

First Description of CTX-M-15-Producing *Klebsiella pneumoniae* in Portugal

The first CTX-M-15 β -lactamase was found in several enterobacterial isolates from India in 1999 (4). Worldwide spread of CTX-M-15 β -lactamases is now well documented (1–5, 7, 8, 12). CTX-M β -lactamases confer high-level resistance to cefotaxime, ceftriaxone, and aztreonam and are well inhibited by clavulanate and tazobactam (10, 11).

Klebsiella pneumoniae 193KFFUL was isolated from a blood culture in September 2003 at the Hospital de Santa Maria. The clinical isolate was resistant to cefotaxime and cefepime (MIC, >256 μ g/ml) and ceftazidime and aztreonam (MIC, 96 μ g/ml) and susceptible to imipenem (MIC, 0.125 μ g/ml). Tazobactam and clavulanate restored the activities of piperacillin, cefotaxime, ceftazidime, and cefepime as determined by E-test strips (Table 1). Genomic DNA was prepared as described elsewhere (6), and PCR experiments were performed using specific primers in order to amplify *bla* genes coding for CTX-M β -lactamases. The set of primers CTX1 (5'-SCS ATG TGC AGY ACC AGT AA-3') and CTX2 (5'-CCG CRA TAT GRT TGG TGG TG-3'), designed in accordance with consensus sequences from the *bla*_{CTX-M} genes available at GenBank, produced an amplicon with 544 bp. In order to perform sequencing of the entire gene, PCR was performed with primers CTX-M-1F (5'-ATG GTT AAA AAA TCA CTG CGY C-3') and CTX-M-1R (5'-TTA CAA ACC GTC GGT G-3'). The amplicon of 876 bp was cloned into the pCR2.1-TOPO vector, resulting in plasmid p193K1, and introduced into *Escherichia coli* TOP10 chemically competent cells. The sequenced gene shared 100% homology with *bla*_{CTX-M-15}. *E. coli* 193K1 revealed MIC profiles similar to those of the parental strain, particularly for cefotaxime, whose MIC was >256 μ g/ml. CTX-M-15 showed increased activity against ceftazidime because of a single nucleotide substitution (A-725→G) that has already been reported in CTX-M-16 (2, 4, 10).

To explore the surrounding regions of *bla*_{CTX-M-15}, PCR was performed with internal primers CTX1 and CTX2 and primers hybridizing to the ends of the insertion sequences *ISEcp1* and *IS903* (2) and to the conserved regions of class 1 integrons,

5'-CS and 3'-CS (6). Positive PCR products were obtained with primers *ISEcp1F* and CTX2 (911 bp) and primers CTX1 and *IS903R* (1,430 bp). Nucleotide sequence analysis indicated that *bla*_{CTX-M-15} was flanked upstream by an *ISEcp1*-like element and downstream by an *IS903*-like element. Insertion sequences such as *ISEcp1* or *IS903* have already been described as flanking regions of *bla*_{CTX-M-14}, *bla*_{CTX-M-17}, and *bla*_{CTX-M-19} (2, 4, 9).

A class 1 integron was identified containing an *aadA1* and an *aadA2* gene not associated with the *bla*_{CTX-M-15} gene.

The –35 and –10 promoter sequences for *bla*_{CTX-M-15} expression are located at the end of an *ISEcp1*-like element upstream of its inverted repeat, which is 48 bp from the start codon ATG (data not shown), as already described for *bla*_{CTX-M-15} from India and Turkey and different from the *bla*_{CTX-M-15} gene described in Poland, in which the distance is 128 bp (4, 9). In addition, analysis of the downstream region of *bla*_{CTX-M-15} showed that 685 nucleotides had 97% similarity to *IS903-C* from *bla*_{CTX-M-17}.

This is the first report identifying an *IS903*-like element downstream of the *bla*_{CTX-M-15} gene in a *K. pneumoniae* isolate from a Portuguese hospital.

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TABLE 1. MICs of β -lactam antibiotics alone or in association with β -lactam inhibitors for *K. pneumoniae* clinical isolate 193KFFUL and *E. coli* 193K1 harboring recombinant plasmid p193K1

β -Lactam	MIC (μ g/ml)	
	<i>K. pneumoniae</i> 193KFFUL	<i>E. coli</i> 193K1
Amoxicillin	>256	>256
Amoxicillin + CL ^a	8	16
Piperacillin	>256	>256
Piperacillin + TZ ^b	32	32
Ceftazidime	96	24
Ceftazidime + CL	0.5	1.0
Cefepime	>256	16
Cefepime + CL	0.19	0.064
Cefotaxime	>256	>256
Cefotaxime + CL	0.125	0.094

^a CL, clavulanic acid.

^b TZ, tazobactam.

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