

**SENSITIVITY PROFILE AND GENOTYPING OF ESBL-PRODUCING *Klebsiella pneumoniae*
ISOLATED FROM PATIENTS WITH NOSOCOMIAL INFECTIONS IN A TERTIARY CARE
HOSPITAL IN CEARÁ, BRAZIL**

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Abstract:

Klebsiella pneumoniae is a Gram-negative bacillus responsible for a significant portion of urinary tract infections, respiratory, and bloodstream of adults in hospitals, besides infections in neonates in intensive care units (ICUs). Its importance has increased due the emergence of extended-spectrum beta-lactamase-producing strains (ESBLs). Outbreaks of nosocomial infections caused by multidrug-resistant *K. pneumoniae* clones have been described in various regions of the country. However, this is the first report of the genetic characterization of ESBL-producing *K. pneumoniae* in the state of Ceará, Brazil. This study aimed to detect the main genes responsible for ESBL production in *K. pneumoniae* strains obtained from patients who developed nosocomial infections in a tertiary support hospital in the northern region of the Ceará state, from November 2013 to August 2014 and to analyze the genetic similarity of these isolates. Thirty-six clinical isolates of ESBL-producing *K. pneumoniae* were evaluated. Bacterial identification, phenotypic detection of ESBL, and antimicrobial susceptibility testing were performed using the Vitek 2 System. The detection of *bla*_{CTX-M} groups 1 and 2, *bla*_{SHV}, *bla*_{TEM}, *bla*_{KPC}, and *bla*_{GES} genes was performed by PCR. Molecular typing of isolates was performed by PFGE. Most isolates were resistant to broad-spectrum cephalosporins such as ceftriaxone (100%), ceftazidime (72.2%), and cefepime (69.4%), but all isolates were sensitive to amikacin, imipenem, meropenem, ertapenem, and tigecycline. Groups 1 or 2 *bla*_{CTX-M} and *bla*_{SHV} genes were detected in 100% of the isolates and *bla*_{TEM}-genes in 55.6%. In addition, 55.6% of CTX-M-producers also produced SHV and TEM. Molecular typing by PFGE showed great diversity between the isolates, although two isolates collected in different wards showed the same banding profile and had the same *bla* genes, and so were considered to belong to a single strain. Detection of *bla*_{CTX-M} genes in 100% of the isolates suggests that CTX-M enzymes are the major ESBLs responsible for the beta-lactam resistance phenotypes of the studied isolates. Data presented in this study call attention to an endemic resistance problem caused by multiclonal strains of multidrug-resistant *K. pneumoniae* whose control passes essentially the improvement of antimicrobial prescription policies and the implementation of prevention and control programs the spread of these pathogens in the studied hospital.

Keywords: Nosocomial Infection, *Klebsiella pneumoniae*, PFGE, Multiclonal Strains.

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