Community-Associated Extended-Spectrum-β-Lactamase Producing *Escherichia coli* Infection in Korea

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Background

Methods

- Extra-intestinal pathogenic *Escherichia coli* infection is a

significant public health problem.

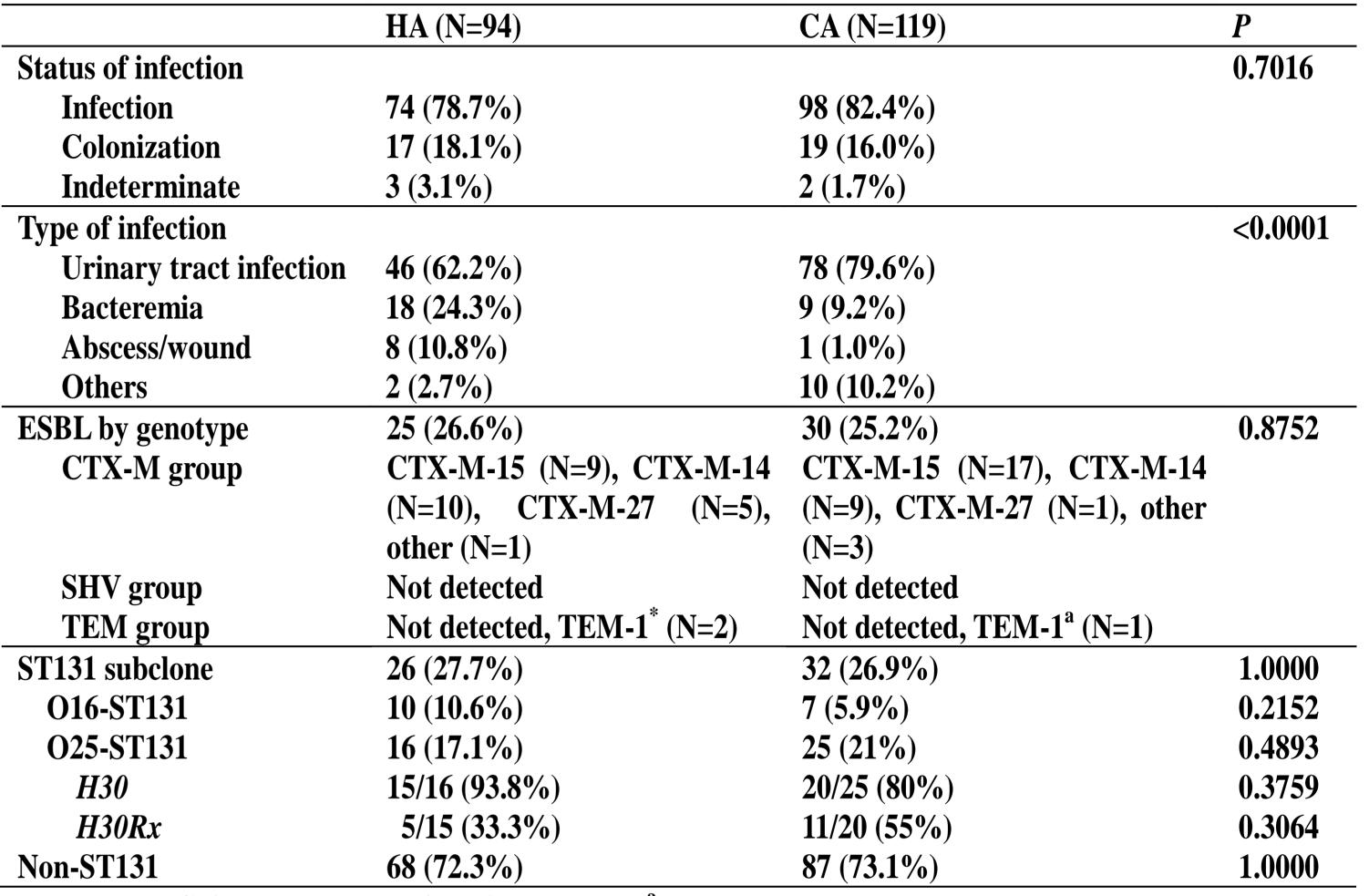
Results

Table 1. Types of infections, extended-spectrum β-lactamase (ESBL) types, and the prevalence of sequence type 131 (ST131) of community-onset healthcare-associated (HA) and community-associated (CA) *Escherichia coli* episodes (N=213)

