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BATTERIOLOGIA

CLONAL DIVERSITY OF CARBAPENEMASE-PRODUCING ENTEROBACTERIACEAE ISOLATED FROM RECTAL SWABS IN HOSPITALISED ADULT PATIENTS

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INTRODUZIONE

The rapid dissemination of carbapenemase-producing Enterobacteriaceae (CPE) represents a serious health problem in hospitals worldwide. The lack of alternative antimicrobial therapy increases the mortality and morbidity rates as well as the costs of prolonged hospitalization. The European Antibiotic Surveillance Network data for 2017 reported frequent carbapenem-resistance for both K. pneumoniae and E. coli with higher levels for the first. This study was aimed to investigate the antibiotic resistance and the genetic features of CPE strains circulating in an Italian hospital.

METODI

Phenotypic tests and molecular typing were performed on 48 carbapenemase-producing isolates of K. pneumoniae and E. coli collected from adult patients of Ospedali Riuniti di Ancona. Antibiotic susceptibility testing was performed using EUCAST guidelines. Carbapenem-resistance was confirmed by PCR detection of resistance genes. All strains were analyzed by PCR-based replicon typing using the PBRT 2.0 kit (Diatheva Srl) and multilocus sequence typing (MLST) was performed for representative isolates of each pattern.

RISULTATI

Of 48 isolates, 45 (94%) were identified as K. pneumoniae whereas the remaining 3 (6%) as E. coli and all of them were CPE. The bla_{KPC} gene was detected in all isolates with the exception of an E. coli strain; bla_{KPC} gene was combined with bla_{VIM} in a single strain of K. pneumoniae. Additional to the carbapenems, other antibiotics were tested and only 7 isolates were susceptible to them. Noteworthy, more than 50% were multidrug-resistant (MDR) strains. The multireplicon status was observed in 39 strains and the most prevalent profiles were FIIK, FIB KQ (33%) and FIIK, FIB KQ, FIB KN (21%). These replicons are frequently associated with the endemic plasmids pKpQIL and pKPN3 carrying bla_{KPC} gene that jumping to different clones support its dissemination. MLST analysis performed on 14 strains revealed 5 different sequence types (STs): 3 STs (ST512, ST101, ST307) were detected in 11 K. pneumoniae strains and 2 STs (ST405, ST131) in 3 E. coli strains. Interestingly, ST512 is the endemic Italian variant of ST258, a high-risk clone responsible for global MDR in K. pneumonia. The emerging ST307 and ST101 clones possess an advantageous adaptation ability to colonize hospital environments. Recent surveillance studies described the emergence of ST307 in the global scenario as a competitive replacement of the clonal group CG258.

CONCLUSIONI

Notwithstanding the modest size of the study, the variability of the genetic repertoire presented by these strains confirmed the dynamic evolution of circulating clones representing a risk for the public health.