Multidrug-Resistant Acinetobacter baumannii Clone, France

To the Editor: Acinetobacter baumannii is an opportunistic pathogen that is a source of nosocomial infections, mostly pneumonia (1). Treatment of infections caused by A. baumannii is becoming a serious clinical concern as this microorganism becomes increasingly resistant to multiple antimicrobial drugs (2). A. baumannii resistance to carbapenems is mostly associated with production of carbapenem-hydrolyzing class D β-lactamases and metallo-β-lactamases (2). New Delhi metallo-β-lactamase 1 (NDM-1) is one of the most recently discovered metallo-β-lactamases among various gram-negative species, including A. baumannii (3). We recently reported the recovery of NDM-1–producing A. baumannii isolates throughout Europe (4). In that study, the genetic background of several strains was identified and corresponded to sequence types (STs) 1, 25 and 85. The ST85 clone was isolated from 2 patients previously hospitalized in Algeria (4,5).

The present study was initiated by the recent isolation of 6 more NDM-1–producing A. baumannii linked with North Africa. To determine the extent of spread of this organism from Africa to Europe, we genetically analyzed 8 other NDM-1–producing A. baumannii isolates collected from different towns in France during 2011–2012. Of these 8 isolates, 6 were from patients previously hospitalized in different cities in Algeria (including Algiers, Setif, Constantine, and Tiemcen), 1 from a patient previously hospitalized in Tunisia, and 1 from a patient previously hospitalized in Egypt. These 8 isolates came from 2 clinical samples (blood cultures and wound) from 6 screening rectal swab samples collected at the time of hospital admission (online Technical Appendix, wwwnc.cdc.gov/EID/article/19/5/12-1618-Techapp1.pdf). Because the 8 samples were recovered from 5 hospitals, nosocomial acquisition can be ruled out.

The isolates were identified by 16S rRNA gene sequencing. Susceptibility testing was performed by disk diffusion (Sanofi-Diagnostic Pasteur, Marnes La Coquette, France) and interpreted according to updated Clinical and Laboratory Standards Institute guidelines (6). The MICs of β-lactams (imipenem, meropenem and doripenem) were determined by the Etest technique (AB bioMérieux, Solna, Sweden) according to the manufacturer’s recommendations. All isolates were resistant to β-lactams, including all carbapenems (MICs >32 mg/L). The isolates were also resistant to fluoroquinolones, gentamicin, sulfonamides, and chloramphenicol but susceptible to amikacin, netilmicin, rifampin, tetracycline, and tigecycline according to Clinical and Laboratory Standards Institute guidelines (6) and colistin according to European Committee on Antimicrobial Susceptibility Testing guidelines (www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Disk_test_documents/EUCAST_breakpoints_v1.3_pdf.pdf).

The production of metallo-β-lactamases was suspected by use of a combined disk test, based on the inhibition of the metallo-β-lactamase activity by EDTA as described (4). All isolates were positive for production of metallo-β-lactamases.

For all 8 isolates, PCRs aimed at detecting carbapenemase genes, using primers described elsewhere (7), followed by sequencing, led to identification of the blaNDM-1 gene. The isolates also carried a naturally-occurring blaOXA-51-like gene, namely blaOXA-51 (online Technical Appendix). The blaOXA-51-like β-lactamase confers a low level of resistance to carbapenems.

Genotypic comparison was performed by multilocus sequence typing as described (8) and by repetitive extragenic palindromic sequence-based PCR by using the DiversiLab system (bioMérieux, La Balme-les-Grottes, France) according to the manufacturer’s instructions. The genomic pattern of all isolates was identical (Figure). Further multilocus sequence typing indicated that all isolates belonged to ST85. This ST was identified in Greece during a nationwide study that focused on carbapenem resistance in clinical isolates of A. baumannii and...
recently, we showed that the blaNDM-1 gene was carried by a composite transposon bracketed by 2 copies of ISAba125 in A. baumannii (10). Cloning and sequencing of the genetic context of the blaNDM-1 in the first isolate showed that transposon Tn125 was truncated at its 3′-end extremity by insertion sequence ISAba14, giving rise to a truncated Tn125 (ΔTn125). PCR mapping of all isolates showed that they possessed this truncated isoform of Tn125, which was therefore probably no longer functional.

The identification of several clinical A. baumannii isolates that possessed the blaNDM-1 gene and originated from North Africa, with no obvious link to the Indian subcontinent, strongly suggests that 1 NDM-producing A. baumannii clone is probably widespread in North Africa and that it might now act as a reservoir for NDM-1. This finding might indicate that control of spread of multidrug-resistant A. baumannii would have a primary role in controlling spread of NDM-1.

This work was funded by a grant from the Institut National de la Santé et de la Recherche Médicale.

Rémy A. Bonnin, Gaëlle Cuzon, Laurent Poirel, and Patrice Nordmann

Author affiliation: Hôpital de Bicêtre, Kremlin-Bicêtre, France

DOI: http://dx.doi.org/10.3201/eid1905.121618

References


Address for correspondence: Patrice Nordmann, Service de Bactériologie-Virologie, Hôpital de Bicêtre, 78 Rue du Général Leclerc, 94275 Le Kremlin-Bicêtre Cedex, France; email: nordmann.patrice@bct.aphp.fr

Genomic Analysis of Salmonella enterica Serovar Typhimurium Definitive Phage Type 104

To the Editor: Salmonella enterica is among the leading causes of foodborne diseases worldwide. Multidrug-resistant S. enterica serovar Typhimurium definitive phage type (DT) 104 emerged during the early 1990s in the United Kingdom and spread worldwide thereafter (1). This phage-type strain harbors a chromosomally encoded genomic island, Salmonella Genomic Island 1, which is typically responsible for resistance to ampicillin, chloramphenicol,
Multidrug-Resistant *Acinetobacter baumannii* Clone, France

Technical Appendix

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Origin of patient</th>
<th>Date of isolation</th>
<th>Specimen</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (Ora-1)</td>
<td>Oran, Algeria</td>
<td>2011 Jul</td>
<td>Rectal swab and blood culture</td>
</tr>
<tr>
<td>2 (StN)</td>
<td>Constantine, Algeria</td>
<td>2011 Aug</td>
<td>Rectal swab</td>
</tr>
<tr>
<td>3 (112)</td>
<td>Tlemcen, Algeria</td>
<td>2011 Dec</td>
<td>Wound</td>
</tr>
<tr>
<td>4 (HAM)</td>
<td>Unknown, Algeria</td>
<td>2012 Apr</td>
<td>Rectal swab</td>
</tr>
<tr>
<td>5 (AYA)</td>
<td>Setif, Algeria</td>
<td>2012 Sep</td>
<td>Rectal swab</td>
</tr>
<tr>
<td>6 (BOU)</td>
<td>Unknown, Tunisia</td>
<td>2012 Aug</td>
<td>Rectal swab</td>
</tr>
<tr>
<td>7 (BER)</td>
<td>Alger, Algeria</td>
<td>2012 Sep</td>
<td>Rectal swab</td>
</tr>
<tr>
<td>8 (ABO)</td>
<td>Gizeh, Egypt</td>
<td>2012 Sep</td>
<td>Blood culture</td>
</tr>
</tbody>
</table>