Phylogeny, Sequence-typing and virulence profile of uropathogenic E. coli (UPEC) strains from Pakistan

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Abstract

Background

Escherichia coli lineage ST131 predominates across various spectra of extra-intestinal infections, including urinary tract infection (UTI). The distinctive resistance profile, diverse armamentarium of virulence factors and rapid global dissemination of ST131 E. coli makes it an intriguing pathogen. However, not much is known about the prevalence and genetic attributes of ST131 lineage in Pakistan.

Methods

We estimated the prevalence and genetic attributes of E. coli ST131 isolates causing UTI among 155 randomly selected samples. Samples were analyzed by phylogenetic grouping, O-typing, fumC/fimH typing. Isolates were further tested for ESBL and virulence factors using PCR.

Results

Overall, 59% of the UPEC isolates belonged to the phylogenetic group B2, followed by D=28%, B1= 8% and A= 5%. Among 18 different Sequence-types, ST131 was the dominant lineage (n=71; 46%) out of which 72% of the isolates were assigned to phylogenetic group B2 while 61% adhered to serogroup O25b. FumC/fimH typing confirmed 49% of the ST131 as H30 sub-types. In this study, significant numbers of the identified ST131 isolates were MDR and 42% showed ESBL phenotypes, out of which 57% carried blaCTX-M-15. Moreover, different virulence factors were detected in following percentages: fimH,155 (100%), iutA 86 (55%), feoB 76 (49%), papC 75 (48%), papGII 70 (45%), kpsMTII 40 (26%), papEF 37 (24%), fyuA 37 (24%), usp 22 (14%), papA 20 (13%), sfa/foc 20 (13%), hlyA 18 (12%), afa 15 (10%), cdtB 11 (7%), papGl 6 (4%), papGIII 6 (4%), kpsMTIII 4 (3%) and bmaE2 (1%).
Conclusion
Conclusively, this study provides important insights into the genetic and virulence attributes of pandemic MDR ST131 strains involved in UTIs. It also highlights high prevalence of ST131-O25b-H30 UPEC isolates in local population, which was previously unreported from this part of globe. Keywords: ST131, VF genes, ESBL, UPEC, MDR

Background
Extra-intestinal *E. coli* is the major cause of urinary tract infections and resistance among UTI strains has been mounting against different antibiotics, including trimethoprim-sulfamethoxazole, fluoroquinolones extended spectrum cephalosporins and amoxicillin clavulanic acid [1-3]. Due to the emergence of specific clonal groups such as ST131, global dissemination of fluoroquinolone-resistance was highlighted across different geographical regions [4-6]. Clonal group ST131 predominates across various spectra of infections including cystitis, pyelonephritis, bacteremia, meningitis, septic shock, epididymo-orchitis and osteoarticular infection. [7, 8]. In addition, ST131 strains harbor diverse armamentarium of virulence factors and their genetic homogeneity regarding virulence potential and resistance profile has been endorsed [8]. Notably, a subgroup of ST131 strains, known as H30-Rx has remarkable tendency to encode *bla-CTX-M-15* gene [7, 9, 10]. In the current scenario of global urgency related to the antibiotic resistance, underlying epidemiological factors related to the fitness and fast emergence of ST131 across different regions are under intensive scrutiny. However, in Pakistan phylogenetic grouping, sequence types, virulence attributes and antibiotic susceptibility profile of UPEC strains remains unexplored [11, 12]. Therefore, data related to the clonal types and
resistance profile of the strains involved in urinary tract infections in Pakistan is extremely scarce. This study fills this gap and provides important insights into the genetic and virulence attributes of pandemic MDR ST131 strains involved in UTIs in Pakistan.

Methods

Sample collection and antibiotic susceptibility testing

Altogether n=155 identified uropathogenic E. coli (UPEC) were collected during the period of August 2012 to August 2014, from Pakistan Institute of Medical Sciences. Ethical Review Board (ERB) of Pakistan Institute of Medical Sciences approved this study. Ethical Review Board approved verbal consent of the patient. Important patient data such as name, age, gender, location was recorded and unique identification number were assigned to each patient. Samples were from community-acquired urinary tract infections. Antibiotic testing and phenotypic detections of ESBL were performed by disc diffusion methods according to the guidelines CLSI, 2014 [13]. Isolates were tested for the susceptibility to 12 different classes of antibiotics including β-lactamase inhibitors (piperacillin tazobactam, amoxicillin-clavulanic acid), cephalosporins (ceftazidime, cefotaxime, ceftriaxone), fluoroquinolone (ciprofloxacin, levofloxacin), aminoglycosides (amikacin), trimethoprim sulfonamides, nitrofurantoin, and fosfomycin were used (BIOANALYSE, Turkey). Control strain E. coli ATCC 25922 was used in this assay.

