عنوان مقاله:

Epidemiology and Genetic Diversity of CTX-M Gene in Klebsiella Pneumoniaein Baghdad City

محل انتشار:

مجله علوم دارویی و شیمی, دوره 6, شماره 6 (سال: 1402)

تعداد صفحات اصل مقاله: 7

نویسندگان:

Hadeel Musafer - *Biology Department, College of Science, University of Mustansiriyah, Baghdad, Iraq*

Majid Al-Bayati - *Biology Department, College of Science, University of Mustansiriyah, Baghdad, Iraq*

Sawsan Kareem - *Biology Department, College of Science, University of Mustansiriyah, Baghdad, Iraq*

خلاصه مقاله:

The enzymes extended spectrum β-lactamases (ESBLs) can hydrolyze oxyimino-cephalosporins. The abuse of new antibiotics leads to the emergence of new types of β-lactamases enzymes; because of the emergence of these reasons, this research aims to investigate Klebsiella pneumoniae-producing ESBLs in patients with urinary tract infection and determine the antibiogram pattern furthermore detect the frequency of mutations in the ctx-m gene. Fifty bacterial isolates of K. pneumoniae were isolated and identified phenotypically and chemically from patients with UTI. All isolates were subjected to an antibiogram using the disc diffusion method. MIC for cefotaxime antibiotic was carried out by microdilution method to all resistant isolates to cefotaxime disc; furthermore, screening of ctx-m gene was carried out by conventional PCR. Sequencing of the ctx-m gene and its mutations was done by the dideoxynucleotide sanger method and BioEdit software, respectively. Fifty bacterial isolates confirm K. pneumoniae; these isolates appeared antibiogram diversity to seventeen antibiotics ranging from high resistance to Ampicillin, Cefazolin, Ceftriaxone, Ampicillin/Sulbactam, Cefepime, and doxycycline while moderate resistance to ciprofloxacin, Moxifloxacin, and Cefotaxime. Furthermore, there is low resistance toward Tobramycin, gentamicin, Amikacin, Meropenem, Imipenem and no resistance toward Ertapenem. The MIC of most resistant isolates is more than ۲۵۶µg/ml of cefotaxime. The PCR detection revealed that twelve of twenty-three isolates harbored the ctx-m gene, while the results of sequencing showed that many mutations occurred. Belong to a high incidence of infection with bacteria K. pneumoniae producing ESBL in the studied population, molecular studies in the field of antimicrobial .resistance of bacteria become emerging to eradicate and prevent the spread of resistance strains

کلمات کلیدی:

MDR K. pneumonia ESBLs Antibiotics resistance ctx, m gene