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Poster Session IV

Molecular epidemiology of MDR Enterobacteriaceae

THE EPIDEMIOLOGY OF EXTENDED SPECTRUM BETA-LACTAMASE PRODUCING KLEBSIELLA PNEUMONIAE THAT CONTAIN QNR GENES IN KUWAIT

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Objectives

Resistance to fluoroquinolones is considered highly important in *Klebsiella pneumoniae*. It arises as a result of alterations in chromosomal DNA gyrase and topoisomerase IV and changes in drug entry efflux. Plasmid mediated qnr genes also contribute to fluoroquinolone resistance. The aim of this study was to investigate the epidemiology of extended spectrum beta-lactamase producing *Klebsiella pneumoniae* that contain qnr genes in Kuwait.

Materials and Methods

Antibiotic susceptibility testing and ESBL production was performed by automated broth micro-dilution method (Vitek2) and disc diffusion according to the CLSI guidelines. PCR was performed for SHV, TEM, CTX-M, NDM, PER, VIM, *aac(6')-Ib Ib-cr*, GEM, gyrA, parC, KPC and qnrA, qnrB & qnrS. PCR products were sequenced and analysed. Pulsed-field gel electrophoresis (PFGE) was used.

Results

From 832 Enterobacteriaceae collected from 2010-2012, 174 were qnr positive ESBL producing *K. pneumoniae* that contained the aminoglycoside-modifying enzyme *aac(6')-Ib Ib-cr*. 74.30% of the isolates harboured qnrB, 14.3% qnrS and in only 2.9% of the isolates; qnrA was present. CTX-M-15 was the most common ESBL followed by CTX-M-2.

Conclusion

Previous studies suggested low prevalence of QnrB determinants among ESBL-producing *K. pneumoniae* isolates and the lack of detection of QnrA and QnrS in Kuwait. We have identified all three qnr genes at a higher rate. For almost all the cases the presence of any of the qnr genes among ESBL producers did not cause resistance to fluoroquinolones even with the presence of *aac(6')-Ib Ib-cr*.