IS*1999* Increases Expression of the Extended-Spectrum --Lactamase VEB-1 in *Pseudomonas aeruginosa*

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The integron-borne $bla_{\text{VEB-1}}$ gene encodes an extended-spectrum β -lactamase. This gene was associated mostly **with IS***1999* **and rarely with an additional IS***2000* **element in** *Pseudomonas aeruginosa* **isolates from Thailand, whereas IS***1999* **was only very rarely associated with** *bla***VEB-1 in** *Enterobacteriaceae***. Expression experiments and promoter study identified promoter sequences in IS***1999* **that increased the expression of VEB-1 in** *P. aeruginosa***.**

Antibiotic resistance in many gram-negative clinical isolates is due to resistance genes that are captured and expressed in class 1 integrons. These integrons possess two conserved regions located on each side of integrated gene cassettes (14). The $5'$ conserved segment ($5'-CS$) includes a gene encoding an integrase, *intI1*, the cassette integration site, *attI1*, and the promoter Pant, sometimes associated with a second promoter P2, which are responsible for the expression of gene cassettes $(6, 14)$. The 3' conserved segment $(3'-CS)$ includes, along with another open reading frame of unknown function, the disinfectant $(qacE\Delta I)$ and the sulfonamide (*sul1*) resistance determinants (14). The expression of the inserted gene cassettes depends not only on sequences of promoters $P_{ant}/P2$ but also on the gene cassette position relative to the 5-CS (2).

The integron-borne bla_{VEB-1} gene encodes the extendedspectrum β-lactamase VEB-1 (Vietnamese extended-spectrum --lactamase) found initially in an *Escherichia coli* clinical isolate from Vietnam (13). Subsequently, the *veb-1* gene cassette was identified in two *Pseudomonas aeruginosa* clinical isolates from Thailand (9, 18). In those strains, $bla_{\text{VEB-1}}$ was associated with either one (IS*1999*) or two (IS*1999*/IS*2000*) insertion sequences (IS) that were inserted upstream of bla_{VEB-1} in the integron-specific recombination site, *attI1*. Bacterial IS may bring promoters located in or near their inverted-repeat sequences (IR) that are capable of modulating the expression of neighboring antibiotic resistance genes (7).

Previous studies performed with ceftazidime-resistant *Enterobacteriaceae* and *P. aeruginosa* strains isolated in 1999 from the Siriraj Hospital, Bangkok, Thailand (3, 4), resulted in reports that out of 37 enterobacterial isolates, 18 were bla_{VEB-1} positive (10 *E. coli*, 4 *Enterobacter cloacae*, 1 *Enterobacter sakazakii*, and 3 *Klebsiella pneumoniae*) and 19 were *bla*_{VEB-1} negative. Out of 33 ceftazidime-resistant *P. aeruginosa* isolates, 31 were $bla_{\text{VEB-1}}$ positive. $bla_{\text{VEB-1}}$ was mostly plasmid located in *Enterobacteriaceae*, whereas this gene was mostly chromosome encoded in *P. aeruginosa* (3, 4). Moreover, spreading of bla_{VEB-1} -containing *P. aeruginosa* strains was detected in several unrelated isolates carrying different integrons of various sizes and structures (3, 4).

Distribution of IS1999 and IS2000 in bla _{VEB-1}-positive iso**lates.** The distribution of IS*1999*, an IS*10*-like element, and IS*2000*, which belongs to the IS*5* family (7, 9), was investigated using the same $bla_{\text{VEB-1}}$ -positive isolates (Table 1). Dot blot hybridizations were performed using whole-cell DNAs (12, 15) of the 18 *Enterobacteriaceae*- and the 31 *P. aeruginosa*-positive isolates (Table 1). Using ECL nonradioactive labeling and detection kits (Amersham Biosciences, Orsay, France), hybridizations were performed under high-stringency conditions. The probes consisted of PCR-generated fragments internal to IS*1999* and IS*2000* (15) (primer sequences are available upon request).

Out of 18 *bla*_{VEB-1}-positive enterobacterial isolates, none possessed IS*2000* and only one *K. pneumoniae* isolate carried IS*1999*. In contrast, IS*1999* was found in 28 out of 31 (90%) bla_{VEB-1} -containing *P. aeruginosa* isolates and 2 out of these 28 isolates had an additional IS*2000* inserted within the IS*1999* sequence.

