

# In vitro activity of ceftolozane-tazobactam against Enterobacter cloacae complex clinical isolates with different $\beta$ -lactam resistance phenotypes

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- In vitro activity of ceftolozane-tazobactam against Enterobacter cloacae complex clinical
- isolates with different β-lactam resistance phenotypes
- Running title: Activity of TOL-TAZ against ECC clinical isolates
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- Supplemental materials. 26
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### **Abstract**

overexpressing ECC isolates.

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The study evaluated the *in vitro* activity of ceftolozane-tazobactam (C/T) against 94 unique 29 30 clinical isolates of Enterobacter cloacae complex (ECC). No difference was observed according to the ECC cluster. The in vitro activity greatly varied depending on the  $\beta$ -31 lactamase-producing profile: 100%, 67% and 19% of wild-type, ESBL-producing, and AmpC-32 overproducing strains were susceptible to C/T, respectively. The use of C/T could be of 33 interest for the treatment of some infections caused by ESBL-producing AmpC-non-34

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The species belonging to the Enterobacter genus are responsible for 5-10% of infections among patients hospitalized in intensive care units (ICUs) and primarily due to the members of the Enterobacter cloacae complex (ECC) (1,2). Actually, ECC is composed of 13 clusters among which three (C-III, VI and VIII) are the most frequently recovered from human clinical specimens (3,4). All ECC members intrinsically harbour a chromosomal ampC gene coding for a cephalosporinase (2,5-7). Among these third generation cephalosporin (TGC)-resistant isolates, approximately one third has acquired plasmid-mediated extended-spectrum  $\beta$ lactamases (ESBLs) while the remaining two thirds express a high-level production of cephalosporinase (HL-CASE) caused by ampC derepression that results from chromosomal mutations (6). Ceftolozane-tazobactam (C/T) is a novel TGC combined with a classical inhibitor of  $\beta$ lactamase (ratio of 2:1), which has recently been approved for the treatment of complicated intra-abdominal and urinary tract infections (8). Although ceftolozane has been developed to be more stable than other TGCs against natural AmpC produced by P. aeruginosa (9), much less is known about its activity against other intrinsically AmpC-producing species, such as ECC. Indeed, previous studies have mainly described the in vitro activity of C/T against Enterobacter spp. with no distinction of species and/or phenotypes of resistance (10-13). In addition, no data is available about the in vitro activity of C/T according to the ECC cluster. The purpose of the study was then to 1) evaluate the in vitro activity of C/T against a collection of ECC clinical isolates representing relevant clusters and exhibiting various phenotypes of  $\beta$ -lactam susceptibility profiles; and 2) compare it to those of commonly-used β-lactams.

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Besides the reference strain of E. cloacae subsp. cloacae ATCC 13047 (belonging to C-XI), a total of 93 ECC clinical isolates (representing 12 clusters) collected from university hospital of Caen were included in the study (3). Note that the strains were identified by MALDI-TOF mass spectrometry (Microflex LT; Bruker Daltonics, Bremen, Germany) and ECC members were clustered by hsp60 sequencing as previously described (7). MICs of C/T (C provided by Cubist Pharmaceuticals and T purchased from Abcam Biochemicals), piperacillin-tazobactam (TZP), cefotaxime (CTX), ceftriaxone (CRO), ceftazidime (CAZ), cefepime (FEP), ertapenem (ETP) and imipenem (IMP) were determined by the broth microdilution reference method in accordance with EUCAST guidelines (http://www.eucast.org/). ECC isolates were classified into four β-lactam susceptibility phenotyes: wild-type [WT] (no resistance to TGCs), ESBL (resistance to at least one TGC with a positive double-disk synergy test), HL-CASE (resistance to at least one TGC with a negative double-disk synergy test and a significant difference in TGC-mediated inhibition with or without cloxacillin 250 mg/L), and ESBL+HL-CASE (resistance to at least one TGC with a positive double-disk synergy test and a significant difference in TGC-mediated inhibition with or without cloxacillin 250 mg/L). To confirm the HL-CASE phenotype (especially in isolates producing ESBLs), we quantified the levels of expression of the chromosomal ampC gene by RT-qPCR using specific primers (Table S1). Total RNAs were extracted as previously described (7). Transcript levels were determined by the DeltaDelta Ct method using the rpoB gene as housekeeping control gene (Table S1), and the fold change (FC) of expression was calculated between TGC-resistant strains and WT strains of the same cluster. HL-CASE was defined if the FC was higher than 2. ESBLs were characterized as previously described (14-16).

