Distribution of Pathogenicity Islands Among Uropathogenic *Escherichia coli* Isolates From Patients With Urinary Tract Infections

Ehsan Asadi¹*, Mohammad Mohammadzadeh², Mohammad Niakan¹*

¹Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran
²Department of Medical Microbiology, School of Medicine, Alborz University of Medical Sciences, Karaj, Iran

Abstract

**Background:** Uropathogenic *Escherichia coli* (UPEC) is one of the most common etiologic agents of urinary tract infection (UTI). The ability of *Escherichia coli* to cause UTI is associated with specific virulence determinants, which are encoded by pathogenicity islands (PAIs).

**Objectives:** This study aimed to investigate the distribution of PAIs among the UPEC isolates collected from patients with UTIs.

**Materials and Methods:** In this study, a total of 100 *E. coli* isolates were collected from patients with UTIs using standard microbiological methods. Polymerase chain reaction (PCR) was used for the identification of the main PAIs of UPEC according to insertion sites and virulence markers.

**Results:** In total, PAI I⁵³⁶, PAI II⁵³⁶, PAI III⁵³⁶, PAI J⁵³⁶, PAI J⁹⁶, PAI J⁹⁶, and PAI I J⁹⁶ were detected in 23, 22, 17, 17, 13, 11, 11, and 8% of isolates. PAI combinations were identified in 15% of isolates.

**Conclusion:** The results showed that PAIs of UPEC are not strain-specific and some strains can carry the PAIs associated with the prototype strains of UPEC simultaneously.

**Keywords:** Pathogenicity island, Insertion site, Urinary tract infections, Uropathogenic *Escherichia coli*.

**Background**

Urinary tract infections (UTIs) are among the most common infections worldwide and Uropathogenic *Escherichia coli* (UPEC) bacteria are known to be the most important cause of UTI, which are involved in more than 80% of these infections.¹ The UPEC strains are a genetically heterogeneous group, which encode various types of virulence factors associated with bacterial colonization and survival of bacteria in the urinary tract.² The main virulence factors of UPEC are iron acquisition systems, adhesins, and cytotoxins. These factors help the bacterial colonization and invasion of bacteria to the urinary tract.³ Virulence factors are encoded by bacterial genes that are located on the plasmid or the chromosome of UPEC. Most of these genes are organized on certain genetic elements that are called “Pathogenicity Islands (PAIs).”⁴ An array of virulence factors were encoded on PAIs. PAI J⁵³⁶ is associated with the well-known virulence factors Alpha-hemolysin, F₁₇-like fimbriae, and CS₁₂-like fimbriae. PAI III⁵³⁶ contains genes for P-related fimbriae, another Alpha-hemolysin gene cluster, the Hek adhesion, and hemagglutinin-like adhesins. PAI III⁵³⁶ encodes S-fimbriae, Iron siderophore system, HmuR-like heme receptor, Sap adhesin, and TSH-like hemoglobin protease. PAI I⁵³⁶ represents the core element of the HPI of pathogenic *Yersinia* spp. It is encoded by the Yersiniabactin siderophore system.⁵ PAI J⁹⁶ contains a hly operon and a pap operon encoding a P-pilus. It is the assembly of the P-pilus and that of type 1 pili. PAI I J⁹⁶ contains a hly operon, as well as a prs operon encoding a different class of pilus and a gene encoding the cytotoxic necrotizing factor 1 (CNF1).⁶ PAI I⁵³⁶ contains a pap operon, encoding P-fimbriae, aerobactin, and genes related to iron transport systems and putative carbohydrate transport systems.⁷ PAI I⁵³⁶ contains a pap operon, iron-regulated genes, mobile genetic elements, and a large number of unknown genes.⁸ PAIs are often associated with tRNA genes and usually located at the downstream of tRNA genes. The tRNA loci are a compatible site for the insertion of PAIs.⁹ Eight PAIs have been identified in three prototype strains of UPEC 536 (4 PAIs), UPEC J⁹⁶ (2 PAIs) and UPEC CFT073 (2 PAIs). These PAIs are commonly associated with selC (PAI 536), leuX (PAI II⁵³⁶), thrW (PAI III⁵³⁶), arsenic resistance (PAI I V⁵³⁶), phosphotransferase system (PAI I J⁹⁶ and PAI I CFT073), and pheU (PAI I J⁹⁶ and PAI I CFT073) tRNA sites.¹⁰

Acquiring data about the genetic structure and the virulence factors which can be encoded by PAIs have a great value for fully understanding UPEC pathogenicity.
Asadi et al

potential. Moreover, the relationship between the pathogen and the host can differ when the different PAI was carried by UPEC strains. The studies on the distribution of PAIs of UPEC isolates can be epidemiologically important, and it can offer useful information for controlling isolates with significant pathogenicity by identifying the virulence of indigenous isolates. This study aimed to evaluate the distribution of PAIs among the isolates of UPEC from patients with UTIs.