Thus, the frequent association mostly of IS*1999*, which is sometimes associated with IS2000, with the $bla_{\text{VEB-1}}$ gene in *P*. *aeruginosa* and its absence from *Enterobacteriaceae*, especially from *E. coli*, led us to study the contribution of these IS on --lactamase expression in both bacterial species.

Influence of IS₁₉₉₉/IS₂₀₀₀ on $bla_{\text{VEB-1}}$ **expression. Using** three *bla*_{VEB-1}-positive *P. aeruginosa* isolates as templates (*P. aeruginosa* 14, 1, and JES), recombinant plasmids were constructed containing $bla_{\text{VEB-1}}$ without any IS (pDA-1), with IS*1999* (pDA-2), and with IS*1999* and IS*2000* (pDA-3) (Fig. 1 and Table 1). Plasmids were constructed by standard recombinant techniques (15). The low-copy-number and broad-hostrange cloning vector pBBR1MCS.3 that replicates in *E. coli* and in *P. aeruginosa* (5) was used for subcloning experiments, generating recombinant plasmids pInt-Veb, pInt-1999-Veb, and pInt-1999-2000-Veb (Fig. 1 and Table 1). Recombinant plasmids were introduced by electroporation into *E. coli* DH10B (12) and *P. aeruginosa* KG2505 (11, 17). *P. aeruginosa* KG2505 does not express the naturally chromosome-encoded AmpC β -lactamase and is deficient for the multidrug efflux system MexAB-OprM (11).

Sequencing was performed using laboratory-designed prim-

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^a Superscript "r," resistance. Abbreviations: Caz, ceftazidime; Kan, kanamycin; Neo, neomycin; Sm, streptomycin; Tet, tetracycline.

ers on an ABI PRISM 3100 automated sequencer (Applied Biosystems, Les Ullis, France). Sequence analysis of inserts of all the recombinant plasmids revealed the presence of the two previously characterized promoters: (i) the weak P_{ant} promoter

and (ii) the P2 promoter that is likely nonfunctional (as previously shown) due to its reduced spacing between the -10 and -35 promoter sequences (14 bp instead of 17 bp) (2, 6).

Using β -lactamase extracts from cultures of *E. coli* DH10B

Specific B-lactamase activity (U/mg)

Specific B-lactamase activity (U/mg)

FIG. 2. Comparative study (using cefepime as the substrate) of the specific activity of β -lactamase VEB-1 from cultures of *E. coli* DH10B (left panel) and *P. aeruginosa* KG2505 (right panel) strains harboring recombinant plasmids. Error bars represent standard deviations calculated from five independent cultures. No measurable activity was detected for *E. coli* DH10B(pVEB) and for *E. coli* DH10B(p1999L-VEB).

and *P. aeruginosa* KG2505 harboring recombinant plasmids (Fig. 2) prepared as previously described (10), $bla_{\text{VEB-1}}$ gene expression was then investigated by measuring the specific β -lactamase activities for cefepime (a β -lactam antibiotic hydrolyzed specifically by VEB-1). Total protein contents and the initial rate of cefepime hydrolysis were determined as previously described (13).

To determine whether IS*1999* and IS*2000* carry active promoter sequences located in their right ends, P_{ant} was deleted from pInt-Veb, pInt-1999-Veb, and pInt-1999-2000-Veb, generating recombinant plasmids pVeb, p1999R-Veb, and p1999R-2000R-Veb, respectively (Fig. 1 and Table 1).

In E . *coli*, the highest β -lactamase activity was measured for *E. coli* DH10B(pInt-Veb), which had *bla*_{VEB-1} located just downstream of the promoter P_{ant} of the class 1 integron (Fig. 1 and 2). Insertion of IS*1999* (pInt-1999-Veb), which moved $bla_{\text{VEB-1}}$ away from P_{ant}, decreased $bla_{\text{VEB-1}}$ expression (50%) decrease). After the removal of the promoter P_{ant} (p1999R-Veb and p1999R-2000R-Veb), significant activity (45%) was still measured, suggesting the presence of an IS*1999-*located promoter. Similar specific activities were obtained for *E. coli* DH10B(pInt-1999-Veb), (p1999R-Veb), (pInt-1999-2000- Veb), and (p1999R-2000R-Veb), suggesting that P_{ant} made only a minor contribution to the overall β -lactamase expression. Thus, the activity measured in *E. coli* DH10B(pInt-1999Veb) and (pInt-1999-2000-Veb) is mostly due to the presence of an IS*1999*-located promoter (and possibly to the presence of IS*2000*).

