First Description of IncX3 Plasmids Carrying \( \text{bla}_{\text{OXA-181}} \) in Escherichia coli Clinical Isolates in Burkina Faso

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Carbapenemase-producing Enterobacteriaceae (CPE) have been increasingly reported worldwide. The few studies available on CPE epidemiology in West and East Africa highlight the identification of carbapenemases in Cameroon (NDM-4), Kenya (NDM-1), Sierra Leone (VIM and DIM-1), Senegal (OXA-48), and Tanzania (KPC, IMP, OXA-48, VIM, and NDM) (1). Although \( \text{bla}_{\text{OXA-48}} \) genes are widely spread in North Africa, \( \text{bla}_{\text{OXA-48}} \) derivatives have been rarely reported in Africa. Indeed, \( \text{bla}_{\text{OXA-48}} \) was detected only twice in Egypt and \( \text{bla}_{\text{OXA-181}} \) (a point mutant analogue of OXA-48) only once in South Africa (1). Here, we describe the first four cases of Escherichia coli carrying the \( \text{bla}_{\text{OXA-181}} \) gene in Burkina Faso.

Four \( E. \text{coli} \) strains (Table 1) were isolated from four patients in two hospitals in Ouagadougou, Burkina Faso. Carbapenem MICs, determined using the Etest (bioMérieux), were 1 to 1.5 mg/liter, 0.125 to 0.75 mg/liter, and 0.25 to 0.5 mg/liter for ertapenem, doripenem, and imipenem, respectively (Table 1). Three patients received antibiotics before strain isolation (Table 1). None of the patients reported recent travel outside Burkina Faso. Multiplex PCR and DNA sequencing targeting the most prevalent extended-spectrum-\(\beta\)-lactamase (ESBL)- and carbapenemase-encoding genes (2, 3) revealed the presence of \( \text{bla}_{\text{CTX-M-15}} \) and \( \text{bla}_{\text{OXA-181}} \) in all four isolates. No other carbapenemase-encoding gene (corresponding to NDM, VIM, IMP, and KPC) was detected. Multi-locus sequence typing (MLST) (http://bigdb.web.pasteur.fr/) showed that the four strains belonged to new sequence type (ST) ST692, which is described here for the first time. Enterobacterial repetitive intergenic consensus sequence PCR (ERIC-PCR) (4) patterns (see Fig. S1 in the supplemental material) and the variable-number tandem-repeat (VNTR) (5) profile determined on the basis of analysis of 7 polymorphic loci \((6-1-5-8-3-5-1)\) gave similar results in all four \( E. \text{coli} \) strains. DNA regions surrounding the \( \text{bla}_{\text{OXA-181}} \) gene are detailed in Fig. 1 and showed that \( \text{bla}_{\text{OXA-181}} \) was part of the \( Tn_{2013} \) transposon, as previously described (10). The same genetic context was recovered in all six \( \text{bla}_{\text{OXA-181}} \)-surrounding sequences available in the GenBank database (GenBank accession numbers KP400525, AB972272, JN205800, NZ_JRKW01000020, JQ996150, and KT005457) (11, 12). The \( repA1 \) gene (encoding a CoE-type replication initiation protein) was downstream of \( Tn_{2013} \). This replicase gene was also found on plasmids pKP3-A (JN205800) and pMR3-OXA181 (NZ_JRKW01000020) that belong to the CoE and IncN incom:}

**Citation**


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patibility groups, respectively. This suggests that blaOXA-181 might have come from a ColE-type scaffold. Fluoroquinolone resistance gene qnrS1 was also detected downstream of blaOXA-181 (Fig. 1).

An IncX3-specific backbone was recovered at the 5′ extremity of blaOXA-181-surrounding regions and included, in addition to the repB replicase gene, the parA partition gene (13) and the umuD gene involved in SOS mutagenesis (14). Large-scale PCR mapping targeting various plasmid regions, including transfer, replication, association with antibiotic resistance, and other genetic elements, was performed.

