, and being almost absent in WT-EC. This finding supports the idea that O25/ST131 owes its success to the ESBL phenotype. Among WT-EC, phylogroups A and B1 were found to be less prevalent among midstream urine isolates and human blood culture isolates as compared with WT-EC obtained from catheter-related urine isolates. This finding supports the hypothesis that these phylogroup isolates need devices like catheters to overcome barriers to cause infection. This phenomenon was not observed in ESBL-EC.

Our results regarding the predominance of phylogroup B2 and O25/ST131 in ESBL-EC are in line with the results of Johnson et al. [13]. Furthermore, the findings regarding the higher prevalence of phylogroup A in ESBL-EC than in WT-EC are comparable. The main limitation of our study is the fact that an O25/ST131-specific real-time PCR was used. Although O25/ST131 constitutes the majority of ST131 isolates, O16 is another serotype associated with ST131 status [14,15].

**TABLE 1.** Distribution of sex and age

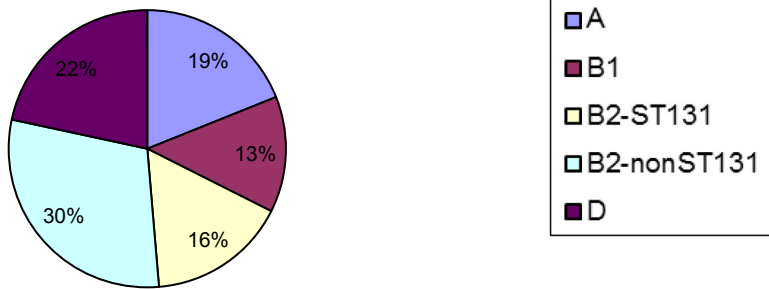
	WT-EC		ESBL-EC	
	Age	Sex	Age	Sex
	Mean (95% CI)	Male (%)	Mean (95% CI)	Male (%)
Rectal colonisation				
Urine culture, midstream*	47.4 (40.3–54.4)	14.8	55.8 (46.4–65.3)	57.9
Urine culture, indwelling catheter†	73.3 (66.4–80.2)	47.6	80.3 (76.2–84.3)	52.6
Blood culture	67.6 (62.0–73.1)	48.5	66.4 (60.3–72.5)	58.8

Mean age with 95% confidence interval and percentage of male subject among wild-type *Escherichia coli* (WT-EC) isolates and extended-spectrum  $\beta$ -lactamase-producing *E. coli* (ESBL-EC) isolates.

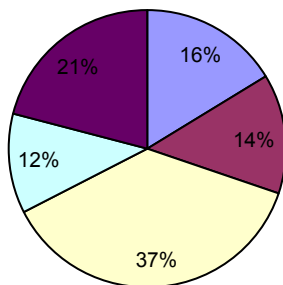
\*Patients with positive midstream urine cultures (both ESBL-EC and WT-EC) were significantly younger than patients with indwelling catheters or with positive blood cultures ( $p$  < 0.001 and  $p$  < 0.001), and were significantly more often female than the patients from whom other cultures were obtained ( $p$  0.001 for WT-EC and  $p$  0.008 for ESBL-EC).

†Patients with indwelling catheters were significantly older than patients with ESBL-EC in their rectal swabs or *E. coli* in their midstream urine cultures ( $p$  0.001 and  $p$  < 0.001, respectively).

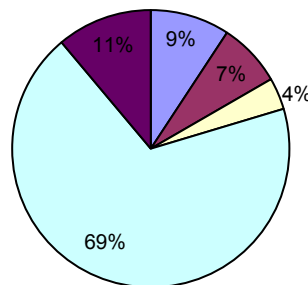
ESBL-EC from rectal cultures (N=38)



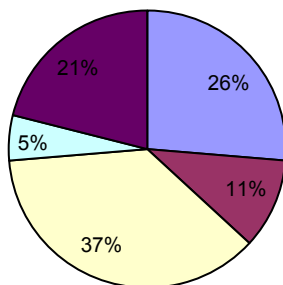
ESBL-EC from midstream urine (N=43)



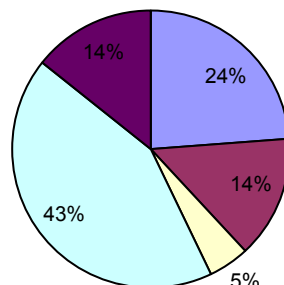
WT-EC from midstream urine (N=54)



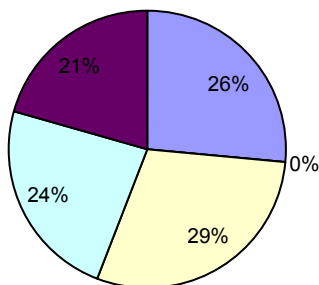
ESBL-EC from Urine Catheters (N=19)



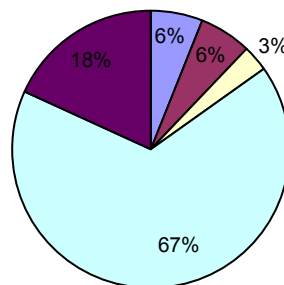
WT-EC from Urine Catheters (N=21)



ESBL-EC from blood cultures (N=34)



WT-EC from blood cultures (N=33)



**FIG. 1.** Distribution of phylogroups and O25/ST131.

In conclusion, our study supports the idea that *E. coli* colonizing the gut are not equally capable of causing infection. For WT-EC, phylogroups B2 and D are more likely to cause infection, whereas other phylogroups need devices such as urinary catheters to overcome barriers and cause infection.

