Extensively Drug-Resistant Pseudomonas aeruginosa Isolates Containing bla(VIM-2) and Elements of Salmonella Genomic Island 2: a New Genetic Resistance Determinant in Northeast Ohio

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Carbapenems are a mainstay of treatment for infections caused by *Pseudomonas aeruginosa*. Carbapenem resistance mediated by metallo-β-lactamases (MBLs) remains uncommon in the United States, despite the worldwide emergence of this group of enzymes. Between March 2012 and May 2013, we detected MBL-producing *P. aeruginosa* in a university-affiliated health care system in northeast Ohio. We examined the clinical characteristics and outcomes of patients, defined the resistance determinants and structure of the genetic element harboring the *bla*<sub>VIM-2</sub> gene through genome sequencing, and typed MBL-producing *P. aeruginosa* isolates using pulsed-field gel electrophoresis (PFGE), repetitive sequence-based PCR (rep-PCR), and multilocus sequence typing (MLST). Seven patients were affected who were hospitalized at three community hospitals, a long-term-care facility, and a tertiary care center; one of the patients died as a result of infection. Isolates belonged to sequence type 233 (ST233) and were extensively drug resistant (XDR), including resistance to all fluoroquinolones, aminoglycosides, and carbapenems. Between March 2012 and May 2013, we detected MBL-producing *P. aeruginosa* isolates containing VIM-2 from patients from community hospitals in northeast Ohio. These isolates displayed an extensively drug resistant (XDR) phenotype, leaving few, if any, treatment options (18). As this was a “sentinel event” in our region, our objective was to define the molecular characteristics of the outbreak strain and to place it in the global context of MBL-producing *P. aeruginosa*. These analyses led us to discover a genetic element that represents a novel recombination event found in *P. aeruginosa*.
MATERIALS AND METHODS

Selection of bacterial isolates. University Hospitals is an integrated health care system consisting of a tertiary care medical center, six community hospitals, and a long-term-care facility located in northeast Ohio, served by a central clinical microbiology laboratory that processes approximately 250,000 cultures a year. A laboratory-based surveillance program was established in 2007 to detect and characterize carbapenem resistance among Gram-negative bacteria across the hospital system (19). Clinical isolates of P. aeruginosa for which the imipenem or meropenem MIC was ≥4 μg/ml were screened for the presence of acquired carbapenemases using a modified Hodge test (mHT) with imipenem and for the presence of MBLs using imipenem-EDTA Etest strips (bioMérieux, Athens, GA). A 3-fold reduction in the imipenem MIC in the presence of EDTA triggered genetic testing for blaMBLs (20, 21). Antimicrobial susceptibility testing (AST) was performed using the MicroScan System (Siemens, Tarrytown, NY), and results were interpreted according to Clinical and Laboratory Standards Institute guidelines (22).

Molecular typing PFGE and rep-PCR. Molecular typing of P. aeruginosa isolates containing VIM-2 was performed with pulsed-field gel electrophoresis (PFGE) using the restriction enzyme SpeI for digestion and previously described analysis criteria (23, 24). Genetic similarity of VIM-2-harboring P. aeruginosa isolates was also investigated by repetitive-sequence-based-PCR (rep-PCR). Bacterial DNA was extracted using an MoBio UltraClean microbial isolation kit (MoBio, Carlsbad, CA) and amplified using a DiversiLab Pseudomonas kit. Amplicons were separated by electrophoresis on microfluidic chips and analyzed on an Agilent 2100 Bioanalyzer (Agilent, Santa Clara, CA). Resulting band patterns were compared via the Pearson correlation method, using DiversiLab software (bioMérieux). Isolates with ≥95% similarity were considered genetically related (17).

MLST. Multilocus sequence typing (MLST) was performed on P. aeruginosa isolates harboring VIM-2 according to the method of Curran et al. (25). Seven housekeeping genes (azaA, aroE, gwaA, mutL, nusD, ppsA, and trpE) were amplified by PCR and sequenced. Sequences were compared to existing alleles, and allelic numbers and sequence types (STs) were assigned according to the Pseudomonas aeruginosa public MLST database (http://pubmlst.org/paeruginosa/).

PCR amplification and sequencing of genes encoding β-lactamases and aminoglycoside resistance enzymes. Among isolates with a positive mHT, PCR amplification of blaIMV, blacPC, blaoXac, and blaNDM genes was performed (26). We also tested for the presence of genes encoding aminoglycoside-modifying enzymes (AME) and 16S rRNA methyltransferases using validated primers and PCR conditions as described previously (27, 28). Amplicons were sequenced at Molecular Cloning Laboratories (MCLAB; San Francisco, CA).

