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Multiple antibiotic-resistance mechanisms including a novel combination of extended-spectrum β-lactamases in a *Klebsiella pneumoniae* clinical strain isolated in Argentina

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***Klebsiella pneumoniae* M1803, isolated from a paediatric patient with chronic urinary infection, presented nine antimicrobial resistance mechanisms harboured on two conjugative megaplasmids, in addition to the chromosomally mediated SHV-1 β-lactamase. These nine antimicrobial resistance mechanisms comprised two extended-spectrum β-lactamases (ESBLs) (PER-2 and CTX-M-2), TEM-1-like, OXA-9-like, AAC(3)-IIa, AAC(6′)-Ib, ANT(3″)-Ia and resistance determinants to tetracycline and chloramphenicol. During fluoroquinolone treatment, a variant derived from M1803 (named M1826) was selected, with an overall increase of MICs, in particular of cefoxitin and carbapenems. No enzymic activity against these latter drugs was found. Mutations in the region analogous to the quinolone resistance-determining region were not found. Strain M1826 was deficient in OmpK35/36 expression, which produced the decrease in the susceptibility to cefoxitin, carbapenems and fluoroquinolones. The $bla_{CTX-M-2}$ gene was located in an unusual class 1 integron, which includes Orf513, as occurred in the recently described In35. In addition, Tn*3* and Tn*1331* were detected in both *K. pneumoniae* isolates. This is the first report of *in vivo* selection of an OmpK35/36 deficiency in a *K. pneumoniae* strain that produced a novel combination of two ESBLs (CTX-M-2 and PER-2) during fluoroquinolone treatment in a paediatric patient with chronic urinary infection.**

Keywords: CTX-M-2, PER-2, In35, Tn*3*, Tn*1331*

Introduction

Klebsiella pneumoniae is a common nosocomial pathogen causing severe morbidity and mortality in paediatric patients. Most *K. pneumoniae* isolates have a chromosomally encoded SHV-1 β-lactamase.[1] Since 1983, plasmid-encoded extended-spectrum β-lactamases (ESBLs) derived from the TEM and SHV families have been extensively reported in Enterobacteriaceae, especially in *Klebsiella* spp.[2,3] Although ESBLs have been identified in Argentina, their prevalences are different from those observed in other countries. A national surveillance of extended-spectrum cephalosporin resistance in *Klebsiella* spp. was performed through the WHONET-Laboratory Network Argentina. The unique ESBLs detected among the 200 isolates analysed in this surveillance were CTX-M-2-like (>60% of isolates) and PER-2-like, SHV-5-like and SHV-2-like (~10% of isolates in each case).[4]

K. pneumoniae producing two or more ESBLs have been reported scarcely, but when they are, in most cases they include TEM- and/or SHV-derived enzymes.[5–11] Herein we report the characterization of a multiresistant *K. pneumoniae* isolate that produces a novel combination of two ESBLs (CTX-M-2 and PER-2) and a derived variant of this strain, which was selected during ciprofloxacin treatment and showed alterations in the expression levels of outer membrane proteins (OMPs).

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Materials and methods

Patient and bacterial strains

K. pneumoniae M1803 and M1826 were isolated from a 1-year-old patient who suffered chronic urinary tract infection due to a posterior urethral valve malformation and bilateral vesicourethral reflux. During a period of 5 months, the child was treated for successive urinary infections with amphotericin (Gador, Buenos Aires, Argentina), ceftriaxone (Roche), furazolidone (nitrofurantoin analogue; Schering-Plough), amoxicillin (Roche), imipenem (imipenem/cilastatin; Merck Sharp & Dohme) and ciprofloxacin (Bayer). During one of these infections, *K. pneumoniae* strain M1803 was isolated. After 10 days of ciprofloxacin therapy, *K. pneumoniae* strain M1826 was isolated.