Materials and Methods

Sample Collection and Identification of Isolates

In this descriptive and cross-sectional study conducted from January 2017 to September 2018, the midstream urine samples were obtained from patients with pyelonephritis and cystitis who referred to the Shahid Modarres Hospital of Tehran. The E. coli isolates were collected from these patients and confirmed by conventional biochemical tests (IMViC).

DNA Extraction, Primer Design, and Detection of Pathogenicity Islands of UPEC

The genomic DNA was extracted using the DNA extraction kit (Roche, Germany) according to the kit protocol. The DNA quality was evaluated based on the OD 260/280 ratio using a NanoDrop spectrophotometer (Quawell, USA). The presence of selC, leuX, thrW, asnT, pheV, pheU tRNA encoding genes was examined using the specific primers designed in this study by Allele ID 6.0 software (Premier Biosoft, USA). Forward primers were designed for the encoding regions of the tRNA genes and reverse primers were designed for the downstream of these genes. In this way, the insertion of PAIs disrupts the genes and results in negative polymerase chain reaction (PCR). Because of the presence of common insertion sites, the primers of iucC and cnf1 virulence genes were used for differentiation of PAIs I and PAIs II J96/CFT073 strains, respectively. The PCR assay was performed in a final volume of 25 μL containing 2.5 μL of buffer (10X), 1 μL of (50 mM) MgCl2, 1 μL (15 pM) of forward and reverse primers, 0.5 μL (5U/μL) of Super Taq DNA Polymerase, 2 μL (500 ng) of bacterial DNA, and 17 μL of sterile distilled water. Thermal conditions included the primary denaturation at 95°C for 5 minutes, followed by 35 cycles (denaturation at 95°C for 30 seconds, annealing at temperatures mentioned in Table 1, for 30 seconds and extension at 72°C for 1 minute). The final extension was carried out at 72°C for 5 minutes. E. coli strain K12 was used as a positive control. The PCR products were evaluated after electrophoresis on 1% agarose gel.

Statistical Analysis

Data of this study were statistically analyzed using the Statistical Package for Social Sciences (SPSS) software version 22.0 (IBM, USA).

Results

A total of 100 UPEC isolates were collected from patients with UTIs. Twenty-two (22%) of isolates were obtained from male patients and 78 (78%) of isolates were isolated from female individuals. Additionally, 7 patients were under 20 years, 40 patients were between 21 and 50, and 53 of the patients were over 50 years old.

The Frequency of Pathogenicity Islands

The tRNA encoding genes leuX, selC, pheV, thrW, asnT, and pheU were positive in 89%, 83%, 79%, 78%, 77% and 72% of UPEC isolates, respectively (Figure 1). The presence of intact tRNA genes indicated that the relevant PAI was not inserted into this site and the genetic structure remained intact. On the other hand, the positive results of the PCR for the tRNA genes indicated the no insertion of the related PAI at the downstream of the tRNA gene. The iucC and cnf1 virulence genes were used for differentiation of PAIs I and PAIs II J96/CFT073 strains, respectively. The PCR assay was performed in a final volume of 25 μL containing 2.5 μL of buffer (10X), 1 μL of (50 mM) MgCl2, 1 μL (15 pM) of forward and reverse primers, 0.5 μL (5U/μL) of Super Taq DNA Polymerase, 2 μL (500 ng) of bacterial DNA, and 17 μL of sterile distilled water. Thermal conditions included the primary denaturation at 95°C for 5 minutes, followed by 35 cycles (denaturation at 95°C for 30 seconds, annealing at temperatures mentioned in Table 1, for 30 seconds and extension at 72°C for 1 minute). The final extension was carried out at 72°C for 5 minutes. E. coli strain K12 was used as a positive control. The PCR products were evaluated after electrophoresis on 1% agarose gel.