Immunoblotting. In order to assess VIM-2 expression, rabbit polyclonal antibodies were raised against purified VIM-2-β-lactamase by New England Peptide and isolated from serum using protein G column purification (Sigma Genosys, The Woodlands, TX). Sample preparation, immunoblotting, and development were performed as previously reported (29, 30).

Mating experiments. To investigate the possibility of conjugal transfer of the blavIM, gene, blavIM-containing P. aeruginosa isolates susceptible to rifampin were selected for by overnight growth in LB medium along with rifampin-resistant Escherichia coli J-53 or P. aeruginosa PAO1 (American Type Culture Collection, Manassas, VA). After overnight culture, cells were plated on Mueller-Hinton agar plates containing 100 mg/liter ampicillin and 100 mg/liter rifampin. Colonies that subsequently grew were replated on the same selective medium and screened by PCR for the presence of blavIM.

Genome sequencing and assembly. Further genomic analysis of the P. aeruginosa wound isolate from case 1 was undertaken. Genomic DNA was extracted using a Wizard genomic DNA purification kit (Promega, Madison, WI). Genomic DNA was fragmented, and genomic libraries were prepared using an Ion Xpress Plus Fragment Library Kit (Life Technologies, Carlsbad, CA). Whole-genome sequencing was performed using the Ion Torrent Personal Genome Machine (PGM) platform per the manufacturer’s instructions (Life Technologies, Carlsbad, CA). Sequencing reads were assembled into a consensus de novo assembly using CLC genomic workbench software (version 5.5.1; CLC Bio, Aarhus, Denmark).

RESULTS

Clinical characteristics and antimicrobial susceptibility testing (AST). In the 2-year period of 2012 and 2013, the laboratory received 3,922 single-patient isolates of P. aeruginosa. Among these strains, the prevalence of carbapenem resistance was 20%. As part of our laboratory-based surveillance program, phenotypic testing with the mHT and imipenem/EDTA identified seven patients with MBL-producing P. aeruginosa, representing 0.9% of carbapenem-resistant P. aeruginosa isolates.

The initial isolate of MBL-producing P. aeruginosa (case 1) was detected in March 2012 from a wound in the foot of a 69-year-old man with type 2 diabetes mellitus who resided at a long-term-care facility; the patient also had asymptomatic bacteriuria with XDR P. aeruginosa. The mHT indicated carbapenemase production, and the imipenem MIC was lowered from >256 μg/ml to 6 μg/ml in the presence of EDTA. MBL-producing P. aeruginosa isolates were similarly detected in isolates from six additional patients (cases 2 to 7) between April 2012 and May 2013 (see Table S1 in the supplemental material). Case 4 had a bloodstream infection and died despite appropriate therapy with aztreonam and colistin. Case 5 was transferred to the tertiary care center from Qatar, in the Persian Gulf. Of note, case 1 was admitted to the same ward in a long-term-care facility; the patient also had asymptomatic bacteriuria with XDR P. aeruginosa and a 3.2-kb Tn402-like class 1 integron fragment was amplified in all isolates with the following primers:
TABLE 1 Antimicrobial susceptibility of VIM-2 producing Pseudomonas aeruginosa

<table>
<thead>
<tr>
<th>Case no.</th>
<th>Date of isolation (mo-day-yr)</th>
<th>Specimen source</th>
<th>MIC (µg/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Aztreonam&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>1</td>
<td>3-24-12</td>
<td>Foot wound</td>
<td>&gt;16</td>
</tr>
<tr>
<td>2</td>
<td>5-4-12</td>
<td>Sputum</td>
<td>4</td>
</tr>
<tr>
<td>3</td>
<td>5-16-12</td>
<td>Urine</td>
<td>&gt;16</td>
</tr>
<tr>
<td>4</td>
<td>9-1-12</td>
<td>Blood</td>
<td>4</td>
</tr>
<tr>
<td>5</td>
<td>9-17-12</td>
<td>Sputum</td>
<td>8</td>
</tr>
<tr>
<td>6</td>
<td>3-12-13</td>
<td>Urine</td>
<td>8</td>
</tr>
<tr>
<td>7</td>
<td>5-7-13</td>
<td>Sputum</td>
<td>8</td>
</tr>
</tbody>
</table>

<sup>a</sup> Isolates were also resistant to piperacillin-tazobactam (MIC > 64/4 µg/ml), cefepime (MIC > 16 µg/ml), ceftazidime (MIC > 16 µg/ml), imipenem (MIC > 8 µg/ml), levofloxacin (MIC > 8 µg/ml), ciprofloxacin (MIC > 2 µg/ml), gentamicin (MIC > 8 µg/ml), tobramycin (MIC > 8 µg/ml), and amikacin (MIC > 32 µg/ml).

<sup>b</sup> The sputum isolate from case 2 and isolates from cases 4, 5, 6, and 7 were interpreted as susceptible.

