of this MRSA strain, as well as qacA/B genes, was much lower in these studies.

MRSA ST239 is found in significantly high numbers in Eastern Australia, and is associated with a broad spectrum of antimicrobial resistance and epidemic potential. The qacA/B genes are thought to be located on multiresistance plasmids, such as pSK1, and co-transmitted with plasmid-mediated antimicrobial resistance genes, hence their association with this multiresistant strain of MRSA is logical.

The high prevalence of this ST239 strain could be due to selective pressure from the use of antiseptic products and/or the widespread use of antimicrobial agents. Our findings suggest the latter, given the absence of a corresponding rise in qacA/B genes with increased antiseptic hand solution use; however, the baseline use of antiseptic agents within the hospital could also explain the high prevalence of qacA/B genes even prior to the hand hygiene campaign.

In either case, the high prevalence of qacA/B-carrying MRSA strains is concerning and carries potential implications for antimicrobial treatment, infection control and also MRSA decolonization regimes that are becoming increasingly popular. Clinical studies evaluating the impact of these resistance genes on hand hygiene treatments are currently lacking. However, a recent study showed that colonization with chlorhexidine-resistant strains of MRSA was associated with an increased risk of treatment failure with these agents exists and warrants further attention.

In conclusion, a high prevalence of qacA/B genes was found in HA-MRSA isolates in this study. These genes correlated closely with the MRSA strain ST239. These findings highlight the need for further evaluation into the clinical implications of these genes in this era of increasing antiseptic use in hand hygiene and decolonization strategies.

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None to declare.

References

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Characterization of a multidrug-resistant Acinetobacter baumannii strain carrying the blaNDM-1 and blaOXA-23 carbapenemase genes from the Czech Republic

Lenka Krizova1–3*, Rémy A. Bonnin3, Patrice Nordmann3, Alexandr Nemec1 and Laurent Poirel3

1Laboratory of Bacterial Genetics, National Institute of Public Health, Prague, Czech Republic; 2Department of Genetics and
Microbiology, Faculty of Science, Charles University in Prague, Prague, Czech Republic; Service de Bactériologie-Virologie, INSERM U914, Hôpital de Bièvres, Assistance Publique/Hôpitaux de Paris, Le Kremlin-Bicêtre, France

*Corresponding author. Laboratory of Bacterial Genetics, National Institute of Public Health, Prague, Czech Republic. Tel: +420-267082266; Fax: +420-267082538; E-mail: amicus@seznam.cz

Keywords: metallo-β-lactamases, Tn125, Tn2008, European clone I

Sir,

Since its discovery in 2008, the metallo-β-lactamase (MBL) NDM-1 has been identified in different Enterobacteriaceae species and recently also in a number of other bacterial species isolated from water supplies in India, such as *Vibrio* species and recently also in a number of other bacterial species. The NDM-1 protein is encoded on a plasmid. Since its discovery in 2008, the metallo-β-lactamase (MBL) NDM-1 has been identified in different Enterobacteriaceae species and recently also in a number of other bacterial species isolated from water supplies in India, such as *Vibrio* species and recently also in a number of other bacterial species.

An MBL Etest (bioMe´rieux) revealed a 24-fold reduction of the MICs of both ceftazidime and cefepime (MICs of both ceftazidime and cefepime >256 mg/L), as well as penicillins in combination with inhibitors (MICs of ampicillin/sulbactam and piperacillin/tazobactam >256 mg/L). The strain was also resistant to fluoroquinolones (MIC of ciprofloxacin 32 mg/L), aminoglycosides (MIC of amikacin 32 mg/L) and broad-spectrum cephalosporins (MICs of both ceftazidime and cefepime 32 mg/L) and broad-spectrum cephalosporins (MICs of both ceftazidime and cefepime >256 mg/L), as well as penicillins in combination with inhibitors (MICs of ampicillin/sulbactam and piperacillin/tazobactam >256 mg/L), as well as penicillins in combination with inhibitors (MICs of ampicillin/sulbactam and piperacillin/tazobactam >256 mg/L).

Transfer of the ticarcillin resistance marker was attempted by both electroporation of the strain ANC 4097 plasmid suspension into *A. baumannii* BM4547 and liquid mating-out assays of the ANC 4097 and BM4547 strains at 37°C. Selection was performed on agar plates supplemented with ticarcillin (100 mg/L). Transformants or transconjugants harbouring the blaNDM-1 and blaOXA-23 genes were not obtained, suggesting a chromosomal location of both genes, as described previously.

This study reports on the first blaNDM-1-positive *A. baumannii* strain in the Czech Republic and adds to the body of evidence of the current spread of multidrug-resistant *Acinetobacter* harbouring this MBL in Europe.

