GEORGIAN MEDICAL NEWS

ISSN 1512-0112

NO 1 (370) Январь 2026

ТБИЛИСИ - NEW YORK

ЕЖЕМЕСЯЧНЫЙ НАУЧНЫЙ ЖУРНАЛ

Медицинские новости Грузии

საქართველოს სამედიცინო სიახლენი

GEORGIAN MEDICAL NEWS

Monthly Georgia-US joint scientific journal published both in electronic and paper formats of the Agency of Medical Information of the Georgian Association of Business Press. Published since 1994. Distributed in NIS, EU and USA.

GMN: Georgian Medical News is peer-reviewed, published monthly journal committed to promoting the science and art of medicine and the betterment of public health, published by the GMN Editorial Board since 1994. GMN carries original scientific articles on medicine, biology and pharmacy, which are of experimental, theoretical and practical character; publishes original research, reviews, commentaries, editorials, essays, medical news, and correspondence in English and Russian.

GMN is indexed in MEDLINE, SCOPUS, PubMed and VINITI Russian Academy of Sciences. The full text content is available through EBSCO databases.

GMN: Медицинские новости Грузии - ежемесячный рецензируемый научный журнал, издаётся Редакционной коллегией с 1994 года на русском и английском языках в целях поддержки медицинской науки и улучшения здравоохранения. В журнале публикуются оригинальные научные статьи в области медицины, биологии и фармации, статьи обзорного характера, научные сообщения, новости медицины и здравоохранения. Журнал индексируется в MEDLINE, отражён в базе данных SCOPUS, PubMed и ВИНИТИ РАН. Полнотекстовые статьи журнала доступны через БД EBSCO.

GMN: Georgian Medical News – საქართველოს სამედიცინო სიახლენი – არის ყოველთვიური სამეცნიერო სამედიცინო რეცენზირებადი ჟურნალი, გამოიცემა 1994 წლიდან, წარმოადგენს სარედაქციო კოლეგიისა და აშშ-ის მეცნიერების, განათლების, ინდუსტრიის, ხელოვნებისა და ბუნებისმეტყველების საერთაშორისო აკადემიის ერთობლივ გამოცემას. GMN-ში რუსულ და ინგლისურ ენებზე ქვეყნდება ექსპერიმენტული, თეორიული და პრაქტიკული ხასიათის ორიგინალური სამეცნიერო სტატიები მედიცინის, ბიოლოგიისა და ფარმაციის სფეროში, მიმოხილვითი ხასიათის სტატიები.

ჟურნალი ინდექსირებულია MEDLINE-ის საერთაშორისო სისტემაში, ასახულია SCOPUS-ის, PubMed-ის და ВИНИТИ РАН-ის მონაცემთა ბაზებში. სტატიების სრული ტექსტი ხელმისაწვდომია EBSCO-ს მონაცემთა ბაზებიდან.

WEBSITE

www.geomednews.com

К СВЕДЕНИЮ АВТОРОВ!

При направлении статьи в редакцию необходимо соблюдать следующие правила:

1. Статья должна быть представлена в двух экземплярах, на русском или английском языках, напечатанная через **полтора интервала на одной стороне стандартного листа с шириной левого поля в три сантиметра**. Используемый компьютерный шрифт для текста на русском и английском языках - **Times New Roman** (**Кириллица**), для текста на грузинском языке следует использовать **AcadNusx.** Размер шрифта - **12**. К рукописи, напечатанной на компьютере, должен быть приложен CD со статьей.

2. Размер статьи должен быть не менее десяти и не более двадцати страниц машинописи, включая указатель литературы и резюме на английском, русском и грузинском языках.

3. В статье должны быть освещены актуальность данного материала, методы и результаты исследования и их обсуждение.

При представлении в печать научных экспериментальных работ авторы должны указывать вид и количество экспериментальных животных, применявшиеся методы обезболивания и усыпления (в ходе острых опытов).

4. К статье должны быть приложены краткое (на полстраницы) резюме на английском, русском и грузинском языках (включающее следующие разделы: цель исследования, материал и методы, результаты и заключение) и список ключевых слов (key words).

5. Таблицы необходимо представлять в печатной форме. Фотокопии не принимаются. **Все цифровые, итоговые и процентные данные в таблицах должны соответствовать таковым в тексте статьи**. Таблицы и графики должны быть озаглавлены.

6. Фотографии должны быть контрастными, фотокопии с рентгенограмм - в позитивном изображении. Рисунки, чертежи и диаграммы следует озаглавить, пронумеровать и вставить в соответствующее место текста **в tiff формате**.

В подписях к микрофотографиям следует указывать степень увеличения через окуляр или объектив и метод окраски или импрегнации срезов.

7. Фамилии отечественных авторов приводятся в оригинальной транскрипции.