Phylogeny, serotyping, and fumC/ fimH Typing
We used the procedure reported by Clermont et al, 2000 to perform phylogenetic analysis of 155 isolates [14]. FumC/fimH typing (CH typing) was performed as previously described [15]. Briefly, PCR amplifications were carried out in 25 µl (12.5 µl GoTaq DNA polymerase (Promega) 7.5 µl water, 1 µl bacterial DNA, 2 µl of each forward and reverse primers). The amplified products were analyzed on 2% agarose gel. The confirmed PCR products were purified using PCR purification kit (QIAquick, PCR Purification Kit, QIAGEN) and all the fragments were sequenced (ABI 3130, Perkin-Elmer Applied Biosystems, Foster City, California). The forward and reverse sequences were aligned, trimmed off using Codon Code Aligner and results were compiled according to the standard procedures [15, 16]. Additionally, by targeting 347bp of pabB gene fragment, clonal group ST131 was scrutinized for serogroup O25b [17]. Previously typed O25b-ST131 and K-12 E. coli strains were included as experimental controls in this study.

Detection of β-lactamases and Virulence factor genes

In order to detect extra-chromosomally encoded ESBL factors, plasmid DNA was isolated by commercially available kit (Thermo-Scientific Gene Jet plasmid Miniprep Kit). ESBL factors including bla_{TEM}, bla_{SHV} and genes bla_{OXA}, bla_{PSE} were also amplified by PCR as described elsewhere [18]. Amplified products were purified (Gel Band Purification Kit, Amersham, USA) and sequencing was done by automated DNA sequencer (ABI 3130, Perkin-Elmer Applied Biosystems, Foster City, California). Sequences were reported to the Gene Bank database (accession number; KX171170-171195). PCR amplifications and sequencing of bla_{CTX-M} allele was carried out, bla_{CTX-M} types were determined by comparing DNA sequences available in the database.
A total of 18 different Virulence factor (VF) genes corresponding to the main classes of extra-intestinal virulence associated genes (VAGs) including adhesins, toxins, siderophores, capsular proteins and uropathogenic-specific protein (usp) were scrutinized in 155 isolates. VF genes were amplified by previously reported sets of primers and amplification conditions [20].

Statistical analysis

The statistical analysis was performed using Graph Pad Prism, version 7. Both Chi square and Fisher exact tests were used to assess differences by assuming cut-off value of $P < 0.05$ as significant.

Results

Phylogeny and sequence typing

Overall, phylogenetic group B2 showed highest representation, 92(59%) followed by D 43 (28%), B1 12 (8%) and A 8(5%) (Table 1). Eighteen different sequence types (STs) among 152 isolates were confirmed, constituting 98% of all the isolates; the remaining 2% of the isolates were un-typeable. Clonal group ST131 comprised 71(46%) of all the isolates, followed by two other lineages, ST405 28(18%) and ST168 16(10%) (Table 3). The majority of the ST131 strains 51(72%) belonged to the phylogenetic group B2, while 43(61%) were assigned to serogroup O25b. CH typing confirmed 35(49%) as ST131-H30 sub-group of strains, out of which 22(31%) belonged to the serogroup O25b.

MDR among ST131 strains

Significant number of the isolates assigned to phylogenetic group B2 and D were multi-drug resistant (Table 3). Similarly, among different STs including ST131,
ST405, ST168, ST29, ST69 and ST89, significant number of the isolates were multi-drug resistant (Table 3). The tendency of ESBL production and the fluoroquinolone resistance was relatively higher among ST131 isolates and majority of the isolates were multi-drug resistant (Table 3). Likewise, resistance against nitrofurantoin was significantly higher among ST131 isolates in comparison to other sequence types (Table 4). One of the frequently prevalent sequence types, ST168 strains showed significant resistance to levofloxacin (Table 4). Resistance against carbapenemes has not been evaluated for the scrutinized strains; hence it is beyond the scope of this discussion.

**Occurrence of β-lactamases among ST131**

Overall, occurrence of ESBL was higher among clonal group ST131, constituting 42% of the total ESBL phenotypes (Table 4). Moreover, 78% of the ESBL phenotypes showed resistance to at least one fluoroquinolone and as expected 95% were resistant to at least one cephalosporin. The occurrence of ESBL genes remained as follows, *bla*\(_{CTX-M-15}\), 57(39%), *bla*\(_{TEM}\) 23(15%), *bla*\(_{SHV}\) 6(4%). Prevalence of other β-lactamases genes such as *bla*\(_{OXA}\) and *bla*\(_{PSE\_1}\) remained 6% and 0.6% respectively. In comparison to other sequence types, overall prevalence of β-lactamases genes was higher among ST131 strains 27(38%) of the *bla*\(_{CTX-M-15}\), followed by *bla*\(_{TEM}\) 8(11%), *bla*\(_{SHV}\) 3(4%) and *bla*\(_{OXA}\) 6(8%). Overall presence of *bla*\(_{CTX-M-15}\) was highest (100%) among ST131 H30-O25b and 91% of the *bla*\(_{CTX-M-15}\) positive ST131 H30-O25b isolates were resistant to fluoroquinolones (Data not shown). ESBL producing isolates were frequently found resistant to ceftazidime, cefotaxime, ceftriaxone, ciprofloxacin, levofloxacin, amoxicillin-clavulanic acid and
Distribution of VF genes among different sequence types