Escherichia coli ER1793 [F^- *fhuA2 Δ(lacZ)r1 glnV44 e14⁻ (McrA⁻) trp-31 his-1 rpsL104(*Str^R*) xyl-7 mtl-2 metB1 Δ(mcrC-mrr)114::IS10*; New England Biolabs, Beverly, MA, USA], resistant to nalidixic acid and rifampicin, was employed as the recipient strain in conjugative assays.

Antimicrobial agents and susceptibility testing

The antimicrobial agents used for susceptibility testing were obtained from standard laboratory powders, and their sources were as follows: amikacin, aztreonam and cefepime (Bristol-Myers Squibb); amoxicillin and clavulanic acid (Smith Kline Beechman and Roemmers, Buenos Aires, Argentina); ampicillin (Temis Lostaló, Buenos Aires, Argentina); chloramphenicol (Parke Davis, Buenos Aires, Argentina); cefotaxime (Argentia, Buenos Aires, Argentina); cefoxitin and imipenem (without cilastatin) (Merck Sharp & Dohme); ceftazidime (Glaxo); ceftibuten, gentamicin, sulfamethoxazole and trimethoprim (Schering Plough); cefalothin, piperacillin and tazobactam (Wyeth Pharmaceuticals); tetracycline (Microsules and Bernabó, Buenos Aires, Argentina); meropenem (Astra Zeneca); and ciprofloxacin (Bagó, Buenos Aires, Argentina). The antimicrobial susceptibility of each isolate and its transconjugants was determined by the disc diffusion and agar dilution methods according to NCCLS guidelines.[12–15] When indicated, clavulanic acid (2 mg/L) or tazobactam (4 mg/L) was used in combination with β-lactams.

Table 1. Primers for PCR analysis of antimicrobial resistance mechanisms

Target	Primer	No.[a]	Oligonucleotide sequence	Ref.
bla$_{CTX-M}$	bla$_{CTX-M}$ F[b]		CGGAATTCATGATGACTCAGAGCATTCG	16
	bla$_{CTX-M}$ R[b]		GCTCTAGATTATTGCATCAGAAACCGTG	
bla$_{PER}$	bla$_{PER}$ F		GTAGTATCAGCCCAATCCCC	16
	bla$_{PER}$ R		CCAATAAAGGCCGTCCATCA	
bla$_{TEM}$	OT-1		TTGGGTGCACGAGTGGGTTA	23
	OT-2		TAATTGTTGCCGGGAAGCTA	
bla$_{SHV}$	OS-1		TCGGGCCGCGTAGGCATGAT	23
	OS-2		AGCAGGGCGACAATCCCGCG	
aac(3)-IIa	aacC2 F		CGCTAAACTCCGTTACC	this work
	aacC2 R		TAGCACTGAGCAAAGCC	
aph(3′)-VIa	aph(3′)-VIa F		GCCGATGTGGATTGCGAAAA	this work
	aph(3′)-VIa R		GCTTGATCCCCAGTAAGTCA	
gyrA	GyrA F		ACGTATTGGCGAYGACTGGA	this work
	GyrA R		AAGAGACGGTCGATTTCGTTG	
Class 1 integrons[c]				
bla$_{CTX-M}$	CTXM-F	1	CGTCGGGATATTCTGGC	30
	CTXM-R	2	TCACTTTATCGGGACCAC	
5′-CS[d]	5′-CS	3	GGCATCCAAGCAGCAAG	22
ant(2″)-Ia	ant(2″)-Ia	4	CCGCAGCTAGAATTTTG	22
	ant(2″)-Ia-COOH	5	ACGTTGAGGTCTTGCGT	this work
sulI	sulIR	6	TTTGAAGGTTCGACAGC	30
orf513	ORF513F	7	ATGGTTTCATGCGGGTT	this work
3′-CS[d]	3′-CS	8	AAGCAGACTTGACCTGA	22
Tn*1331*[c]				
tnpA	Tn3F	9	AAGTTCATCGGGTTCGC	this work
aac(6′)-Ib	aac(6′)-Ib[e]	10	TGTGACGGAATCGTTGC	22
bla$_{OXA-9}$	bla$_{OXA-9}$	11	GAACACCAACATATGCA	this work
ant(3″)-Ia	ant(3″)-Ia[e]	12	TCGATGACGCCAACTAC	22
	ant(3″)-Ia-COOH[e]	13	CGCAGATCAGTTGGAAG	this work

