Global Incidence of Carbapenemase-Producing Escherichia coli ST131

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We characterized Escherichia coli ST131 isolates among 116 carbapenemase-producing strains. Of isolates from 16 countries collected during 2008–2013, 35% belonged to ST131 and were associated with bla_kpc, H30 lineage, and virotype C. This study documents worldwide incidences of resistance to "last resort" antimicrobial drugs among a common pathogen in a successful sequence type.

Escherichia coli sequence type 131 (ST131) was identified as pathogenic to humans in 2008; retrospective research suggests that its isolates have been present since at least 2003. The group has spread extensively and has been linked to the rapid global increase in the prevalence of antimicrobial resistance among E. coli strains (1). The intercontinental dissemination of this sequence type has contributed immensely to the worldwide emergence of fluoroquinolone-resistant and CTX-M–producing E. coli (1,2). Recent surveillance studies have shown that its overall prevalence ranges from 12.5% to 30% of all E. coli clinical isolates, from 70% to 80% of fluoroquinolone-resistant isolates, and from 50% to 60% of extended spectrum β-lactamase-producing isolates (3).

The development of resistance to carbapenems among E. coli is of particular concern because these agents are often the last line of effective therapy available for the treatment of persons with serious infections (4). New Delhi metallo-β-lactamase (NDM) and carbapenem-hydrolyzing oxacillinase-48 (OXA-48) are the most common carbapenemases among E. coli worldwide (5).

The Study

This study describes the characteristics of ST131 isolates among carbapenemase-producing E. coli strains collected globally by 2 research groups during 2008–2013. The Merck Study for Monitoring Antimicrobial Resistance Trends (SMART) (http://www.merck.com/about/featured-stories/infectious_disease.html) started in 2002 and AstraZeneca’s global surveillance study of antimicrobial resistance (unpublished data) began in 2012, to monitor global antimicrobial resistance trends among gram-negative bacteria (online Technical Appendix, wwwnc.cdc.gov/EID/article/20/11/14-1388-Techapp1.pdf). Antimicrobial susceptibilities of different antimicrobial agents (Table 1, wwwnc.cdc.gov/EID/article/20/11/14-1388-T1.htm) were determined by using frozen broth microdilution panels according to 2013 Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing guidelines (6). Established PCR and sequencing methods were used to identify β-lactamases (7,8) and define O25b:H4, O16:H5 ST131, fimH30 lineage, H30-Rx sublineage (9–11), and virotypes (12).

Overall, 47,843 E. coli isolates were collected and tested for susceptibility; 407 were found to be nonsusceptible to ertapenem or imipenem and were molecularly characterized for β-lactamases genes. A total of 116 of the 407 isolates were positive for NDM, KPC, OXA-48-like, VIM, and IMP types of carbapenemases. Various gene types were identified: 44 (38%) were positive for blaNDM, 38 (33%) for blaKPC, 30 (26%) for blaOXA-48-like, 2 (2%) for blaVIM, and 2 (2%) were positive for blaIMP (Table 1).

The countries from which the E. coli isolates were obtained are shown in Table 2. The isolates were cultured from intraabdominal specimens (37%), peritoneal fluid (16%), biliary fluid (10%), urine (30%), and from miscellaneous sources such as sputum and tissue (9%).

PCR testing for O25b:H4, O16:H5, and MLST showed that 41/116 (35%) belonged to the sequence type ST131. Antimicrobial susceptibilities, types of β-lactamases, the presence of the fimH30 lineage, and virotypes are shown in Table 1. ST131 strains were more likely than non-ST131 strains to be nonsusceptible to ciprofloxacin and to be positive for blaKPC, the H30 lineage, and virotype C; non-ST131 isolates were more likely to be positive for blaNDM.

The majority, i.e., 24 (58%), of ST131 strains were positive for blaKPC, 13 (32%) for blaOXA-48-like, 3 (7%) for blaNDM, and 1 (2%) for blaIMP. ST131 was present in 16 countries spanning 5 continents (Table 2). The distribution of ST131 during 2008–2013 is shown in Table 3.

Various fimH alleles were identified among ST131 isolates: 24 H30 (58%), 3 H41 (7%), 3 H54 (7%), 2 H22 (5%), 2 H27 (5%), and 2 H191 (5%); and 1 each (2%) belonging to H24, H32, H65, and the new fimH alleles
*NDM, New Delhi metallo-β-lactamase-1; KPC, Klebsiella pneumoniae carbapenemase; USA, United States of America; OXA, oxacillinase; UAE, United Arab Emirates; IMP, imipenemase; VIM, Verona integron-encoded metallo-β-lactamase.
†PCR-based screening of *E. coli* ST131 may infrequently identify isolates that belong to the 131 Clonal Complex as ST131 and rarely misidentifies non-ST131 *E. coli* as ST131.
<table>
<thead>
<tr>
<th>Year</th>
<th>Total no. E. coli</th>
<th>No. nonsusceptible E. coli</th>
<th>No. (%) carbapenemase-producing E. coli</th>
<th>Type of carbapenemases (no.)</th>
<th>No. ST131 fimH30</th>
<th>Type of carbapenemases among ST131 (no.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2008</td>
<td>3,739</td>
<td>45</td>
<td>10 (0.3)</td>
<td>NDM-1 (9), IMP-1 (1)</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2009</td>
<td>5,913</td>
<td>63</td>
<td>21 (0.4)</td>
<td>NDM-1 (16), NDM-4 (2), NDM-6 (1), OXA-48 (2)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2010</td>
<td>8,951</td>
<td>71</td>
<td>17 (0.2)</td>
<td>KPC-2 (7), OXA-48 (10)</td>
<td>17</td>
<td>10</td>
</tr>
<tr>
<td>2011</td>
<td>10,009</td>
<td>81</td>
<td>21 (0.2)</td>
<td>NDM-1 (5), OXA-48 (5), OXA-163 (1)</td>
<td>8</td>
<td>2</td>
</tr>
<tr>
<td>2012</td>
<td>14,275</td>
<td>97</td>
<td>35 (0.2)</td>
<td>KPC-2 (n12), KPC-3 (2), NDM-1 (7), NDM-5 (1), OXA-48 (11), OXA-244 (1), IMP-14 (1)</td>
<td>9</td>
<td>5</td>
</tr>
<tr>
<td>2013</td>
<td>4,956</td>
<td>50</td>
<td>12 (0.2)</td>
<td>KPC-2 (4), KPC-3 (3), NDM-1 (2), NDM-5 (1), VIM-1 (2)</td>
<td>6</td>
<td>5</td>
</tr>
</tbody>
</table>

*No. = number; ST131 = Escherichia coli sequence type 131.

References


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