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<sub>KPC</sub>, 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started in 2002 and AstraZeneca’s global surveillance study of antimicrobial resistance (unpublished data) began in 2012, to monitor global antimicrobial resistance trends among gram-negative bacteria (online Technical Appendix,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-lactamase 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 bla<sub>NDM</sub>, 38 (33%) for bla<sub>KPC</sub>, 30 (26%) for bla<sub>OXA-48-like</sub>, 2 (2%) for bla<sub>VIM</sub>, and 2 (2%) were positive for bla<sub>IMP</sub> (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 bla<sub>KPC</sub>, the H30 lineage, and virotype C; non-ST131 isolates were more likely to be positive for bla<sub>NDM</sub>.

The majority, i.e., 24 (58%), of ST131 strains were positive for bla<sub>KPC</sub>, 13 (32%) for bla<sub>OXA-48-like</sub>, 3 (7%) for bla<sub>NDM</sub>, and 1 (2%) for bla<sub>IMP</sub>. 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.

DOI: http://dx.doi.org/10.3201/eid2011.141388
Among ST131 strains (i.e., 58%) it was associated with spread of ST131 E. coli H30-Rx sublineages have contributed substantially to the presence of carbapenemases had been carefully monitored but has been limited to the presence of carbapenemases from combined Merck Study for Monitoring Antimicrobial Resistance Trends (MERIT) and MBW surveillance programs*. Of note, 24/38 (63%) of 14 Hangzhou, Zhejiang Province, China (13) and Pittsburgh, Pennsylvania, USA (14). Of note, 24/38 (63%) of E. coli strains with blaKPC belonged to ST131, as opposed to 3/44 (7%) for NDMs and 13/30 (43%) for OXA-48-like strains. Our results suggest that ST131 is most likely responsible for the global distribution of E. coli with blaKPC.

The expansion of the H30 lineage and its H30-R and H30-Rx sublineages have contributed substantially to the spread of ST131 E. coli (11,15). In our study, H30-R, which belongs to virotype C, was the most common lineage among ST131 strains (i.e., 58%); it was associated with blaKPC and was especially prominent during 2012–2013. The increase of the ST131 H30 lineage with blaKPC during 2012–13 is cause for concern.

E. coli ST131 has received comparatively less attention than other antimicrobial-resistant pathogens. Retrospective molecular surveillance studies have shown that ST131 with blaCTX-M-15 was rare during the early 2000s, but that an explosive global increase followed during the mid-to-late 2000s (I). The results of this study show a similar scenario with E. coli ST131 and blaKPC∗: a low prevalence combined with a global distribution. This study is of special concern because we documented resistance to “last resort” antimicrobial drugs (i.e., carbapenems) in most regions of the world, in a common community and hospital pathogen (i.e., E. coli) among a very successful sequence type (i.e., ST131). We urgently need well-designed epidemiologic and molecular studies to clarify the dynamics of transmission, risk factors, and reservoirs for ST131.

The medical community can ill afford to ignore E. coli ST131 strains with carbapenemases. This sequence type poses a major threat to public health because of its worldwide distribution and association with the dominant H30 lineage. This sequence type among E. coli has the potential to cause widespread resistance to carbapenems.

This work was supported by a research grant from the Calgary Laboratory Services (#10006465).

J.D.D.P. had previously received research funds from Merck and AstraZeneca. PAB is an employee of AstraZeneca. K.M.K., R.E.B., M.H. and D.J.H. are employees of International Health Management Associates, which is under contract by Merck and AstraZeneca.

### Table 2. Escherichia coli with carbapenemases from combined Merck Study for Monitoring Antimicrobial Resistance Trends and AstraZeneca surveillance programs*

