

## TEM-103/IRT-28 $\beta$ -Lactamase, a New TEM Variant Produced by *Escherichia coli* BM4511

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**Clinical isolate *Escherichia coli* BM4511 was resistant to broad-spectrum penicillins in the presence or in the absence of  $\beta$ -lactamase inhibitors but remained susceptible to cephalosporins. Resistance was due to production of a new TEM-type  $\beta$ -lactamase, designated TEM-103/IRT-28, characterized by the Arg<sub>275</sub>Leu substitution and encoded by the ca. 62-kb pIP845 conjugative plasmid of the IncI1 incompatibility group.**

Among the mechanisms responsible for resistance of *Escherichia coli* to  $\beta$ -lactam- $\beta$ -lactamase inhibitor combinations, hyperproduction of TEM-1 penicillinase and alteration in the outer membrane proteins limiting the entry of the drugs were reported first (16, 19). Inhibitor-resistant TEM (IRT)  $\beta$ -lactamases have been isolated since the beginning of the 1990s and are mostly produced by strains of *E. coli* but also by clinical isolates of *Klebsiella* spp. and *Proteus mirabilis* (2). These enzymes confer resistance to penicillins and their combinations with  $\beta$ -lactamase inhibitors (3, 6, 13). IRT variants are derivatives of TEM  $\beta$ -lactamases, with mutations at various amino acid positions (69, 130, 244, 275, and 276, according to Ambler's numbering [1]) that have been shown, or postulated, to play a role in determining resistance to inhibitors. These substitutions decrease the affinity for  $\beta$ -lactams and alter the way in which the enzymes interact with suicide inactivators (9). We report the genetic characterization of a new TEM variant, TEM-103/IRT-28, in a clinical isolate of *E. coli* resistant to amoxicillin-clavulanate and susceptible to cephalosporins.

*E. coli* BM4511 was isolated from the surgery wound of an 82-year-old woman suffering from colon cancer and hospitalized in Hospital de Basurto, Bilbao, Spain. The MICs of various  $\beta$ -lactams, alone or in combination with  $\beta$ -lactamase inhibitors used at fixed concentrations (clavulanic acid, 2  $\mu$ g/ml; tazobactam, 4  $\mu$ g/ml; sulbactam, 8  $\mu$ g/ml), were determined by the microdilution method in Mueller-Hinton broth (Difco) with an inoculum of approximately  $5 \times 10^4$  cells/well. BM4511 was resistant to penicillins (MICs  $\geq 1,024$   $\mu$ g/ml) but susceptible to cephalosporins (MICs  $\leq 4$   $\mu$ g/ml). Clavulanic acid was unable to restore susceptibility of the strain to penicillins, but tazobactam reduced significantly the piperacillin MIC (Table 1). These data were compatible with the production of an IRT  $\beta$ -lactamase. The presence of a *bla*<sub>TEM</sub> gene in BM4511 was revealed by PCR amplification (data not shown) using primers TEM-C and TEM-H (12).

To determine the pI of the enzyme, crude sonic bacterial extracts were applied to Phast-gels with different pH gradients in a Phast System (Pharmacia) and compared with TEM-30/IRT-2 (pI 5.2), TEM-1 (pI 5.4), and TEM-2 (pI 5.6). The strain was shown to produce a  $\beta$ -lactamase with an isoelectric point of 5.2 (data not shown). All IRT-type  $\beta$ -lactamases reported so far, except for TEM-59/IRT17 (pI 5.6), have a pI of either 5.2 or 5.4.

Resistance to amoxicillin-clavulanate was transferred by conjugation from BM4511 to *E. coli* JM83 at an approximate frequency of  $10^{-7}$  per donor. Analysis of the donor and of a transconjugant after digestion with *EcoRI* revealed the presence of a single plasmid, pIP845, with a size of approximately 62 kb. By reciprocal conjugation with *E. coli* BM21 (5) containing plasmids belonging to various incompatibility groups, pIP845 was found to be of incompatibility group I1; the size of these plasmids ranges between 55 and 80 kb (A. Labigne, personal communication).