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82 Twelve of the 13 clusters were represented in the study (Table S2). Among them, C-III (21%, 20/94), C-VI (20%, 19/94) and C-VIII (28%, 26/94) were predominant, as previously described 83 (Table S2) (4). Note that none of the studied clusters expressing a WT phenotype exhibited 84 an intrinsic resistance to the C/T in spite of the genetic variability of the ampC gene (7). 85 Among the 94 isolates, four antimicrobial susceptibility phenotypes were distinguished: WT 86 34% (32/94), ESBL alone 10% (9/94), ESBL+HL-CASE 20% (19/94) and HL-CASE 36% (34/94) 87 (Tables 1 and S2). By using the disk method with or without cloxacillin (250 mg/L), the HL-88 89 CASE phenotype was not highlighted in 21% of isolates (4/19) presenting an ESBL+HL-CASE 90 combined phenotype. By contrast, the expression of ampC allowed to accurately discriminate between all ESBL and ESBL+HL-CASE phenotypes (P < 0.0001) (Figure 1). Among 91 the 28 isolates expressing an ESBL phenotype (ESBL alone and ESBL+HL-CASE), four genes 92 encoding such β-lactamases were identified: bla<sub>CTX-M-15</sub> (17/28, 61%), bla<sub>SHV-12</sub> (9/28, 32%), 93  $bla_{\text{CTX-M-9}}$  (2/28, 7%) and  $bla_{\text{TEM-15}}$  (1/28, 4%). Note that one isolate co-produced  $bla_{\text{CTX-M-15}}$ 94 and bla<sub>SHV-12</sub> genes (Table S3). The distribution of ESBLs was similar to that recently 95 96 described in French E. cloacae isolates (CTX-M-15, 52%; SHV-12, 38%; CTX-M-9, 10%) (17). Besides ESBL production, plasmid-mediated AmpC β-lactamase genes were also identified in 97 two isolates ( $bla_{CMY-4}$  and  $bla_{DHA-1}$ ) and one strain harboured the acquired OXA-48-like 98 carbapenemase OXA-204 (Table S3). 99 For the 32 isolates with a WT phenotype, all were categorized as susceptible for all tested β-100 101 lactams except one strain that was not susceptible to CAZ (MIC = 2 mg/L) according to 102 EUCAST breakpoints (Table 1). MICs of C/T ranged from 0.12 to 0.5 mg/L with MIC<sub>50</sub> and 103  $MIC_{90}$  at 0.25 and 0.5 mg/L, respectively (Table 1). These MIC values were identical to  $MIC_{50}$ (0.25 mg/L) and MIC<sub>90</sub> (0.5 mg/L) published for ceftazidime-susceptible Enterobacter strains 104 105 (12,18).

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For the nine isolates expressing an ESBL phenotype, all were resistant to TGCs (CTX, CRO and CAZ) while TZP and FEP retained an activity against 22% and 44% of strains, respectively (Table 1). Six isolates (67%) were categorized as susceptible to C/T, with MICs comprised between 0.25 and 4 mg/L (Table 1). MIC<sub>50</sub> and MIC<sub>90</sub> were at 1 and 2 mg/L, which is similar to values (2 and 4 mg/L, respectively) reported in a previous study on 15 ESBL-producing Enterobacter strains (19). Also, a recent study reports a proportion at 85% (40/47) of Enterobacter isolates susceptible to C/T (20). This is in accordance with the fact that tazobactam inhibits most of class A  $\beta$ -lactamases (including ESBLs) and that C/T remains active against >80% of ESBL-producing Escherichia coli clinical isolates (11-13,18). All the 53 isolates showing a HL-CASE phenotype, including 19 that co-produced an ESBL, were categorized as resistant to TGCs (CTX, CRO and CAZ) and only 19% were susceptible to C/T (Table 1). The percentages of susceptible strains were comparable between ESBL+HL-CASE and HL-CASE isolates for TZP (0 vs 3%), ETP (53 vs 47%) and IMP (95 vs 100%) but different for FEP (11 vs 35%) (Table 1). MIC<sub>50</sub> and MIC<sub>90</sub> of C/T were higher for ECC isolates with an ESBL+HL-CASE phenotype (8 and 128 mg/L, respectively) than those for HL-CASE strains (4 and 16 mg/L, respectively) (Table 1). Consequently, eight isolates (24%) were categorized as susceptible to C/T among HL-CASE isolates whereas only two (11%) remained susceptible to the combination in the group of ESBL+HL-CASE strains (Table 1). As compared to ESBL producers, this poorer activity of C/T against HL-CASE ECC isolates is due to the fact that tazobactam is not effective against AmpC  $\beta$ -lactamases (8). In this subgroup (HL-CASE ECC), the percentage of strains inhibited by ≤1 mg/L (corresponding to the EUCAST breakpoint) of C/T varied between 14 and 36% (11-13,18), which is similar to our results. Surprisingly, for the two studies where resistance mechanisms were specified (12,20), 50 to 75% of HL-CASE strains remained susceptible to C/T, which is much higher that proportions

reported here. Interestingly, 30% (28/94) of ECC isolates were not susceptible to ETP 130 (including one not susceptible to IMP) of which only two were susceptible to C/T (MIC = 1 131 132 mg/L), suggesting that C/T is likely not a good option for the treatment of caused by non-CPE 133 strains showing reduced carbapenem susceptibility. 134 In summary, there is no difference in  $\beta$ -lactamase-producing profile to C/T according to the 135 ECC cluster. By contrast, the in vitro activity of C/T greatly varies depending of the  $\beta\mbox{-lactam}$ 136 137 susceptibility profile. 138 139 **Funding information** 