<sup>c</sup> The wound isolate from case 1, both isolates from case 2, and isolates from cases 4, 5, 6, and 7 were interpreted as susceptible.

<sup>d</sup> All isolates were interpreted as susceptible.

intII forward, 5′-GCAAGCGCCGACGCGACG-3′; mtc reverse, 5′-GAAACCAACTGGGCGATC-3′. Analysis of this molecular genetic element revealed two aminoglycoside-modifying enzyme (AME) genes: aacA7, a gene conferring resistance to amikacin and tobramycin, and aacC-A5, conveying resistance to gentamicin. Other AME or 16S rRNA methyltransferase genes were not detected. Steady-state protein expression assessed by Western blot analysis revealed that the VIM-2 ß-lactamase was expressed at similar levels in all isolates tested (data not shown).

Structure of a bla<sub>VIM-2</sub>-harboring genomic island. Further analysis of the genetic environment of the VIM-2-producing P. aeruginosa wound isolate from case 1 revealed a genomic island harboring bla<sub>VIM-2</sub> that is 34,954 bp in length and harbors 37 predicted ORFs (Fig. 2). This genomic island is integrated into the chromosome within a gene encoding the phosphate ABC transporter substrate-binding protein (PA5101 in P. aeruginosa PAO1). The whole region is bounded by 38-bp Tn3-like transposon-associated invert repeats (IRs), flanked by 6-bp duplications (TTTTC) of the target sequence (target site duplications [TSD]). This recombinant element carries resistance to ß-lactams (bla<sub>VIM-2</sub> and bla<sub>OXA-4</sub>), aminoglycosides (aadA2, aacA7, and aacC-A5), tetracycline [tetA(G)], chloramphenicol (cmlA6 and cmlA9), trimethoprim (dfrB5), antiseptics (qacE), sulfonamides (sul1), and mercury (a mer operon) (Fig. 2).

The upstream 19-kb region is a Tn5021-like transposon (~93% identical to Tn501) that includes genes encoding a transposase (tnpA) and a resolvase (tnpR), an inserted bla<sub>VIM-2</sub>-harboring class 1 integron, and a mer operon (Fig. 2). The tnpA (2,967 bp) and tnpR (561 bp) genes are 97.4% and 99.8% identical, respectively, to those of Tn501 from P. aeruginosa plasmid pVS1 (GenBank accession number Z00027). The Tn402 like class 1 integron, carrying an aacA7-bla<sub>VIM-2</sub>-dfrB5-aacC-A5 gene cassette array, is inserted downstream of the tnpR gene, generating a 5-bp duplication sequence (GCCCT) adjacent to the IR at the integrase end.
Integron in SGI2

FIG 2  Tn501-like transposon containing bla_VIM proximal to an integron-like element very similar to SGI2 (GenBank accession no. KJ463833) from Salmonella enterica subsp. enterica serovar Emek (GenBank accession no. AT963803). Open reading frames (ORFs) are represented by arrows. The genes located in the Pseudomonas aeruginosa chromosome are illustrated with black arrows. The genes encoding transposase or resolvase, or within IS elements are indicated by green arrows, and the genes in the mer operon are represented with purple arrows. Shading with light blue indicates >99.5% nucleotide identity. Antimicrobial resistance genes are shown with red arrows, and the intI1 integrase gene is shown with yellow arrows. The target duplicated sequences (TTTTCA) and In559 are conserved segment and the fragment from TNI2 found in SGI2. The rest of this region (including the 5'-flank ISPa54 in tniC denote its 5-bp (TTAGG) direct repeats.

(IR) and the IR at the transposon end (IRt). BLAST results show only four nucleotide differences (>99.9% identity) with the partial sequence of integron In559 (GenBank accession number KC821786) and a novel IS element, designated ISPa54, present in the tniC gene. The mer operon (4.5 kb), located downstream of the blaVIM-harboring integron, is nearly identical (>99.9% identity) to that from a P. aeruginosa strain C79 genomic island (GenBank accession number JF826498), suggesting a hybrid transposon structure.

The downstream region is a 16-kb integron-like element, with its overall structure resembling that of the integron-like element identified in Salmonella enterica genomic island 2 (SGI2) in Salmonella enterica subsp. enterica serovar Emek (32). The only difference between the two integrons is that in the isolate from this study, a bla\textsubscript{OXA-4-\textsubscript{a}}\textsubscript{aadA2-cmlA6} gene array replaces the dfrA1-orfC gene array found in SGI2. The rest of this region (including the 5' conserved segment and the fragment from qacEΔ1 to IS6100 [12.5 kb]) shows >99.9% identity to that of the SGI2. There is also an extra IRt close to IS6100 in an In4-like structure.