8. При оформлении и направлении статей в журнал МНГ просим авторов соблюдать правила, изложенные в «Единых требованиях к рукописям, представляемым в биомедицинские журналы», принятых Международным комитетом редакторов медицинских журналов - http://www.spinesurgery.ru/files/publish.pdf и http://www.nlm.nih.gov/bsd/uniform_requirements.html
В конце каждой оригинальной статьи приводится библиографический список. В список литературы включаются все материалы, на которые имеются ссылки в тексте. Список составляется в алфавитном порядке и нумеруется. Литературный источник приводится на языке оригинала. В списке литературы сначала приводятся работы, написанные знаками грузинского алфавита, затем кириллицей и латиницей. Ссылки на цитируемые работы в тексте статьи даются в квадратных скобках в виде номера, соответствующего номеру данной работы в списке литературы. Большинство цитированных источников должны быть за последние 5-7 лет.

9. Для получения права на публикацию статья должна иметь от руководителя работы или учреждения визу и сопроводительное отношение, написанные или напечатанные на бланке и заверенные подписью и печатью.

10. В конце статьи должны быть подписи всех авторов, полностью приведены их фамилии, имена и отчества, указаны служебный и домашний номера телефонов и адреса или иные координаты. Количество авторов (соавторов) не должно превышать пяти человек.

11. Редакция оставляет за собой право сокращать и исправлять статьи. Корректура авторам не высылается, вся работа и сверка проводится по авторскому оригиналу.

12. Недопустимо направление в редакцию работ, представленных к печати в иных издательствах или опубликованных в других изданиях.

При нарушении указанных правил статьи не рассматриваются.

REQUIREMENTS

Please note, materials submitted to the Editorial Office Staff are supposed to meet the following requirements:

1. Articles must be provided with a double copy, in English or Russian languages and typed or compu-ter-printed on a single side of standard typing paper, with the left margin of **3** centimeters width, and **1.5** spacing between the lines, typeface - **Times New Roman** (**Cyrillic**), print size - **12** (referring to Georgian and Russian materials). With computer-printed texts please enclose a CD carrying the same file titled with Latin symbols.

2. Size of the article, including index and resume in English, Russian and Georgian languages must be at least 10 pages and not exceed the limit of 20 pages of typed or computer-printed text.

3. Submitted material must include a coverage of a topical subject, research methods, results, and review.

Authors of the scientific-research works must indicate the number of experimental biological species drawn in, list the employed methods of anesthetization and soporific means used during acute tests.

4. Articles must have a short (half page) abstract in English, Russian and Georgian (including the following sections: aim of study, material and methods, results and conclusions) and a list of key words.

5. Tables must be presented in an original typed or computer-printed form, instead of a photocopied version. **Numbers, totals, percentile data on the tables must coincide with those in the texts of the articles.** Tables and graphs must be headed.

6. Photographs are required to be contrasted and must be submitted with doubles. Please number each photograph with a pencil on its back, indicate author's name, title of the article (short version), and mark out its top and bottom parts. Drawings must be accurate, drafts and diagrams drawn in Indian ink (or black ink). Photocopies of the X-ray photographs must be presented in a positive image in **tiff format**.

Accurately numbered subtitles for each illustration must be listed on a separate sheet of paper. In the subtitles for the microphotographs please indicate the ocular and objective lens magnification power, method of coloring or impregnation of the microscopic sections (preparations).

7. Please indicate last names, first and middle initials of the native authors, present names and initials of the foreign authors in the transcription of the original language, enclose in parenthesis corresponding number under which the author is listed in the reference materials.

8. Please follow guidance offered to authors by The International Committee of Medical Journal Editors guidance in its Uniform Requirements for Manuscripts Submitted to Biomedical Journals publication available online at: http://www.nlm.nih.gov/bsd/uniform_requirements.html
http://www.icmje.org/urm_full.pdf
In GMN style for each work cited in the text, a bibliographic reference is given, and this is located at the end of the article under the title "References". All references cited in the text must be listed. The list of references should be arranged alphabetically and then numbered. References are numbered in the text [numbers in square brackets] and in the reference list and numbers are repeated throughout the text as needed. The bibliographic description is given in the language of publication (citations in Georgian script are followed by Cyrillic and Latin).

9. To obtain the rights of publication articles must be accompanied by a visa from the project instructor or the establishment, where the work has been performed, and a reference letter, both written or typed on a special signed form, certified by a stamp or a seal.

10. Articles must be signed by all of the authors at the end, and they must be provided with a list of full names, office and home phone numbers and addresses or other non-office locations where the authors could be reached. The number of the authors (co-authors) must not exceed the limit of 5 people.

11. Editorial Staff reserves the rights to cut down in size and correct the articles. Proof-sheets are not sent out to the authors. The entire editorial and collation work is performed according to the author's original text.

12. Sending in the works that have already been assigned to the press by other Editorial Staffs or have been printed by other publishers is not permissible.

Articles that Fail to Meet the Aforementioned Requirements are not Assigned to be Reviewed.

ავტორთა საყურადღებოდ!

