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Multidrug Resistance Mechanisms among Gram Negative Clinical Isolates from Egypt

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Abstract : Multidrug resistant (MDR) bacteria have become a significant public health threat. The prevalence rates, of Gram negative MDR bacteria, are in continuous increase. However, few data are available about these resistant strains. Since, third generation cephalosporins are one of the most commonly used antimicrobials, we set out to investigate the prevalence, different mechanisms and clonal relatedness of multidrug resistance among third generation resistant Gram negative clinical isolates. A total of 114 Gram negative clinical isolates, previously characterized as being resistant to at least one of 3rd generation cephalosporins, were included in this study. Each isolate was tested, using Kirby Bauer disk diffusion method, against its assigned categories of antimicrobials. The role of efflux pump in resistance development was tested by the efflux pump inhibitor-based microplate assay using chloropromazine as an inhibitor. Detecting different aminoglycosides, β-lactams and quinolones resistance genes was done using polymerase chain reaction. The genetic diversity of MDR isolates was investigated using Random Amplification of Polymorphic DNA technique. MDR phenotype was detected in 101 isolates (89%). Efflux pump mediated resistance was detected in 49/101 isolates. Aminoglycosides resistance genes; armA and aac(6)-Ib were detected in one and 53 isolates, respectively. The aac(6)-Ib-cr allele, that also confers resistance to floroquinolones, was detected in 28/53 isolates. β-lactam resistance genes; blaTEM, blaSHV, blaCTX-M group 1 and group 9 were detected in 52, 29, 61 and 35 isolates, respectively. Quinolone resistance genes; qnrA, qnrB and qnrS were detectable in 2, 14, 8 isolates respectively, while qepA was not detectable at all. High diversity was observed among tested MDR isolates. MDR is common among 3rd generation cephalosporins resistant Gram negative bacteria, in Egypt. In most cases, resistance was caused by different mechanisms. Therefore, new treatment strategies should be implemented.

Keywords : gram negative, multidrug resistance, RAPD typing, resistance genes
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