Nucleotide sequence of the gene encoding the SHV-2 β-lactamase (bla_{SHV-2}) of *Klebsiella ozaenae*

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SHV-type β-lactamases are the most frequently encountered plasmid-encoded β-lactam hydrolyzing enzymes in Klebsiella species. SHV-2 β-lactamase was first characterized (1) as an extended spectrum enzyme conferring to its original *Klebsiella ozaenae* 2180 host a reduced susceptibility to methoxyimino cephalosporins (minimum inhibitory concentration for cefotaxime: 4 mg/l). Its gene is located on a conjugative 45 kb plasmid designated pBP60. The amino acid sequence of the mature protein was published (2). We cloned the gene encoded on two adjacent PstI fragments into pBGS18 (3) and determined the complete nucleotide sequence.

The underlined parts of the 2354 bp sequence represent consecutively: the sequence segments homologous to the −35 and −10 boxes of the bla_{LEN-1} promoter (4), the Shine-Dalgarno sequence, start and stop codons and, inverted repeats for putative transcription termination.

bla_{SHV-2} is situated between bases 931 and 1788 of the complete sequence.

Comparison to the only nucleotide sequence of an SHV-type enzyme published so far, SHV-3 (5), exhibits 7 nucleotide exchanges, two of which are found in the leader peptide region. The deduced amino acid sequences differ in two positions, Trp for Leu at position 17 within the leader peptide and Leu for Arg at position 201, a mutation affecting the pI and because of its position next to the rim of the pouch of the active site, in some cases the affinity for side chains of newer cephalosporins. Since amino acid 136 (Ala) and 137 (Thr) are in the same arrangement in SHV-3 and LEN-1, we think the sequence given by Barthelemy *et al.* is erroneous at this point. There is no homology on the 80% level of the upstream and downstream sequences of SHV-2 to published sequences of bacterial transposon genes. Thus, the reason for the existence of highly related resistance genes on different plasmids (1, 5) or on the chromosome (4) cannot be ascribed to the action of well-characterized transposons.

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CTGCAGTTCC TAAGCGGCAT CAGAGCAGCC GGCAGGCGAT TTGCAGCCGG GGGGGGTGAC GATCGAGGGG CGAACGCTCC CCGGACCACA TCATATTCTC CAGACCGCCC TCTTCGCTGA  120
TAAACCCCGA AAGCCTGCCC TCAGCGGCAG CGGTCAGCAG GTGGATGGCG TTATAAATAT TGGATTTACC GCAGCCGTTA GGGCCGAAGA CAATGTTCAG CGGCCCGAGC TCCAGCGCGA  240
TATCCTTTAC TGAGCGAAAA TTTTGAATAC GAATGTACTG AATCATTATG CGTTCGGCCC TGGAAATAGA AGGCTGCCAC AGTAGCACAG CGGCGCCCGG CATACCCTCT TACGCCCCCT  360
TTCGGGCAGG GTTTAACAGA ACATTTTTTT CATTCCACGG GTCAGGGCGA CCCGCGTTCA CTTATCGCTA TCCTGATGGG CGTCGCTGAA AACGCCAAAA AAATAGCGTT CATCGTCAAT  480
GGTTTGGCTA ACAATTCGGT AGCTCAACGA TTGCCCGGAT AGCGCACCGT ACTGCGCAGG CGTCACCGAG ACTTCGGTCG CGTCATCGGC GACGCTGACC AACAGCCCGT CCGCCTTACC  600
GCCCACCAGC ATGACCTTAA TTATCGGGTG CACCAGTTCC TCCCGGGATG GCATATAGCG TTGGCGAACC GCAGGGACCG GCGGGCGTGG TGATCGGCAA ACAGCGACGC CCGACAGAGT  720
GCGGTATTTA GTACTTTCTT ATAGTTCATC ACGGCCTTGA GTCAAAAAAT AGCGTGCTTA GGCAGGGCTA GATATTGATT ATTCGAAATA AAAGATGAAA AATGATGAAG GAAAAAAGAG  840
GAATTGTGAA TCAGCAAAAC GCCGGGTTAT TCTTATTTGT CGCTTCTTTA CTCGCCTTTA TCGGCCCTCA CTCAAGGATG TATTGTGGTT ATGCGTTATA TTCGCCTGTG TATTATCTCC  960
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CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG ACGAACAGCT GGAGCGAAAG 1200
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CGGGTCGCCG GACCGTTGAT CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTA GCGAGCGGGG TGCGCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA 1680
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