

ROLE OF PATHOGENICITY ISLANDS AND INTEGRONS WITH HORIZONTAL TRANSFER MULTIPLE DRUG RESISTANCE OF UPEC ISOLATES : A MOLECULAR STUDY

Noor M. Faisal*, Ahmed D. Jabbar, Aya A. Hussein and Zainab A. Bachay

Wasit University, Iraq.

*e-mail: noormuhanad941@gmail.com

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ABSTRACT : Sixty UPEC isolates were collected from female suffered from recurrent urinary tract infections. Antibiotic resistance profile was determined by VITEK2. Results showed ampicillin resistance was most prevalent 83.3% (41/60), followed by ceftriaxone, 71.7% for, while cefoxitine relative, cefazolin shows moderate resistant since 60% of UPEC isolates. This work demonstrates that 48% of isolates were positive for integron (Int I). 90.9% of UPEC were *intI* positive isolates, which accounts of MDR-UPEC isolates. From the *IntI* positive mentioned above, 35(87.5%) of MDR-UPEC isolates were positive for type 1 integron signified by *intII*, whereas a little lower results obtained with integrin II represented by *intI2*, 30 (75%) isolates. About 51.3% of isolates have PAI markers. The most prevalent PAI among MDR-UPEC was PAI IV 58(96.6%), followed by PAI III 42 (70%), PAI II 563 3(5%), PAI II J96 5(8.3%) and PAI I 6352(3.3%). PAIs are considered to be a subclass of genomic islands that are acquired by horizontal gene transfer via transduction, conjugation and transformation, and provide ‘quantum leaps’ in microbial evolution. The MDR-UPEC isolate were screen for replication regions of IncFI and IncFII plasmid. The present study established a high incidence of repFIA plasmid was found statistically associated with *papC*, *sfaA* and *fimH*. No obvious role found for CRISPR’s associated genes (for both class 1 and class 2) in association with antibiotic resistance.

Key words : Pathogenicity island (I, II, III, IV), integrons (I, II), MDR-UPEC, microRNA.

INTRODUCTION

The spread and appearance of antimicrobial resistance caused desirous an increasing and concern health problem. *E. coli* strains are part of the normal flora in the gastrointestinal tract in the diverse animal and humans (Pitout, 2012). However, they are also the major cause of extra intestinal infection like meningitis, UTIs, and infection relate “with intravascular devices” (Chamberlain, 2009). As extraintestinal pathogenic *E. coli* (ExPEC), including UPEC, yearly affects a large proportion of the population, being responsible of as many as 80% of UTI in otherwise healthy people, so they are a major target of antimicrobial therapy (Poey *et al*, 2012). The management of infections caused by ExPEC has been complicated by the emergence of antimicrobial resistance. Resistance genes are disseminated by plasmids or by transposons and can be integrated into DNA elements designated integrons (Cambray *et al*, 2011).

Integrons are compose of a site-specific recombination system capable of integrating and expressing genes in cassettes. Both antibiotic resistances and virulence factors can be encoded by mobile elements.

If co-integration occurs, antibiotic pressure also selects for virulence factors, which in turn could lead to more virulent antibiotic-resistant strains (Rijavec *et al*, 2006). Certainly, plasmids belonging to the IncF incompatibility group encoding both antibiotic resistance and virulence factors have to be examined (Carattoli, 2009).

CRISPR or clustered regularly interspersed short palindromic repeats, is quit new field of study and the possible link between this system and pathogenicity of bacteria is not understood.

We try to find the involvement of the type of PAI, CRISPR system and integrons in the pathogenicity of UPEC and antibiotic resistance.

MATERIALS AND METHODS

Antibiotic sensetivity test

Antibiotic sensitivity was determined by Automated VITEK2 system, Biomerieux.

2.2 Molecular study

2.2.1 Bacterial Nucleic Acid Extraction:

Total genomic bacterial nucleic acid was extracted as recommended by the manufacturer. Cat. # GBB100