F, forward; R, reverse.
[a]Numeration corresponding to primers employed in PCR mapping (see Figure 3).
[b]Used to obtain the sequenced amplimer.
[c]Different primer combinations were made in PCR cartography for detection of class 1 integrons and Tn*1331* transposon.
[d]5′ and 3′ conserved segments of class 1 integrons.
[e]These primers were also used in the PCR cartography of class 1 integrons.[22]

Nalidixic acid and rifampicin (both for use in molecular biology applications) were from Sigma (St Louis, MO, USA).

Isoelectric focusing and microbiological method for detection of β-lactamases

β-Lactamase preparation and analytical isoelectric focusing (IEF) were performed as described previously.[16] β-Lactamase bands were visualized by the iodometric method described by Labia & Barthélémy.[17] For β-lactamase inhibition procedures the gel was covered with a piece of filter paper impregnated with 1 mM clavulanic acid, aztreonam or cefoxitin as indicated, and incubated for 10 min at room temperature before developing as described above. Crude preparations from bacteria possessing β-lactamases of known isoelectric points (pI) were used as standards: TEM-1 (pI 5.4), PER-2 (pI 5.4), SHV-2 (pI 7.6), P99 (pI 7.8), CTX-M-2 (pI 7.9) and SHV-5 (pI 8.2).

The hydrolytic activity against cefoxitin and carbapenems was determined by the microbiological method.[18]

OMP analysis

OMPs were isolated as sodium lauroyl sarcosynate-insoluble material from cell envelopes after sonication (20 pulses of 30 s in ice at 30 s intervals) and centrifugation of lysed cells at 100 000**g** for 1 h at 4°C.[19] Electrophoretic analysis of OMPs was performed as previously reported,[19] using 12% SDS–PAGE gels and broad molecular weight markers (unstained; Bio-Rad, Hercules, CA, USA) as standards.

Conjugative assays

Biparental conjugations were performed by mixing the donor and recipient strains on Luria–Bertani agar in a ratio of 5:1, and incubating the mixture for 18 h at 35°C. Transconjugants were selected on Mueller–Hinton agar supplemented with nalidixic acid (50 mg/L) plus cefotaxime (8 mg/L), or nalidixic acid plus ceftazidime (15 mg/L).

General molecular biology procedures

The relatedness of *K. pneumoniae* M1803 and M1826 was assessed by pulsed-field gel electrophoresis (PFGE) of the *Xba*I-digested DNA using conditions already described.[20] Plasmid DNA was extracted from *K. pneumoniae* and *E. coli* transconjugant cells as described previously,[21] and were analysed by electrophoresis in 0.7% agarose gels (Tris–acetate buffer), employing plasmids of known size as standards.

PCR assays

Detection of antimicrobial resistance genes was performed by PCR using the forward and reverse primers listed in Table 1. DNA templates were prepared by lysing one or two colonies of each *K. pneumoniae* isolate, or each *E. coli* transconjugant, in 50 μL of boiling water, and 2 μL was used for the PCRs. Amplifications were performed with a Biometra thermal cycler (Whatman Biometra GmbH, Göttingen, Germany) in a final volume of 50 μL containing 20 pmol of each primer (purchased from Gibco-BRL, Gaithersburg, MD, USA), 25 μM of each dNTP, 1.5 mM $MgCl_2$ and 2.5 U of *Taq* polymerase (Promega, Madison, WI, USA). Previously described conditions for cycling were used.[16,22,23]