რედაქციაში სტატიის წარმოდგენისას საჭიროა დავიცვათ შემდეგი წესები:

1. სტატია უნდა წარმოადგინოთ 2 ცალად, რუსულ ან ინგლისურ ენებზე,დაბეჭდილი სტანდარტული ფურცლის 1 გვერდზე, 3 სმ სიგანის მარცხენა ველისა და სტრიქონებს შორის 1,5 ინტერვალის დაცვით. გამოყენებული კომპიუტერული შრიფტი რუსულ და ინგლისურენოვან ტექსტებში - **Times New Roman (Кириллица)**, ხოლო ქართულენოვან ტექსტში საჭიროა გამოვიყენოთ **AcadNusx.** შრიფტის ზომა – 12. სტატიას თან უნდა ახლდეს CD სტატიით.

2. სტატიის მოცულობა არ უნდა შეადგენდეს 10 გვერდზე ნაკლებს და 20 გვერდზე მეტს ლიტერატურის სიის და რეზიუმეების (ინგლისურ, რუსულ და ქართულ ენებზე) ჩათვლით.

3. სტატიაში საჭიროა გაშუქდეს: საკითხის აქტუალობა; კვლევის მიზანი; საკვლევი მასალა და გამოყენებული მეთოდები; მიღებული შედეგები და მათი განსჯა. ექსპერიმენტული ხასიათის სტატიების წარმოდგენისას ავტორებმა უნდა მიუთითონ საექსპერიმენტო ცხოველების სახეობა და რაოდენობა; გაუტკივარებისა და დაძინების მეთოდები (მწვავე ცდების პირობებში).

4. სტატიას თან უნდა ახლდეს რეზიუმე ინგლისურ, რუსულ და ქართულ ენებზე არანაკლებ ნახევარი გვერდის მოცულობისა (სათაურის, ავტორების, დაწესებულების მითითებით და უნდა შეიცავდეს შემდეგ განყოფილებებს: მიზანი, მასალა და მეთოდები, შედეგები და დასკვნები; ტექსტუალური ნაწილი არ უნდა იყოს 15 სტრიქონზე ნაკლები) და საკვანძო სიტყვების ჩამონათვალი (key words).

5. ცხრილები საჭიროა წარმოადგინოთ ნაბეჭდი სახით. ყველა ციფრული, შემაჯამებელი და პროცენტული მონაცემები უნდა შეესაბამებოდეს ტექსტში მოყვანილს.

6. ფოტოსურათები უნდა იყოს კონტრასტული; სურათები, ნახაზები, დიაგრამები - დასათაურებული, დანომრილი და სათანადო ადგილას ჩასმული. რენტგენოგრამების ფოტოასლები წარმოადგინეთ პოზიტიური გამოსახულებით **tiff** ფორმატში. მიკროფოტოსურათების წარწერებში საჭიროა მიუთითოთ ოკულარის ან ობიექტივის საშუალებით გადიდების ხარისხი, ანათალების შეღებვის ან იმპრეგნაციის მეთოდი და აღნიშნოთ სურათის ზედა და ქვედა ნაწილები.

7. სამამულო ავტორების გვარები სტატიაში აღინიშნება ინიციალების თანდართვით, უცხოურისა – უცხოური ტრანსკრიპციით.

8. სტატიას თან უნდა ახლდეს ავტორის მიერ გამოყენებული სამამულო და უცხოური შრომების ბიბლიოგრაფიული სია (ბოლო 5-8 წლის სიღრმით). ანბანური წყობით წარმოდგენილ ბიბლიოგრაფიულ სიაში მიუთითეთ ჯერ სამამულო, შემდეგ უცხოელი ავტორები (გვარი, ინიციალები, სტატიის სათაური, ჟურნალის დასახელება, გამოცემის ადგილი, წელი, ჟურნალის №, პირველი და ბოლო გვერდები). მონოგრაფიის შემთხვევაში მიუთითეთ გამოცემის წელი, ადგილი და გვერდების საერთო რაოდენობა. ტექსტში კვადრატულ ფჩხილებში უნდა მიუთითოთ ავტორის შესაბამისი N ლიტერატურის სიის მიხედვით. მიზანშეწონილია, რომ ციტირებული წყაროების უმეტესი ნაწილი იყოს 5-6 წლის სიღრმის.

9. სტატიას თან უნდა ახლდეს: ა) დაწესებულების ან სამეცნიერო ხელმძღვანელის წარდგინება, დამოწმებული ხელმოწერითა და ბეჭდით; ბ) დარგის სპეციალისტის დამოწმებული რეცენზია, რომელშიც მითითებული იქნება საკითხის აქტუალობა, მასალის საკმაობა, მეთოდის სანდოობა, შედეგების სამეცნიერო-პრაქტიკული მნიშვნელობა.

10. სტატიის ბოლოს საჭიროა ყველა ავტორის ხელმოწერა, რომელთა რაოდენობა არ უნდა აღემატებოდეს 5-ს.

