## Genetic Characterization of a Composite Transposon Carrying armA and Aac(6)-Ib Genes in an Escherichia coli Isolate from Egypt

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**Abstract :** Aminoglycosides are used in treating a wide range of infections caused by both Gram-negative and Gram positive bacteria. The presence of 16S rRNA methyl transferases (16S-RMTase) is among the newly discovered resistance mechanisms that confer high resistance to clinically useful aminoglycosides. Cephalosporins are the most commonly used antimicrobials in Egypt; therefore, this study was conducted to determine the isolation frequency of 16S rRNA methyl transferases among third generation cephalosporin-resistant clinical isolates in Egypt. One hundred and twenty three cephalosporin resistant Gramnegative clinical isolates were screened for aminoglycoside resistance by the Kirby Bauer disk diffusion method and tested for possible production of 16S-RMTase. PCR testing and sequencing were used to confirm the presence of 16S-RMTase and the associated antimicrobial resistance determinants, as well as the genetic region surrounding the armA gene. Out of 123 isolates, 66 (53.66%) were resistant to at least one aminoglycoside antibiotic. Only one Escherichia coli isolate (E9ECMO) which was totally resistant to all tested aminoglycosides, was confirmed to have the armA gene in association with blaTEM-1, blaCTX-M-15, blaCTX-M-14 and aac(6)-Ib genes. The armA gene was found to be carried on a large A/C plasmid. Genetic mapping of the armA surrounding region revealed, for the first time, the association of armA with aac(6)-Ib on the same transposon. In Conclusion, the isolation frequency of 16S-RMTase was low among the tested cephalosporin-resistant clinical samples.

Keywords : aminogloosides, armA gene,  $\beta$  lactmases, 16S rRNA methyl transferases

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1