DNA sequencing

DNA sequencing of amplicons obtained with primers specific to $bla_{CTX\text{-}M}$, bla_{PER} and *gyrA* [including the region analogous to the quinolone resistance-determining region (QRDR)] genes (Table 1) was performed on both strands by the method of Sanger *et al.*,[24] using the BigDye terminators methodology (Applied Biosystems/Perkin Elmer, Foster City, CA, USA). The sequences were analysed in an ABI Prism 377 DNA Sequencer (Applied Biosystems/Perkin Elmer).

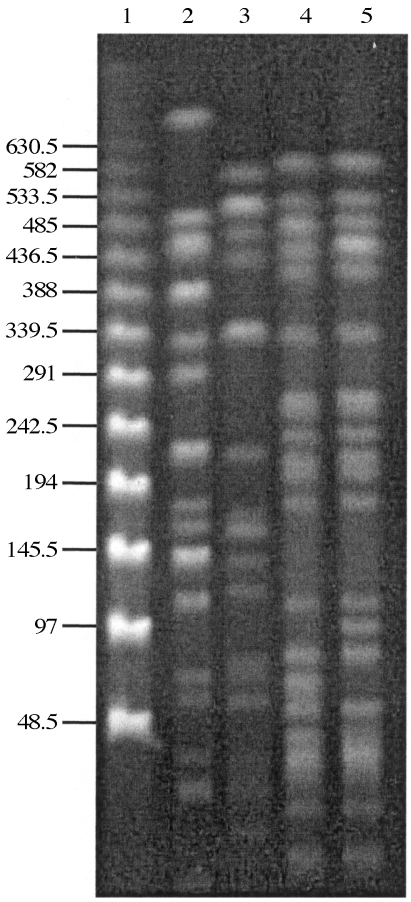

Figure 1. PFGE patterns of *K. pneumoniae* strains. Chromosomal DNA was digested with *Xba*I endonuclease. Lane 1, λ ladder; lane 2, *K. pneumoniae* ATCC 700603; lane 3, *K. pneumoniae* ATCC 10031; lane 4, *K. pneumoniae* M1803; lane 5, *K. pneumoniae* M1826.

Results and discussion

Antibiotic susceptibility and plasmid profiles of K. pneumoniae M1803 and M1826, and E. coli transconjugants

K. pneumoniae M1803 and M1826 showed less than three differences according to PFGE profiling, indicating the clonal relationship between both isolates (Figure 1).[25] In contrast to M1803, isolate M1826 was resistant to cefoxitin and ceftibuten, showing a 4–32× increase in the MICs of extended-spectrum cephalosporins, carbapenems, aztreonam, piperacillin–tazobactam, chloramphenicol and ciprofloxacin. In addition, clavulanic acid produced almost no reduction in the MICs of extended-spectrum cephalosporins against isolate M1826 (Table 2).

For strains M1803 and M1826, two different types of *E. coli* transconjugants were obtained, named type 1 and type 2 (Table 2). Type 1 transconjugants (M3089 and M3090, derived from M1803 and M1826 strains, respectively) were selected with nalidixic acid plus cefotaxime, and were resistant to cefotaxime, cefepime and gentamicin. Type 2 transconjugants (M3129 and M3130, derived from M1803 and M1826 strains, respectively) were selected with nalidixic acid plus ceftazidime, and were resistant to ceftazidime, ceftibuten, chloramphenicol, tetracycline and gentamicin, and showed

Table 2. Antibiotic susceptibility [MIC (mg/L)], plasmid content, IEF of β-lactamases and PCR mapping of antimicrobial resistance mechanisms in *K. pneumoniae* isolates and *E. coli* transconjugants

