



Publications Template

#	Research Title	Field	Abstract	Year of Publication Publishing	Publishing Link "URL"
1	Potential Co-prevalence of Plasmid-Mediated Quinolone Resistance Determinant qepA and 16S rRNA Methylase rmtB among <i>E.coli</i> Clinical Isolates from Alexandria- Egypt	Micobiology	<p>Background: Fluoroquinolone-resistant Gram-negative pathogens have been increasingly reported from most regions of the world over the last decade. A new plasmid-mediated fluoroquinolone efflux pump gene (qepA) is known to be associated with the 16S rRNA methylase gene (rmtB) that confers resistance to aminoglycosides.</p> <p>Aim: To investigate the potential co-prevalence of qepA and rmtB genes in Escherichia coli (<i>E. coli</i>) clinical isolates collected from Egyptian medical facilities.</p> <p>Material and methods: A total of 225 non-duplicate <i>E. coli</i> isolates were collected between 2008 and 2009 from two hospitals in Alexandria. Isolates were initially tested for their antibiotic susceptibility by disc diffusion method. Isolates exhibited quinolone and aminoglycosides co-resistance profile were screened for the presence of qepA and rmtB genes. The effect of efflux pump inhibitor, phenylarginine-beta-naphthylamide (PAβN) on the minimum inhibitory concentration (MIC) of ciprofloxacin, levofloxacin and gentamicin against these strains was tested and log activity index was calculated. Using checkerboard titration method, the combinations of gentamicin with ciprofloxacin against the strains harboring qepA and rmtB genes were tested and the fractional inhibitory concentrations (FIC) were calculated.</p>	2010	https://pubmed.ncbi.nlm.nih.gov/22054101/

Marketing Department

إدارة التسويق

			<p>Results: Forty-five E. coli isolates exhibited quinolone and aminoglycosides co-resistance profile. Of them, two E. coli isolates were positive for qepA, and three harbored rmtB genes. No association between both genes was detected. The calculated log activity index revealed a reduction in MIC of the fluoroquinolones with PAβN but not of gentamicin. FIC calculated here for gentamicin/ciprofloxacin combinations reflected either antagonism or indifference against the strains harboring qepA and rmtB genes.</p> <p>Conclusion and recommendations: qepA as well as rmtB genes-carrying E. coli strains could become a greater nosocomial infection problem with appropriate foci of selective pressure. Therefore, public health support for active surveillance for plasmid mediated fluoroquinolones, aminoglycosides resistance determinants among clinical E. coli isolates should be encouraged. In addition, the effect of efflux pumps needs to be considered in the design of future antibiotics as their synergistic role may pave the way to novel combination therapies that could be used against these strains.</p>		
2	Association of Sulphonamide Resistance with Integron-bearing Uropathogenic Escherichia coli in Alexandria, Egypt	Microbiology	<p>Introduction: Escherichia coli is by far one of the most common Enterobacteriaceae associated with community- and hospital-acquired infections. The dissemination of sulphonamide resistance is causing serious problems in the treatment of infections worldwide. Of additional concern, some sulphonamide resistance genes are related to the presence of integrons which leads to transfer of these antibiotic resistance genes among other bacterial isolates. This study aimed to investigate the prevalence of sulphonamide resistance and to reveal the relatedness between sul genes with integron-associated int genes.</p> <p>Materials and Methods: Fifty-five uropathogenic Escherichia coli isolates were collected and their resistance to 27 antimicrobial agents was tested. PCR analysis was carried out to observe integron-</p>	2019	<p>https://www.ijamhr.com/downloads/pdf/Ali-GH.pdf</p>

Marketing Department

إدارة التسويق

			<p>associated int genes (both int1 and int2) and also 2 different sul genes, namely sul1 and sul2. Results: Forty-eight (87.3%) isolates were multidrug-resistant, with the highest resistance (89%) detected against beta lactams. Among the 55 isolates, 31 (56.4%) were sulfonamide resistant. Of these sulfonamide resistant isolates, 25 (80.6%) carried sul genes, where 23 (74.2%) and 22 (71%) contained sul1 and sul2, respectively. Twenty-one of 23 (91.3%) harboring the sul1 gene, whilst 20 of 22 strains (90.9%) positive for sul2 gene, were positive for int1. Class II integrase was not detected among the isolates. To the best of our knowledge, this is the first study in Egypt revealing the strong association of sul genes with class I integrase among uropathogenic E. coli isolates. Conclusion: Multidrug resistant E. coli are increasingly being reported worldwide mainly in developing countries like Egypt. The occurrence and prevalence of integron was found to play an essential role in the dissemination of sulphonamide resistance genes.</p>		
3	<p>Multidrug Resistance in Integron Bearing <i>Klebsiella pneumoniae</i> isolated from Alexandria University Hospitals, Egypt</p>	Micobiology	<p><i>Klebsiella pneumoniae</i> is by far one of the most common Enterobacteriaceae associated with hospital-acquired infections. The dissemination of multi drug resistant <i>Klebsiella pneumoniae</i> is causing difficulty to treat infections worldwide. Of additional concern, multi drug resistant <i>Klebsiella pneumoniae</i> acquires and transfers antibiotic resistance genes among other bacterial isolates. Integrons have the main role in the acquisition as well as dissemination of resistance genes. Accordingly we aimed to investigate the frequency of resistance genes <i>sul1</i>, <i>sul2</i>, <i>tetA</i>, <i>tetB</i> and <i>aac (3) Ila</i>, class one (<i>int1</i> gene) and class two integrons (<i>int2</i> gene) in <i>Klebsiella pneumoniae</i> clinical isolates from four major hospitals in Alexandria, Egypt using Polymerase Chain Reaction. In addition we aimed to evaluate the association between multidrug resistance and presence of integrons in hospital-acquired <i>Klebsiella pneumoniae</i> in our hospitals. To the best of our knowledge, there is little information about integrons and acquisition of multiple antibiotic resistance in <i>Klebsiella pneumoniae</i> in hospitals in Alexandria, Egypt. In this study</p>	2020	<p>https://link.springer.com/article/10.1007/s00284-020-02217-7</p>



Marketing Department

إدارة التسويق

			<p>76 isolates were resistant to sulphamethoxazole /trimethoprim. Of these 38 isolates (50%) harbored both genes <i>sul1</i> and <i>sul2</i> genes. 42 isolates out of the 60 (70%) isolates that showed resistance to tetracycline were <i>tetA</i> or <i>tetB</i> positive. The prevalence of <i>int1</i> gene among all isolates tested was 90%, while only one isolate harbored the <i>int2</i> gene (1%). Our results were indicative of the high prevalence of multidrug resistant <i>Klebsiella pneumoniae</i> as well as integrons that were found to play an essential role in the dissemination of antibiotic resistance genes in our hospitals.</p>		
--	--	--	--	--	--