### TABLE 1

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>EC187</th>
<th>EC187 (T)</th>
<th>EC292</th>
<th>EC292 (T)</th>
<th>EC309</th>
<th>EC309 (T)</th>
<th>EC327</th>
<th>EC327 (T)</th>
<th>E. coli J53</th>
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<td>Patient</td>
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<td>M, 2 yrs old</td>
<td>F, 65 yrs old</td>
<td>F, 21 yrs old</td>
<td></td>
<td></td>
<td></td>
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<tr>
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<td>Suppuration</td>
<td>Suppuration</td>
<td>Urine</td>
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<td>Clinical symptom or diagnosis</td>
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<td>Abdominal pain</td>
<td>Peritonitis</td>
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<tr>
<td>Use of antibiotics in the previous 3 mo</td>
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<td>CFM, CRO, GE</td>
<td>AMC, GE</td>
<td>CRO, GE</td>
<td></td>
<td></td>
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<tr>
<td>VNTR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>6-1-5-8-3-5-1</td>
<td>6-1-5-8-3-5-1</td>
<td>6-1-5-8-3-5-1</td>
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<td>MIC (mg/liter)</td>
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<td>0.5</td>
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<td>0.38</td>
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<td>0.75</td>
<td>ND</td>
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<tr>
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<td>CTX-M-15</td>
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<tr>
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<td>CIP, GE, SXT, TE</td>
<td>ND</td>
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<td>CIP, GE, SXT, TE</td>
<td>ND</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> (T), transformant; F, female; M, male; ND, not determined; AMX, amoxicillin; AMC, amoxicillin-clavulanic acid (co-amoxiclav); CFM, cefixime; CIP, ciprofloxacin; CRO, ceftriaxone; GE, gentamicin; SXT, sulfamethoxazole-trimethoprim; TE, tetracycline.

<sup>b</sup> Data represent CNV1, CNV2, CNV3, CNV4, CNV7, CNV14, and CNV15.

![Genetic map of the four plasmids harboring blaOXA-181](image)

**FIG 1** Genetic map of the four plasmids harboring blaOXA-181 described in this report. Purple arrows represent the replicase genes. Light-gray arrows represent genes encoding hypothetical proteins. Yellow arrows represent genes encoding partition systems. Dark-gray arrows represent accessory genes. Green arrows represent transposase-encoding genes and insertion sequences. Red arrows represent antimicrobial resistance genes. Blue arrows represent genes implicated in plasmid transfer. The genetic context of blaOXA-181 is visually extended at the bottom. Plasmid pOXA181_EC14828 was harbored by an *E. coli* isolate in China (GenBank accession no. KP400525) and was used as a model to map the four blaOXA-181–carrying plasmids described in this report. Thin black lines represent the 25 oligonucleotide pairs used for PCR mapping in all four plasmids. All amplicons were fully sequenced and displayed 100% identity to those of plasmid pOXA181_EC14828.
and partition systems, was also performed and covered a total of 29,569 bp, which amounts to ca. 55% coverage compared to the estimated size of the plasmid (Fig. 1; see also Table S1 in the supplementary material). All PCR products displayed 100% identity to those encoded by the respective regions of plasmid pOXA181_EC14828 (Fig. 1).

Since the first description in Indian hospitals in 2011, OXA-181-positive Enterobacteriaceae have been reported worldwide (1, 11). Their emergence in West Africa in IncX3 plasmids is of particular concern because these plasmids mediate the spread of carbapenemases in Enterobacteriaceae (15, 16). Moreover, a recent study found an IncX3 plasmid harboring blaOXA-181 in a Klebsiella variicola isolate in fresh vegetables imported to Switzerland from Asia (12). This plasmid, named pKS22 (KT005457), is highly similar to pOXA181_EC14828 (100% coverage and 99% identity) and therefore to the four IncX3 plasmids described in our report. The presence of highly similar IncX3 plasmids in Asia, Africa, and Europe might suggest the epidemic potential of the members of this plasmid lineage and their role in worldwide dissemination of OXA-181.

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REFERENCES