HIGH PREVALENCE OF BLA_{CTX-M} , BLA_{SHV} E BLA_{TEM} B-LACTAMASES GENES IN Klebsiella pneumoniae NOSOCOMIAL STRAINS ISOLATED FROM PATIENTS IN A TERTIARY CARE HOSPITAL IN CEARÁ, BRAZIL

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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 strains producing extended spectrum beta-lactamases (ESBLs). These enzymes are produced by some Gram-negative bacilli and mediate resistance to oxyimino-β-lactams. In this pathogen, most of the identified ESBL are of the types TEM, SHV and CTX-M. In addition, β-lactamases that hydrolyze carbapenems of types KPC and GES has been frequently detected in these isolates. Hospital infection outbreaks caused by multiresistant K. pneumoniae have been described in various regions of the country. However, this is the first report of the genetic characterization of isolates of ESBL-producing K. pneumonia in the state of Ceará. This study aimed to detect the main genes responsible for ESBL production in K. pneumoniae strains obtained from patients with nosocomial infection admitted to a tertiary support hospital in the northern region of the state of Ceará, from November 2013 to August 2014. Thirty-six clinical isolates of ESBL-producing K. pneumoniae were evaluated. The detection of genes bla_{CTX-M-1/2}, bla_{SHV}-like, bla_{TEM}-like, bla_{KPC}-like and bla_{GES}-like was performed by PCR. The genes bla_{CTX-M-1/2} and bla_{SHV}-like were detected in 100% of the isolates and bla_{TEM}-like gene in 55.6%. In addition, 55.6% of the producers of CTX-M also produced SHV and TEM. No bla_{GES}-like and bla_{KPC}-like gene was detected. Despite the high incidence of genes blashv.like and blatem-like, we could not tell whether they were responsible for ESBL-producing, since some variants of these families such as blaTEM-1. bla_{TEM-2}, bla_{SHV-1} and bla_{SHV-11} are narrow-spectrum beta-lactamases that do not have activity against extended-spectrum cephalosporin. The detection of gene bla_{CTX-M-1/2} in 100% of the samples suggests that CTX-M enzyme is the major ESBL responsible for multidrug resistance phenotype of the studied isolates.

Keywords: Klebsiella pneumoniae, Nosocomial infection, ESBL, CTX-M.

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