<table>
<thead>
<tr>
<th>Carbenapenemase (no.)</th>
<th>Total: country (no.)</th>
<th>ST131: country (no.)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>NDM (44)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NDM-1 (39)</td>
<td>India (25), Vietnam (10), Serbia (1), Philippines (1), Thailand (1), China (1)</td>
<td>Philippines (1), India (1), Thailand (1)</td>
</tr>
<tr>
<td>NDM-2 (2)</td>
<td>India (2)</td>
<td>None</td>
</tr>
<tr>
<td>NDM-5 (n2)</td>
<td>Saudi Arabia (1), Kuwait (1)</td>
<td>None</td>
</tr>
<tr>
<td>NDM-6 (n1)</td>
<td>India (1)</td>
<td>None</td>
</tr>
<tr>
<td>KPC (38)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>KPC-2 (32)</td>
<td>Argentina (1), Brazil (2), Colombia (9), China (5), Ecuador (2), Italy (1), Jordan (1), Panama (1), Puerto Rico (5), USA (2), Vietnam (3)</td>
<td>Argentina (1), Colomibia (5), China (4), Ecuador (1), Italy (1), Panama (1), Puerto Rico (4), USA (2), Vietnam (2)</td>
</tr>
<tr>
<td>KPC-3 (6)</td>
<td>Puerto Rico (1), Israel (1), USA (4)</td>
<td>USA (3)</td>
</tr>
<tr>
<td>OXA-48-like (30)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OXA-48 (28)</td>
<td>Egypt (1), Jordan (1), Lebanon (3), Morocco (2), Turkey (18), Vietnam (3), UAE (1)</td>
<td>Jordan (1), Morocco (1), Turkey (10), UAE (1)</td>
</tr>
<tr>
<td>OXA-163 (1)</td>
<td>Argentina (1)</td>
<td>None</td>
</tr>
<tr>
<td>OXA-244 (1)</td>
<td>Tunisia (1)</td>
<td>None</td>
</tr>
<tr>
<td>IMP (2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IMP-1 (1)</td>
<td>India (1)</td>
<td>None</td>
</tr>
<tr>
<td>IMP-14 (1)</td>
<td>Thailand (1)</td>
<td>Thailand (1)</td>
</tr>
<tr>
<td>VIM-1 (2)</td>
<td>Italy (1), Greece (1)</td>
<td>None</td>
</tr>
<tr>
<td>Total</td>
<td>116</td>
<td>41</td>
</tr>
</tbody>
</table>

*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.
Dr Peirano is a research associate at Calgary Laboratory Services and the University of Calgary. Her main research interests are related to the detection and molecular epidemiology of antimicrobial drug resistance mechanisms among Gram-negative bacteria.

References


9. Banerjee R, Robicsek A, Kuskowski MA, Porter S, Johnston BD, Sokurenko E, et al. Molecular epidemiology of *Escherichia coli* sequence type 131 and its K50-R sublineage. It is likely that this institution housed an outbreak during that time. If the 2010 isolates were removed from consideration, there was a substantial increase in ST131 toward the latter part of this study.


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The Studies

The Merck Study for Monitoring Antimicrobial Resistance Trends (SMART) and AstraZeneca program antimicrobial drug surveillance program combine global surveillance with molecular characterization to monitor the prevalence of different resistance determinants and sequence types among Gram negative bacteria. The SMART surveillance program included 237 institutions from 56 countries and the AstraZeneca surveillance program included 180 institutions from 39 countries present in Africa (5%), Asia (25%), Latin America (27%), Europe (13%), North America (17%), the South Pacific (5%) and the Middle East (8%). Countries that are represented include Argentina, Australia, Brazil, Canada, China, Chili, Colombia, Dominican Republic, Ecuador, Egypt, Greece, Costa Rica, Czech Republic, Estonia, France, Germany, Guatemala, Israel, India, Italy, Japan, Jordan, Honduras, Hong Kong, Korea, Kuwait, Lebanon, Latvia, Lithuania, Mexico, Morocco, New Zealand, Panama, Poland, Oman, the Philippines, Paraguay, Portugal, Puerto Rico, Romania, Saudi Arabia, Serbia, Singapore, Slovenia, Slovakia, Spain, Switzerland, Taiwan, Thailand, Turkey, Tunisia, United Arab Emirates, United Kingdom, Uruguay, USA, Venezuela, and Vietnam.

Each investigator from both programs was instructed to collect 100 consecutive clinically relevant Gram-negative aerobes from intra-abdominal infections and 50 from urinary tract infections. All isolates that were deemed to be colonizers were not collected. Astra-Zeneca specifically targeted E. coli, Klebsiella spp., Proteus spp., Enterobacter spp., Citrobacter spp., and Serratia spp. and also collected gram-negative bacteria responsible for skin and soft tissue infections and lower respiratory tract infections.

The bacteria with carbapenemases were collected during 2008–2013. Of 47,843 E. coli isolates, 4% were from Africa, 28% from Asia, 32% from Latin America, 9% from Europe, 14% from North America, 5% from the South Pacific and 8% the Middle East (8%).