	K. pneumoniae		*E. coli*		
	M1803	M1826	type 1[a]	type 2[b]	ER1793
(i) Antimicrobial susceptibility					
ampicillin	>1024	>1024	>1024	>1024	4
co-amoxiclav	16	32	16	8	4
cefalothin	>1024	>1024	>1024	512	8
cefoxitin	2	64	4	8	4
cefotaxime	64	512	256	4	<0.03
cefotaxime–clavulanic acid	0.12	256	0.12	0.03	<0.03
ceftazidime	64	256	8	>256	0.12
ceftazidime–clavulanic acid	0.25	64	0.25	0.25	0.12
cefepime	32	512	64	8	<0.5
cefepime–clavulanic acid	<0.5	128	<0.5	≤0.25	0.5
ceftibuten	16	128	2	64	<0.25
ceftibuten–clavulanic acid	<0.25	64	<0.25	≤0.12	<0.25
aztreonam	64	512	32	128	0.06
piperacillin	>1024	>1024	1024	256	8
piperacillin–tazobactam	64	512	1	ND	1
amikacin	16	32	0.25	4	0.25
gentamicin	256	256	128	16	≤0.12
imipenem	0.12	1	0.25	0.12	0.25
meropenem	0.03	1	≤0.015	0.015	≤0.015
tetracycline	256	256	1	128	1
SXT	128	>256	≤0.12	≤0.12	≤0.12
chloramphenicol	128	512	4	256	4
ciprofloxacin	0.032	0.25	0.25	ND	0.25
(ii) Plasmid content (kb)	140, 60, 4, 3	140, 60	140	140	–
(iii) IEF band (pI)	5.4, 7.6, 7.9	5.4, 7.6, 7.9	5.4, 7.9	5.4	–
(iv) PCR mapping					
bla_{SHV}-like	+	+	–	–	–
bla_{TEM}-like	+	+	+	+	–
bla_{PER-2}	+	+	–	+	–
$bla_{CTX-M-2}$	+	+	+	–	–
ant(2″)-Ia	+	+	+	–	–
aac(3)-IIa	+	+	+	+	–
Tn*1331*	+	+	–	+	–
Tn*3*	+	+	+	–	–

SXT, trimethoprim–sulfamethoxazole; ND, not determined.
[a]Features shown were the same for M3089 and M3090 transconjugants.
[b]Features shown were the same for M3129 and M3130 transconjugants.

decreased susceptibility to amikacin. The results of the plasmid profile analysis are summarized in Table 2. It is noteworthy that the segregation of different non-β-lactam susceptibility profiles into type 1 and 2 transconjugants occurred in the absence of any selective pressure. The most probable explanation for this fact would be the co-existence of two different megaplasmids of the same size (i.e. 140 kb) in each of the two parental *K. pneumoniae* isolates, each carrying a different complement of β-lactam and non-β-lactam resistance genes.

Characterization of β*-lactamases produced by K. pneumoniae M1803 and M1826*

By IEF analysis, with the β-lactamase bands being visualized by an iodometric method using ampicillin plus cefaloridine as substrate, three bands were detected in both *K. pneumoniae* strains, with pIs of 5.4, 7.6 (corresponding to the chromosomal SHV-1 β-lactamase) and 7.9 (Table 2). In contrast, when visualizing the β-lactamase bands with ceftazidime, two bands were detected, with pIs of 5.4 and 7.9. All bands were susceptible to clavulanic acid inhibition. The nature of a broad-spectrum β-lactamase activity with a pI of 5.4 could not be specifically determined in these standard IEF assays because of an overlapping ESBL band at the same pI. Accordingly, *in situ* β-lactamase inhibition using cefoxitin was performed on the IEF gel, as described previously.[16] The ESBL activity with a pI of 5.4 was inhibited with cefoxitin, whereas the broad-spectrum β-lactamase activity with a pI of 5.4 and the ESBL activity with a pI of 7.9 were not. This property, of cefoxitin inhibition of the ESBL band at pI 5.4, indicated it was most likely to be the PER-2 enzyme. These results are in agreement with those obtained by PCR assays, which yielded amplification products with primers specific to TEM, SHV, CTX-M and PER families of β-lactamases genes. Therefore, the presence of four β-lactamase genes, bla_{PER-2}-like, $bla_{CTX-M-2}$-like, bla_{SHV-1}-like