A total of 18 different virulence factors were scrutinized among 155 isolates. Overall percentages of VF genes were as follows: *fimH*, 155 (100%), *iutA*, 86 (55%), *feoB*, 76 (49%), *papC*, 75 (48%), *papGII*, 70 (45%), *kpsMTII*, 40 (26%), *papEF*, 37 (24%), *fyuA*, 37 (24%), *usp*, 22 (14%), *papA*, 20 (13%), *sfa/foc*, 20 (13%), *hlyA*, 18 (12%), *afa*, 15 (10%), *cdtB*, 11 (7%), *papGI*, 6 (4%), *papGIII*, 6 (4%), *kpsMTIII*, 4 (3%) and *bmaE2*, 1 (1%).

Some virulence factors such as *sfa/foc*, *fyuA* and *feoB* were detected frequently among ST131 isolates whereas VF-genes *papEF*, *sfa/foc* and *hlyA* were frequently associated with *H30* sub-clone (Table 5). Overall, virulence genes such as *sfa/foc*, *fyuA* and *feoB* were associated significantly (*p* < 0.05) with strains ST131, while *papEF* had significant presence among clonal group ST131-*H30*.

Discussion

*E. coli* ST131 was reported from three different continents [8]. However, recently it has become the most predominant lineage associated with variety of infections around the globe. ST131 strains have a tendency to harbor ESBL enzymes such as *bla* -CTX-M-15, which play a significant role in mounting resistance to β-lactam class of antibiotics [8]. Moreover, ST131 strains show remarkable resistance to fluoroquinolones and demonstrate greater abilities to adhere bladder, kidneys and epithelial cells [4, 5]. In this study, clonal group ST131 was the most prevalent lineage, comprising 46% of the isolates and majority of these isolates (59%) belonged to the phylogenetic group B2. Prevalence of two other lineages ST405 and
ST168 were 18% and 10% respectively. Involvement of these lineages in UTIs has been described earlier and recently ST405 was confirmed as an emerging uropathogenic *E. coli* clone in Saudi Arabia [21, 22]. Urinary tract infections caused by *E. coli* pose considerable challenge and are associated with high morbidity and mortality [5]. Due to their resistance against variety of antibiotics, including β-lactams, aminoglycosides and fluoroquinolones, infections caused by pandemic clonal group ST131 are challenging to treat [23, 24]. In this context, epidemiological significance of a sub group ST131 H30-Rx has been well described [5, 25]. In this study, 50% of the ST131 strains carried H30 variant of *fimH* gene and 61% belonged to the serogroup O25b. Moreover, all the isolates belonging to sub-group ST131-H30-O25b carried ESBL *bla*\textsubscript{CTX-M-15} however, overall prevalence of these strains constituted 10% of the total isolates. In this study overall resistance against fluoroquinolones remained 60%, which was remarkably higher among ST131 isolates (60% vs 82%). Generally, for the treatment of UTIs commonly prescribed antibiotics include sulphamethoxazole-trimethoprim and fluoroquinolones. Due to the emerging resistance to these antibiotics alternative therapeutic choices such as nitrofurantoin, fosfomycin and β-lactam inhibitors can be used.

In this study, prevalence of ESBL genes was higher among ST131 isolates and 90% of the ST-131 isolates were resistant to ceftazidime and cefotaxime. Likewise, resistance to ceftriaxone was confirmed in 77% of these isolates. Because of their favorable safety, cephalosporins are considered important therapeutic choice for the treatment of uncomplicated UTIs among pregnant women [26]. Nitrofurantoin is a fluoroquinolone-sparing alternative antibiotic used for uncomplicated cystitis [27]. In recent years use of nitrofurantoin has increased steadily, due to resistance against trimethoprim/sulfamethoxazole and
aminopenicillins. Contraindication of ciprofloxacin in pregnancy and adverse impact on gut flora favored the use of nitrofurantoin as a treatment option for UTIs. In this study 13% of the ST-131 isolates were resistant to nitrofurantoin.

We found that majority of the isolates belonging to the lineages ST405, ST168, ST29, ST69 and ST89 were multi-drug resistant. However, the MDR percentage was particularly higher among fluoroquinolones-resistant ST131 strains. Overall 59% of the isolates belonged to the phylogenetic group B2. A previous study from Pakistan confirmed that 50% of the UPEC isolates belonged to the phylogenetic group B2 [28]. Interestingly however, another study conducted in Pakistan reported that only 12% of the strains belonged to phylogenetic group B2. These findings suggest that prevalence of phylogenetic group B2 may vary across different regions [29].