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References

Emergence of NDM-1-producing Acinetobacter baumannii in Belgium

Pierre Bogaerts1,*, Roberta Rezende de Castro1, Sandrine Roisin2, Ariane Deplano2, Te-Din Huang1, Marie Hallin2, Olivier Denis2 and Youri Glupczynski1

1 National Reference Laboratory of Antimicrobial Resistance in Gram-negative Bacteria, Cliniques universitaires UCL de Mont-Godinne, Yvoir, Belgium; 2 Associated National Reference Laboratory of Antimicrobial Resistance in Gram-negative Bacteria, Hôpital Universitaire Erasme, Université Libre de Bruxelles (ULB), Brussels, Belgium

*Corresponding author. Laboratory of Bacteriology, Cliniques Universitaires, UCL de Mont-Godinne, Av. Dr Therasse 1, 5530 Yvoir, Belgium. Tel: +32-(0)81-42-32-41; Fax: +32-(0)81-42-32-04; E-mail: pierre.bogaerts@uclouvain.be

Keywords: metallo-β-lactamases, carbapenemases, resistance, New Delhi

Sir,

New Delhi metallo-β-lactamase (NDM) is a class B β-lactamase that confers resistance to virtually all β-lactams, including carbapenems. Initially reported in Sweden in Enterobacteriaceae isolates from a patient transferred from India, NDM-1 is currently spreading worldwide, including Belgium, especially in Enterobacteriaceae.1 Recently the presence of blaNDM-1 was also reported in Acinetobacter baumannii isolates from India, China and Germany, suggesting a broad host range distribution of this gene.1-3 Here, we report an NDM-1-producing A. baumannii detected in Belgium that was isolated from a patient following medical repatriation from Algeria.

In early 2011, a young male patient was admitted to the emergency ward of an Algerian hospital for severe cranial and thoracic trauma following a road traffic accident. He presented with a Glasgow Coma Score (GCS) of 07/15 and was rapidly intubated, ventilated and transferred to the intensive care unit (ICU).

While hospitalized in Algeria, he experienced three successive, distinct episodes of bloodstream infection, due to Acinetobacter spp., Candida albicans and Klebsiella pneumoniae, but no clinical information was available concerning the possible sources of these infections. In August, the patient was transferred, in a vegetative state (GCS of 02/15), to the ICU of a Belgian hospital. He was immediately placed in a single room with contact isolation precautions.

Screening for asymptomatic intestinal carriage of carbapenemase producers was carried out upon admission, by rectal swabbing cultured by direct plating on ChromID™ ESBL Agar (bioMérieux, Marcy l’Étoile, France). The recovered isolate was identified as A. baumannii (Ab 11314) by MicroFlex LT (Bruker Daltonik, Bremen, Germany). By disc diffusion, Ab 11314 was found to be multiresistant and synergy was observed in a double disc test using imipenem and EDTA (420 μg), suggesting involvement of a metallo-β-lactamase in resistance to β-lactams. Use of the CLSI microdilution method confirmed that the isolate was resistant to β-lactams including ceftazidime (MIC >64 mg/L), cefepime (MIC >64 mg/L), imipenem (MIC 4 mg/L; Etest MIC >32 mg/L), meropenem (MIC 4 mg/L; Etest MIC >32 mg/L), amikacin (MIC >32 mg/L) and ciprofloxacin (MIC >32 mg/L), and susceptible to tigecycline (MIC 0.125 mg/L), colistin (MIC 0.5 mg/L) and minocycline (MIC <2 mg/L).

Analysis of β-lactamase-coding genes by an MDR CT102 array (Check-Points, Wageningen, The Netherlands) and by PCR sequencing targeting metallo-β-lactamases and OXA-carbapenemases revealed the presence of blaNDM-1. Plasmid extraction was performed with a QiaGen plasmid kit, and this revealed a single 174 kb untypeable plasmid.3 This plasmid was efficiently electroporated and transferred by mating experiments to the A. baumannii recipient strain N9040364, and it conferred resistance to aminoglycosides (gentamicin, tobramycin and amikacin) only (data not shown). The blaNDM-1 gene was not associated with this plasmid suggesting that it was located in the chromosome. PCR mapping and sequencing revealed that blaNDM-1 was located between two direct repeats of the IS element Aba125. These genes were identical to those recovered in the NDM-1-expressing A. baumannii Ab 161/07 reported from Germany (accession no. HG857107).3 Nevertheless, a PCR experiment performed with Ab 161/07 as a positive control revealed that in Ab 11314, in contrast, the mfs gene (a shikimate-transporter-coding gene belonging to the major facilitator superfamily) was not disrupted, indicating that the ISAba125 transposon was inserted elsewhere in the chromosome. By multilocus sequence typing (MLST) (http://pubmlst.org/abaumannii/), A. baumannii Ab 11314 was shown to belong to sequence type (ST) 92 (allelic profile: 1-3-3-2-2-7-3), the founding genotype of the international clone (CC) 92, which includes European clone 2 (EU2) and worldwide lineage 2 (WW2). CC92 is one of the most prevalent CCs worldwide, mostly represented by OXA-23-producing strains. Sequencing analysis of the intrinsic blaOXA-51-like and blaADC genes showed that this strain harboured blaOXA-64 and blaADC-26, neither of which was downstream of ISAba1 or ISAba125. These two intrinsic genes were identical to those recovered in the NDM-1-expressing A. baumannii Ab 161/07, but nevertheless presented a very different MLST profile (1-15-2-28-1-new allele-32), not related to any CC described up to now.

This clinical isolate is the first characterized NDM-1-producing A. baumannii from Belgium. As yet, there have been only a few reports of NDM-producing A. baumannii, and the only case reported in Europe was from Germany in a patient transferred from Serbia in 2007.2 In the present case, the NDM-1-producing A. baumannii isolate originated from North Africa (Algeria) where NDM-1 has not yet been described in A. baumannii, although another single case of A. baumannii producing an NDM-1 variant (NDM-2) was recently reported from Egypt.5 This brief report further highlights the wide distribution of NDM-producing organisms around the world, their constant evolving spread.