

## CTX-M Expression and Selection of Ertapenem Resistance in *Klebsiella pneumoniae* and *Escherichia coli*<sup>∇</sup>

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**In vitro selection of mutants with decreased susceptibility to ertapenem was performed using *Escherichia coli* and *Klebsiella pneumoniae* clinical strains producing either the  $bla_{\text{CTX-M-2}}$ ,  $bla_{\text{CTX-M-3}}$ ,  $bla_{\text{CTX-M-9}}$ , or  $bla_{\text{CTX-M-15}}$  gene. Frequencies of mutants with decreased susceptibilities to ertapenem were similar for all  $\beta$ -lactamases expressed.**

Extended-spectrum  $\beta$ -lactamases (ESBLs) of the CTX-M type are emerging worldwide mostly in *Enterobacteriaceae* as a source of community-acquired and nosocomial infections (11).

Most CTX-M-type  $\beta$ -lactamases hydrolyze cefotaxime at a higher level than that of ceftazidime. However, several amino acid substitutions result in an increased hydrolytic activity against ceftazidime, as seen for the CTX-M enzyme that has spread worldwide, CTX-M-15, a variant of CTX-M-3 (14). Specific substitutions at Ambler positions 167 (P167S/T/Q) and 240 (D240G) in CTX-M-2 (21) and in CTX-M-3 (6, 14) conferring resistance to ceftazidime have been selected in vitro after a ceftazidime selection. Although rare ESBLs such as several GES-like enzymes may hydrolyze carbapenems (12), no CTX-M enzyme has been reported to possess carbapenemase activity. Among  $\beta$ -lactam molecules, carbapenems (imipenem, ertapenem, and meropenem) are the drugs of choice for treating infections by ESBL-producing *Enterobacteriaceae* (16, 17, 18).

The objective of this study was to determine if CTX-M  $\beta$ -lactamases with carbapenemase activity may be selected in vitro.

Therefore, the frequency of in vitro selection of mutant strains with reduced susceptibility to ertapenem was evaluated with *Escherichia coli* and *Klebsiella pneumoniae* strains expressing different CTX-M  $\beta$ -lactamases. The risk of selection of mutated  $bla_{\text{CTX-M}}$  genes and the level of porin expression were investigated also.

The  $bla_{\text{CTX-M}}$  genes were expressed under the same promoter and in the same genetic background. The  $bla_{\text{CTX-M}}$  genes ( $bla_{\text{CTX-M-2}}$ ,  $bla_{\text{CTX-M-3}}$ ,  $bla_{\text{CTX-M-9}}$ , and  $bla_{\text{CTX-M-15}}$ ) were amplified from clinical isolates without their promoter sequence (primer sequence in Table 1), cloned into the low-copy-number pACYC184 plasmid (New England Biolabs, Ozyme, Saint-Quentin-en-Yvelines, France), and expressed in clinical isolates of *E. coli* Wi and *K. pneumoniae* M (Hôpital Bicêtre strain collection). Transformants were selected over-

night at 37°C on Trypticase soy agar (bioMérieux, Craponne, France) containing chloramphenicol (Euromedex, Souffelweyersheim, France) at 30  $\mu\text{g/ml}$ .

Mutant strains with decreased susceptibilities to ertapenem were selected as described previously (6), on Trypticase soy agar containing ertapenem (Merck Sharp & Dohme-Chibret, Paris, France) at a concentration fourfold higher than the MICs (6). After overnight incubation at 37°C for 18 h, mutation frequencies were calculated, taking plate counts of viable bacteria on drug-free agar (6). Comparison of the means was performed by Student's *t* test on three independent experiments. In *E. coli* as well as in *K. pneumoniae* isolates, mean frequencies of selection of ertapenem-reduced susceptibility were not related to the  $bla_{\text{CTX-M}}$  content ( $P > 0.1$ ) (Table 2).