Phylogenetic group B2 strains are equipped with various VF genes related to the extra-intestinal infections. These genes include P-fimbriae, S-fimbriae, haemolysin, aerobactin, K1 and K5 antigens and capsular antigen genes [30, 31]. A previous report focusing on UPEC, in Pakistan described prevalence of various VF genes, including hlyA, sfaDE, papC,cnf1, eaeAand afaBC[29] While another study conducted on rectal flora isolates of Pakistani children confirmed that virulence factors such as S-fimbriae, haemolysin, K-1 antigens and class III PapGAdhesins are either very rare or completely absent [29]. Among UPEC strains of phylogenetic group B2 wide range of the virulence factors including genes for adhesins (fimH 100%, papA13%, papC 47%, papEF 21% papGI 3%, papGII 40%,papGIII 4% , sfa/foc14%, afa 11%, bmaE 1%), toxins (hlyA 7%, cdtB 7%) iron acquisition system (iutA 57%, feoB 43%, fyuA 23%) capsular proteins (kpsMTII 26% , kpsMTIII 3%) and uropathogenic specific protein (usp 14%) were detected. Moreover, we observed that gene papGIIwas significantly associated with phylogenetic group B2 strains.
Association of the gene *papGII* with pyelonephritis and bacteraemia in human has been confirmed previously [32-34]. In the current study, fimbriae associated gene *fimH* was detected among 100% of the UPEC isolates consistent with previous work. Role of *fimH* in adhesion, invasion and formation of intracellular bacterial communities (IBCs) has been described previously and its importance in the host pathogen interaction was confirmed by higher vulnerabilities of premenopausal women to UPEC infections [35]. Genes related to the adhesins (*papEF, sfa/foc*) and toxins (*hlyA*) were found to be strongly associated with ST131 *H30* sub-clone. Recently HlyA in interaction with natural killer (NK) cells of urinary bladder was described [36]. Likewise, significant association of iron acquisition genes (*fyuA* and *feoB*) was witnessed among ST131 lineage. The importance of genes related to the iron acquisition system was shown by strong upregulation of these genes during UTIs [37]. Generally, *E. coli* strains causing UTI share similar properties in terms of phylogeny, sero-grouping and VF genes. Moreover, other than genetic attributes of the virulence strains host factors may play important role in the outcome of infection [38].

**Conclusion**

In conclusion it is the first report that highlights MDR ST131 as predominant lineage associated with UTI in Pakistan. ST131 and other scrutinized sequence types having MDR status among UTI isolates in Pakistan indicate considerable constraints on the empirical choice for the treatment of UTI. Alternative therapies and identification of effective prevention strategies—including antibiotic stewardship – are needed. As antibiotic resistance can be transferred from UPEC to other pathogens, more judicious use of antibiotics is required.
Abbreviations

UTI, Urinary tract infections; ST, Sequence type; UPEC, Uropathogenic *E. coli*; MDR, Multidrug resistance; ESBL, Extended spectrum beta lactamases; VF, virulence factors; IBCs, intracellular bacterial communities; NK, natural killer.

Declarations

**Ethics approval and consent to participate**

Upon informed consent of the participants, Ethical Review Board (ERB) of Pakistan Institute of Medical Sciences approved this study.

**Consent for publication**

Right to publish this information was obtained by informed consent of the participants.

**Availability of data and material**

The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

**Competing interests**

We declare that there is no conflict of interest.

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**Author’s contributions**

AI and RZ conducted the research, data analysis and interpretation and drafted the manuscript. TF helped in MIC determination. AI, GES, SB and ES helped in statistical and bioinformatics analysis. DIJ and FB designed and co-supervised the study, helped in acquiring the data and improved the manuscript. All authors have read, contributed and approved the final manuscript.

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Tables

Table 1: Distribution of ESBL factors, antibiotic resistance and VF genes in MDR UPEC.

