

## RAPID DETECTION OF UROPATHOGENIC *ESCHERICHIA COLI* VIRULENCE FACTORS IN IRAQI PATIENTS BY MULTIPLEX POLYMERASE CHAIN REACTION

Esam. G. M. Salih, Mohammed. I. Nader\*, Maarib. N. Rasheed

Ministry of Higher Education and Scientific Research-University of Baghdad-Genetic Engineering and Biotechnology Institute for Postgraduate Studies. Iraq-Baghdad.

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### \*Correspondence for

#### Author

**Mohammed. I. Nadeer**

Ministry of Higher  
Education and Scientific  
Research-University of  
Baghdad-Genetic  
Engineering and  
Biotechnology Institute  
for Postgraduate Studies.  
Iraq-Baghdad.

### ABSTRACT

The aim of the study was to determine the occurrence of virulence genes expressing fimbriae among a hundred and twelve *Escherichia coli* isolates obtained from outpatients of seven Iraqi hospitals, between November 2014 and February 2015, showing clinical and laboratory signs of urinary tract infection (UTI). Primers to amplify the genes encoding the virulence factors of uropathogenic *Escherichia coli*, such as type 1 fimbriae (*fimH*), S fimbriae (*sfa*), pilus associated with pyelonephritis (*pap*) and afimbrial adhesin (*afa*) genes were combined to develop a multiplex polymerase chain reaction (MPCR) for detection of the respective Virulence factors and for the identification of uropathogenic *E. coli*. Among the isolates studied, the prevalence of genes coding for fimbrial adhesive systems was 91.071%, 75%, 51.785% and 5.357% for *fim H*, *sfa*, *pap* and *Afa* respectively. The various combinations of detected genes were

designated as virulence patterns. A rapid assessment of the bacterial pathogenicity characteristics may contribute to a better medical approach of the patients with urinary tract infections. The multiplex PCR developed was therefore, concluded to be a useful, sensitive and rapid assay system to identify uropathogenic *E. coli*. Thus, this assay can be recommended for clinical use to detect virulent urinary *E. coli* strains, as well as for epidemiological studies.

**KEYWORDS:** Uropathogenic *Escherichia coli* (UPEC), Virulence factors, Multiplex polymerase chain reaction (MPCR), Urinary tract infections (UTIs), Iraq.

## INTRODUCTION

6 to 90% of urinary tract infections (UTIs) in humans are caused by Gram-negative, rod-shaped, flagellated and facultative anaerobic bacterium of the family Enterobacteriaceae with name *Escherichia coli* (*E. coli*) (Cheesbrough, 2012). The UTIs comprise of a range of disorders, including cystitis (infection of the bladder) and pyelonephritis (infection of the kidney), which are defined by the presence of microorganisms like *E. coli* in urinary tract (Kulkarni *et al.*, 2009). previous Investigations have indicated that the distribution of various virulence factors, such as type 1 fimbriae (*fimH*), S fimbriae (*sfa*), pilus associated with pyelonephritis (*pap*) and afimbrial adhesin (*afa*) Were useful markers for the detection of uropathogenic *E.coli* and could, therefore, be used in the diagnosis of UTI (Yamamoto *et al.*, 1995a; Usein *et al* 2001; Tiba *et al.*, 2008; Tarchouna *et al.*, 2013; Momtaz *et al.*, 2013).

In this study, we assessed the utility of Multiplex polymerase chain reaction (MPCR) for rapid Detection of the virulence factors of Uropathogenic *E.coli* (UPEC) isolated from Iraqi patients with UTIs by a mixture of previously reported primers (Le Bouguenec *et al.*, 1992; Yamamoto *et al.*, 1995b; Struve and Krogfelt, 1999).