11. რედაქცია იტოვებს უფლებას შეასწოროს სტატია. ტექსტზე მუშაობა და შეჯერება ხდება საავტორო ორიგინალის მიხედვით.

12. დაუშვებელია რედაქციაში ისეთი სტატიის წარდგენა, რომელიც დასაბეჭდად წარდგენილი იყო სხვა რედაქციაში ან გამოქვეყნებული იყო სხვა გამოცემებში.

აღნიშნული წესების დარღვევის შემთხვევაში სტატიები არ განიხილება.

GEORGIAN MEDICAL NEWS
NO 1 (370) 2026

Содержание:

GEORGIAN MEDICAL NEWS
No 1 (370) 2026

PREVALENCE, PHYLOGENETIC DIVERSITY, AND ANTIMICROBIAL RESISTANCE OF UROPATHOGENIC *ESCHERICHIA COLI IN* GEORGIA

Rigvava Sophio[1,2]*, Kusradze Ia[1,3], Karumidze Natia[1,3], Kharebava Shorena[4], Tchgkonia Irina[1], Tatrishvili Nino[1], Goderdzishvili Marina[1].

[1]*Laboratory of General Microbiology, George Eliava Institute of Bacteriophages, Microbiology and Virology, Tbilisi, Georgia.*

[2]*Caucasus International University, Faculty of Medicine, Tbilisi, Georgia.*

[3]*European University, Tbilisi, Georgia.*

[4]*Zurich Medical Research Centre, Tbilisi, Georgia.*

Abstract.

Background: Uropathogenic *Escherichia coli* (UPEC) represents the leading cause of urinary tract infections (UTIs) worldwide and remains a growing clinical concern due to increasing antimicrobial resistance. Data describing the molecular epidemiology of UPEC in Georgia are limited.

Methods: Ninety *E. coli* isolates obtained from patients with genitourinary infections were analyzed. Species identification was confirmed by 16S rRNA gene sequencing. UPEC strains were identified by PCR detection of virulence-associated genes (c3509, c3686 (yrbH), and chuA). Phylogenetic grouping was performed using the Clermont multiplex PCR method. Antimicrobial susceptibility testing was carried out by disk diffusion in accordance with EUCAST guidelines.

Results: Eighty-one isolates (90%) were classified as UPEC based on the presence of at least one virulence marker. Twenty-nine strains carried all three genes, whereas 22 harbored a single marker. Phylogenetic analysis demonstrated a predominance of group B2, with additional representation from groups A, B1, F, and clade I/II; several isolates remained unclassified. Resistance rates among UPEC strains were highest for trimethoprim (55%), ciprofloxacin (47%), and ceftriaxone (42%). Nitrofurantoin (5% resistance) and fosfomycin (3% resistance) remained highly effective. Notably, B2 strains exhibited higher frequencies of trimethoprim and ciprofloxacin resistance compared with non-B2 strains.
Conclusion: UPEC strains circulating in Georgia exhibit marked phylogenetic diversity but relatively low levels of multidrug resistance. Continued surveillance is warranted to support evidence-based antimicrobial therapy and stewardship.

Key words. Uropathogenic *Escherichia coli*, UPEC, phylogenetic groups, antimicrobial resistance.

Introduction.

Urinary tract infections are among the most frequently diagnosed bacterial infections in both community and hospital settings, imposing a substantial burden on healthcare systems worldwide affecting about 150 million people globally each year [1]. The majority of UTIs are caused by uropathogenic *Escherichia coli*, a subgroup of extraintestinal pathogenic *E. coli* characterized by specific virulence determinants that facilitate colonization and persistence within the urinary tract [2,3]. These determinants include adhesins, toxins, iron-acquisition systems, and the ability to form biofilms, all of which contribute to disease severity and recurrence. 11% of women over the age of 18 have a UTI episode every year, and that 40% of women will have at least one UTI in their lifetime. The three different types of symptomatic UTIs, such are: urosepsis syndrome, pyelonephritis, and cystitis—are categorized according to severity. Factors that increase an individual's susceptibility to UPEC infections include female anatomy (shorter urethra), sexual activity, the use of certain contraceptives, urinary tract abnormalities, and compromised immune function. UPEC can cause a range of UTI symptoms, including frequent and painful urination, cloudy or bloody urine, and lower abdominal discomfort. UPEC possesses a variety of virulence factors that enable it to adhere to and invade the cells lining the urinary tract. These factors include fimbriae (such as type 1 and P fimbriae), which allow the bacteria to attach to specific receptors on the surface of bladder cells. UPEC produces a range of virulence factors that contribute to its ability to cause infection. These factors include toxins, such as hemolysin and cytotoxic necrotizing factor 1 (CNF1), which can damage host cells and promote bacterial survival. UPEC has the ability to form biofilms, which are complex communities of bacteria encased in a protective matrix [4,5]. Biofilms provide UPEC with increased resistance to antibiotics and host immune responses, making them more difficult to eradicate. UPEC strains have shown an increasing resistance to commonly used antibiotics, making treatment more challenging. This resistance is often mediated by the presence of antibiotic resistance genes carried on plasmids or other mobile genetic elements [6,7].