| Resistance traits          | Total Isolates (n=155)n (%) | Group A (n=8) n(%) | Group B1 (n=12) n(%) | Group B2 (n=92) n(%) | Group B3 (n=92) n(%) |
|----------------------------|----------------------------|--------------------|----------------------|----------------------|----------------------|
| ESBL phenotypes            | 65(42)                     | 1(13)              | 3(25)                | 36(39)               | 25                   |
| blaCTX-M-15                 | 57(37)                     | 1(13)              | 3(25)                | 32(35)               | 21                   |
| blaTEM                     | 23(15)                     | 1(13)              | 3(25)                | 13(14)               | 6                   |
| blaSHV                     | 6(4)                       | 0                  | 0                    | 3(3)                 | 3                   |
| blaOXA                     | 10(6)                      | 0                  | 1(8)                 | 4(4)                 | 5                   |
| blaOXA                     | 10(6)                      | 0                  | 1(8)                 | 4(4)                 | 5                   |
| blaOXA                     | 10(6)                      | 0                  | 1(8)                 | 4(4)                 | 5                   |
| Piperacillin tazobactam    | 7(5)                       | 0                  | 1(8)                 | 4(4)                 | 2                   |
| Ceftazidime                | 96(62)                     | 3(38)              | 7(58)                | 54(59)               | 32                  |
| Cefotaxime                 | 101(65)                    | 3(38)              | 7(58)                | 59(64)               | 32                  |
| Drug                  | Column 1 (N) | Column 2 (N) | Column 3 (N) | Column 4 (N) | Column 5 (N) |
|-----------------------|-------------|-------------|-------------|-------------|-------------|
| Ceftriaxone           | 99 (64)     | 3 (38)      | 8 (67)      | 59 (64)     | 29          |
| Ciprofloxacin         | 95 (61)     | 6 (75)      | 7 (58)      | 56 (90)     | 26          |
| Levofloxacin          | 97 (63)     | 7 (88)      | 8 (67)      | 56 (90)     | 26          |
| Amikacin              | 7 (5)       | 1 (13)      | 0           | 5 (5)       | 1 (9)       |
| Gentamicin            | 47 (30)     | 4 (50)      | 6 (50)      | 24 (26)     | 13          |
| Amoxicillin-clavulanic acid | 111 (72) | 5 (63)      | 7 (58)      | 66 (72)     | 26          |
| Trimethoprim sulfonamides | 130 (84) | 7 (88)      | 11 (92)     | 77 (84)     | 35          |
| Nitrofurantoin        | 9 (6)       | 1 (13)      | 1 (8)       | 6 (7)       | 1 (9)       |
| Fosfomycin            | 15 (10)     | 1 (13)      | 2 (17)      | 8 (9)       | 4 (14)      |
| fimH                  | 155 (100)   | 8 (100)     | 12 (100)    | 92 (100)    | 43          |
| papA                  | 20 (13)     | 1 (13)      | 1 (8)       | 12 (13)     | 6 (14)      |
| papC                  | 75 (48)     | 2 (25)      | 8 (67)      | 43 (47)     | 22          |
| papEF                 | 37 (24)     | 0           | 6 (50)      | 19 (21)     | 12          |
| papGI                 | 6 (4)       | 0           | 0           | 3 (3)       | 3 (4)       |
| papGII                | 70 (45)     | 2 (25)      | 7 (58)      | 37 (40)     | 24          |
| papGIII               | 6 (4)       | 0           | 0           | 4 (4)       | 2 (3)       |
| sfa/foc               | 20 (13)     | 2 (25)      | 1 (8)       | 13 (14)     | 4 (14)      |
| Afa                   | 15 (10)     | 0           | 1 (8)       | 10 (11)     | 4 (14)      |
| bmaE                  | 2 (1)       | 0           | 1 (8)       | 1 (1)       | 0           |
| fyuA                  | 37 (24)     | 1 (13)      | 2 (17)      | 21 (23)     | 13          |
| iutA                  | 86 (55)     | 5 (63)      | 5 (42)      | 52 (57)     | 24          |
| feoB                  | 76 (49)     | 3 (38)      | 6 (50)      | 40 (43)     | 27          |
| kpsmtII               | 40 (26)     | 0           | 4 (33)      | 21 (23)     | 15          |
| kpsmtIII              | 4 (3)       | 0           | 1 (8)       | 3 (3)       | 0           |
| Usp                   | 22 (14)     | 2 (25)      | 2 (17)      | 14 (15)     | 4 (14)      |
| hlyA                  | 18 (12)     | 1 (13)      | 3 (25)      | 6 (7)       | 8 (10)      |
| cdtB                  | 11 (7)      | 0           | 3 (25)      | 6 (7)       | 2 (3)       |
| Resistance traits                      | All isolates (n=155); n(%) | Non ESBL producers (n=90) n(%) | ESBL producers (n=65) n(%) |
|----------------------------------------|----------------------------|--------------------------------|---------------------------|
| Piperacillin tazobactam                | 7(5)                       | 4(4)                           | 3(5)                      |
| Ceftazidime                            | 96(62)                     | 36(40)                         | 60(92)                    |
| Cefotaxime                             | 101(65)                    | 40(44)                         | 61(94)                    |
| Ceftriaxone                            | 99(64)                     | 49(54)                         | 50(77)                    |
| Ciprofloxacin                          | 95(61)                     | 45(50)                         | 50(77)                    |
| Levofloxacin                           | 97(63)                     | 48(53)                         | 49(75)                    |
| Amikacin                               | 7(5)                       | 4(4)                           | 3(5)                      |
| Gentamicin                             | 47(30)                     | 30(33)                         | 17(26)                    |
| Amoxicillin-clavulanic acid            | 111(72)                    | 50(56)                         | 61(94)                    |
| Trimethoprim sulfonamides              | 130(84)                    | 67(74)                         | 63(97)                    |
| Nitrofurantoin                         | 9(6)                       | 6(7)                           | 3(5)                      |
| Fosfomycin                             | 15(10)                     | 8(9)                           | 7(11)                     |
| *fimH*                                 | 155 (100)                  | 90 (100)                       | 65 (100)                  |
| *papA*                                 | 20 (13)                    | 12 (13)                        | 8 (12)                    |
| *papC*                                 | 75 (48)                    | 42 (47)                        | 33 (51)                   |
| *papEF*                                | 37 (24)                    | 18 (20)                        | 19 (29)                   |
| *papGI*                                | 6 (4)                      | 3 (3)                          | 3 (5)                     |
| *papGII*                               | 70 (45)                    | 33 (37)                        | 37 (57)                   |
| *papGIII*                              | 6 (4)                      | 4 (4)                          | 2 (3)                     |
| *sfa/foc*                              | 20 (13)                    | 11 (12)                        | 9 (14)                    |
| *Afa*                                  | 15 (10)                    | 7 (8)                          | 8 (12)                    |
| *bmaE*                                 | 2 (1)                      | 1 (1)                          | 1 (2)                     |
| *fyuA*                                 | 37 (24)                    | 20 (22)                        | 17 (26)                   |
| *iutA*                                 | 86 (55)                    | 45 (50)                        | 41 (63)                   |
| *feoB*                                 | 76 (49)                    | 40 (44)                        | 36 (55)                   |
| *kpsmtII*                              | 40 (26)                    | 19 (21)                        | 21 (32)                   |
| *kpsmtIII*                             | 4 (3)                      | 2 (2)                          | 2 (3)                     |
| *Usp*                                  | 22 (14)                    | 10 (9)                         | 12 (18)                   |
| *hlyA*                                 | 18 (12)                    | 7 (8)                          | 11 (17)                   |
| *cdtB*                                 | 11 (7)                     | 6 (7)                          | 5 (8)                     |

