

Letters to the Editor

Characterization of *bla*_{TEM-3} and *bla*_{SHV-4} β-Lactamase-Encoding Genes in *Citrobacter diversus*

Citrobacter diversus (also called *Citrobacter koseri*) is an opportunistic pathogen which causes various infections (4). *C. diversus* is intrinsically sensitive to all antibiotics active against gram-negative bacilli, except for penicillins (7). Additional resistances, to β-lactam antibiotics in particular (2), have rarely been reported. Between 1989 and 1991, we isolated three clinical strains of *C. diversus* (Cd2, Cd3, and Cd4) resistant to most β-lactam agents, including expanded-spectrum cephalosporins and aztreonam (Table 1); β-lactamase inhibitors were highly synergistic with these antibiotics against the isolates. These isolates were also resistant to most aminoglycosides, chloramphenicol, sulphonamides, and trimethoprim.

β-Lactam resistance of the three *C. diversus* strains was transferable to *Escherichia coli* by conjugation or transformation. Analytical isoelectric focusing on polyacrylamide gels indicated that the three *C. diversus* isolates produced two types of β-lactamases: one enzyme with a pI of ~5 (pI of 4.8 for Cd2 and Cd3 and pI of 5.4 for Cd4), likely to be the species-specific constitutive penicillinase (7), and one additional enzyme with a pI of 6.3 (Cd2 and Cd3) or 7.8 (Cd4), the single β-lactamase synthesized by the transformants or the transconjugants, expected to be an extended-spectrum β-lactamase (ESBL) (Table 1). Plasmid DNA extracted from the transformants in *E. coli* (pCd2, pCd3, and pCd4) demonstrated the presence of a single large plasmid. Plasmids pCd2 and pCd3 (~150 kb) gave the same patterns after restriction by *Bgl*II and *Ssp*I; an internal *bla*_{TEM-1} probe hybridized with the same *Bgl*II fragment (~20 kb). Plasmid pCd4 (between 40 and 60 kb) gave a distinct restriction pattern with both enzymes; an internal *bla*_{SHV-3} probe hybridized with an *Ssp*I fragment (2.7 kb).

It is highly probable that the ESBL produced by Cd4 was an SHV-4 enzyme, as SHV-4 is the only SHV-derived enzyme with a pI of 7.8 described at present. However, the identity of

the ESBL produced by Cd2 and Cd3 was more uncertain, since several TEM-derived ESBLs have a pI of 6.3 (TEM-3, TEM-18, and TEM-22) (8). Consequently, the structural genes of the ESBLs synthesized by Cd2 and Cd4 were amplified by polymerase chain reaction by using a set of oligonucleotide primers complementary to both strands of the TEM-1 (10) and the SHV-1 (5) genes and directly sequenced. The nucleotide sequence of the *bla*_{TEM}-encoding gene of Cd2 differed from that of the *bla*_{TEM-1} gene (10) at seven nucleotide positions: four of them were silent and the remaining three caused substitutions of amino acids (Gln 39→Lys, Glu 104→Lys, Gly 238→Ser) (Table 1) as previously described for TEM-3 (9). The nucleotide sequence of the *bla*_{SHV}-encoding gene of Cd4 differed from that of the *bla*_{SHV-1} gene by three base changes, all of which resulted in amino acid substitutions: Arg 205→Leu, Gly 238→Ser, and Glu 240→Lys; the *bla*_{SHVpCd4} sequence was identical to that of *bla*_{SHV-4} except for one silent mutation (G→A, Lys-240) (6) (Table 1).

The present study is the first genetic characterization of ESBLs in *C. diversus* and the first report of an SHV-type ESBL in this species.

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TABLE 1. MIC, pI, and nucleotide and amino acid substitutions in *bla*_{TEM} and *bla*_{SHV} genes

β-Lactamase	MIC ^a (mg/liter)			pI	Amino acid and substitution at position ^b :					Reference
	CTX	CAZ	ATM		39	104	205	238	240	
TEM-1	0.125	0.25	0.06	5.4	Gln	Glu	Gln	Gly	Glu	10
TEM-2	0.125	0.25	0.125	5.6	GAG	GAG	CAA	GGT	GAG	3
TEM-3	32	64	32	6.3	Lys	Lys		Ser		9
TEM pCd2 ^c	8	16	2	6.3	AAG	AAG		AGT		This study
SHV-1	0.125	0.125	0.06	7.6	Lys	Lys		Ser		
SHV-4	32	128	256	7.8	AAG	AAG		AGT		
SHV pCd4 ^d	4	32	32	7.8	Gln	Asp	Arg	Gly	Glu	5
					CAG	GAC	CGG	GGC	GAG	
							Leu	Ser	Lys	6
							CTG	AGC	AAG	
							Leu	Ser	Lys	This study
							GTG	AGC	AAA	

^a CTX, cefotaxime; CAZ, ceftazidime; ATM, aztreonam.

^b The number refers to the position of the amino acid according to Ambler et al. (1).

^c From *C. diversus* Cd2.

^d From *C. diversus* Cd4.

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