Epidemiological typing of multidrug-resistant Klebsiella pneumoniae, which causes paediatric ventilator-associated pneumonia in Egypt

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Abstract:

Purpose. Multidrug-resistant Klebsiella pneumoniae is a common nosocomial pathogen that plays an important role in ventilator-associated pneumonia (VAP). This study aimed to define the clonal relatedness of K. pneumoniae strains isolated from paediatric VAP in addition to those isolated from environmental samples. Methodology. This study included 19 clinical and 4 environmental K. pneumoniae isolates recovered from the paediatric intensive care unit (PICU) in Assiut University Children's Hospital. The K. pneumoniae isolates were confirmed by biotyping using API strips and subjected to antimicrobial susceptibility testing. The genes coding K1 and K2 capsular types were detected by PCR. The clonal relationships between the K. pneumoniae isolates were determined by pulsed-field gel electrophoresis (PFGE). Results. Ten resistotypes were detected among all the K. pneumoniae isolates, while PFGE identified seventeen K. pneumoniae pulsotypes. Similar PFGE patterns were found between environmental and clinical isolates and between isolates recovered from different patients, suggesting the circulation of K. pneumoniae pathogens in the PICU and the role of the environment in the spread of infection. No correlation was found between the resistotypes and pulsotypes of the K. pneumoniae isolates. PFGE showed higher discriminatory power for the typing of nosocomial K. pneumoniae [Simpson's diversity index (DI)=0.96] than resistotyping (DI=0.72). Conclusion. As far as we know, this is the first report of the isolation of the same multidrug-resistant (MDR) K. pneumoniae pulsotype from patients and environmental samples in the same hospital ward in Egypt. This study provides a step on the way to understanding the genotyping and epidemiology of MDR K. pneumoniae for enhanced prevention of bacterial transmission.

Keywords:

PFGE, VAP, clonal relatedness

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