Title: Prevalence of ESBL/AmpC genes and specific clones among the third-generation cephalosporin-resistant *Enterobacteriaceae* from canine and feline clinical specimens in Japan

Authors: Yoshihiko Maeyama, Yui Taniguchi, Wataru Hayashi, Yusuke Ohsaki, Shunsuke Osaka, Shota Koide, Kiyoko Tamai, Yukiko Nagano, Yoshichika Arakawa, Noriyuki Nagano

PII: S0378-1135(18)30048-8
DOI: https://doi.org/10.1016/j.vetmic.2018.02.020
Reference: VETMIC 7884

To appear in: *VETMIC*

Received date: 12-1-2018
Revised date: 14-2-2018
Accepted date: 15-2-2018

Please cite this article as: Maeyama Y, Taniguchi Y, Hayashi W, Ohsaki Y, Osaka S, Koide S, Tamai K, Nagano Y, Arakawa Y, Nagano N, Prevalence of ESBL/AmpC genes and specific clones among the third-generation cephalosporin-resistant *Enterobacteriaceae* from canine and feline clinical specimens in Japan, *Veterinary Microbiology* (2010), https://doi.org/10.1016/j.vetmic.2018.02.020

Prevalence of ESBL/AmpC genes and specific clones among the third-generation cephalosporin-resistant *Enterobacteriaceae* from canine and feline clinical specimens in Japan

Yoshihiko Maeyama[a,b, 1], Yui Taniguchi[a, 1], Wataru Hayashi[a, 1], Yusuke Ohsaki[a], Shunsuke Osaka[a], Shota Koide[a], Kiyoko Tamai[b], Yukiko Nagano[c], Yoshichika Arakawa[c], and Noriyuki Nagano[a,]*

[a]Department of Health and Medical Sciences, Shinshu University Graduate School of Medicine, 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan; [b]Miroku Medical Laboratory Inc., 659-2 Innai, Saku, Nagano 384-2201 Japan; [c]Department of Bacteriology, Nagoya University Graduate School of Medicine, 65 Tsurumai-cho, Showa-ku, Nagoya, Aichi 466-8550, Japan.

***Corresponding author at:** Department of Health and Medical Sciences, Shinshu University Graduate School of Medicine
Phone: 81-263-37-2381 FAX: 81-263-37-2370
E-mail address: naganon@shinshu-u.ac.jp

[1]These authors contributed equally to this work.

Highlights

- In *E. coli*, *bla*$_{\text{CTX-M-27}}$ and *bla*$_{\text{CMY-2}}$ were predominant, followed by *bla*$_{\text{CTX-M-15}}$.
- In *K. pneumoniae*, 10 *bla* gene types including *bla*$_{\text{CTX-M-15}}$ and *bla*$_{\text{CTX-M-2}}$ were found.
- High prevalence of *bla*$_{\text{CTX-M-27}}$ among *E. coli* isolates of *H*30R/non-Rx lineage.
- Newly emerging virulent and resistant *E. coli* lineage ST1193 was confirmed.
- The *fosA3* and/or *armA* genes were detect in *E. coli* and *K. pneumoniae* isolates.

Abstract

In recent years, besides the widespread occurrence of extended-spectrum β-lactamase (ESBL)- and/or plasmid-mediated AmpC (pAmpC)-producing *Enterobacteriaceae* in both healthcare and community settings of humans, the third-generation cephalosporin (3GC)-resistant microbes have also been reported from companion animals worldwide. Here, we characterized ESBL- and/or pAmpC-producing *Enterobacteriaceae* clinical isolates from companion animals. Among the 487 clinical isolates mainly from urine of dogs and cats between May and September 2016, 104 non-repetitive isolates were resistant to the 3GC, and they consisted of 81 of 381 (21.3%) *Escherichia coli*, 21 of 50 (42.0%) *Klebsiella pneumoniae*, and 2 of 56 (3.6%) *Proteus mirabilis* isolates. In the 81 *E. coli*, the predominant *bla* genes were *bla*$_{\text{CTX-M-27}}$ and *bla*$_{\text{CMY-2}}$ (n=15 each), followed by *bla*$_{\text{CTX-M-15}}$ (n=14), *bla*$_{\text{CTX-M-14}}$ (n=10), and *bla*$_{\text{CTX-M-55}}$ (n=5). In 21 *K. pneumoniae*, 10 *bla* gene types including *bla*$_{\text{CTX-M-15}}$ (n=4), *bla*$_{\text{CTX-M-2}}$ (n=4), and *bla*$_{\text{CTX-M-14}}$ (n=3) were found. The *bla*$_{\text{CTX-M-2}}$ was identified in 2 *P. mirabilis*. Twenty-four of the 42 *E. coli* belonging to phylogroup B2 were O25b-ST131 clone, mostly associated