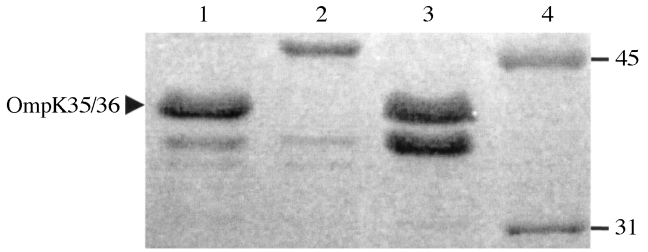

Figure 2. OMP profiles of *K. pneumoniae* M1803 and M1826. Numbers on the right indicate molecular weight markers (in kDa); the arrow shows the relative mobility of OmpK35/36 porins. Lane 1, *K. pneumoniae* M1803; lane 2, *K. pneumoniae* M1826; lane 3, *K. pneumoniae* ATCC 10031; lane 4, molecular weight standard.

and bla_{TEM-1}-like, was confirmed. These results were replicated using both types of transconjugant strains to determine which β-lactamase gene is encoded for on which plasmid (Table 2). The identity of bla_{PER-2} and $bla_{CTX-M-2}$ genes was unequivocally established by sequencing of the corresponding amplicons (data not shown).

Non-transferable antibiotic resistance caused by an OmpK35 and OmpK36 deficiency in K. pneumoniae M1826

K. pneumoniae isolates that are resistant to cefoxitin have been described previously, with resistance caused by either the production of a plasmid-mediated AmpC-like β-lactamase[26,27] or the loss of OMPs, such as OmpK35 and OmpK36.[19,28] Indeed, reduced expression of both porins has been reported in *K. pneumoniae* strains with high MICs of cefoxitin (>32 mg/L).[28] Moreover, increase in the levels of resistance to extended-spectrum cephalosporins, carbapenems and also fluoroquinolones other than cefoxitin, has been associated to the loss of both OmpK35 and OmpK36.[19,29,30]

In this study, the genetic determinants of *K. pneumoniae* M1826 conferring resistance to cefoxitin and carbapenems could not be transferred to *E. coli* by conjugation. Furthermore, incubation of the IEF gels with aztreonam (an AmpC-like β-lactamase inhibitor), prior to β-lactamase visualization using ampicillin plus cefaloridine, did not result in inhibition of any of the β-lactamase bands produced by *K. pneumoniae* M1826 (data not shown). This fact suggests the absence of enzymic activity against cefoxitin in this isolate. Indeed, using a microbiological method, no enzymic activity against cefoxitin and carbapenems was detected in *K. pneumoniae* M1826. In this assay, the parallel control was a crude extract containing the known AmpC MIR-1, and this showed a positive result for cefoxitin hydrolysis. All this information suggests the absence of AmpC-type enzymes in *K. pneumoniae* M1826, and that cefoxitin resistance was chromosomal.

Accordingly, OMP analysis for *K. pneumoniae* M1803 and M1826 (cefoxitin MICs of 2 and 64 mg/L, respectively) was performed and showed that the latter was deficient in OmpK35/36 expression (Figure 2). Our results are in agreement with the previous reports mentioned above, suggesting that the deficiency in OmpK35/36 expression is responsible for the higher overall resistance levels displayed by the M1826 isolate (particularly to cefoxitin and carbapenems) as compared with those of the pretreatment M1803 isolate (Table 2).

