

Comparision Study of Presence Eight Correlated Gene with Avian Pathogenic *Escherichia coli* in Human Uropathogenic *Escherichia coli*

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Background & Objectives: A wide range of extra intestinal infections in humans and vertebrate animals are created by the Extra intestinal *E.coli* strains (EXPEC). Including the APEC (Avian pathogenic *Escherichia coli*) and urinary tract infection (Uropathogenic *Escherichia coli*) noted in humans. Recent studies indicate that *E.coli* of the animal is the suitable source for emergency presence of UPEC. The aim of study is evaluation of the presence virulence factors between APEC in UPEC.

Methods: This study investigated the presence of associated genes (*astA*, *iss*, *Iranp2*, *papC*, *iucD*, *tsh*, *vat*, *cva / cvi*) with APEC in UPEC of isolated from patients with UTI west of Tehran by using multiplex PCR. The correlation was evaluated by chi-square test.

Results: All isolates of urinary tract infection were having with different genes *astA* (13 of 100), *iss* (11 of 100), *Iranp2* (33 of 100), *papC* (3 of 100). None of these genes isolated *iucD*, *tsh*, *vat*, *cva / cvi* carrying did not. While the 28 isolates of APEC study of genes were required *astA* (24 of 28), *iss* (27 of 28), *Iranp2* (15 of 28), *papC* (23 of 28), *iucD* (24 of 28), *tsh* (24 of 28), *vat* (24 of 28), *cva / cvi* (14 of 28).

Conclusion: The results showed that there are meaningful relationships between the presence of genes for virulence *astA*, *iss*, *Iranp2*, *papC*, in APEC and UPEC. genes *iss*, having the highest frequency in both strains as well as the frequency of 33% gene *irp2* in strains of UPEC are proposed likely the most important factors that contributing in the presence of extra intestinal *Escherichia coli* live.

Keywords: *E.coli*; Human; Avian