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

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Background: *Escherichia coli* (*E.coli*) is most predominant organism causing 95% of community acquired urinary tract infection. 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 virulent factors, clinical characteristics according to phylogenetic group.

Material/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. Phylogenetic group and 29 virulence factors were identified by muptiplex PCR.

Results: The phylogenetic group analysis reveals that most of uropathogenic E. coli are group B2 and D: B2 (101, 75.9%), D (27, 20.3%), B1 (3, 2.3%), A (2, 1.5%). Among the Virulence factors, *fimH*, *fyuA, traT, iutA, papC, papG, papA* were most frequently observed. We compared clinical presentations and virulent factors of group B2 (n=101) and D (n=27).

Phylogenetic group B2 was more related with virulent factors which were *sfa/focED, focG, fyuA, hlyA, cnf1*. Group D was more related with *nfa*. 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. Group D was mostly community origin infection. 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.

Conclusions: 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.

	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