

1   **Correspondence**

2  
3   *Escherichia coli* O25b-ST131 is an important cause of antimicrobial-resistant  
4   infections in women with uncomplicated cystitis

5  
6   Pak-Leung Ho\*, Wai U Lo, Eileen L. Lai, Kin-Hung Chow, Wing-Cheong Yam

7  
8   <sup>1</sup>*Department of Microbiology and Carol Yu Centre for Infection, The University of Hong*  
9   *Kong, Queen Mary hospital, Hong Kong*

10  
11   Running title:

12   Keywords: fluoroquinolone resistance; cefotaximases; *Escherichia coli*

13  
14   \*Corresponding author. Mailing address: Division of Infectious Diseases, Department of  
15   Microbiology, The University of Hong Kong, Queen Mary hospital, Pokfulam Road,  
16   Pokfulam, Hong Kong SAR, CHINA. Tel: +852-2855 4897; Fax: +852-2855 1241; E-mail:  
17   [plho@hkucc.hku.hk](mailto:plho@hkucc.hku.hk)

18   Word count = 522 (excluding references)

20 Sir,  
21 Worldwide, the *Escherichia coli* serotype O25b-sequence type (ST) 131 clonal group is  
22 emerging and represent an important cause of antimicrobial-resistant infections that ranges  
23 from uncomplicated cystitis to life-threatening bacteraemia.<sup>1</sup> Nonetheless, there is only  
24 limited epidemiological information about this clonal group in Asia.<sup>1-3</sup> In this study, we  
25 investigated the presence of this clonal group among 271 *E. coli* isolates recovered from a  
26 prospective cohort of female outpatients with uncomplicated cystitis in Hong Kong during  
27 2006-2008.<sup>4</sup> The patient demographics and antimicrobial susceptibility of the isolates have  
28 previously been published.<sup>4</sup> In brief, all patients had community-acquired infections. Prior  
29 urinary tract infection (UTI) history was present in 78 (28.8%) patients and 38 (14.0%) had  
30 been treated with antibiotics in the preceding six weeks.<sup>4</sup> The major *E. coli* phylogenetic  
31 groups (A, B1, B2 and D) were determined by multiplex PCR.<sup>3,5</sup> Subsequently, O25b-ST131  
32 isolates were identified by PCRs for the O25b-ST131-specific single nucleotide  
33 polymorphism in *pabB* and the O25b *rfb* variant.<sup>5,6</sup>

34 The isolates were found to have the following phylogenetic group distribution: B2  
35 (66.9%, 181/271), D (17.7%, 48/271), A (10.3%, 28/271) and B1 (5.2%, 14/271). Twenty-  
36 three of the B2 isolates were PCR positive for both *pabB* and O25b and were identified as  
37 O25b-ST131 isolates. All other isolates were PCR-negative for the two targets. Thus, O25b-  
38 ST131 accounted for 8.5% (23/271) of the total *E. coli* population. The 23 isolates were  
39 recovered from patients with residence in 13 of the 18 geographic districts in Hong Kong.  
40 The O25b-131 clonal group accounted for the following proportions of *E. coli* infections in  
41 the different age groups: 18-35 years (4.3%, 3/71), 36-50 years (6.5%, 7/107), 51-64 years  
42 (9.3%, 5/54) and  $\geq 65$  years (20.5%, 8/39). The proportion of O25b-ST131 isolates in patients  
43 aged  $\geq 65$  years was significantly higher than that among patients aged 18-64 years ( $P =$   
44 0.004). O25b-ST131 isolates were significantly more likely than non-O25b-ST131 isolates to

be ciprofloxacin-resistant (69.6%, 16/23 vs. 7.7%, 19/248;  $P < 0.001$ ), cotrimoxazole-resistant (52.2%, 12/23 vs. 28.6%, 71/248;  $P = 0.02$ ) and gentamicin-resistant (52.2%, 12/23 vs. 14.9%, 37/248;  $P < 0.001$ ). Table 1 showed that O25b-ST131 isolates accounted for 45.7% and 41.7% of the ciprofloxacin-resistant, and dually ciprofloxacin and cotrimoxazole-resistant *E. coli* populations, respectively. The incidence of O25b-ST131 among antimicrobial-susceptible (as defined by susceptibility to all of ciprofloxacin, cotrimoxazole and gentamicin) isolates was low (2.9%, 5/175). PCR and sequencing showed that the only ESBL-producing O25b-ST131 isolate had *bla*<sub>CTX-M-14</sub>.