Table 1. Characteristics of Primers Used in the Study

| Target | Primer Sequence (5’→3’) | Amplicon Size | Annealing Temperature | Accession Numbers | References |
|--------|--------------------------|---------------|-----------------------|-------------------|------------|
| selC   | F: GGTGAGCCCCGGCTGCACTTC R: TGCCAGTACGGTGGCTGAG | 324 bp        | 62°C                  | CP017979.1       | This study |
| leuX   | F: GAATTGCGAATACGCTTAGAC R: CATCGTAATCTCCCCCTGTTGG | 270 bp        | 61°C                  | CP014272.1       | This study |
| thrW   | F: TCGTAATGCGAATCGCTGAGG R: ACGATTAGTAGCTAAGCCAGCC | 194 bp        | 63°C                  | LN832404.1       | This study |
| asnT   | F: TAATCCGTATGCCTTCTGCGG R: CTCCACTTCCTTCCTGAG | 379 bp        | 60°C                  | CP000948.1       | This study |
| pheV   | F: CATCTGCTGAAATGGCGGATGGG R: GTGTTGCTATCCAGCCGATG | 408 bp        | 60°C                  | AP005048.1       | This study |
| pheU   | F: ACCAGGGACACGGGGATTGTCG R: GAAGCCGCAACGCCGATG | 526 bp        | 58°C                  | CP042184.1       | This study |
| iucA   | F: AAACCTGCTTACGAACACTTG R: ACCCCTG CTCAATCGGAT | 269 bp        | 59°C                  | -                 | 12         |
| cnf1   | F: AAGATGGAGTTTTCTATGCGGAGG R: CATTGGAGTCTGCAAGTCAT | 498 bp        | 62°C                  | -                 | 12         |
The presence of PAIs in the downstream region of these tRNA genes was investigated. However, due to the failure of the identification of these sites by reverse primers, no amplification was observed in PCR. In some studies, the PAIs have been identified based on their insertion sites in tRNA loci.17-19

The UPEC 536 related PAIs were the most prevalent PAIs among isolates, while PAIs associated with J96 and CFT073 strains showed almost similar abundance in this study. Moreover, 15% of isolates had PAI combination. Sabaté et al20 reported PAI IV536, PAI ICFT073, PAI IICFT073, PAI IIJ96, PAI I536, PAI II536, and PAI III536 in 89%, 73%, 46%, 34%, 33%, 20%, and 2%, respectively, and PAI IIJ96 was not detected among 100 isolates of E. coli isolated from the urine of patients with UTI. PAI combination was shown in their study. In other words, different types of PAIs (536, J96, and CFT073) were found simultaneously in 75% of isolates. Moreover, in a study by Navidinia et al21 in 2013, on 100 isolates of E. coli collected from the urine of children with UTI, the prevalence rates were reported to be 19%, 11%, and 18% for PAI ICFT073, PAI II536, and PAI I536, respectively, which are very close to those found in the present study. Dobtindt et al1 reported in their study that 64.5% of the isolates caused UTI and 39.3% of the

distribution of PAIs in the current study. The identification of the PAIs was based on the detection of their insertion sites in tRNA loci. The forward primers were designed for the coding region of tRNA and reverse primers were designed for downstream of these sites in this study. The presence of PAIs in the downstream region of these tRNA genes was investigated. However, due to the failure of the identification of these sites by reverse primers, no amplification was observed in PCR. In some studies, the PAIs have been identified based on their insertion sites in tRNA loci.17-19

The UPEC 536 related PAIs were the most prevalent PAIs among isolates, while PAIs associated with J96 and CFT073 strains showed almost similar abundance in this study. Moreover, 15% of isolates had PAI combination. Sabaté et al20 reported PAI IV536, PAI ICFT073, PAI IICFT073, PAI IIJ96, PAI I536, PAI II536, and PAI III536 in 89%, 73%, 46%, 34%, 33%, 20%, and 2%, respectively, and PAI IIJ96 was not detected among 100 isolates of E. coli isolated from the urine of patients with UTI. PAI combination was shown in their study. In other words, different types of PAIs (536, J96, and CFT073) were found simultaneously in 75% of isolates. Moreover, in a study by Navidinia et al21 in 2013, on 100 isolates of E. coli collected from the urine of children with UTI, the prevalence rates were reported to be 19%, 11%, and 18% for PAI ICFT073, PAI II536, and PAI I536, respectively, which are very close to those found in the present study. Dobtindt et al1 reported in their study that 64.5% of the isolates caused UTI and 39.3% of the

