

عنوان مقاله:

Genetic characterization of Klebsiella pneumoniae: Five year experience in ICU admitted patients

محل انتشار:

بیست و سومین کنگره بین المللی میکروب شناسی ایران (سال: 1401)

تعداد صفحات اصل مقاله: 2

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خلاصه مقاله:

Background and Aim : Klebsiella pneumoniae being widely recognized as a nosocomial, multidrug-resistant and a heterogeneous pathogen which requires critical genetic characterization to be discovered to provide more comprehensions about the characterization of this pathogen in various infections. We aimed at to characterize 124 ESBL producing, carbapenem and quinolone resistant clinical K. pneumoniae isolates collected over a five year period, through serotyping, determination of virulence factors, antibiotic resistance testing, and enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR). Methods : All typical colonies of K. pneumoniae isolated were initially confirmed by PCR and tested for being hyper virulent phenotypically followed by antimicrobial susceptibility test. MIC of ciprofloxacin was determined by E-test. Multiplex PCR based screening was done for plasmid mediated quinolone resistance (PQMR), integrase genes and efflux pump genes. The Mast® DFC test detected the presence of ESBLs and AmpCs phenotypically, and later presence of ESBL and AmpC genes was observed by PCR. Presence of carbapenemase genes were evaluated by PCR. Capsular serotyping and capsule-associated virulence genes were studied using the molecular method. All strains were fingerprinted by ERIC-PCR. Results : All K. pneumoniae isolates had a positivity for the internal transcribed spacer region (K. pneumoniae 16S-23S) confirming as K. pneumoniae. Of all isolates, 59% were typeable. Majority of isolates (88.9%) were resistant to cephalosprins while, ciprofloxacin and carbapenem resistance was evident in 41.3% and 24% strains respectively. ESBL production was observed in 73% isolates. Frequency of qnrA, qnrB and qnrS was 3.7%, 10.5% and 9.2% respectively while 47.6% and 4.8% isolates were positive for aac(6')-Ib and 4.8% qepA respectively. Integron 1 and 2 and both 1 and 2 were noticed in 38.1%, 17.5 and 6.3% respectively. We identified 17 different ERIC patterns. Frequency of blaOXA-48, blaKPC, blaNDM, blaVIM and blaIMP genes was found as 78.8%, 14.75%, 19.67%, 11.47% and 4.91

respectively. Our study evidenced virulence-associated genes including, capsules, encoding lipopolysaccharides, regulators of hypermucoviscosity, adhesins, iron acquisition systems, enterobactin, allantoin metabolism and those which help to overcome innate host immunity. Conclusion : Our findings highlight the importance of surveillance of *K. pneumoniae* in clinical infections. The genetic surveillance is important in understanding the pathogenic characteristics of *K. pneumoniae* isolates.

کلمات کلیدی:

Klebsiella pneumoniae; Serotyping; Virulence factors; Antibiotic resistance; ERIC-PCR

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