Both strands of the  $bla_{\text{CTX-M}}$  genes were sequenced from five of each  $bla_{\text{CTX-M}}$ -harboring *E. coli* and *K. pneumoniae* mutant strain. All mutants had a wild-type  $bla_{\text{CTX-M-2}}$ ,  $bla_{\text{CTX-M-3}}$ ,  $bla_{\text{CTX-M-9}}$ , or  $bla_{\text{CTX-M-15}}$  sequence, thus indicating that the reduced susceptibility to ertapenem was not due to point mutations located in the  $bla_{\text{CTX-M}}$  genes.

The outer membrane protein (OMP) profiles of the *E. coli* and *K. pneumoniae* isolates before and after ertapenem selection were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis as described previously (15). Comparison of the OMP profiles of *E. coli* mutant strains selected on ertapenem-containing plates showed mainly a decrease in OmpC expression (Fig. 1). Similarly, comparison of the OMP profiles of *K. pneumoniae* isolates showed mainly a decrease in OmpK36 expression in ertapenem-selected isolates expressing a CTX-M  $\beta$ -lactamase or not (Fig. 1).

In order to quantify expression of the *ompC* and *ompF* genes in *E. coli* isolates and of the *ompK35* and *ompK36* genes in *K. pneumoniae* isolates, the two-step quantitative reverse transcription-PCR was used as recommended by Fey et al. (3). Expression level results were standardized relative to the transcription level of the constitutively expressed *gapA* (D-glyceraldehyde-3-phosphate dehydrogenase) gene in *E. coli* (19) and the 16S rRNA genes in *K. pneumoniae* (Fig. 2). Transcript quantification was performed by using the LightCycler FastStart DNA Master<sup>PLUS</sup> kit SYBR-Green I on a LightCycler 1.0 instrument (Roche Diagnos-

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TABLE 1. Nucleotide sequences of primers used for amplification and sequence analysis

Primer	Sequence (5'→3')	Reference or GenBank accession no.
CTX-M-2F <sup>a</sup>	AATGTATATTGAAGGCCG AGGG	This study
CTX-M-2R	ATACCTCGCTCCATTTATTGC	This study
CTX-M-3F	TCGTCTCTTCCAGAATAAG	This study
CTX-M-3R	TACCTATTACAAACCGTC GGTG	This study
CTX-M-9F	CTGATGTAACACGGATTGAC	This study
CTX-M-9R	AGCGCCCATTTATTGAGAG	This study
CTX-M-15F <sup>b</sup>	TCGTATCTTCCAGAATAAGG	This study
EcOmpC-F	GTTAAAGTACTGTCCCTCCTG	15
EcOmpC-R	TAACCGGTGAGCTGGTCA GTAA	This study
EcOmpF-F	TCGTATCTTCCAGAATAAGG	AM040706
EcOmpF-R	CAGGTAAGTCAAACGCTGC	15
GapA-F	TATGACTGGTCCGTCTAAAG ACAA	19
GapA-R	GGTTTTCTGAGTAGCGGTAG TAGC	19
OmpK35-F	TGATCCCTGCCCTGCTGGT	8
OmpK35-R	TCCATGTTGTATTCCACTGG	This study
OmpK36-F	TTAGACCTGTACGGCAAA ATCG	Z33506
OmpK36-R	AATGCCAGACGAGTCCATGC	Z33506
Kp16S rRNA-F	GGCAGGGTGAGTAATGTC	EU048272
Kp16S rRNA-R	TCTCAGACCAGCTAGGGATCG	EU048272

<sup>a</sup> Expected sizes of PCR products with combinations of forward (F) and reverse (R) primers: 943 bp for the *bla*<sub>CTX-M-2</sub> gene, 916 bp for the *bla*<sub>CTX-M-3</sub> gene, 932 bp for the *bla*<sub>CTX-M-9</sub> gene, 904 bp for the *bla*<sub>CTX-M-15</sub> gene, 215 bp for the *ompC* gene, 204 bp for the *ompF* gene, and 201 bp for the *gapA* gene of *E. coli* and 202 bp for the *ompK36* gene, 222 bp for the *ompK35* gene, and 193 bp for the 16S rRNA gene of *K. pneumoniae*.