UPEC strains are distributed across multiple phylogenetic lineages, with certain groups. The phylogeny of *E. coli* is based on genetic variations and evolutionary relationships among different strains. While UPEC strains can be found within different phylogroups, particularly phylogroup B2 and D being more commonly associated with extraintestinal infections and B2 is considered highly virulent. B2 strains often possess multiple virulence factors, allowing them to effectively colonize and invade the urinary tract. UPEC strains belonging to phylogroup D are also commonly associated with urinary tract infections. While they may not possess the same extensive array of virulence factors as B2 strains, they still exhibit urovirulence traits.

The phylogenetic background of UPEC has been linked to both virulence potential and antimicrobial resistance patterns, highlighting the importance of molecular epidemiological studies. In parallel, the global increase in antimicrobial resistance among UPEC strains has complicated the management of UTIs and emphasized the need for region-specific surveillance data. It's important to keep in mind that our understanding of the

phylogenetic diversity of UPEC is constantly expanding as new research emerges [8,9].

Despite the clinical relevance of UTIs, information on the prevalence, phylogenetic structure, and antibiotic susceptibility of UPEC isolates in Georgia remains scarce. The present study was designed to characterize UPEC strains isolated from genitourinary infections in Georgian patients, focusing on virulence gene carriage, phylogenetic distribution, and antimicrobial resistance profiles.

Materials and Methods.

Bacterial strains: A total 90 *E. coli* isolates collected over a three-month period from patients with genitourinary infections were included. *E. coli* bacterial strains were provided by the Zurich Medical Research Centre and "Diagnosis 90" LLC,. The isolates were obtained from a day clinic diagnostic center, primarily from patients with chronic genitourinary infections. Reference strains: *Escherichia coli* ATCC 25922, ATCC8739, O111 and O26 (G. Eliava Institute Collection) were used as control strains. All strains were cultured on Luria-Bertani (LB) medium (Becton Dickinson) at 37°C for 24 hours.

Identification and Genetic characterization of *E.coli*. DNA Isolation by 16s rRNA Sequencing: Genomic DNA was extracted using Commercial purification kit Invitrogen PureLink Genomic DNA Mini Kit according to the manufacturer's recommendation. Species confirmation was performed by amplification and sequencing of the v1-v4 region of the 16S rRNA gene. PCR was performed with the following conditions: initial incubation for 30 min at 95°C followed by 35 cycles of 15 s at 94°C, 15 s at 55°C, 30 s at 72°C with a final incubation for 10 min at 72°C. PCR products were purified and Sanger sequencing was performed. Sequenced data were analyzed and assembled by CodonCode Aligner 11.0.1. Blastn was used for comparison of all 90 bacterial strains 16s eRNA sequencing fasta with a nucleotide database. MEGA-X (v10.0.1) software was used for construction of phylogenetic tree (Neighbor-joining, bootstrap method – 500 replications).

Detection of Uropathogenic *E.coli*: Isolates were screened for the presence of virulence genes: c3509, c3686 (yrbH) and chuA by PCR. Detection of at least one marker gene was considered indicative of uropathogenic strain [3]. For detection of those genes, PCR reactions were performed under the following condition: initial denaturation for 30 s. at 95 °C; 30 cycles consisting of 7 s. at 95 °C, 12 s. at 60 °C, and 12 s. at 75°C; and extension for 30 s. at 75°C. All amplification products were analyzed by electrophoresis in 1.0% (wt/vol) agarose gels, followed by ethidium bromide staining, distaining (1× Tris-acetate) and visualization under UV.

Phylo-grouping of uropathogenic *E. coli*: The distribution of phylogenetic groups among *E. coli* isolates was determined as described by Clermont and colleagues [3,10,11]. All PCR reactions were carried out in a 20 ml volume containing 2 ml of 10X buffer (supplied with Taq polymerase), 2 mM each dNTP, 2 U of Taq polymerase, 3 ml of bacterial lysate or 2 ml of DNA (at approximately 100 ng ml-1) and the appropriate primers. PCR reactions were performed under the following conditions: denaturation 4 min at 94°C, 30 cycles of 5 s at 94°C and 20 s at 57°C (group E) or 59°C (quadruplex and group C), and a final extension step of 5 min at 72°C. Primers used in this study are listed in supplementary table 1.

Antibiotic susceptibility testing: The antibiotic susceptibility of the *E. coli* strains was evaluated using the disc diffusion method. The following antibiotics were tested: Ceftriaxone (30 μg), Ciprofloxacin (5 μg), Trimethoprim (5 μg), Nitrofurantoin (100 μg), Norfloxacin (10 μg), Fosfomycin (200 μg), and Gentamicin (10 μg). The results were interpreted according to the EUCAST clinical breakpoints.

Results.

