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Difference of virulence factors, clinical presentation according to phylogenetic group in uropathogenic *E. coli* strains isolated Korean patients

Hyun Ah Kim[1*], Won-ki Baek[2], Seong-yeol Ryu[1]

[1] *Department of Infectious Diseases, Keimyung University Dongsan Medical Center, Daegue, Korea*

[2] *Department of Microbiology, Keimyung University school of Medicine, Daegue, Korea*

*Hyun Ah Kim
E-mail :hyunah1118@hanmail.net
Phone : +82 53 250 7892
Fax : +82 53 250 7434

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Introduction

- *Escherichia coli* (*E.coli*) is most predominant organism causing 95% of community acquired urinary tract infection.
- *E. coli* is made up of four phylogenetic groups; A, B1, B2, D. It has been demonstrated that most uropathogenic *E. coli* belong to phylogenetic group B2 and D.
- But there are only a few studies about the difference of virulence factors, clinical characteristics according to phylogenetic group.
- We aimed to find out the prevalence of virulence factors of uropathogenic *E. coli* and difference of clinical manifestation according to phylogenetic group in Korean urinary tract infection patients.

Methods

- The study was performed on 133 *E. coli* isolates recovered from blood, urine specimens from patients with urinary tract infections who were diagnosed at Keimyung university of Dongsan medical center from February 2015 through May 2016.
- The bacteria were confirmed as E. coli by VITEK system.
- Phylogenetic analysis was conducted by targeting three genetic markers *chuA, yjaA, TSPE4.C2*.
- Twenty nine virulence factors were identified by muptiplex PCR.
- Primers' sequence were as published, provided by other investigators.

Primers were sorted into 5 pools according to amplicon size.

Pool 1: *PAI, papA, fimH, kpsMT III, papEF, and ibeA*

Pool 2: *fyuA, bmaE, sfa/focDE, iutA, papG allele III*, and K1

Pool 3: *hlyA, rfc, nfaE, papG allele I, kpsMT II, and papC*

Pool 4: *gafD, cvaC, cdtB, focG, traT*, and *papG allele II*

Pool 5: *papG allele I, papG alleles II and III, afa/draBC, cnf1, sfaS, K5*

Results

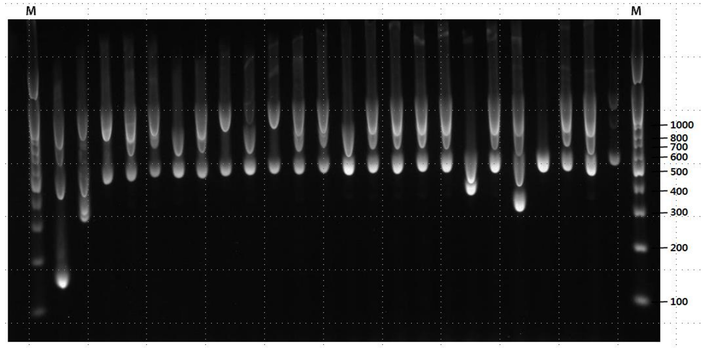

Figure 1. Agarose gel showing polymerase chain reaction (PCR) products from multiplex virulence factors PCR of pool 1 set.

- The phylogenetic group analysis reveals that most of uropathogenic *E. coli* are group B2 and D.
- The proportion of phylogenetic group of uropathogenic *E. coli* as follows: B2 (101, 75.9%), D (27, 20.3%), B1 (3, 2.3%), A (2, 1.5%).

Gene name	N (%)	Gene name	N (%)	Gene name	N (%)
fimH	131(98%)	*K5*	41(31%)	*kpsMT III*	3(2%)
fyuA	129(97%)	*hlyA*	40(30%)	*papG allele III*	3(2%)
traT	102(77%)	*cnf1*	40(30%)	*bmaE*	2(2%)
PAI	99(74%)	*K1*	35(26%)	*rfc*	2(2%)
iutA	95(71%)	*sfa/focED*	18(14%)	*nfaE*	2(2%)
papC	92(69%)	*focG*	15(11%)	*sfaS*	1(1%)
papG	91(68%)	*afa/draBC*	13(10%)	*gafD*	0
papA	88(66%)	*cvaC*	10(8%)	*cdtB*	0
papG allele II	88(66%)	*papEF*	8(6%)	*papG allele I*	0
kpsMT II	77(58%)	*ibeA*	8(6%)		

Table 1. Prevalence of virulence factors of uropathogenic *E. coli*

- Among the Virulence factors, *fimH, fyuA, traT, PAI, iutA, papC, papG, papA* were most frequently observed.

Results

- We compared clinical presentations and virulence factors of group B2 (n=101) and D (n=27).
- Phylogenetic group B2 was more related with virulence factors which were *sfa/focED, focG, fyuA, hlyA, cnf1*. Group D was more related with *nfa* (Table 2). Number of virulence factor was higher in group B2 (11(7-12) vs. 8(6-10), p=0.001).
- Group B2 and D were showed similar clinical presentation and complication. But, Group D was mostly community origin infection (26(96.3%) vs. 80(79.2%), p=0.043). Group B2 was more related with healthcare-associated infection and antimicrobial resistance.
- Most of extended spectrum β-lactamase producing *E.coli* was gorup B2 (42/45, 93%). K1 serotype was prevalent in group B2 and K5 was higher in group D.

	Virulence factor	Group B2 n=101	Group D n=27	*p*		Virulence factor	Group B2 n=101	Group D n=27	*p*
Adhesion	*papA*	70 (69.3%)	16 (59.3%)	0.36	**Iron metabolism**	*fyuA*	101 (100%)	26 (96.3%)	0.211
	fimH	100 (99%)	26 (96.3%)	0.379		*iutA*	74 (73.3%)	19 (70.4%)	0.81
	papEF	5 (5%)	3 (11.1%)	0.364	**Toxin**	*hlyA*	38 (37.6%)	1 (3.7%)	0.001
	sfa/focED	18 (17.8%)	0	0.013		*cvaC*	9 (8.9%)	0	0.203
	nfaE	0	2 (7.4%)	0.043		*cnf1*	40 (39.6%)	0	0.001
	afa/draBC	8 (7.9%)	5 (18.5%)	0.146	**Protection**	*kpsMTIII*	2 (2.0%)	1 (3.7%)	0.512
	focG	15 (14.9%)	0	0.039		*kpsMTII*	60 (59.4%)	17 (63%)	0.827
	papC	73 (72.3%)	17 (63%)	0.353		*traT*	81 (80.2%)	19 (70.4%)	0.299
	papG	73 (72.3%)	17 (63%)	0.353	**Others**	*PAI*	96 (95%)	3 (11.1%)	0.001
	papG alleleII	70 (69.3%)	17 (63%)	0.643		*ibeA*	8 (7.9%)	0	0.202

Table 2. Association of virulence factors of uropathogenic *E. coli* according to phylogenetic group B2 and D.

conclusion

- In our study, phylogenetic group B2 and D show different characteristics.
- Phylogenetic group B2 has more virulence factors than group D. Group B2 showed high presentation of adhesion related virulence factors(S fimbriae, F fimbriae). Higher presentation of resistance and healthcare-associated infection also noted.
- Presentation of virulence factors in Korean patients was different from other geographic regions. We need more studies to find out the microbiologic characteristics of uropathogenic *E. coli*. It may help to find out new target of therapy for urinary tract infection.