Determination of specific activity of *P. aeruginosa* KG2505 cultures showed that surprisingly, the highest activity was measured for *P. aeruginosa* KG2505(pInt-1999-Veb) [a 60% increase compared to the activity of cultures of *P. aeruginosa* KG2505pInt-Veb)] (Fig. 2). However, insertion of IS*2000* (pInt-1999-2000-Veb) or deletion of the P_{ant} promoter along with the left end(s) of IS*1999* and/or IS*2000* (p1999R-Veb and p1999R-2000R-Veb) led to a decrease in β-lactamase activity. Thus, the right end of IS*1999*, which includes the left IR (IRL), most likely carried a functional outward-directed promoter capable of driving *bla*_{VEB-1} transcription in *P. aeruginosa*.

To determine whether the left end of IS*1999* carried additional promoter sequences, plasmid p1999L-Veb was constructed. This plasmid contained two-thirds of the IS*1999* sequence, including the right IR (IRR) located upstream of bla_{VEB-1} (Fig. 1). Strains harboring p1999L-Veb plasmid had very low levels of β -lactamase activity similar to those observed for strains harboring pVeb, suggesting the absence of functional promoter sequences in the left end of IS*1999*.

To determine whether the functional transposase of IS*1999* can influence $bla_{\text{VEB-1}}$ expression, the plasmid pInt-1999^{*}-Veb, which contains an interrupted open reading frame en-

FIG. 1. Schematic map of the constructs used in this study. Constructs 1 (pDA-1, pInt-Veb, and pVeb), 2 (pDA-2, pInt-1999-Veb, pInt-1999*- Veb, p1999R-Veb, p1999-Veb, and p1999L-Veb), and 3 (pDA-3, pInt-1999-2000-Veb, and p1999R-2000R-Veb) were cloned from genomic DNAs of *P. aeruginosa* clinical isolates 14, 1, and JES, respectively. The $bla_{\text{VEB-1}}$ gene was inserted in opposite orientation to P_{lac} , thus removing any contribution of promoter P_{lac} in β -lactamase expression. The stop codon resulting from a site-directed mutagenesis experiment is shown by an asterisk (construct pInt-1999*-Veb). Restriction sites that were used at each cloning step are underlined. The coding regions are shown as boxes, with an arrow indicating the orientation of their transcription. The IR of IS*1999* and IS*2000* are shown by filled and empty triangles, respectively. IRL and IRR of IS*1999* are indicated for pDA-2. The broken arrows indicate the promoter P*lac.* Thin dashed lines indicate ligation in the multiple-cloning site of the shuttle vector pBBR1MCS.3.

coding the IS*1999* transposase, was generated. No significant modification of bla_{VEB-1} expression was measured for strains harboring pInt-1999*-Veb compared to those harboring pInt-1999-Veb (Fig. 2). Thus, the transposase had no or little effect on β-lactamase expression in *E. coli* and *P. aeruginosa*.

Mapping of promoter Pout of IS*1999***.** The precise location of the right-end-located promoter of IS*1999* was determined with a primer extension system-AMV reverse transcriptase kit (Promega, Charbonnières, France). Total RNAs were extracted with a Qiagen RNeasy Maxi kit (Qiagen, Courtaboeuf, France). cDNAs were synthesized using 32P end-labeled primers Vebprom and Vebprom 1999, which annealed to the left end of *veb-1* gene cassette and to the right end of IS*1999*. Using a