<sup>b</sup> The CTX-M-3R primer was also used for the amplification of the *bla*<sub>CTX-M-15</sub> gene.

tics, Neuilly, France) at an annealing temperature of 57°C. The calibration curves were generated with serially diluted cDNA from in vitro-obtained RNA standards (10) for each gene with primers listed in Table 1. The slope of each calibration curve was used to compare the number of copies of each *omp* gene in *E. coli* and *K. pneumoniae* isolates before and after ertapenem selection. Real-time quantitative reverse transcription-PCR experiments showed that the *E. coli* isolates with decreased susceptibilities to ertapenem had similarly decreased expression of the *ompC* and *ompF* genes whatever the CTX-M expressed (Fig. 2), the converse of what was observed with sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Similarly, *K. pneumoniae* isolates with decreased susceptibilities to ertapenem had decreased expression of the *ompK35* and *ompK36* genes whatever the CTX-M expressed (Fig. 2). The level of *ompK35* transcript was 10-fold lower than that of *ompK36* in the same RNA extracts, and the decrease in transcript level upon ertapenem selection was then less significant for *ompK35* (two- to sixfold) than for *ompK36* (up to 30-fold) (Fig. 2).

Resistance to carbapenems in *Enterobacteriaceae* may be related to carbapenemases (13, 20) or to dual mechanisms associating the outer membrane permeability defect and β-lactamases such as AmpCs and ESBLs (2, 5, 7). In the absence of β-lactamase, no defect in outer membrane per-

TABLE 2. Mean frequencies of mutation to ertapenem decrease susceptibility for *Escherichia coli* and *Klebsiella pneumoniae* strains producing no CTX-M (wild type) and producing the ESBLs CTX-M-2, CTX-M-3, CTX-M-9, and CTX-M-15

Strain	Ertapenem selection (μg/ml) <sup>b</sup>	Frequency of selection of mutants with decreased susceptibility to ertapenem (10 <sup>-8</sup> ) <sup>a</sup>
<i>K. pneumoniae</i>		
M (wild type)	0.032	4 ± 1.7
M (CTX-M-2)	0.064	7 ± 6
M (CTX-M-3)	0.064	5 ± 3
M (CTX-M-9)	0.048	1.8 ± 1.2
M (CTX-M-15)	0.064	4.2 ± 2.5
<i>E. coli</i>		
Wi (wild type)	0.032	0.8 ± 0
Wi (CTX-M-2)	0.092	3 ± 1.4
Wi (CTX-M-3)	0.092	2.4 ± 1.3
Wi (CTX-M-9)	0.064	2.7 ± 0.6
Wi (CTX-M-15)	0.092	1.2 ± 0.5

<sup>a</sup> Mutation frequencies are arithmetic means from three independent experiments, each performed in triplicate.

<sup>b</sup> Ertapenem selection was performed at concentrations of four times the MICs.

meability is sufficient to lead to carbapenem resistance (1). Previous studies reported ertapenem resistance in CTX-M-producing *K. pneumoniae* (2, 9) and CTX-M-producing *E. coli* (7) isolates exhibiting a permeability defect. Here, we show that ertapenem selects for mutant strains with decreased susceptibility by modification of porin expression whatever the content in CTX-M β-lactamases.