Genetic Characterization of *E. coli*:

All 90 isolates were confirmed as *E. coli* by 16S rRNA sequencing. The phylogenetic groups of all 90 *E. coli* strains were determined using specific primers and the Clermont method for assigning isolates to phylogroups. The frequency of each phylogenetic group among the 90 strains was as follows: 6 strains (6.6%) belonged to the A phylogroup, 4 strains (4.4%) belonged to the B1 phylogroup, 58 strains (64.4%) belonged to the B2 phylogroup, 3 strains (3.3%) belonged to the F phylogroup, and 7 strains (7.7%) belonged to Clade I/II. Additionally, 12 strains (13.3%) could not be classified (Figure 1). These unclassified strains may represent atypical or divergent lineages of *E. coli*, highlighting the genetic diversity within isolates from the genitourinary tract. Their presence underscores the need for continuous evaluation of phylogenetic schemes, as some strains may not fit traditional Clermont categories. These results indicate that although all strains were isolated from the genitourinary system over a three-month period, they show considerable phylogenetic diversity.

All 90 *E. coli* genomes were screened for UPEC-specific virulence factor markers. Of these, 81 strains (90%) contained at least one of the three UPEC-specific genes (c3508, c3686, or chuA), and were classified as UPEC. The remaining 9 strains (10%) did not carry any UPEC-specific genes. The distribution of these virulence genes among the 81 UPEC strains is shown in Figure 2. Percentages related to virulence gene presence are calculated using 81 UPEC strains (Figure 2 and Table 2S).

Antibiotic susceptibility testing:

Antibiotic susceptibility was studied on 90 strains of *Escherichia coli*. The following antibiotics were used: (ceftriaxone (30 μg); ciprofloxacin (5 μg); trimethoprim (5 μg); nitrofurantoin (100 μg); norfloxacin (10 μg); fosfomycin (200 μg); gentamicin (10 μg)). It should be noted that antibiotic susceptibility testing of isolated bacteria showed that complete resistance to antibiotics was rare, only 2 strains showed resistance to 6 of the antibiotics, but retained sensitivity to nitrofurantoin. The least resistance was revealed to nitrofurantoin (2 out of 90 strains were only resistant) (Figure 3 and Table 1S).

Discussion.

Uropathogenic *Escherichia coli* remains the predominant causative agent of urinary tract infections, owing to its ability to persist outside the intestinal environment and adapt to the conditions of the urinary tract. While *E. coli* is a natural component of the gut microbiota, UPEC strains possess specialized virulence attributes that distinguish them from

Table 1. *Primers used in this study.*

primers of UPEC					
Target strain	**primer name**	**primer sequence**	**protuct size**	**target gene**	**reference**
Uropathogenic E. coli	8F	ACAATCCGCCACCATCCAG	208	c3509	[3]
	8R	CTCTCCACCGGAGAGTGTT			
	9F	TTGCACCAACAACGTCTACC	259	c3686	
	9R	TCTGCGTCTTCTACCATCAC			
	10F	GCTACCGCGATAACTGTCAT	221	chuA	
	10R	TGGAGAACCGTTCCACTCTA			
E. coli quadruplex phylo-typing					
E. coli groups	primer name	primer sequence	protuct size	target gene	reference
Quadruplex	chuA.1b	ATGGTACCGGACGAACCAAC	288	chuA	[10]
	chuA.2	TGCCGCCAGTACCAAAGACA			
	yjaA.1b	CAAACGTGAAGTGTCAGGAG	211	yjaA	
	yjaA.2b	AATGCGTTCCTCAACCTGTG			
	TspE4C2.1b	CACTATTCGTAAGGTCATCC	152	TspE4.C2	
	TspE4.C2.2b	AGTTTATCGCTGCGGGTCGC			
	AceK.f	AACGCTATTCGCCAGCTTGC	400	arpA	
	ArpA1.r	TCTCCCCATACCGTACGCTA			
Group E	ArpAgpE.f	GATTCCATCTTGTCAAAATATGCC	301	arpA	
	ArpAgpE.r	GAAAAGAAAAAGAATTCCCAAGAG			
Group C	trpAgpC.1	AGTTTTATGCCCAGTGCGAG	219	trpA	
	trpAgpC.2	TCTGCGCCGGTCACGCCC			
Internal control	trpBA.f	CGGCGATAAAGACATCTTCAC	489	trpA	
	trpBA.r	GCAACGCGGCCTGGCGGAAG			
16s rRNA sequencing v1-v4 region					
Target strain	primer name	primer sequence	protuct size	target gene	reference
	27F	AGRGTTTGATCMTGGCTCA	800	16s rRNA	[11]
	806R	GGACTACNVGGGTWTCTAAT			