FIG. 3. (A) Structure of IS*1999*. The IS*1999* IR are shown by filled triangles. The arrows indicate the orientation of transcription. The outward-directed promoter, P_{out}, and the promoter of the transposase gene, P_{in} , are indicated by broken arrows. The -10 and -35 regions for P_{in} and P_{out} are underlined. Nucleotide position 115 (according to the sequence GenBank AF133697) in IS*1999* corresponds to the transcription start of P_{out}. The IRL sequence is boxed. (B) Mapping of transcription initiation. Primer Vebprom was extended using RNAs from cultures of *E. coli* DH10B(pInt-1999-Veb) (lane 1) or *P. aeruginosa* KG2505(pInt-1999-Veb) (lane 2) as the templates. Equal volumes $(2 \mu l)$ of the extension product obtained from *P. aeruginosa* and *E. coli* were loaded onto the gel. Size markers were from sequencing reactions generated from pInt-1999-Veb DNA primed with Vebprom. G-, A-, T-, and C-specific lanes are indicated. The nucleotide sequences on the left side correspond to that of the complementary strand, which was deduced from the sequencing reaction. The -10 and -35 promoter sequences of P_{out} regions are shown, and the $+1$ tran-scriptional initiation site is indicated by an arrowhead. Similar results were obtained for RNA extracted from *E. coli* DH10B and *P. aeruginosa* KG2505 harboring pInt-1999-2000-Veb recombinant plasmid (data not shown).

Sequenase version 2 DNA sequencing kit (Amersham Biosciences), manual sequencing was performed with the same primers. Sequencing and extension products were separated on an 8% polyacrylamide gel and were visualized by autoradiography after overnight exposure at -80° C.

Primer extension experiments (performed with Vebprom primer and RNAs from *E. coli* DH10B and *P. aeruginosa* KG2505 strains containing recombinant plasmids pInt-1999- Veb and pInt-1999-2000-Veb) generated a cDNA starting at a thymidine at nucleotide position 115 (Fig. 3). Analysis of the sequence located upstream of bp 115 revealed a putative -35 promoter region (CAGTAT) separated by 17 bp from a -10 region (TAGGAT) (Fig. 3). This promoter was located close to the IRL of IS*1999* at a position similar to that of the promoter P_{out} (-35 [CAGAAT] and -10 [TAAAAT]) identified in the related IS element, IS*10* (16). Using the primer Vebprom 1999, which annealed upstream of P_{out} , no extension product was identified, indicating that no promoter sequence was located further inside of IS*1999* or in IS*2000*.

Conclusions. This work identified a functional outward-directed promoter, P_{out}, of IS1999 that was capable of driving bla_{VEB-1} expression in *E. coli* and in *P. aeruginosa*. The level of expression obtained from P_{ant} or P_{out} was about fourfold higher in *E. coli* than in *P. aeruginosa*. Furthermore, our results suggest that an association between IS1999 and the P_{ant} promoter enhances $bla_{\text{VEB-1}}$ expression by about 60% in *P. aerugi-*

nosa but not in *E. coli*. An increase in β-lactamase expression may change bacteria from being susceptible to being intermediate or even resistant. This is the case for *P. aeruginosa* harboring plasmid pInt-1999-Veb, for which certain β -lactams, such as piperacillin and cefepime, that are extensively prescribed in hospitals display a twofold increase in MICs (data not shown). Thus, in a hospital environment, where bacteria may be under constant antibiotic pressure, IS*1999* (by enhancing the $bla_{\text{VEB-1}}$ gene expression) might bring a selective advantage to *P. aeruginosa*, at least when it is present on a lowcopy-number plasmid (pBBR1MCS). Future experiments will be directed towards determination of $bla_{\text{VEB-1}}$ gene expression in its native environment, i.e., the chromosome of *P. aeruginosa* isolates, to see whether our plasmid-mediated system mimics the chromosomal situation.

An increase of *bla*_{VEB-1} expression in *P. aeruginosa* KG2505 (pInt-1999-Veb) might be the result of a cooperative effect between P_{out} and P_{ant} promoters. Indeed, the maximum amount of expression was obtained only when both promoters were present. In *E. coli*(pInt-1999-Veb), however, both promoters were present and still the expression decreased compared to that seen with *E. coli*(pInt-Veb). These data may reflect major differences in transcriptional properties between *P. aeruginosa* and *E. coli.* The role of IS2000 in the $bla_{\text{VFR-1}}$ containing integron remains unclear, but decrease of bla_{VEB-1} expression after IS*2000* insertion into IS*1999* argues against its role in β-lactamase expression.

Most of the genes inserted in class 1 integrons are expressed from a common promoter region ($P_{ant}/P2$). In a few cases, however, other promoters of the expression of gene cassettes have been reported (1, 8). This work identified for the first time an IS-located promoter capable of driving expression of downstream-located gene cassettes in an integron structure.

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