Fragments of pIP845 DNA generated by double digestion with *EcoRI* and *BamHI* were inserted into pBGS18+ (17), and the resulting recombinant plasmids were introduced into *E. coli* TOP10 (Invitrogen) with selection on ampicillin at 100  $\mu$ g/ml. The smallest plasmid able to confer resistance to amoxicillin-clavulanate to the new host, pAT779, had a 1.3-kb insert. Direct sequencing of the resistance gene, designated *bla*<sub>TEM-103</sub>, using an automated sequencer (CEQ 2000 DNA analysis system; Beckman Coulter) revealed that it was identical to *bla*<sub>TEM1-B</sub> except for a single G-to-T change at position 1020 (according to Sutcliffe's numbering [18]) (Table 2), which leads to the amino acid substitution of Arg to Leu at position 275 (according to Ambler's numbering [1]). The change of arginine, a basic positively charged amino acid, to leucine, an uncharged amino acid, accounts for the decrease in pI from 5.4 to 5.2 (9). Substitutions that lead to an inhibitor-resistant phenotype occur at a few specific sites within the TEM enzymes: Met-69, Arg-244, Arg-275, and Asn-276 (14). To the best of our knowledge, the Arg<sub>275</sub>Leu substitution has not yet been observed alone in TEM-type  $\beta$ -lactamases, and the enzyme was designated TEM-103/IRT-28 according to the TEM and IRT nomenclature (G. Jacoby and K. Bush, Amino acid sequences for TEM, SHV, and OXA extended-spectrum

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TABLE 1. MICs of  $\beta$ -lactams against strains

<i>E. coli</i> strain	MIC ( $\mu\text{g/ml}$ ) <sup>a</sup>										
	AMX	AMX + CLA	TIC	TIC + CLA	AMP	AMP + SUL	PIP	PIP + TZB	CEF	CFZ	FOX
BM4511, <i>bla</i> <sub>TEM-103</sub>	>1,024	64	>1,024	64	>1,024	32	64	16	8	4	4
JM83	8	8	4	4	8	4	2	2	4	2	2
JM83 (pIP845), <i>bla</i> <sub>TEM-103</sub>	>1,024	32	>1,024	32	>1,024	32	64	8	8	4	4
TOP10	4	4	4	4	4	4	4	4	4	1	2
TOP10 (pAT779), <i>bla</i> <sub>TEM-103</sub>	>1,024	1,024	>1,024	>1,024	>1,024	>1,024	128	16	16	8	4

<sup>a</sup> AMP, ampicillin; AMX, amoxicillin; CEF, cephalothin; CFZ, cefazolin; CLA, clavulanic acid (2  $\mu\text{g/ml}$ ); FOX, cefoxitin; PIP, piperacillin; SUL, sulbactam (8  $\mu\text{g/ml}$ ); TIC, ticarcillin; TZB, tazobactam (4  $\mu\text{g/ml}$ ).

$\beta$ -lactamases [http://www.lahey.org/studies/webt.html; last accessed 10 July 2002]).

The Arg<sub>275</sub>Leu substitution has been detected in TEM-38/IRT-9 associated with Met<sub>69</sub>Val (9) and in TEM-68 associated with Gly<sub>238</sub>Ser, Glu<sub>240</sub>Lys, and Thr<sub>265</sub>Met (7). Another mutation at this position, Arg<sub>275</sub>Gln, was found in TEM-45/IRT-14 (4), TEM-82/IRT-24 (11), and TEM-83/IRT-25 (11) enzymes associated with Met<sub>69</sub>Leu, Met<sub>69</sub>Val, and Met<sub>69</sub>Ile substitutions, respectively; TEM-83 has, in addition, a Trp<sub>165</sub>Cys substitution. These  $\beta$ -lactamases, except for TEM-68, are enzymes with strong inhibitor-resistant activity because the Arg<sub>275</sub> substitution is associated with substitutions at position 69 known to confer resistance to inhibitors (10). Therefore, the contribution of the Arg<sub>275</sub> mutation to the IRT phenotype was not known.