The partial sequencing of *gyrA* from *K. pneumoniae* M1826, including the QRDR, did not reveal mutations at codons 83 and 87, indicating that the increased levels of fluoroquinolone resistance in this mutant are not associated with these target site alterations, and are probably a result of the observed loss of OmpK35/36. Increased expression of efflux mechanisms cannot be completely discounted, however.

Detailed analysis of the transferable resistance genes carried by K. pneumoniae M1803 and M1826

Very recently, the $bla_{CTX-M-2}$ gene has been reported as being located in unusual class I integrons In35 and InS21, in clinical isolates of *Proteus mirabilis* and *Salmonella enterica* ser. Infantis, respectively.[30,31] This unusual class 1 integron contains a partial duplication of the 3′ conserved segment, and a region that includes $bla_{CTX-M-2}$ and the Orf513 between both 3′ conserved segments. In addition, In35-related integrons having $bla_{CTX-M-2}$ in conjunction with different resistance cassettes such as *aac(6′)-Ib-ant(3″)-Ia*, *orfD*, *ant(2″)-Ia-ant(3″)-Ia*, *ant(3″)-Ia* and *aac(6′)-Ib* within the variable region of class 1 integrons were detected in clinical isolates of Enterobacteriaceae.[30] In the present work, by PCR mapping of both *K. pneumoniae* isolates and the type 1 transconjugants, the $bla_{CTX-M-2}$ gene was located in an unusual class 1 integron having *ant(2″)-Ia-ant(3″)-Ia* gene cassettes within the variable region (Figure 3a). The co-existence of $bla_{CTX-M-2}$ and *ant(2″)-Ia* genes in the same genetic structure (a complex *sulI*-type integron) and harboured, in turn, in a conjugative megaplasmid, may explain the high prevalence in our bacterial population of both extended-spectrum cephalosporin and gentamicin resistance. The widespread distribution of CTX-M-2-like enzymes among clinical isolates of *K. pneumoniae* in Argentina (60%)[4] could be explained by the fact that ceftriaxone and cefotaxime are the most used cephalosporins in our country. Another gene conferring resistance to gentamicin, *aac(3)-IIa*, was found in both type 1 and type 2 transconjugants. The finding of two gentamicin resistance genes [*ant(2″)-Ia* and *aac(3)-IIa*] in type 1 transconjugants correlated well with an MIC of gentamicin 8-fold higher than that observed for type 2 transconjugants (Table 2).

TEM-1 is the most widespread plasmid-mediated β-lactamase around the world, because its structural gene is harboured on the Tn*3* transposon. Tn*1331* is a transposable element belonging to the Tn*3* family that carries, in addition to bla_{TEM-1}, another β-lactamase gene (bla_{OXA-9}) and two genes encoding aminoglycoside-modifying enzymes: *aac(6′)-Ib* and *ant(3″)-Ia* (Figure 3b).[32] By PCR mapping, three amplification products of Tn*1331* were produced using templates from both *K. pneumoniae* isolates in this study (Table 2; Figure 3b). Interestingly, Tn*1331* was only detected in the type 2 transconjugants, while in the type 1 transconjugants, the bla_{TEM-1}-like gene was located in Tn*3* by PCR with primers to *tnpA* and bla_{TEM} (OT-2) genes (Table 2). These data also support the hypothesis of the existence of two different megaplasmids of the same size in each of the two parental *K. pneumoniae* isolates (one of them harbouring Tn*1331* and the other Tn*3*), which can be separately transferred by conjugation into *E. coli*. The presence of the Tn*1331*-encoded *aac(6′)-Ib* gene conferring amikacin resistance only in type 2 transconjugants may explain the 16-fold increase in the MIC of amikacin observed for type 2 as compared with those for type 1 (Table 2). The *aph(3′)-VIa* gene, which also confers amikacin resistance, was not detected by PCR in the *K. pneumoniae* parental isolates.

