

POSTER PRESENTATION

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# Molecular epidemiology of KPC-producing *Klebsiella pneumoniae* clinical isolates in hospitals in North-Western Tuscany

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## Introduction / objectives

The emergence and spread of carbapenem-resistant *Enterobacteriaceae* represents a major clinical and public health challenge, especially concerning those organisms that produce *Klebsiella pneumoniae* carbapenemase (KPC)-type b-lactamase. In this study, we examined the molecular epidemiology of KPC-producing *Klebsiella pneumoniae* strains, isolated during sporadic or epidemic cases in different hospitals of North-Western Tuscany (NWT).

## Methods

Starting from April 2010, an outbreak of clinical infection caused by multiresistant *Klebsiella pneumoniae*, occurred in the University Hospital of Pisa and in other hospitals from the surrounding area; during this period we isolated 57 *Klebsiella pneumoniae* strains in our hospital and 23 from other health-care facilities; all strains, isolated mostly from different patients hospitalized over protracted periods of time, showed reduced susceptibility to carbapenems and were assayed for KPC detection.

## Results

60 out of 61 tested strains produced KPC type 2; molecular typing results indicated the spread of a prevalent clone during the outbreak in Pisa. The PFGE method allowed to identify 7 variants clonally related (pt A1-A7), sharing the same MLST sequence type (ST 258).

## Conclusion

Molecular characterization confirmed the higher discriminatory power of PFGE compared to MLST and it may be useful in local and short-time outbreaks; however MLST, providing unequivocal and comparable data, remains the gold standard for molecular typing.

## Disclosure of interest

None declared.

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