Dissemination of Klebsiella pneumonia and Klebsiella oxytoca Harboring bla TEM genes isolated from different clinical samples in Erbil City

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Abstract

Background: *Klebsiella spp*. is an opportunistic nosocomial pathogen causing a variety of infections including urinary tract infections, pneumonia, septicemia, wound infections, distributed between patient results from producing ESBL enzymes lead to multiresistance against antibiotic encoded by some genes like blaTEM.

Objective: To identify *Klebsiella pneumonia* and Klebsiella *oxytoca* isolates harboring gene encoding for ESBL enzyme and multiresistance antibiotics such as blaTEM.

Patients and Methods: Three hundred samples were collected from (urine, wound, sputum), Klebsiella spp. isolated and identified by using microscopical, morphological, biochemical tests and Vitek 2 compact system. Antibiotic susceptibility testing was screening according to the CLSI guideline and Vitek 2 compact system. Phenotypic screening of ESBLs was undertaken using (Double disk diffusion and Standard disk diffusion) Methods, also PCR technique was used for genotypic detection of ESBL genes (blaTEM) according to the standard protocol.

Results: We obtained in this study 88 (29.33%) total positive results of Klebsiella spp.84 isolates for *Klebsiella* pneumonia and 4 isolates for Klebsiella oxytoca isolated from 300 different clinical specimens (urine, wound and sputum) ,from patient attending public hospitals in Erbil province (Rizgary, Teaching hospital, Laboratory center, Raparin, Nanakaly hospitals at a period from September 2014 to March 2015.Susceptibility profilehas been done for all *Klebsiella spp* isolated by using 13 antimicrobial agent,our multifinding pointed out that highest resistance ,most of *Klebsiella spp* isolates were resistance to more than three antibiotics belonging to different classes used and these were considered to be multidrug resistant (MDR) isolates. The incidence rate of ESBL-producing Klebsiella spp was 51 (57.95%) by Standard disk diffusion Method,48 (54.85%) by Double disk diffusion . Remarkably,dissemination of blaTEM 13 (11.09%) genes among ESBLs-positive isolates and the length of amplified genes (840) bp for blaTEM genes.

Conclusion: It can be said that the incidence rate of *Klebsiell asp* carring genes encoding for ESBL enzyme representing their commonness in our institute and multi resistance to many classes of antibiotic, resulting in limited treatment options.

Key words: *Klebsiella spp*, antimicrobial resistance extend spectrum β-lactamase, Bla TEM gene, PCR.

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