Discussion

UTI is recognized as one of the common infections, both in the hospital and in the community, which is associated with human health problems in the world.14 Various epidemiological studies on UTI have reported that UPEC is the cause of 80% of these infections.15 Different virulence factors are encoded by the UPEC PAIs. By overcoming the host defense mechanisms, these factors play important roles in the pathogenesis of UPEC strains and causing the disease.14 The PAIs usually enter the tRNA encoding gene loci such as selC, pheU, pheV, etc, and each locus is associated with a particular PAI.16 The UPEC isolates from patients with UTIs were examined in terms of the distribution of PAIs in the current study. The identification of the PAIs was based on the detection of their insertion sites in tRNA loci. The forward primers were designed for the coding region of tRNA and reverse primers were designed for downstream of these sites in this study. The presence of PAIs in the downstream region of these tRNA genes was investigated. However, due to the failure of the identification of these sites by reverse primers, no amplification was observed in PCR. In some studies, the PAIs have been identified based on their insertion sites in tRNA loci.17-19

The UPEC 536 related PAIs were the most prevalent PAIs among isolates, while PAIs associated with J96 and CFT073 strains showed almost similar abundance in this study. Moreover, 15% of isolates had PAI combination. Sabaté et al20 reported PAI IV536, PAI ICFT073, PAI IICFT073, PAI IIJ96, PAI I536, PAI II536, and PAI III536 in 89%, 73%, 46%, 34%, 33%, 20%, and 2%, respectively, and PAI IIJ96 was not detected among 100 isolates of E. coli isolated from the urine of patients with UTI. PAI combination was shown in their study. In other words, different types of PAIs (536, J96, and CFT073) were found simultaneously in 75% of isolates. Moreover, in a study by Navidinia et al21 in 2013, on 100 isolates of E. coli collected from the urine of children with UTI, the prevalence rates were reported to be 19%, 11%, and 18% for PAI ICFT073, PAI II536, and PAI I536, respectively, which are very close to those found in the present study. Dobtindt et al1 reported in their study that 64.5% of the isolates caused UTI and 39.3% of the

Table 2. Distribution of Pathogenicity Islands in UPEC Isolates Collected from Patients with UTI

| PAI Composition | Total Frequency (%) | Patients (n=100) Female (%) | Male (%) |
|-----------------|---------------------|---------------------------|---------|
| PAI IJ96        | 17                  | 13%                       | 67%     |
| PAI II536       | 11                  | 11%                       | 89%     |
| PAI III536      | 10                  | 10%                       | 90%     |
| PAI IV536       | 8                   | 8%                        | 92%     |
| PAI IICFT073    | 7                   | 7%                        | 93%     |
| PAI IIJ96       | 6                   | 6%                        | 94%     |
| PAI II536 + PAI III536 | 5 | 5% | 95% |
| PAI III536 + PAI IV536 | 4 | 4% | 96% |
| PAI IICFT073 + PAI IIJ96 | 3 | 3% | 97% |
| PAI IICFT073 + PAI II536 | 3 | 3% | 98% |
| PAI IIJ96 + PAI IICFT073 | 2 | 2% | 98% |
| PAI IIJ96 + PAI IICFT073 | 2 | 2% | 98% |
| PAI II536 + PAI III536 | 2 | 2% | 98% |
| PAI III536 + PAI IV536 | 2 | 2% | 98% |
| PAI IICFT073 + PAI IIJ96 | 2 | 2% | 98% |
| PAI IICFT073 + PAI II536 | 2 | 2% | 98% |
| PAI IIJ96 + PAI IICFT073 | 2 | 2% | 98% |
non-pathogenic bacteria were PCR-positive for a specific region of PAIV536 and concluded that PAI II536 was more prevalent than PAI I1536 or PAI 1536, which, like our study, outlined the prevalence and frequency of these PAIs. However, the frequency rates in some studies were different from our study. For example, in a study conducted by Navидinia et al., the PAI III536 was present in 3% of isolates that were less than the frequency rate of PAI III536 (22%) in our study. Additionally, in the report of Sabaté et al., the frequency rate of the PAI II1536 was 2%, which is lower compared to our study (22%). A remarkable point in our study was the low prevalence of PAI IJ96, which is common in all the aforementioned studies.