Furthermore, our results show a significant association of O25/ST131 with ESBL production, with this strain being almost absent in WT-EC isolates. Overall, phylogroup B2 is less frequently seen in ESBL-EC than in WT-EC, whereas for phylogroup A the opposite was found.

## Transparency declaration

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Jan Kluytmans received consultancy fees from Pfizer, Biomerieux and 3M. The other authors have nothing to declare.

## References

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- [1] Sobel JD, Kaye D. Urinary tract infections. In: Mandell GL, Bennett JE, Dolin R, editors. Principles and practice of infectious diseases. 6th ed. New York: Elsevier; 2005. p. 875–905.
- [2] Pitout JDD. Extraintestinal pathogenic *Escherichia coli*: an update on antimicrobial resistance, laboratory diagnosis and treatment. *Expert Rev Anti Infect Ther* 2012;10:1165–76.
- [3] López-Cerero L, Navarro MD, Bellido M, Martín-Peña A, Viñas L, Cisneros JM, et al. *Escherichia coli* belonging to the worldwide emerging epidemic clonal group O25b/ST131: risk factors and clinical implications. *J Antimicrob Chemother* 2014;69:809–14.
- [4] Herzer PJ, Inouye S, Inouye M, Whittam TS. Phylogenetic distribution of branched RNA-linked multicopy single-stranded DNA among natural isolates of *Escherichia coli*. *J Bacteriol* 1990;172: 6175–81.
- [5] Pitout JDD. Extraintestinal pathogenic *Escherichia coli*: a combination of virulence with antibiotic resistance. *Front Microbiol* 2012;3:1–7.
- [6] Picard B, Garcia JS, Gouriou S, Duriez P, Brahimi N, Bingen E, et al. The link between phylogeny and virulence in *Escherichia coli* extra-intestinal infection. *Infect Immunol* 1999;67:546–53.
- [7] Bush K. Extended-spectrum beta-lactamases in North America, 1987–2006. *Clin Microbiol Infect* 2008;S1:134–43.
- [8] Cantón R, Novais A, Valverde A, Machado E, Peixe L, Baquero F, et al. Prevalence and spread of extended-spectrum  $\beta$ -lactamase-producing *Enterobacteriaceae* in Europe. *Clin Microbiol Infect* 2008;S1:144–53.
- [9] Peirano G, Pitout JDD. Molecular epidemiology of *Escherichia coli* producing CTX-M  $\beta$ -lactamases: the worldwide emergence of clone ST131 O25:H4. *Int J Antimicrob Agents* 2010;35:316–21.
- [10] Xu L, Shabir S, Bodah T, McMurray C, Hardy K, Hawkey P, et al. Regional survey of CTX-M-type extended-spectrum  $\beta$ -lactamases among *Enterobacteriaceae* reveals marked heterogeneity in the distribution of the ST131 clone. *J Antimicrob Chemother* 2011;66:505–11.
- [11] Doumith M, Day MJ, Hope R, Wain J, Woodford N. Improved multiplex PCR strategy for rapid assignment of the four major *Escherichia coli* phylogenetic groups. *J Clin Microbiol* 2012;50:3108–10.
- [12] Dhanji H, Doumith M, Clermont O, Denamur E, Hope R, Livermore DM, et al. Real-time PCR for detection of the O25b-ST131 clone of *Escherichia coli* and its CTX-M-15-like extended-spectrum  $\beta$ -lactamases. *Int J Antimicrob Agents* 2010;36:355–8.
- [13] Johnson JR, Johnston B, Clabots C, Kuskowski MA, Castanheira M. *Escherichia coli* sequence type ST131 as the major cause of serious multidrug-resistant *E. coli* infections in the United States. *Clin Infect Dis* 2010;51:286–94.
- [14] Banjeree R, Johnson JR. A new clone sweeps clean: the enigmatic emergence of *Escherichia coli* sequence type 131. *Antimicrob Agents Chemother* 2014;58:4997–5004.
- [15] Johnson JR, Clermont O, Johnston B, Clabots C, Tchesnokova V, Sokurenko E, et al. Rapid and specific detection, molecular epidemiology, and experimental virulence of the O16 subgroup within *Escherichia coli* sequence type 131. *J Clin Microbiol* 2014;52:1358–65.