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Paper Poster Session V

Recent epidemiological data on carbapenem-resistant Enterobacteriaceae

The spread of carbapenemase-producing Enterobacteriaceae (CPE): experience in a paediatric hospital in northern Italy between 2013 and 2014

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Objectives: A retrospective study was conducted to evaluate both the spread of carbapenemase producers Enterobacteriaceae (CPE) and their resistance mechanisms in pediatric patients admitted to the Institute G. Gaslini of Genoa, Italy, between October 2013 and September 2014

Methods: Between October 2013 and September 2014, according to CPE screening guidelines followed in the Institute, 2694 pediatric patients (chronic diseases that require several hospitalizations and antibiotic treatments, immunocompromised patients and the admissions to Neonatal or Pediatric Intensive Care Units) were screened for CPE by rectal swabs, at the admission to the hospital. The swabs were directly plated onto MacConkey agar with meropenem disk. The bacterial colonies grown in a zone diameter within 30 mm. were investigated for carbapenemases production using Xpert Carba-R Assay (GeneXpert-Cepheid, USA). This test is an automated real-time polymerase chain reaction (PCR) for rapid detection and differentiation of the *bla*KPC, *bla*NDM, *bla*VIM, *bla*OXA48 and *bla*IMP-1 gene sequences associated with carbapenem-non-susceptibility in gram negative bacteria. The clonality analysis was conducted on the genomes sequences, determined by Ion Personal Genome Machine (PMG) system (Life tecnologies), using opensource softwares and different bioinformatics tools. The identification and the antimicrobial susceptibility testing of CPE were performed by Phoenix (BD, USA).

Results: A total of 5 patients (5/2694 – 0.19 %) had a positive CPE screening with the following isolated species: 2 *Klebsiella oxytoca* both producers of Verona integron-mediated metallo-beta-lactamase (VIM); 1 *Klebsiella pneumoniae* producer of *Klebsiella pneumoniae* carbapenemase (KPC); 1 *Escherichia coli* producer of New Delhi metallo beta-lactamase (NDM) and 1 *Escherichia coli* producer of OXA-48. The genomes investigation revealed that the sequence types (ST) of *Klebsiella pneumoniae* was ST512 and it carried *bla* KPC_3 gene, while 2 strains of *Klebsiella oxytoca* were attributed to sequence type MLST 6-6-19-1-46-7-9 and MLST 3-8-17-2- new allele -17-29. Both the strains carried *bla*VIM_1 gene but on different plasmid.

Conclusions: The rate of CPE carriers among pediatric patients is lower (0.19%) than data found among adult patients (EARSS 2012). The introduction in the diagnostic algorithm of Xpert Carba-R Assay has allowed a rapid confirmation and typing of possible carbapenemase production. The genome investigation revealed that *Klebsiella pneumoniae* was ST512, already described in clonal spread in three acute care hospitals in Northern Italy (Migliavacca R, New Microbiologica, 2013). Moreover, *Klebsiella oxytoca* isolates showed different sequence types. We can exclude both the CPE spread and the clonality among these patients. In conclusion the implementation of screening tests to different risk categories and the contact isolation precautions have prevented the spread of CPE in our Institute.