Carbapenem-resistant *Klebsiella pneumoniae* carriage, colonization and infection in Intensive Care Units in Catania, Italy

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Background:

Carbapenem-Resistant *Klebsiella pneumoniae* (CRKP) is becoming increasingly common in Europe, and especially in Italy as reported by the Italian surveillance of healthcare infections in ICUs network (SPIN-UTI project; Agodi et al., 2015). Our study aimed to describe the epidemiological and molecular relationships of CRsKP in four Intensive Care Units (ICUs) in Catania.

Materials and methods:

During the period from the 1st October 2014 to the 31st March 2015, in the framework of the SPIN-UTI project, all the consecutive isolates of *K. pneumoniae* from any site were collected. Resistance to carbapenems was defined according with the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines. Patterns of *K. pneumoniae* acquisition in ICU were carriage, colonization and infection. PCR screening for carbapenemase encoding gene of bla_{KPC}, for extended-spectrum β-lactamases encoding gene bla_{CTX-M} and for plasmid-mediated quinolone resistance (PMQR) genes *qnr*B and *aac(6')-Ib-cr* was performed. Molecular typing of *K. pneumoniae* isolates by PFGE analysis of the XbaI-digested genomic DNA, according to the PulseNet protocol, and MLST analysis using the Institute Pasteur MLST scheme, were evaluated.

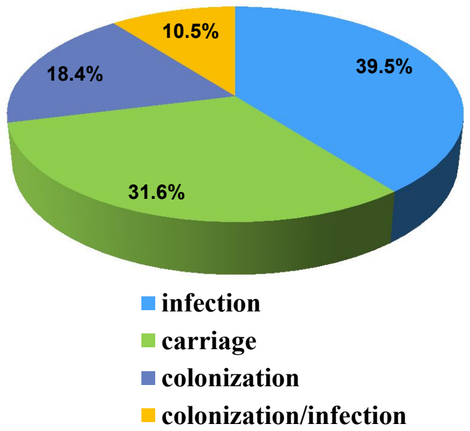

Fig 1. Patterns of CRKP acquisition

Results:

A total of 123 *K. pneumoniae* were collected and 50 of them (41%), from 35 patients, were CRsKP. Using standard definitions, infection was associated to 39.5% of isolates, carriage to 31.6%, colonization to 18.4%, and colonization/infection to 10.5% of isolates (Fig. 1). Among the resistance genetic determinants under screening, KPC3-type enzymes were detected in all *K. pneumoniae* isolates as a single determinant of β-lactam resistance (76.3%) or in association with CTX-M-15 (23.7%).

Among the PMQR genes, aac(6′)-Ib-cr and qnrB were found in 78.9% and 42.1% isolates, respectively. PFGE analysis led to the identification of 6 different PFGE-types (named A to F) (Fig. 2).

A major clone was identified, involving 51.47% of isolates, showing intra-ICU and inter-hospital spread. Besides, some clones spread within single ICUs. MLST analysis of representative isolates with same PFGE-type and resistance genetic determinants pattern, recognized 4 different STs: ST 258, ST 512, ST 35 and ST 307.

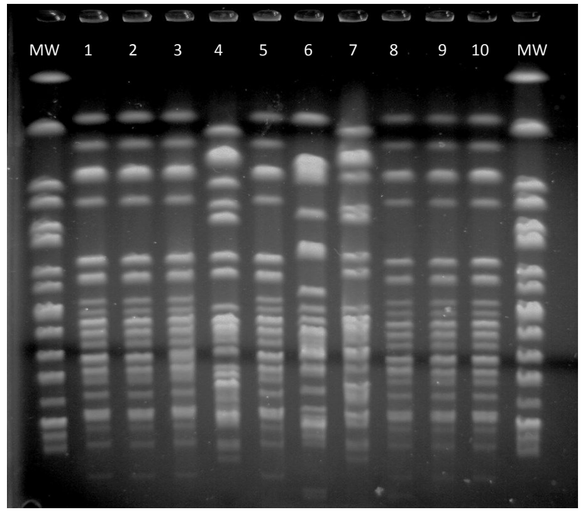

Figure 2. PFGE-type, 1-10 isolates; MW, molecular weight marker

Conclusions:

Our study indicates that multiple CRsKP clones were disseminated through different hospitals, suggesting clonal spread of some PFGE-types and STs and lateral transmission of genetic resistance determinants. These local findings suggest the need to extend the systematic surveillance of CRsKP acquisition at the nationwide level while implementing infection control strategies in order to evaluate their effectiveness in minimising the risk of transmission between ICUs and the spread of this dramatic antimicrobial resistance trait.

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- References: Agodi et al., Antibiotic consumption and resistance: results of the SPIN-UTI project of the GISIO-SItI. Epidemiol Prev. 2015
- http://bigsdb.web.pasteur.fr/klebsiella/klebsiella.html

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