Finally, this study may indicate that the frequency of selection of ertapenem resistance is not higher in isolates expressing CTX-Ms. In addition to the alteration of membrane permeability, CTX-M β-lactamases most probably contribute to the decreased ertapenem susceptibility by binding with a high affinity to this molecule. Indeed, even if poorly hydrolyzed by CTX-Ms, ertapenem has been shown to have a strong inhibitory effect (low *K<sub>i</sub>*) on these β-lactamases as exemplified with CTX-M-15 (4). This finding shall be added to the current debate on usage of ertapenem for treating infections due to ESBL-producing *K. pneumoniae* and *E. coli* isolates.

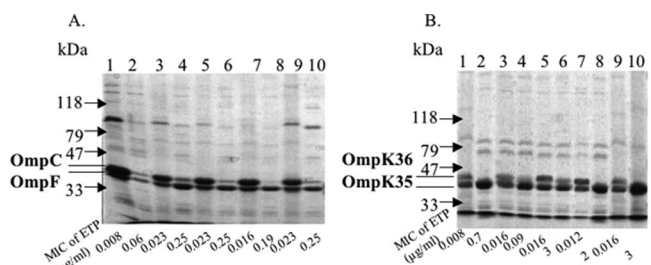


FIG. 1. OMP profiles of *E. coli* Wi (A) and *K. pneumoniae* M (B) isolates expressing no CTX-M (lanes 1 and 2) or expressing CTX-M-2 (lanes 3 and 4), CTX-M-3 (lanes 5 and 6), CTX-M-9 (lanes 7 and 8), or CTX-M-15 (lanes 9 and 10). Lanes 1, 3, 5, 7, and 9 correspond to OMPs extracted from isolates cultured without ertapenem (ETP); lanes 2, 4, 6, 8, and 10 correspond to OMPs extracted after a single-step ertapenem selection (4× MIC for each).

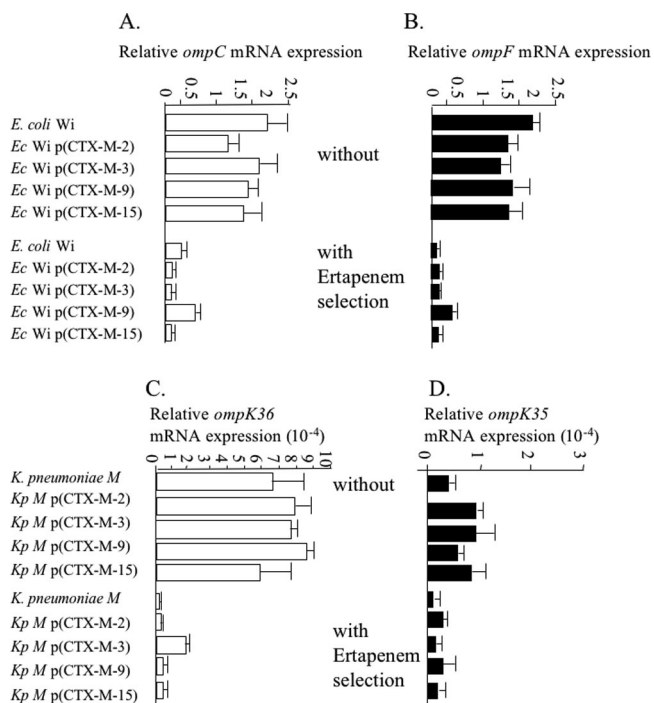


FIG. 2. Effects of one-step selection of ertapenem ( $4\times$  MIC) on transcription of *ompC* (A) and *ompF* (B) genes in *E. coli* and of *ompK36* (C) and *ompK35* (D) genes in *K. pneumoniae*. Isolates expressing no CTX-M, CTX-M-2, CTX-M-3, CTX-M-9, or CTX-M-15 were used as templates. Data are expressed as the amount of target mRNA relative to the control value, i.e., the *gap* gene of *E. coli* and the 16S rRNA genes of *K. pneumoniae*. Upper lanes of each diagram correspond to the *omp* transcript level in isolates cultured without ertapenem, and lower lanes correspond to the *omp* transcript level after one-step selection of ertapenem.

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