A 913-bp fragment, located between the above-described Tn501-like transposon and the 16-kb integron-like element, is identical to part of P. aeruginosa strain C plasmid pKLC102 transposon TNC23 (GenBank accession number AT257539), carrying a putative resolvase gene, res. Interestingly, the res gene of the strain in this study was disrupted by the mer operon at 826 bp downstream of the start codon. A third 38-bp Tn3-like transposon IR was found immediately abutting this truncated res gene. PCR assays confirmed the presence of the same genomic island in all isolates.

**DISCUSSION**

Through laboratory-based surveillance, we uncovered the presence of genetically related XDR P. aeruginosa harboring VIM-2 in seven patients from a regional hospital system in northeast Ohio. Alarmingy, the XDR phenotype expressed by some of these isolates precluded any reliable antibiotic treatment since they even displayed intermediate resistance to colistin, an “agent of last resort.” Aztreonam, a monobactam usually stable against MBLs, was not consistently active either. Patients who were affected had multiple comorbidities, endured prolonged colonization, required long-term care, and, in one instance, had a lethal outcome from a bloodstream infection. The epidemiological link among these genetically related isolates appears to be admission to a community hospital and residence in long-term-care facilities in northeast Ohio, with the exception of a patient who was transferred to the tertiary medical center from Qatar. After the detection of MBL-producing P. aeruginosa by the clinical microbiology laboratory, enhanced infection control precautions and contact isolation were implemented. Despite ongoing surveillance 12 months after the last case, no additional cases have been detected.

All P. aeruginosa isolates in this report belonged to ST233 and contained bla\textsubscript{VIM-2} in the In559 cassette array. The gene array in this class 1 integron is almost identical to genes characterized in P. aeruginosa isolates from an outbreak in 2003 at John H. Stroger, Jr., Hospital of Cook County in Chicago, IL (isolate 7052; GenBank accession number AT943084) (12). The same genetic element was detected in Norway (GenBank accession number FM165436) in P. aeruginosa ST233 imported from Ghana (33), in a P. aeruginosa isolate from Taiwan (isolate S1-36) (34), and in P. aeruginosa ST235 from Russia (GenBank accession number DO522233). We note that P. aeruginosa ST233 and ST235 do not share any alleles (http://pubmlst.org/paeruginosa). Recently, the widespread dissemination of P. aeruginosa ST235 harboring bla\textsubscript{VIM-2} in a similar array was described in Russia and its neighboring region, as well as in several Asian countries (35, 36). Other high-risk clones of VIM-producing P. aeruginosa have also spread successfully (37); for instance, P. aeruginosa ST175 harboring VIM-2 has been detected in Spain, France, and Central Europe (23, 38–41).
Further in-depth analyses of our strains revealed that the blaVIM-2 gene was located in a complex 35-kb genomic island, consisting of integron In559 embedded in a Tn501-like transposon, and located in the chromosome of P. aeruginosa. Adjacent to this structure we found genetic elements homologous to SG12, a large genetic element first seen in Salmonella. Horizontal gene transfers between Salmonella and other nonfermenters have been previously documented in clinical isolates, but none of these transfers resulted in a genetic element with the size and complexity of the one we found (42). Mobile genetic elements similar to those of Salmonella found in our P. aeruginosa strain have also been identified in the chromosome of Acinetobacter baumannii (43). Our finding raises concerns about recombination events between bacterial species of diverse clinical, animal, and environmental origins that may result in the propagation of antibiotic resistance determinants (44). Salmonella enterica carrying the VIM-2 MBL has been detected in Morocco, where the multidrug-resistant (MDR) S. enterica serovar Kentucky is prevalent (45).

The detection of an international clone of VIM-2-producing P. aeruginosa in different components of a health care system in our region heralds the potential threat of widespread dissemination of MBLs in northeast Ohio and beyond. The presence of a single clone and the epidemiological association with patients affected by multiple comorbidities and heavily exposed to health care are reminiscent of outbreaks of two other frequently carbapenem-resistant species, A. baumannii and Klebsiella pneumoniae, which emerged in the United States during the past decade (46, 47). The dissemination of these highly resistant pathogens underscores the vulnerability of our patients and health care system, made more urgent by the lack of effective antibiotic therapies and the current crisis in antibiotic development (19, 48).

At present, disciplined adherence to infection control practices and prudent use of antibiotics remain the best strategies to prevent the emergence of VIM-producing P. aeruginosa. Although efforts and resources in this regard are increasingly deployed in the acute-care setting, significant challenges are faced in community and long-term-care facilities (49). This report highlights the important role of laboratory surveillance enhanced with detailed genetic characterization in identifying emerging resistant phenotypes at the local and regional levels (50). These efforts led to the identification of a novel recombination event resulting from a Tn501-like transposon and SG12, expanding our understanding of the molecular epidemiology of MBL-producing P. aeruginosa.

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