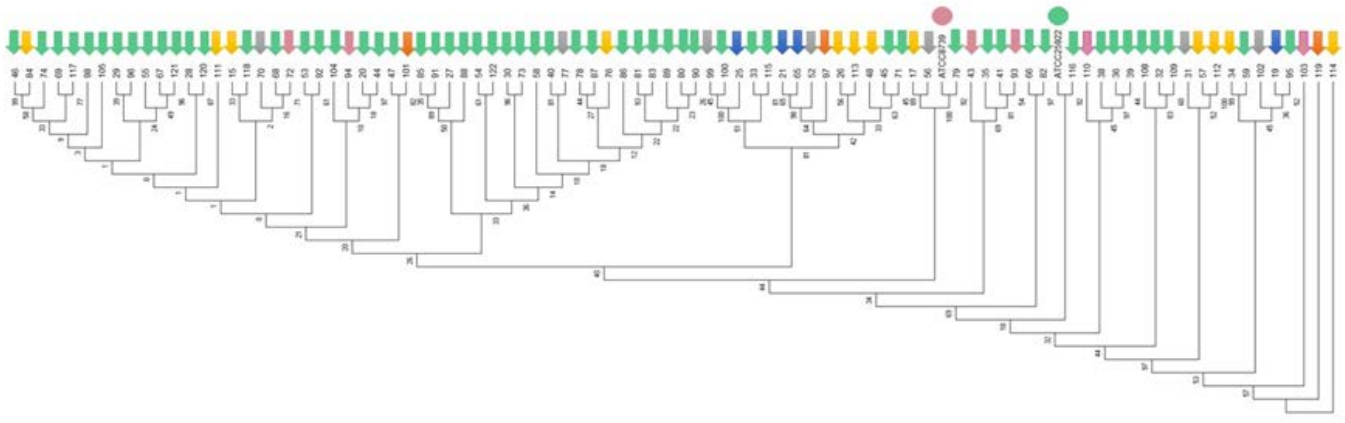

Figure 1. *Phylogenetic tree of 90 bacterial strains of E. coli contracted by v1-v4 region of 16s rRNA. Phylo groups are color-coded: green- B2; pink - A; orange-F; blue-B1; grey- clade I/II; yellow- unclassified.*

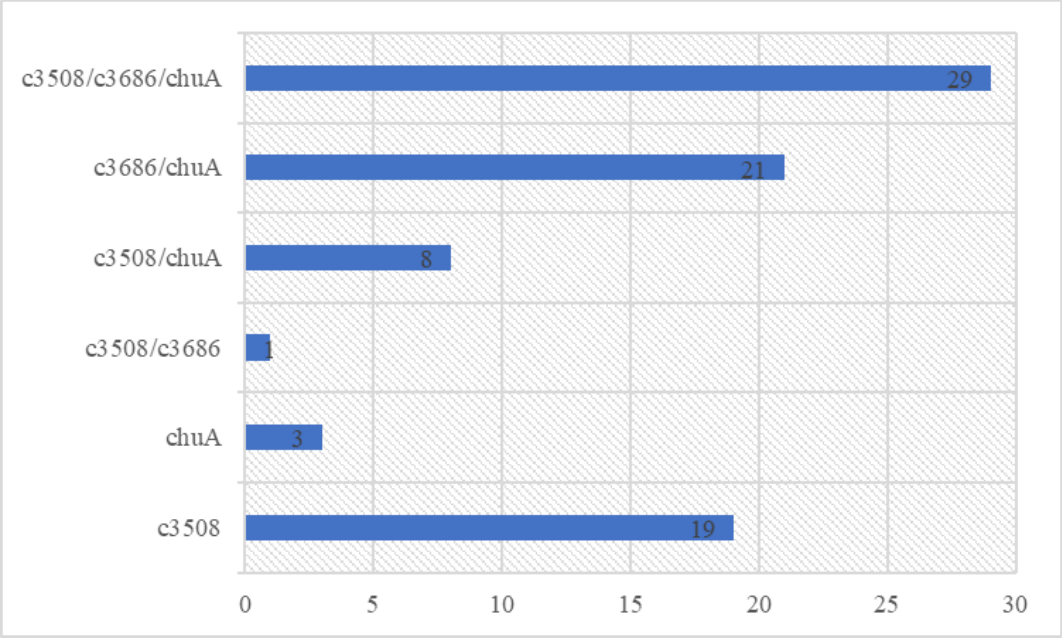

Figure 2. *Distribution Genes determining uropathogenicity in E. coli bacterial strains.*

