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Unusual Detection of an *Acinetobacter* Class D Carbapenemase Gene, bla_{OXA-23}, in a Clinical *Escherichia coli* Isolate

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Carbapenem resistance in *Acinetobacter baumannii* is typically mediated by the acquisition of class D β-lactamases belonging to gene clusters of bla_{OXA-23}-like, bla_{OXA-40}-like, and bla_{OXA-58}-like (1). In the *Enterobacteriaceae*, carbapenem-hydrolyzing class D β-lactamases are encoded by a dissimilar set of genes, the bla_{OXA-48}-like genes (2). The presence of bla_{OXA-23} in *Enterobacteriaceae* is exceptional and has been described once in *Proteus mirabilis*, where it was chromosomally encoded (3).

As a result of national surveillance efforts to characterize non-carbapenem-susceptible *Enterobacteriaceae* isolates, we detected a case of bla_{OXA-23} in *Escherichia coli*, which to the best of our knowledge is the first description of plasmid-borne bla_{OXA-23} in *E. coli*.

The isolate was recovered from the urine sample of an elderly woman. However, the isolate was not likely to be a cause of infection, as urine microscopy did not show an increased number of white blood cells. The isolate exhibited resistance to β-lactams, fluoroquinolones, and chloramphenicol. Sensitivity to tigecycline, colistin, and aminoglycosides was observed (Table 1).

Comprehensive PCR screening and sequencing for β-lactamase genes was performed (4, 5). The isolate carried bla_{OXA-23}, which had 100% identity with *A. baumannii* bla_{OXA-23}. It was also positive for TEM-1, OXA-1, and CMY-2 but was negative for other carbapenemases and extended spectrum β-lactamases. The isolate had a multilocus sequence type of ST471. (http://www.pasteur.fr/recherche/genopole/PF8/mlst/EColi.html).

Two large plasmids of approximately 50 and 100 kb were detected (6), with Southern blot hybridization localizing bla_{OXA-23} to the 50-kb plasmid.

Solid-medium conjugation assays were performed to assess the transferability of bla_{OXA-23} from the clinical isolate to the azide-resistant recipient *E. coli* J53 and to a spontaneous rifampin-resistant mutant of *A. baumannii*, ATCC 17978. However, we did not manage to isolate any transconjugants, suggesting that bla_{OXA-23} was harbored on a non-self-conjugative plasmid.

The immediate nucleotide sequences flanking bla_{OXA-23} were determined by inverse PCR and the primer walking approach (7). *E. coli* bla_{OXA-23} is flanked by two copies of insertion sequence IS*1* (Fig. 1). In contrast, in *A. baumannii*, bla_{OXA-23} is found as part of a transposon (Tn*2006*, Tn*2007*, Tn*2008*) associated with insertion sequence IS*Aba1* or IS*Aba4* (8, 9) (Fig. 1).

One hundred eighty-three bases upstream, the *E. coli* bla_{OXA-23} start codon was completely identical to IS*Aba1* (GenBank accession number GQ861438.1). Within this region, −35 and −10 IS*Aba1*-associated promoters were identified and likely to be functional (10) (Fig. 1). The 764-bp stretch after the bla_{OXA-23} stop codon comprised a partially truncated putative AAA ATPase identical to that in *A. baumannii* Tn*2006*, Tn*2007*, and Tn*2008* (Fig. 1).

TABLE 1 MICs of antibiotics for the *Escherichia coli* isolate harboring bla_{OXA-23}

Antibiotic	MIC (mg/liter)
Aztreonam	32
Piperacillin-tazobactam	>256
Cefoxitin	128
Cefotaxime	32
Ceftazidime	16
Imipenem	3
Meropenem	4
Ertapenem	6
Tigecycline	0.125
Tetracycline	86
Levofloxacin	>32
Ciprofloxacin	>32
Amikacin	0.125
Gentamicin	2
Chloramphenicol	16
Colistin	0.125

We hypothesized that *E. coli* bla_{OXA-23} may be carried within a transposon, not unlike those identified in *A. baumannii* but interrupted by IS*1*. However, attempts to PCR map the region using both IS*Aba1* and IS*Aba4* as reference sequences did not yield amplicons, suggesting that it was in a genetic configuration different from that found in *A. baumannii*.

In summary, we describe the novel detection of an *E. coli* isolate carrying an *Acinetobacter* bla_{OXA-23} gene associated with *Enterobacteriaceae* IS*1* on a 50-kb non-self-conjugative plasmid. The discovery highlights the potential for the tremendous spread of carbapenemases.

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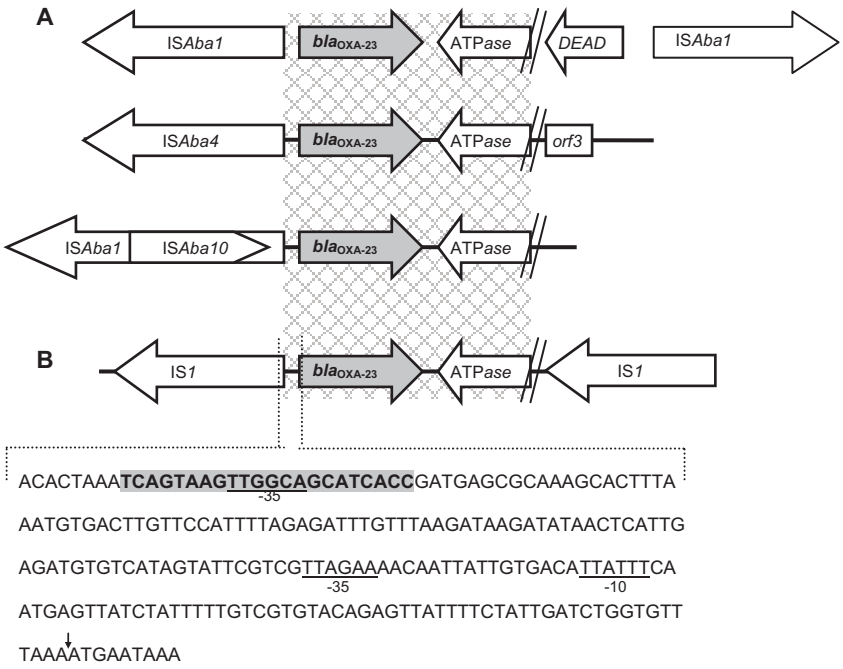

FIG 1 Schematic representation of the genetic organization of bla_{OXA-23}. (A) In *Acinetobacter baumannii*, IS*Aba* insertion sequence elements are typically found immediately upstream of bla_{OXA-23} (8, 9). (B) In the clinical *Escherichia coli* isolate, bla_{OXA-23} is flanked by two copies of *Enterobacteriaceae* insertion sequence IS*1*. The terminal left inverted repeat (IRL) of IS*1* is indicated by the boldface nucleotides with gray shading. The putative −35 promoter of the IRL is underlined and may form hybrid promoters with existing −10 promoters, enabling transcription (11). The IS*Aba1*-associated −35 and −10 promoters are underlined (10). The ATG start codon of OXA-23 is indicated by the vertical arrow (↓). Gray checked regions represent 100% identity between *E. coli* and *A. baumannii*. ATPase, gene encoding putative AAA ATPase; DEAD, gene encoding the putative DEAD (Asp-Glu-Ala-Asp) helicase.

Nucleotide sequence accession number. The bla_{OXA-23} sequence from the clinical *E. coli* isolate has been deposited into GenBank under accession number KJ716226.

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We have no conflicts of interest to declare.

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