Emergence of OXA-48-producing Enterobacteriaceae in Switzerland

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DOI : 10.1016/j.ijantimicag.2012.07.003
PMID : 23040008
Table 1
Oritavancin MICs versus vancomycin MICs for Staphylococcus aureus and coagulase-negative staphylococci (CoNS).

<table>
<thead>
<tr>
<th>No. of isolates</th>
<th>VAN MIC (µg/mL)</th>
<th>ORI MIC range (µg/mL)</th>
<th>ORI modal MIC (µg/mL)</th>
<th>ORI MIC50 (µg/mL)</th>
<th>ORI MIC90 (µg/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Staphylococcus aureus</td>
<td>51</td>
<td>≤0.25</td>
<td>≤0.004–0.25</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>3648</td>
<td>0.5</td>
<td>≤0.004–0.25</td>
<td>0.03</td>
<td>0.03</td>
<td>0.12</td>
</tr>
<tr>
<td>5298</td>
<td>1</td>
<td>≤0.004–4</td>
<td>0.06</td>
<td>0.06</td>
<td>0.12</td>
</tr>
<tr>
<td>78</td>
<td>2</td>
<td>0.03–1</td>
<td>0.25</td>
<td>0.12</td>
<td>0.25</td>
</tr>
<tr>
<td>CoNS</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>≤0.25</td>
<td>≤0.004–0.06</td>
<td>0.015</td>
<td>0.015</td>
<td>0.06</td>
</tr>
<tr>
<td>98</td>
<td>0.5</td>
<td>≤0.004–0.25</td>
<td>0.015</td>
<td>0.03</td>
<td>0.06</td>
</tr>
<tr>
<td>853</td>
<td>1</td>
<td>0.008–1</td>
<td>0.06</td>
<td>0.06</td>
<td>0.5</td>
</tr>
<tr>
<td>697</td>
<td>2</td>
<td>0.015–1</td>
<td>0.12</td>
<td>0.12</td>
<td>0.25</td>
</tr>
<tr>
<td>1</td>
<td>4</td>
<td>1</td>
<td>N/D</td>
<td>N/D</td>
<td>N/D</td>
</tr>
</tbody>
</table>

VAN, vancomycin; ORI, oritavancin; MIC, minimum inhibitory concentration; MIC50, MICs for 50% and 90% of the organisms, respectively; N/D, not determined (as <10 isolates).

Acknowledgments

The authors thank the scientific support personnel at The Medicines Company (Ville Saint Laurent, QC, Canada) and Eurofins Medinet (Chantilly, VA) for their contributions to this research.

Funding: This study was funded by Targanta Therapeutics.

Competing interests: This study was funded by Targanta Therapeutics, which is now a wholly owned subsidiary of The Medicines Company. The Medicines Company authors have no significant declarations to make with respect to external funding, ownership of company stocks or shares, and reimbursement for preparing this article. The Medicines Company authors were Targanta Therapeutics employees at the time the work was conducted.

Ethical approval: Not required.

References


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Emergence of OXA-48-producing Enterobacteriaceae in Switzerland

Sir,

The carbapenem-hydrolysing β-lactamase OXA-48 is increasingly reported as a source of carbapenem resistance in Enterobacteriaceae [1]. First identified in Turkey, OXA-48-producers have been identified in many countries of the Mediterranean area [1]. This resistance determinant is at least endemic in Turkey and now in several North African countries [1]. Additional scattered cases or related outbreaks have been reported in many other countries [1,2]. The blaOXA-48 gene has been detected in various Enterobacteriaceae species and its spread is mainly associated with the Tn1999-like transposon inserted into a single 62-kb InclM-type plasmid [1]. Here we report the identification of OXA-48-producers in another European country.

Klebsiella pneumoniae AEL was recovered in March 2010 from a rectal swab of a 64-year-old man. Strain carriage persisted until April 2010 when it became complicated by urinary catheter-related cystitis. Escherichia coli ZAN was recovered in February 2011 from a urine catheter of a 46-year-old patient without causing active infection.

Susceptibility testing was performed by disk diffusion assay (Sanofi-Diagnostic Pasteur, Marnes-la-Coquette, France), and minimum inhibitory concentrations (MICs) were determined by Etest (bioMérieux, La Balme-les-Grottes, France) and were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines [3]. Both isolates displayed an extended-spectrum β-lactamase (ESBL)-producing phenotype. Klebsiella pneumoniae AEL was resistant to all penicillins, extended-spectrum cephalosporins, ertapenem (MIC = 6 mg/L) and fluoroquinolones. It was susceptible to imipenem (MIC = 0.5 mg/L), meropenem (MIC = 0.75 mg/L) and gentamicin (MIC = 0.19 mg/L) and of intermediate susceptibility to tigecycline (MIC = 2 mg/L). Escherichia coli ZAN was resistant to all penicillins, cefotaxime and aztreonam and of intermediate susceptibility to cefepime, ceftazidime (MIC = 1.5 mg/L) and tigecycline (MIC = 2 mg/L). MICs of imipenem, meropenem and ertapenem were, respectively, 0.75, 1.5 and 24 mg/L for E. coli ZAN. It was also resistant to trimethoprim/sulfamethoxazole.
sulfonamides, tobramycin and gentamicin and was susceptible to amikacin (MIC = 1 mg/L), chloramphenicol, tetracycline and fluoroquinolones. PCR experiments with primers designed to detect Ambler class A, B and D genes, followed by sequencing, identified the bla_{OXA-48} carbapenemase gene in both isolates [2]. Klebsiella pneumoniae AEL also possessed the ESBL bla_{CTX-M-15} gene together with bla_{OXA-48} and bla_{SHV-28} genes, whereas E. coli ZAN co-harbour the ESBL bla_{CTX-M-24} gene and the bla_{TEM-1} gene.

