

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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