Conclusions

Generally, in *Vibrio cholerae*[16] and Enterobacteriaceae[4,33,34] from Argentina, ESBLs and TEM-1-like enzymes are encoded on the

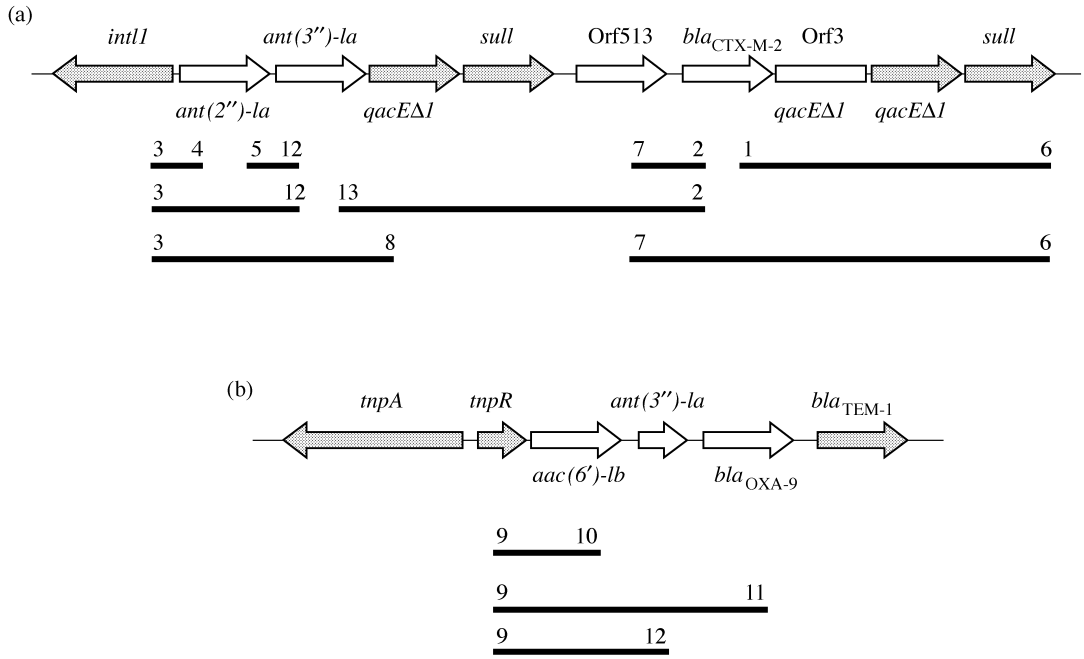

Figure 3. PCR mapping strategy of relevant resistance determinants. Numbers represent the primers employed (see Table 1). (a) $bla_{CTX\text{-}M\text{-}2}$ gene and its surrounding regions inner of In35; (b) Tn*1331*.

same megaplasmid, which, additionally, harbours genetic determinants conferring resistance to other kinds of antibiotics, such as aminoglycosides, trimethoprim–sulfamethoxazole, chloramphenicol and tetracycline. Therefore, the use of any of these drugs in nosocomial acquired infections may lead to cross-selection of extended-spectrum cephalosporin resistance.

Worldwide, few descriptions of strains with two or more ESBLs have been reported, and all of those that have been reported involve TEM- or SHV-derived enzymes. We identified here two ESBLs, CTX-M-2 and PER-2, in a single multiresistant isolate, the first report of this ESBL combination in the same strain. The fact that $bla_{CTX\text{-}M\text{-}2}$ and $bla_{PER\text{-}2}$ were harboured in two different megaplasmids suggests a differential spread of these genes, which correlates well with their different prevalences (60% versus 10%, respectively[4,33,34]) observed in the Argentinean isolates. After successive antibiotic treatments, the last of them with ciprofloxacin, *K. pneumoniae* M1826 could be selected. The selection of these multiresistant bacteria in the hospital environment could be due, amongst other factors, to excessive and/or inappropriate antibiotic use, particularly of empirically prescribed broad-spectrum agents.

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