Our results showed that O25b-ST131 exhibited a wide range of susceptibility patterns. Similar to previous studies,<sup>1,5</sup> our findings showed that O25b-ST131 isolates were often multidrug-resistant and one was a CTX-M producer. However, the only ESBL-producing O25b-ST131 isolate was found to have *bla*<sub>CTX-M-14</sub> instead of *bla*<sub>CTX-M-15</sub>.<sup>1,5</sup> Among blood culture *E. coli* isolates collected in 2007-2008, our recent work showed that O25b-ST131 accounted for 25.6% of the ESBL-producing isolates.<sup>3</sup> All ESBL-producing O25b-ST131 isolates had *bla*<sub>CTX-M-14</sub> and none had *bla*<sub>CTX-M-15</sub>.<sup>3</sup> As our previous studies revealed, the dissemination of *bla*<sub>CTX-M-14</sub> in O25b-ST131 isolates was associated with the acquisition of an epidemic pHK01 plasmid with FII replicon.<sup>3</sup> In conclusion, this study showed that the O25b-ST131 clonal group is widely distributed among *E. coli* isolates causing community-acquired urinary tract infection in the region. The finding highlights the importance of clonal expansion in dissemination of antimicrobial resistance involving first-line drugs commonly used for treatment of urinary tract infections.

**Funding:** This study is supported by the Research Fund for the Control of Infectious Diseases (RFCID) of the Health and Food Bureau of the Hong Kong SAR Government.

**Transparency declaration:** None to declare.

70 **Table 1.** Contribution of O25b-ST131 to antimicrobial-resistant *E. coli* populations, 2006-  
71 2008

Resistance phenotype	% (number/total) of with phenotype	Fraction due to O25b-ST131, % (number/subtotals)
ESBL-positive	5.2 (14/271)	7.2 (1/14)
Cip-R	12.9 (35/271)	45.7 (16/35)
Sxt-R	30.6 (83/271)	14.4 (12/83)
Gen-R	18.1 (49/271)	24.5 (12/49)
Cip-R and Sxt-R	8.9 (24/271)	41.7 (10/24)
Cip-S, Gen-S and Sxt-S	64.6 (175/271)	2.9 (5/175)

72 Cip-R/S, ciprofloxacin-resistant/sensitive; Gen-R, gentamicin-resistant/sensitive; Sxt-R/R,  
73 cotrimoxazole-resistant/sensitive; ESBL, extended-spectrum  $\beta$ -lactamase

74

75

76

77

78

79

80

81

82

83

84

85

86

87

88

89

90

91

92

93

94

95

96

97

98

99

## References

1. Rogers BA, Sidjabat HE, & Paterson DL. *Escherichia coli* O25b-ST131: a pandemic, multiresistant, community-associated strain. *J Antimicrob Chemother* 2011; **66**, 1-14.
2. Zong Z & Yu R. bla(CTX-M)-carrying *Escherichia coli* of the O25b ST131 clonal group have emerged in China. *Diagn Microbiol Infect Dis* 2011; **69**, 228-31.
3. Ho PL, Yeung MK, Lo WU *et al*. Predominance of pHK01-like incompatibility group FII plasmids encoding CTX-M-14 among extended-spectrum beta-lactamase-producing *Escherichia coli* in Hong Kong, 1996-2008. *Diagn Microbiol Infect Dis* 2012.
4. Ho PL, Yip KS, Chow KH *et al*. Antimicrobial resistance among uropathogens that cause acute uncomplicated cystitis in women in Hong Kong: a prospective multicenter study in 2006 to 2008. *Diagn Microbiol Infect Dis* 2010; **66**, 87-93.
5. Clermont O, Lavollay M, Vimont S *et al*. The CTX-M-15-producing *Escherichia coli* diffusing clone belongs to a highly virulent B2 phylogenetic subgroup. *J Antimicrob Chemother* 2008; **61**, 1024-8.
6. Clermont O, Dhanji H, Upton M *et al*. Rapid detection of the O25b-ST131 clone of *Escherichia coli* encompassing the CTX-M-15-producing strains. *J Antimicrob Chemother* 2009; **64**, 274-7.