Table 2: Distribution of drug resistance and VF genes among ESBL producers and non ESBL UPEC.
Table 3: Distribution of MDR and fluoroquinolone resistant MDR strains in different phylogroups and ST-types.

| No of isolates in group n (%) | No of MDR isolates n (%) | ESBL+FQR-MDR isolates n (%) | p value |
|-------------------------------|--------------------------|------------------------------|---------|
| Group A 8(5)                  | 7(88)                    | 2(25)                        | 0.0117  |
| Group B1 12(8)                | 10(83)                   | 5(42)                        | 0.0350  |
| Group B2 92(59)               | 71(77)                   | 33(36)                       | <0.0001 |
| Group D 43(28)                | 36(84)                   | 11(26)                       | <0.0001 |
| ST131 71(46)                  | 57(82)                   | 22(31)                       | <0.0001 |
| H30 35(49)                    | 28(80)                   | 10(29)                       | <0.0001 |
| Non H30 36(51)                | 29(81)                   | 12(33)                       | <0.0001 |
| ST405 28(18)                  | 24(86)                   | 10(36)                       | 0.0001  |
| ST168 16(10)                  | 14(88)                   | 7(44)                        | 0.0092  |
| ST29 13(8)                    | 9(69)                    | 5(38)                        | 0.1156  |
| ST69 5(3)                     | 5(100)                   | 2(40)                        | 0.0384  |
| ST95 2(1)                     | 2(100)                   | 0.00                         |         |
| ST31 2(1)                     | 0(0)                     | 0.00                         |         |
| ST10 2(1)                     | 1(50)                    | 0.00                         |         |
| ST448 2(1)                    | 1(50)                    | 0.00                         |         |
| ST89 2(1)                     | 2(100)                   | 1(50)                        | 0.2482  |
| ST703 2(1)                    | 2(100)                   | 0.00                         |         |
| ST910 1(1)                    | 1(100)                   | 0.00                         |         |
| ST545 1(1)                    | 0(0)                     | 0.00                         |         |
| ST971 1(1)                    | 0(0)                     | 0.00                         |         |
| ST153 1(1)                    | 0(0)                     | 0.00                         |         |
| ST152 1(1)                    | 1(100)                   | 0.00                         |         |
| ST12 1(1)                     | 1(100)                   | 0.00                         |         |
| ST838 1(1)                    | 0(100)                   | 0.00                         |         |
| NSC 3(2)                      | 2(67)                    | 2(67)                        | >0.9999 |

