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# First Report of $bla_{NDM-1}$ in *Raoultella ornithinolytica*

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The genus *Raoultella* is composed of Gram-negative, aerobic, oxidase-negative, catalase-positive, nonmotile, capsulated rods belonging to the *Enterobacteriaceae* family (1). *Raoultella ornithinolytica* is found in aquatic and hospital environments (2). Occurrence of *Raoultella* in human infections is rare, but it has been reported to cause bloodstream and soft tissue infections (2–5).

A 67-year-old man was admitted to a tertiary care hospital in Pune, India, after having sustained injury to the perineum. He was diagnosed as having a ruptured urethra. Injury to the urethra was repaired, and patient was treated with intravenous cefotaxime and amikacin postoperatively. He developed pus discharge from the surgical site after 72 h of hospital admission. Pus culture on two consecutive days grew Gram-negative, nonmotile bacilli in pure culture, which was identified as *R. ornithinolytica* by biochemical properties and confirmed by the Vitek-2 system (bioMérieux, Marcy l'Etoile, France). Antimicrobial susceptibility was performed on Mueller-Hinton agar plates by the standard Kirby Bauer disk diffusion method as per the guidelines of the Clinical and Laboratory Standards Institute (CLSI) (6). MICs of antibiotics were determined by Vitek-2 and by Etest. Both isolates showed similar antibiograms and had sensitivity to tigecycline and colistin (Table 1).

Screening for metallo-β-lactamase (MBL) production was determined by the MBL (IP/IPI) Etest method (AB Biodisk, Solna, Sweden), as per the manufacturer's instructions, and the isolates were found to be positive. PCR amplification for $bla_{KPC}$, $bla_{IMP}$, $bla_{VIM}$, $bla_{SPM}$, $bla_{GIM}$, $bla_{SIM}$, $bla_{OXA-23}$, and $bla_{OXA-24}$ was conducted on the isolates by using the Gene Amp 9700 PCR system (Applied Biosystems, Singapore) and the PCR conditions and primers described previously (7–9), and the isolates were found to be negative for these genes. PCR for detection of $bla_{NDM-1}$ was carried out using primers as described previously (10) that amplify an 813-bp fragment. The amplicon after purification (Qiagen, GmbH, Hilden, Germany) was sequenced with the ABI 3730XL capillary sequencer (Applied Biosystems, Foster City, CA) and was identified as the $bla_{NDM-1}$ gene by analysis of sequencing result with BLAST software (www.ncbi.nlm.nih.gov). The patient was successfully treated with tigecycline. After 1 week of intensive daily wound care and tigecycline therapy, the patient recovered well and was discharged from the hospital.

*Raoultella* is an emerging pathogen that causes hospital infections (3–5). Carbapenems are the most frequently used antimicrobial in cases of nosocomial and mixed bacterial infections. In our case, this isolate was multidrug-resistant requiring therapy with tigecycline. The presence of $bla_{NDM-1}$ in *R. ornithinolytica* poses a serious threat for the spread of hospital-acquired infections. Carbapenem resistance due to $bla_{KPC}$ has been reported in *R. ornithinolytica* (3). However, our isolate was negative for $bla_{KPC}$ and other carbapenemases except $bla_{NDM-1}$. Carbapenem-resistant *Enterobacteriaceae* pose a serious threat of treatment failure for hospitalized patients. Their early recognition and proper infection control measures are mandatory for controlling their spread.

**TABLE 1** Antibiogram of $bla_{NDM-1}$-positive *R. ornithinolytica*

| Antibiotic[a] | MIC (μg/ml) for isolate PC/452/12 |
|---|---|
| IPM | 4 |
| MEM | 4 |
| ETP | >8 |
| AMK | >64 |
| GEN | >16 |
| TOB | >16 |
| CIP | >4 |
| MXF | >8 |
| TGC | <0.5 |
| SXT | >320 |
| SAM | >32 |
| TZP | >128 |
| FEP | >64 |
| AMP | >64 |
| CRO | >64 |
| CAZ | >64 |
| CS | <0.5 |

[a] IPM, imipenem; MEM, meropenem; ETP, ertapenem; AMK, amikacin; GEN, gentamicin; TOB, tobramycin; CIP, ciprofloxacin; MXF, moxifloxacin; TGC, tigecycline; SXT, trimethoprim-sulfamethoxazole; SAM, ampicillin-sulbactam; TZP, piperacillin-tazobactam; FEP, cefepime; AMP, ampicillin; CRO, ceftriaxone; CAZ, ceftazidime; CS, colistin.

**Nucleotide sequence accession number.** The sequence of $bla_{NDM-1}$ determined in this study has been assigned GenBank accession no. JX680686.

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