## MATERIALS AND METHODS

### Bacterial strains

A total of 112 *E. coli* strains isolated from patients of both sex and different ages presenting symptomatic UTIs were studied. Patients were visited the emergence room of seven Hospitals are AL-Muthana Military Hospital, AL-Yarmouk Teaching Hospital, AL-Karkh General Hospital, AL-Karama Teaching Hospital, AL-Imamein AL-Kadhemein Medical City, Medical City/ Teaching Laboratories and AL-Hilla Teaching Hospital in Baghdad city and Hilla city, Iraq. The strains were isolated in pure cultures and identified in the Molecular Biology Laboratory at the Institute Genetic Engineering & Biotechnology for Post Graduate Studies/University of Baghdad. Strains biochemically confirmed as *E. coli* were kept in Luria-Bertani (LB) broth/lycerol at -20°C.

### DNA isolation

Bacterial strains were subcultured overnight in LB broth (Merck, Germany) and genomic DNA was extracted by using DNA extraction kit (Presto™ Mini gDNA Bacteria Kit, Geneaid, Thailand) according to manufacturer's instruction.

### Detection of urovirulence genes in *E. coli*

In this study, one reaction of the multiplex PCR were used for detection of four virulence factors of *E.coli* isolates from patients with urinary tract infection in Iraq. Table 1 showed the primers used for detection of UPEC virulence genes and the multiplex PCR program was comprised of the following three steps: initial denaturation at 94°C for 3 min, followed by 35 cycles of denaturation at 94°C for 1 min. annealing at 57°C for 70s, and extension at 72°C for 70s and the final extension for 6 min at 72°C. In multiplex PCR reaction, for cycling, a DNA thermo-cycler (Eppendorf Master cycler, Eppendorf-Nethel-Hinz GmbH, Hamburg, Germany) was used. A multiplex PCR was performed in total volume of 25µl and components are shown in Table 2. The amplified products were visualized by ethidium bromide staining after gel electrophoresis of 10µL of the final reaction mixture in 2% agarose (see Figuer 1).

**Table 1. Primers used for detection of virulence genes in Uropathogenic *E. coli* isolates.**

Gene	Primer name	Primer sequence (5'-3')	Size of product (bp)	Annealing temperature (°C)	References
<i>fimH</i>	fimH-F	GAGAAGAGGTTTGGATTAACTTATTG	559	58	(Struve and Krogfelt,1999)
	fimH-R	AGAGCCGCTGTAGAACTGAGG			
<i>sfa</i>	Sfa-F	CTCCGGAGA AACTGGGTGCATCTTAC	410	55	(Le Bouguenec <i>et al.</i> ,1992)
	Sfa-R	CGGAGGAGTAATTACAAACCTGGCA			
<i>pap</i>	Pap-F	GCAACAGCAACGCTGGTTGCATCAT	336	63	(Yamamoto <i>et al.</i> ,1995b)
	Pap-R	AGAGAGAGCCACTCTTATACGGACA			
<i>afa</i>	Afa-F	CATCAAGCTGTTTGTTCGTCGCCCG	750	55.5	(Le Bouguenec <i>et al.</i> ,1992)
	Afa-R	GCTGGGCAGCAA AACTGATAACTCTC			

**Table 2. Multiplex PCR reaction components.**

Components	Volume (µl)
Forward primer of four genes (IDT, USA)	4 (one of each gene, con. 10 pmol/ml)
Reverse primer of four genes (IDT, USA)	4 (one of each gene, con. 10 pmol/ml)
DNA template	2
Deionized Distilled water (Bioneer, Korea)	2.5
GoTaq® Green Master Mix (Promega, USA)	12.5
<b>volume</b>	<b>25</b>

## RESULTS AND DISCUSSION

Non- properly managed from their onset, urinary tract infection can in time, become a real threat, capable of leading to renal failure. A better knowledge of the virulence characteristics of the micro organism causing the infection allows the clinician to anticipate the evolution of infection in the host (Santo *et al.*, 2006).