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Figure 1. Fold change of expression of the ampC chromosomal gene according to the 224 resistant phenotype: production of an extended-spectrum  $\beta$ -lactamase (ESBL), AmpC 225 overproduction (HL-CASE), ESBL+HL-CASE. The fold change (expressed as Log<sub>10</sub> values) was 226 calculated between resistant strains and wild-type strains of the same cluster. HL-CASE was 227 defined if the fold change was higher than 2. 228

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Table 1. MICs of different  $\beta$ -lactams against a collection of 94 strains (93 clinical isolates and ATCC13047) of Enterobacter cloacae complex (ECC) according to resistance phenotypes

ECC clinical isolates (no.)	MIC (mg/L)			EUCAST susceptibility	% of susceptible strains
	MIC <sub>50</sub>	MIC <sub>90</sub>	Range	breakpoint (mg/L)	
All ECC (94)					
Ceftolozane-tazobactam	1	16	0.12-128	≤1	51
Imipenem	0.25	0.5	0.12-4	≤2	99
Ertapenem	0.25	2	0.01-32	≤0.5	70
Cefepime	0.5	16	0.03->256	≤1	54
Ceftazidime	64	256	0.25->256	 ≤1	33
Cefotaxime	64	>256	0.25->256	= <del>-</del> ≤1	34
Ceftriaxone	128	>256	0.25->256	<u>=1</u> ≤1	34
Piperacillin-tazobactam	64	256	2-256	<u> </u>	37
Wild-type ECC (32)					
Ceftolozane-tazobactam	0.25	0.5	0.12-0.5	≤1	100
Imipenem	0.25	0.5	0.12-0.5	≤2	100
Ertapenem	0.06	0.12	0.01-0.25	≤0.5	100
Cefepime	0.03	0.06	0.03-0.06	≤1	100
Ceftazidime	0.5	1	0.25-2	 ≤1	97
Cefotaxime	0.5	1	0.25-1	<u></u> ≤1	100
Ceftriaxone	0.5	1	0.25-1	<u>=1</u> ≤1	100
Piperacillin-tazobactam	2	4	2-8	≤8	100
ESBL alone (9)					
Ceftolozane-tazobactam	1	2	0.25-4	≤1	67
Imipenem	0.25	0.5	0.12-0.5	≤2	100
Ertapenem	0.125	0.5	0.03-1	≤0.5	89
Cefepime	4	256	0.06-64	≤1	44
Ceftazidime	64	128	32-128	<u></u> ≤1	0
Cefotaxime	256	>256	4->256	<u>≤1</u> ≤1	0
Ceftriaxone	256	>256	2->256	<u>=1</u> ≤1	0
Piperacillin-tazobactam	64	128	8-128	≤s ≤8	22
ESBL+HL-CASE (19)					
Ceftolozane-tazobactam	8	128	1-128	≤1	11
Imipenem	0.5	1	0.25-4	≤2	95
Ertapenem	0.5	8	0.12-32	≤0.5	53
Cefepime	4	256	0.12->256	≤1	11
Ceftazidime	128	256	32->256	≤1	0
Cefotaxime	256	>256	64->256	 ≤1	0
Ceftriaxone	256	>256	128->256	<u></u> ≤1	0
Piperacillin-tazobactam	128	256	32->256	<u>≤1</u> ≤8	0
HL-CASE (34)				-	
Ceftolozane-tazobactam	4	16	0.25-32	≤1	24
Imipenem	0.25	0.5	0.12-1	≤2	100
Ertapenem	1	2	0.03-4	≤0.5	47
Cefepime	2	8	0.12-16	≤1	35
Ceftazidime	128	256	2->256	= <del>-</del> ≤1	0
Cefotaxime	256	>256	16->256	≤1 ≤1	0
Ceftriaxone	256	>256	32->256	≤1 ≤1	0
Piperacillin-tazobactam	128	256	8-256	≤8	3

 ${\small \textbf{ESBL}, Extended-spectrum $\beta$-lactamase; HL-CASE, High-level production of cephalosporinase.} \\$ 