Previous studies have identified strains 536, J96, and CFT073 as the UPEC prototype and some associated PAIs were identified in these strains. In the current study, it was found that some isolates carry PAIs of different UPEC prototypes simultaneously. Similar results were reported by other studies. The structure of the PAI is very similar to other mobile genetic elements such as bacteriophages and integrons. Furthermore, the possibility of horizontal PAI transfer between different strains of UPEC is not unexpected. According to earlier studies, the highest number of PAI combination was associated with PAIs of 536 and CFT073 strains. In the present study, PAIs of these two strains were found simultaneously in some isolates, which may confirm the higher rate of genetic exchange between these two strains. Previous studies have shown that PAI IJ96/CFT073 and PAI IIJ96/CFT073 have similar insertion sites in the bacterial genome. Pittard et al. reported that E. coli has only two target tRNA phcV and phcU genes. It can increase the level of competition between these two PAIs. Therefore, the results suggest that PAIs of CFT073 have a greater affinity than PAIs of IJ96 to be located in the target area. This may be the reason that PAIs of CFT073 are more prevalent than PAIs of J96 among UPEC clinical isolates. Mixed bacterial infection is not common in the sterile areas of the body and it is usually caused by one type of bacteria in these areas. However, evidence of infection with more than one bacterial species has been reported. Given this condition, the simultaneous isolation of two strains of a species may not be unexpected. This may be a reason for the simultaneous identification of PAIs of different UPEC strains in a patient with a UTI.

Conclusion
The presence of PAI combination was shown among the UPEC isolates from patients with UTIs in our region. These results revealed that the PAIs of well-known strains of UPEC is not strain-specific and different PAIs can be present simultaneously in some clinical isolates. However, the possibility of mixed infection with two strains simultaneously should be refused, which requires further studies.

Authors’ Contributions
EA: Sample collection, project administration; MM: Conceptualization, software, review & editing; MN: Original draft, review & editing.

Ethical Approval
This study was approved by the Ethics Committee of Shahed university (IR.Shahed.REC.1395.119).

Conflict of Interest Disclosures
The authors report no conflicts of interest.

Financial Support
None.

Acknowledgements
We would like to appreciate the collaboration of Shahed University of Medical Sciences and Laboratory of Shahid Modarres Hospital.