The prevalence of virulence genes ranged from 91.071% for *fimH* to 5.357% for *afa* (Table 3). Of the adhesin coding genes, *fimH* was the most prevalently detected (102 strains), followed by *sfa* (84 strains), *pap* (58 strains) and *afa* (6 strains), respectively.

**Table 3. Distribution of various virulence genes of UPEC strains isolated from patients with UTIs in Iraq.**

No. <i>E. coli</i> isolates	Virulence genes (%)			
	<i>fimH</i>	<i>sfa</i>	<i>pap</i>	<i>afa</i>
112	102 (91.071)	84 (75)	58 (51.785)	6 (5.357)

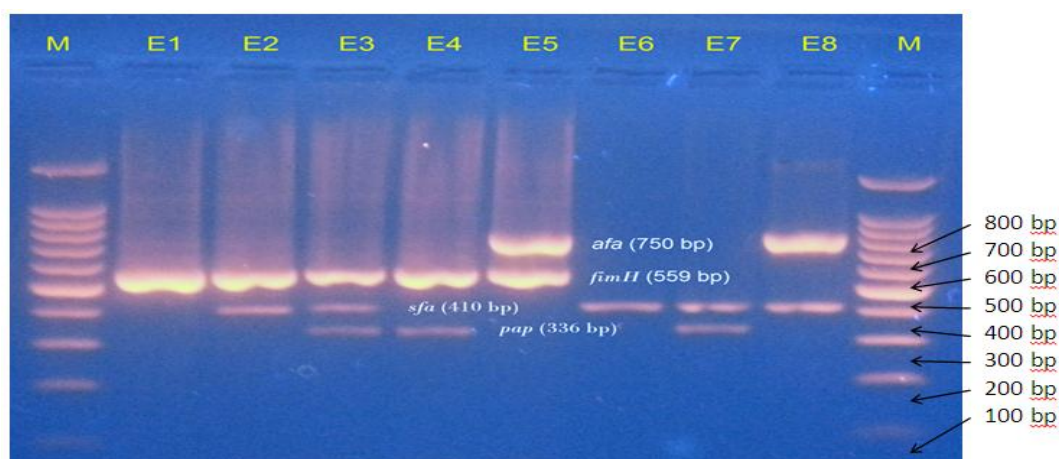
These results agree with published reports (Johnson and Stell, 2000), (Mihaylova *et al.*, 2012), (Ribero *et al.*.,2008), (Tiba *et al.*, 2008), (Köves, 2014), (Ananias and Yano, 2008), (Wang *et al.*, 2002), (Momtaz *et al.*, 2013), (Usein *et al.*, 2001), (Karimian *et al.*, 2012), (Reza *et al.*, 2011), (Abass *et al.*, 2014), (Tarchouna *et al.*, 2013) and (Jadhav *et al.*, 2011), which emphasize the predominance of fimbriae type 1 among the UPEC strains. The distribution of the S fimbriae-encoding operons found among the isolates studied was higher than previously reported (Momtaz *et al.*, 2013), (Rahman and Deka, 2014), (Tarchouna *et al.*, 2013), (Tiba *et al.*.,2008), (Bashir, 2010), (Oliveira *et al.*, 2011), (AL-Alak, 2012), (Santo *et al.*, 2006), (Farshad *et al.*, 2010), (Farshad and Emamghorashi, 2009) and (Arisoy *et al.*, 2006).Regarding P fimbriae, pooled results from other studies indicate that among *E.coli* isolates from patients with UTIs, approximately 80% and 30% respectively, possess P fimbriae (Johnson, 1991; Donnenberg and Welch, 1996). These results agree with our findings. A small number of UTI strains possessing *afa*-afimbrial adhesions have been reported (AL-Alak, 2012), (Bashir, 2010), (Usein *et al.*.,2001), (Rahman and Deka, 2014), (Santo *et al.*, 2006), (Arisoy *et al.*, 2006), (Karimian *et al.*, 2012), (Momtaz *et al.*, 2013), (Tiba *et al.*, 2008), (Oliveira *et al.*, 2011) and (Abe *et al.*, 2008). These results agree with our findings. The results showed that there were no negative samples for virulence genes of *E.coli* isolated from Iraqi patients with UTIs.