Arginine 275 is located at the beginning of the C terminus of the  $\alpha$ -11 helix, and its side chain is close to the guan-

dinium group of Arg<sub>244</sub>. A kinetic study of the Arg<sub>275</sub>Leu variant has shown the involvement of this change in resistance of the TEM  $\beta$ -lactamases to inactivation by clavulanic acid (15). This could be related to electrostatic interactions with Arg<sub>244</sub> and/or to a possible displacement of the water molecule involved in the inactivation process of clavulanic acid (6). Variant TEM-68 (7) combines mutations responsible for the enlargement of the substrate profile (Gly<sub>238</sub>Ser, Glu<sub>240</sub>Lys, and Thr<sub>265</sub>Met) with a change (Arg<sub>275</sub>Leu) conferring resistance to inhibitors. Fielt et al. (7) attributed the inhibitor-resistant activity of TEM-68 to the Arg<sub>275</sub>Leu substitution.

Functional characterization of this new inhibitor-resistant  $\beta$ -lactamase should provide further insight into the understanding of the heterogeneity of IRT-type enzymes and into structure-activity relationships of the expanding family of TEM proteins.

TABLE 2. Substitutions in *bla*<sub>TEM</sub> genes and derived  $\beta$ -lactamases

Region and nucleotide no. <sup>a</sup> (amino acid no.) <sup>b</sup>	Nucleotide (amino acid) in the following gene (protein):							
	<i>bla</i> <sub>TEM-1A</sub>	<i>bla</i> <sub>TEM-1B</sub>	<i>bla</i> <sub>TEM-2</sub>	<i>bla</i> <sub>TEM-45</sub>	<i>bla</i> <sub>TEM-68</sub>	<i>bla</i> <sub>TEM-82</sub>	<i>bla</i> <sub>TEM-83</sub>	<i>bla</i> <sub>TEM-103</sub>
Promoter region	P3	P3	Pa and Pb	P4		Pa and Pb	P4	P3
32	C	C	T	C	ND <sup>d</sup>	T	C	C
162	G	G	G	T	ND	G	T	G
175	A	G	A	A	ND	A	A	G
Coding region								
226 <sup>c</sup>	C (Phe)	T	C	C	T	C	C	T
317 (39)	C (Gln)	C	A (Lys)	C	C	C	C	C
346 <sup>c</sup>	A (Glu)	A	G	G	A	A	G	A
407 (69)	A (Met)	A	A	A	A	G (Val)	T (Ile)	A
409 (69)	G (Met)	G	G	T (Leu)	G	G	G	G
436 <sup>c</sup>	C (Gly)	T	T	T	T	C	T	T
604 <sup>c</sup>	G (Ala)	T	G	G	G	G	G	T
682 <sup>c</sup>	T (Thr)	T	C	C	C	T	C	T
697 (165)	G (Trp)	G	G	ND	G	G	T (Cys)	G
914 (238)	G (Gly)	G	G	ND	A (Ser)	G	G	G
917 (240)	G (Glu)	G	G	ND	A (Lys)	G	G	G
925 <sup>c</sup>	G (Gly)	G	A	A	A	G	A	G
929 (244)	C (Arg)	C	C	ND	C	C	C	C
990 (265)	C (Thr)	C	C	ND	T (Met)	C	C	C
1020 (275)	G (Arg)	G	G	A (Gln)	T (Leu)	A (Gln)	A (Gln)	T (Leu)
1022 (276)	A (Asn)	A	A	ND	A	A	A	A
Source or reference	18	8	8	4	7	11	11	This study

<sup>a</sup> Nucleotide numbering is according to J. G. Sutcliffe (18).

<sup>b</sup> Amino acid numbering is according to Ambler et al. (1).

<sup>c</sup> Positions at which only silent mutations occur.

<sup>d</sup> ND, no data.

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