The genetic environment of the bla_{OXA-48} gene was determined by PCR mapping using specific primers for the insertion sequence IS199, located upstream and downstream of the gene in Tn199 [2]. Tn199 was identified in E. coli ZAN isolate whereas Tn199,2, differing from Tn199 by the insertion of an IS1R element, was identified in K. pneumoniae AEL. In K. pneumoniae AEL, mating-out assays and plasmid DNA analysis performed as described previously [2] allowed identification of the bla_{OXA-48} gene in a 62-kb conjugative plasmid similar to that of the prototypic OXA-48-positive K. pneumoniae 11978 strain from Turkey and other OXA-48-producers from other geographical origins [1]. Mating-out assays using E. coli ZAN were unsuccessful. To search for a possible chromosomal location of the bla_{OXA-48} gene, the technique using the endonuclease I-CeuI was performed as described previously [4] and confirmed the chromosomal location of the bla_{OXA-48} gene (data not shown).

Multilocus sequence typing (MLST) performed as described previously [2] showed that K. pneumoniae AEL belonged to a new sequence type ST900 (allelic profile 1-6-1-5-4-1-6). Noticeably, ST900 is a single-locus variant of ST101 (allelic profile 2-6-1-5-4-1-6), and OXA-48-producing K. pneumoniae belonging to ST101 have been reported in Tunisia, Turkey and South Africa (personal data), highlighting the wide dissemination of this sequence type [2,5]. Escherichia coli ZAN belonged to ST38, similar to other OXA-48-producing E. coli isolates reported in France from patients coming from Egypt and Turkey [1]. Interestingly, those recently identified isolates co-produced the same β-lactamases as E. coli ZAN, namely TEM-1 and CTX-M-24, suggesting their clonal spread in various European countries.

Although recent data suggest that the current spread of the bla_{OXA-48} gene is mainly linked to the transfer of a single epidemic IncI/M-type plasmid, K. pneumoniae ST101 and ST395 together with E. coli ST38 may be considered as epidemic strains and likely contribute to the spread of that resistance determinant [1]. Interestingly, we report here for the first time a chromosomal acquisition of the bla_{OXA-48} gene. This report underlines that importation of carbapenemase-producers and their potential subsequent diffusion may occur despite strict control of antibiotic stewardship and high quality of hand hygiene as reported in the University Hospital of Geneva (Geneva, Switzerland).

Acknowledgments

The authors thank platform Genotyping of Pathogens and Public Health (Institut Pasteur, Paris, France) for coding MLST alleles and profiles and making them available at http://www.pasteur.fr/mlst.

Funding: This work was supported by a grant from the Ministère de la Recherche, Université Paris XI (Paris, France) and by INSERM (France). The research leading to these results has also received funding from the European Community’s Seventh Framework Programme FP7/2007-2013 under grant agreement no. 241742 (TEMPOtest-QC) and no. 282512 (R-GNOSIS).

Competing interests: None declared.

Ethical approval: Not required.

References


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6 July 2012
doi:10.1016/j.jantimicag.2012.07.003

Low prevalence of vancomycin heteroresistance among meticillin-resistant Staphylococcus aureus causing bacteraemia in Hong Kong

Sir,

Infections caused by meticillin-resistant Staphylococcus aureus (MRSA) with heterogeneous resistance to vancomycin (hVISA) are more likely to fail treatment with vancomycin, leading to persistent bacteraemia, relapse and the emergence of vancomycin-intermediate S. aureus (VISA) [1]. This study investigated 249 consecutive bacteraemia MRSA isolates recovered from inpatients treated in four healthcare districts (designated A–D) in Hong Kong in 2009. The hospitals in the healthcare districts together served approximately one-half of the 7 million population in Hong Kong. Vancomycin minimal inhibitory concentrations (MICs) were determined by the broth microdilution method using an arithmetic dilution (0.094, 0.125, 0.19, 0.25, 0.38, 0.5, 0.75, 1, 1.5, 2, 3 and 4 mg/L). Quality control strains (including S. aureus ATCC 29213 and 12 in-house MRSA internal control strains with vancomycin MICs of 0.5–4 mg/L) were included on each day of testing. Antimicrobial susceptibility testing was performed by the Clinical and Laboratory Standards Institute (CLSI) disk diffusion method [2].