

## Evaluation of carbapenem-resistant *Enterobacteriaceae* in an Italian setting: Report from the trench

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### Abstract

The spread of carbapenem resistant *Enterobacteriaceae* (CRE) has recently become a matter of concern in public health, mainly due to the wide distribution of carbapenemase genes. Italy is a country considered endemic for the spread of blaKPC *Klebsiella pneumoniae* (KP). The aim of this study was to depict the epidemiological trend of CRE in one Italian hospital over a long period (3 years surveillance, from May 2011 to April 2014).

Based on defined MIC cut-off for specific carbapenems, 164 strains isolated from 146 different patients were analyzed both phenotypically and genotypically to establish the resistance genes. Molecular typing was performed using the RAPD technique. 77 strains were demonstrated to harbor the blaKPC gene (73 KP, 4 *Escherichia coli* - EC), 51 strains the blaVIM gene (44 KP, 3 EC, 2 *Enterobacter cloacae* and 2 *Klebsiella oxytoca*), 8 the blaNDM gene (3 KP, 4 EC and one *Providencia stuartii*), 3 the blaOXA-48 gene (2 KP, 1 EC), whereas 25 out of the 164 isolates (of different genera and species) had a negative multiplex-PCR amplification for all the targets tested. 39 out of the 164 strains analyzed (23.8%) revealed discrepancies between the MICs obtained with automated instrument and gradient MICs of more than two logs of difference; the broth microdilution provided a better agreement with the results obtained with the gradient MIC. The use of RAPD allowed to distinguish different clusters, closely related, both for blaKPC and for blaVIM KP.