- Sequence type 131 (ST131) *E. coli* has played a major part in the global dissemination.
- ST131-O25*H30Rx* is associated with fluoroquinolone resistance and CTX-M type extended-spectrum β -lactamase .
- Recently ST131-O16 sub-clone was reported.
- The aims of study are to evaluate the recent molecular

epidemiology of ESBL-producing E. coli and to assess the

differences between community-associated and community-onset healthcare-associated isolates in a prospective, multicenter, observational study.



N, number.; Chi-square test or Fisher's exact test; ^aNarrow-spectrum β-Lactamase

Table 2. Extended-spectrum β-lactamase (ESBL) types and the prevalence of sequence type 131 (ST131) in community-onset *Escherichia coli* episodes (N=58)

- Bacterial isolates: non-duplicated *E. coli* isolates from consecutive, sequentially encountered patients with communityonset episodes between March and April 2016 in two community hospitals (742 beds, Goyang-si; 132 beds, Yongin-si).

Definition: sites of acquisition (community-associated or healthcare-associated) were determined as described by Friedman with some modifications¹ and diagnosis of infection was made based on clinical, bacteriological, and radiological investigations.
Microbiological analysis: ESBL genotype was determined by PCR and sequencing². For the detection of ST131, all isolates were screened by PCR for O16-ST131 and O25-ST131³. *FimH* type and *H30Rx* were determined by PCR and sequencing⁴.

	ST131 (025+016)	025	H30	H30Rx	016
ESBL positive (%)	28/58 (48.3%)	23/41 (56.1%)	20/35 (57.1%)	13/16 (81.3%)	5/17 (29.4%)
CTX-M group					0
CTX-M-15	16	16	14	13	0
CTX-M-14	9	4	4	0	5
CTX-M-27	3	3	2	0	0
N, number					

Table 3. Antimicrobial resistance rate (%) of *Escherichia coli* isolated from two community hospitals

Antimicrobial agents	Resistance rate (%) of									
	Site of acquisition		Sequence type (ST)							
	HA (n=93)	CA (n=119)	ST131- O25-H30	ST131-O25- H30Rx (n 10)	ST131- 016	All ST131 (59)	Other STs (n=154)			
Ampicillin	70	68	$\frac{(n=35)}{83}$	(n=16) 94	(n=17) 65	(n=58) 79	65			
Piperacillin	69	64	80	88	65	78	62			
Ampicillin/sulbactam	33	25	40	44	29	35	27			
Cefoxitin	4	2	3	6	0	3	3			
Cefotaxime	30	27	60	88	29	50	20			
Ceftazidime	30	24	57	81	24	47	19			
Meropenem	0	0	0	0	0	0	0			
Imipenem	0	0	0	0	0	0	0			
Ciprofloxacin	39	44	100	100	18	67	32			
Gentamicin	23	25	51	56	35	43	17			
Tobramycin	13	11	31	38	24	28	6			
Amikacin	0	0	0	0	0	0	0			
Cotrimoxazole	33	25	49	44	41	45	23			

- Statistical analysis: Chi-square test or Fisher's exact test with the

level of significance set as P value <0.05.

Reference

- 1. Park YS. et al. Yonsei Med J 2014;55:467-75.
- 2. Sidjabat HE, et al. AAC 2009;53:4733–9.
- 3. Johnson JR, et al. JCM 2014;52:1358-65.
- 4. Price LB, et al. mBio 2013;17:1–10.

HA, community-onset healthcare-associated; CA, community-associated; all ST131, O25-H30, O25nonH30, and O16; ^aOne isolate was excluded from the antimicrobial susceptibility test

Conclusions and Discussion

In this study, considerable ST131 *E. coli* isolations in the community were observed and about half of them were related to the history of visit to the healthcare facilities, indicating the spread of multidrug resistance *E. coli* to the community via healthcare facilities.