Based on the distribution of the various targeted sequences all the studied strains exhibited 8 virulence gene patterns, referred to as E followed by an Arabic numeral (Table 4).

**Table 4. Virulence patterns identified among the studied strains.**

Pattern	Virulence gene				No. of strains	%
	<i>fimH</i>	<i>sfa</i>	<i>pap</i>	<i>afa</i>		
E1	+	-	-	-	12	10.7
E2	+	+	-	-	34	30.4
E3	+	+	+	-	40	35.7
E4	+	-	+	-	14	12.5
E5	+	-	-	+	2	1.8
E6	-	+	-	-	2	1.8
E7	-	+	+	-	4	3.6
E8	-	+	-	+	4	3.6
<b>Total</b>	<b>102</b>	<b>84</b>	<b>58</b>	<b>6</b>	<b>112</b>	<b>100%</b>

Two of the virulence gene patterns designated as E1 and E6 were characterized by the presence of only one gene, which was either *fimH* (12 strains) or *sfa* (2 strains). Five patterns (E2, E4, E5, E7 and E8) were represented by strain possessing a two gene association (58 strains). The patterns E3 which included strains presenting three virulence genes were the best represented (40 strains). Among all the studied strains, there were no strains having four genes. The maximum number of detected amplicons in one strain was three virulence gene region targeted. This result agrees with those reported by Usein *et al.* (2001) in Romania, Santo *et al.* (2006) in Brazil and Tarchouna *et al.* (2013) in Tunisia. Also, there was no simultaneous presence of *pap* gene and *afa* gene in a same strain, compatible with others (Daigle *et al.*, 1994; Santo *et al.*, 2006). Instead the presence of *afa* together with *sfa* gene and *fimH* gene was commonly detected in the same strain, as in E8 and E5 patterns, respectively. This result agrees with those reported by Blanco *et al.* (1997) and Usein *et al.* (2001) in Romania.



**Fig.1. Detection of *fimH*, *sfa*, *pap*, *afa* genes by Multiplex PCR (MPCR). Lane M: DNA ladder (100 bp); Lane E1: Sample of *E. coli* isolates that contain *fimH* gene only; Lane E2: Sample of *E. coli* isolates that contain two genes (*fimH* and *sfa*); Lane E3: Sample of *E. coli* isolates that contain three genes (*fimH*, *sfa* and *pap*); Lane E4: Sample of *E.***

*coli* isolates that contain two genes (*fim H* and *pap*); Lane E5: Sample of *E. coli* isolates that contain two genes (*fim H* and *afa*); Lane E6: Sample of *E. coli* isolates that contain *sfa* gene only; Lane E7: Sample of *E. coli* isolates that contain two genes (*sfa* and *pap*); Lane E8: Sample of *E. coli* isolates that contain two genes (*sfa* and *afa*).

A Co-dependence of these virulence factors in a particular pathogenic pathway, which may differ from that use by the *E. coli* strains expressing fimbrial adhesions and was suspected (Zhang *et al.*, 1997; Lalioui and Le Bouguéneq, 2001). Some of the virulence patterns found in the studied strains could be suggestive for the presence of pathogenicity islands described in uropathogenic *E. coli* (Hacker *et al.*, 1990; Blum *et al.*, 1995). This first molecular study of *E. coli* strains isolated from Iraqi patients with UTI was meant as a step towards improving the knowledge regarding their virulence determinants. The molecular features of *E. coli* extraintestinal strains revealed by its results may contribute to a better medical approach of the patients concerned. From these results it was concluded that the multiplex PCR reported in this study is a useful method for the rapid concurrent detection of virulence factors and thereby the identification of *E. coli* causing UTIs.

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