Table 4: Chi-squared distribution of ESBL factors and antibiotic resistance in
different ST-types.
| Resistancer traits | All isolates (n=155) | All ST131 (n=71) | Non H30 (n=36) | H30 (n=36) | ST405 (n=28) | ST168 (n=16) | ST29 (n=13) | ST69 (n=5) | ST95 (n=2) | ST31 (n=2) | ST10 (n=2) |
|-------------------|---------------------|-----------------|--------------|----------|------------|------------|----------|----------|-----------|-----------|-----------|
| ESBL phenotypes   | 65(42)              | 30(42)          | 15(43)       | 15(42)   | 13(46)     | 8(50)      | 7(54)    | 2(40)    | 00        | 00        | 1(50)     |
| blaCTX-M-15       | 57(39)              | 27(38)          | 12(34)       | 15(42)   | 11(39)     | 8(50)      | 6(46)    | 2(40)    | 00        | 00        | 1(50)     |
| blaTEM            | 23(15)              | 8(11)           | 5(14)        | 3(8)     | 5(18)      | 5(31)      | 3(23)    | 2(40)    | 00        | 00        | 00        |
| blaSHV            | 6(4)                | 3(4)            | 1(3)         | 2(6)     | 1(4)       | 2(13)      | 00       | 00       | 00        | 00        | 00        |
| blaOXA            | 10(6)               | 6(8)            | 3(9)         | 3(8)     | 3(11)      | 1(6)       | 00       | 00       | 00        | 00        | 00        |
| blaPS             | 1(0.6)              | 00              | 00           | 00       | 00         | 00         | 00       | 00       | 00        | 00        | 00        |
| Pipericillin      | 7(5)                | 3(4)            | 2(6)         | 0(0)     | 3(11)      | 2(13)      | 00       | 00       | 1(50)     | 00        | 00        |
| Tazobactam        | 99(64)              | 46(65)          | 25(71)       | 21(58)   | 21(75)     | 10(63)     | 9(69)    | 2(40)    | 1(50)     | 00        | 00        |
| Ceftazidime       | 96(62)              | 43(61)          | 20(57)       | 23(64)   | 20(71)     | 10(63)     | 9(69)    | 5(100)   | 1(50)     | 00        | 00        |
| Cefotaxime        | 101(65)             | 46(65)          | 22(63)       | 24(67)   | 20(71)     | 10(63)     | 9(69)    | 5(100)   | 2(100)    | 00        | 1(50)     |
| Ceftiraxone       | 99(64)              | 46(65)          | 25(71)       | 21(58)   | 21(75)     | 10(63)     | 9(69)    | 2(40)    | 1(50)     | 00        | 00        |
| Ciprofloxacin     | 95(61)              | 45(63)          | 23(66)       | 22(61)   | 18(64)     | 13(81)     | 6(46)    | 4(80)    | 2(100)    | 1(50)     | 1(50)     |
| Levofloxacin      | 97(63)              | 45(63)          | 24(69)       | 21(58)   | 19(68)     | 14* (88)   | 6(46)    | 4(80)    | 2(100)    | 1(50)     | 2(100)    |
| Amikacin          | 7(5)                | 4(6)            | 2(6)         | 2(6)     | 00         | 1(6)       | 1(8)     | 1(20)    | 00        | 00        | 00        |
| Gentamicin        | 47(30)              | 21(30)          | 11(31)       | 10(28)   | 10(36)     | 5(31)      | 3(23)    | 1(20)    | 2(100)    | 00        | 1(50)     |
| Amoxicillin-clavulanic acid | 111(72) | 48(68) | 25(71) | 23(64) | 22(79) | 10(63) | 9(69) | 2(40) | 00 | 00 | 00 |
| Trimethoprim sulfonamide | 130(84) | 61(86) | 30(86) | 31(86) | 24(86) | 13(81) | 10(77) | 4(80) | 2(100) | 1(50) | 1(50) |
| Nitrofurantoin    | 9(6)                | 9(13)*          | 6(17)*       | 3(8)     | 00         | 00         | 00       | 00       | 00        | 00        | 00        |
| Fosfomycin        | 15(10)              | 9(13)           | 3(9)         | 6(17)    | 00         | 2(13)      | 00       | 00       | 00        | 1(50)     | 00        |
Table 5: Chi-squared distribution of virulence factor genes in different ST-types.

*P < 0.05, ** P ≤ 0.01, *** P ≤ 0.001
Number of the isolates with traits n(%)  