References
1. Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. Nat Rev Microbiol. 2015;13(5):269-284. doi:10.1038/nrmicro3412
2. Tiba MR, Yano T, Leite Dda S. Genotypic characterization of virulence factors in Escherichia coli strains from patients with cystitis. Rev Inst Med Trop Sao Paulo. 2008;50(5):255-260. doi:10.1590/s0036-46652008000500001
3. Janke Jj, Osterstock JB, Washburn KE, Bissett WT, Roussel AJ, Hooper RN. Use of Walpole’s solution for treatment of goats with urolithiasis: 25 cases (2001–2006). J Am Vet Med Assoc. 2009;234(2):249-252. doi:10.2460/jvma.234.2.249
4. Koga VL, Tomazetto G, Cydia PS, et al. Molecular screening of virulence genes in extraintestinal pathogenic Escherichia coli isolated from human blood culture in Brazil. Biomed Res Int. 2014;2014:465054. doi:10.1155/2014/465054
5. Dobrindt U, Blum-Oehler G, Nagy G, et al. Genetic structure and distribution of four pathogenicity islands (PAI I/536) to PAI IV(536) of uropathogenic Escherichia coli strain 536. Infect Immun. 2002;70(11):6365-6372. doi:10.1128/iai.70.11.6365-6372.2002.
6. Sarowar S, Hu OJ, Werneburg GT, Thanassi DG, Li H. The Escherichia coli P and type 1 pilus assembly chaperones PapD and FimC are monomeric in solution. J Bacteriol. 2016;198(17):2360-2369. doi:10.1128/jb.00366-16
7. Cydia PS, Rodrigues GR, Nishio EK, et al. Presence of virulence genes and pathogenicity islands in extraintestinal pathogenic Escherichia coli isolates from Brazil. J Infect Dev Ctries. 2015;9(10):1068-1075. doi:10.3855/jidc.6683
8. Sarowska J, Futoma-Koloch B, Jama-Kmiecik A, et al. Virulence factors, prevalence and potential transmission of extraintestinal pathogenic Escherichia coli isolated from different sources: recent reports. Gut Pathog. 2019;11:10. doi:10.1186/s13099-019-0290-0
9. Waldhuber A, Puthia M, Wieser A, et al. Uropathogenic Escherichia coli strain CFT073 disrupts NLRP3 inflammasome activation. J Clin Invest. 2016;126(7):2425-2436. doi:10.1172/jci81916
10. Hacker J, Kaper JB. Pathogenicity Islands and the Evolution of Pathogenic Microbes. Springer Science & Business Media; 2013.
11. Najafi A, Hasanpour M, Askary A, Aziemzadeh M, Hashemi N. Distribution of pathogenicity island markers and virulence
factors in new phylogenetic groups of uropathogenic Escherichia coli isolates. Folia Microbiol (Praha). 2018;63(3):335-343. doi:10.1007/s12223-017-0570-3
12. Watt S, Lanotte P, Mereghetti L, Moulin-Schouleur M, Picard B, Quentin R. Escherichia coli strains from pregnant women and neonates: intraspecies genetic distribution and prevalence of virulence factors. J Clin Microbiol. 2003;41(5):1929-1935. doi:10.1128/jcm.41.5.1929-1935.2003
13. Birosová E, Siegfried L, Knet'ová M, et al. Detection of virulence factors in alpha-haemolytic Escherichia coli strains isolated from various clinical materials. Clin Microbiol Infect. 2004;10(6):569-573. doi:10.1111/j.1469-0691.2004.00922.x
14. Klumpp DJ, Rycyk MT, Chen MC, Thumbikat P, Sengupta S, Schaeffer AJ. Uropathogenic Escherichia coli induces extrinsic and intrinsic cascades to initiate urothelial apoptosis. Infect Immun. 2006;74(9):5106-5113. doi:10.1128/iai.00376-06
15. Heydari Chaleshtori M, Tajbakhsh E, Arbab Soleymani N. Determination of phylogenetic groups in uropathogenic Escherichia coli in Shahrekord. Pajoohandeh Journal. 2016;21(2):93-98. [Persian].
16. Agarwal J, Srivastava S, Singh M. Pathogenomics of uropathogenic Escherichia coli. Indian J Med Microbiol. 2012;30(2):141-149. doi:10.4103/0255-0857.96657
17. Mohammadzadeh M, Oloomi M, Bouzari S. Genetic evaluation of Locus of enterocyte effacement pathogenicity island (LEE) in Enteropathogenic Escherichia coli isolates (EPEC). Iran J Microbiol. 2013;5(4):345-349.
18. Del Canto F, Valenzuela P, Canto L, et al. Distribution of classical and nonclassical virulence genes in enterotoxigenic Escherichia coli isolates from Chilean children and tRNA gene screening for putative insertion sites for genomic islands. J Clin Microbiol. 2011;49(9):3198-3203. doi:10.1128/jcm.02473-10
19. Asadi Karam M, Bouzari S, Oloomi M, Aslani M, Jafari A. Phenotypic and genotypic characterization of Enteropathogenic Escherichia coli (EPEC) strains in Tehran, Iran. Iran J Microbiol. 2010;2(1):3-7.
20. Sabaté M, Moreno E, Pérez T, Andreu A, Prats G. Pathogenicity island markers in commensal and uropathogenic Escherichia coli isolates. Clin Microbiol Infect. 2006;12(9):880-886. doi:10.1111/j.1469-0691.2006.01461.x
21. Navidinia M, Najär Peerayeh S, Fallah F, Bakhshi B. Phylogenetic groups and pathogenicity island markers in Escherichia coli isolated from children. Jundishapur J Microbiol. 2013;6(10):e8362. doi:10.5812/jjm.8362
22. Waldhuber A, Puthia M, Wieser A, et al. Uropathogenic Escherichia coli strain CFT073 disrupts NLRP3 inflammasome activation. J Clin Invest. 2016;126(7):2425-2436. doi:10.1172/jci81916
23. da Silva LC, de Mello Santos AC, Silva RM. Uropathogenic Escherichia coli pathogenicity islands and other ExPEC virulence genes may contribute to the genome variability of enteroinvasive E. coli. BMC Microbiol. 2017;17(1):68. doi:10.1186/s12866-017-0979-5
24. Schmidt H, Hensel M. Pathogenicity islands in bacterial pathogenesis. Clin Microbiol Rev. 2004;17(1):14-56. doi:10.1128/cmrr.17.1.14-56.2004
25. Che D, Hasan MS, Chen B. Identifying pathogenicity islands in bacterial pathogenomics using computational approaches. Pathogens. 2014;3(1):36-56. doi:10.3390/pathogens3010036
26. Pittard J, Praszkier J, Certoma A, et al. Evidence that there are only two tRNA(Phe) genes in Escherichia coli. J Bacteriol. 1990;172(10):6077-6083. doi:10.1128/jb.172.10.6077-6083.1990
27. Kline KA, Lewis AL. Gram-positive uropathogens, polymicrobial urinary tract infection, and the emerging microbiota of the urinary tract. Microbiliol Spectr. 2016;4(2). doi:10.1128/microbiolspec.UlT-0012-2012.