| Traits | Total n=155 | ST-131 n=71 | Non H30 n=35 | H30 n=36 | ST-05 n=28 | ST-168 n=16 | ST-29 n=13 | ST-69 n=5 | ST-95 n=2 | ST-31 n=2 | ST-10 n=2 | ST-44 n=1 |
|--------|-------------|-------------|--------------|----------|------------|-------------|------------|----------|----------|----------|----------|----------|
| fimH   | 155 (100)   | 71 (100)    | 35 (100)     | 36 (100) | 28 (100)   | 16 (100)    | 13 (100)   | 5 (100)  | 2 (100)  | 2 (100)  | 2 (100)  | 2 (100)  |
| papA   | 20 (13)     | 12 (17)     | 5 (14)       | 7 (19)   | 4 (14)     | 1 (6)       | 0          | 0        | 0        | 0        | 0        | 1 (†)    |
| papC   | 75 (48)     | 33 (46)     | 17 (49)      | 16 (44)  | 15 (54)    | 9 (56)      | 5 (38)     | 3 (60)   | 1 (50)   | 1 (50)   | 0        | 0        |
| papEF  | 37 (24)     | 20 (28)     | 7 (20)       | 13* (36) | 7 (25)     | 3 (19)      | 3 (23)     | 1(20)    | 0        | 0        | 0        | 1(†)     |
| papGI  | 6 (4)       | 2 (3)       | 0           | 2 (6)    | 1 (4)      | 1 (6)       | 0          | 1(20)    | 0        | 0        | 0        | 0        |
| papGII | 70 (45)     | 32 (45)     | 17 (49)     | 15 (42)  | 12 (43)    | 6 (38)      | 4 (31)     | 4(80)    | 2 (100)  | 0        | 2 (100)  | 1(†)     |
| sfa/loc| 20 (13)     | 13* (18)    | 4 (11)      | 9* (25)  | 2 (7)      | 1 (6)       | 1 (8)      | 0        | 1(50)    | 0        | 1(50)    | 0        |
| afa    | 15 (10)     | 7 (10)      | 4 (11)      | 3 (8)    | 6* (21)    | 1 (6)       | 1 (8)      | 0        | 0        | 0        | 0        | 0        |
| bmaE   | 2 (1)       | 1 (1)       | 1 (3)       | 0        | 0          | 1 (6)       | 0          | 0        | 0        | 0        | 0        | 0        |
| fyuA   | 37 (24)     | 12* (17)    | 7 (20)      | 5 (14)   | 10 (36)    | 6 (38)      | 2 (15)     | 2(40)    | 0        | 0        | 2(100)   | 0        |
| iutA   | 86 (55)     | 41 (58)     | 22*** (63)  | 19 (53)  | 14 (50)    | 10 (63)     | 5 (38)     | 3 (60)   | 2 (100)  | 1 (50)   | 2 (100)  | 1(†)     |
| feoB   | 76 (49)     | 28* (39)    | 13 (37)     | 15 (42)  | 12 (43)    | 10 (63)     | 6 (46)     | 4(80)    | 2 (100)  | 1 (50)   | 2 (100)  | 1(†)     |
| kpsmtII| 40 (26)     | 20 (28)     | 9 (26)      | 11 (31)  | 8 (29)     | 2 (13)      | 2 (15)     | 2(40)    | 0        | 0        | 0        | 1(†)     |
| kpsmtIII| 4 (3)       | 2 (3)       | 0           | 2 (6)    | 0          | 0           | 0          | 1(20)    | 0        | 0        | 0        | 0        |
| usp    | 22 (14)     | 13 (18)     | 5 (14)      | 8 (22)   | 2 (7)      | 3 (19)      | 1 (8)      | 0        | 0        | 0        | 1(50)    | 0        |
| hlyA   | 18 (12)     | 8 (11)      | 1 (3)       | 7* (32)  | 5(18)      | 1 (6)       | 1 (8)      | 0        | 1(50)    | 0        | 0        | 0        |
| cdtB   | 11 (7)      | 4 (6)       | 1 (3)       | 3 (8)    | 4(14)      | 1 (6)       | 0          | 0        | 0        | 1(50)    | 0        | 0        |

*P < 0.05, ** P ≤ 0.01, *** P ≤ 0.001

Table 1: Distribution of resistance and virulence traits among different phylogroups of uropathogenic E. coli (N = 155). The p values were calculated by comparing different traits among phylogroups.

Table 2: Distribution of resistance and virulence traits among ESBL and non-ESBL
producing uropathogenic *E. coli* (N = 155). The *p* values were calculated by comparing different traits among ESBL producer’s and non-ESBL producers.

**Table 3:** Phylogenetic and sequence type distribution of co-resistance among uropathogenic *E. coli* (N = 155). The *p* values were calculated by comparing total number of MDR producers and ESBL producers FQR MDR.

**Table 4:** Distribution of antibiotic resistance of uropathogenic *E. coli* (n=155) among different sequence types. The *p* values were calculated by comparing individual STs with each other. The table correlates different traits in vertical columns among different sequence types. The percentages were calculated with reference to total number of sequence types.

**Table 5:** Distribution of virulence traits of uropathogenic *E. coli* (n=155) among different sequence types. The *p* values were calculated by comparing individual STs with each other. The table correlates different traits in vertical columns among different sequence types. The percentages were calculated with reference to total number of sequence types. Table 6:

**Supplementary Files**

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ST, VF and resistance-updated.xlsx