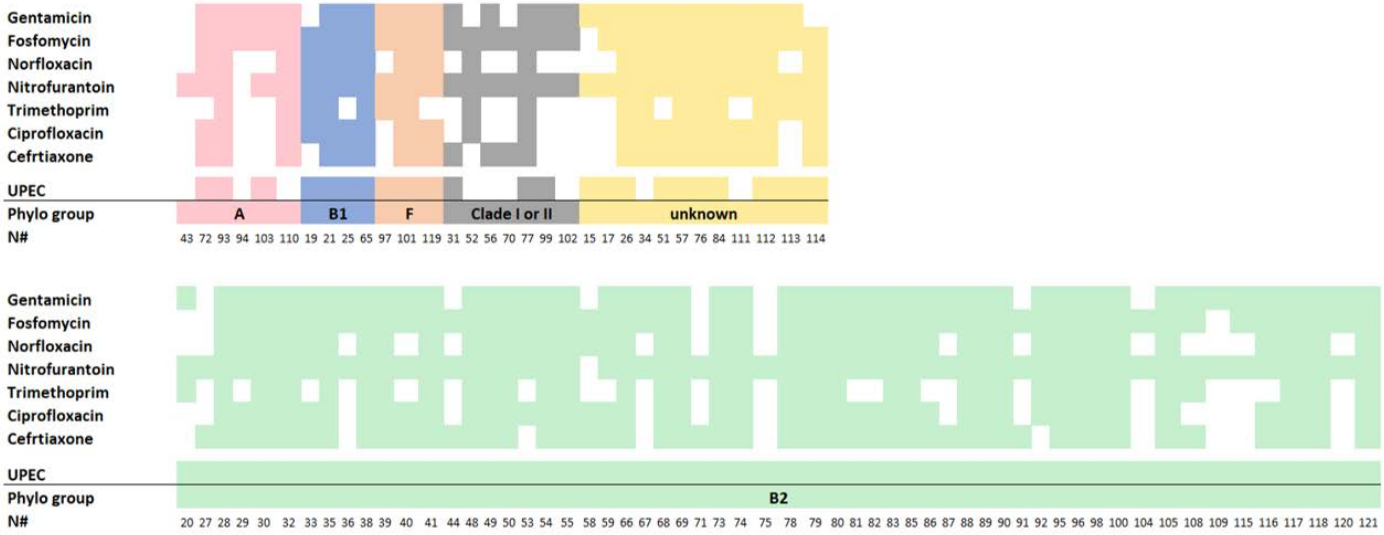

Figure 3. *Antibiotic susceptibility of 90 clinical strains of E. coli. White boxes indicated of Resistance and colored one-Sensitive strains.*

commensal isolates and enable successful colonization, invasion, and survival within the host urinary system. These characteristics underline the importance of studying UPEC not only as a clinical pathogen but also as a genetically and phenotypically diverse subgroup of *E. coli* [12].

In the present study, 90 *E. coli* isolates obtained from genitourinary infections in Georgia were investigated to determine their uropathogenic potential, phylogenetic background, and antimicrobial susceptibility. Using a virulence gene-based approach, 81 isolates were classified as UPEC [10], indicating a high prevalence of uropathogenic strains among clinical *E. coli* isolates. Notably, a substantial proportion of these strains carried multiple UPEC-associated genes, suggesting an increased pathogenic capacity and supporting their clinical relevance.

The chuA gene, which encodes an outer membrane protein involved in heme utilization, was detected in the majority of UPEC isolates. This finding is consistent with previous reports highlighting the role of iron acquisition systems in UPEC survival and colonization within the urinary tract [3,13]. The frequent presence of chuA among Georgian isolates suggests that iron metabolism represents an important virulence strategy in this regional UPEC population and may contribute to infection persistence.

Phylogenetic analysis revealed considerable diversity among the studied isolates. As anticipated, phylogroup B2 predominated, reflecting its well-established association with extraintestinal pathogenic *E. coli*. Nevertheless, UPEC strains were also distributed among several other phylogenetic groups, including A, B1, F, and clade I/II, emphasizing the

heterogeneous nature of UPEC populations. The presence of uropathogenic strains outside the classical B2 lineage indicates that urovirulence is not restricted to a single evolutionary background and may arise through the acquisition of virulence determinants across diverse lineages [13-15].

The observation that non-uropathogenic isolates were largely confined to phylogroup A and clade I/II further supports the link between phylogenetic background and pathogenic potential [12,16]. However, the inability to classify a subset of isolates also highlights the limitations of PCR-based phylogrouping methods and suggests the existence of genetically divergent strains within the local *E. coli* population.

Phylogenetic group distributions and antimicrobial resistance patterns of UPEC have been characterized in several countries adjacent to Georgia. In Iran [17], systematic reviews have shown that phylogroups B2 and D are predominant among UPEC isolates and that certain phylogroups exhibit higher antibiotic resistance than others, underscoring differences in epidemiological traits across regions. Whole genome sequencing data from Armenia have identified ESBL producing UPEC lineages (such as ST127) carrying both virulence and resistance genes, indicating the presence of genetically related UPEC strains across the Caucasus region [18]. Additionally, global analyses demonstrate that phylogenetic background often correlates with virulence gene carriage and resistance profiles, particularly in groups B2 and D [19]. Our findings from Georgian isolates — showing B2 predominance and specific resistance trends — align with these regional and global patterns, while also highlighting the need for localized surveillance and statistical association analyses between phylogeny, virulence markers, and phenotypic resistance.

Antimicrobial susceptibility testing demonstrated that, despite global concerns regarding increasing resistance, UPEC isolates in this study were not characterized by extensive multidrug resistance. Resistance was most frequently observed to trimethoprim, ciprofloxacin, and ceftriaxone, reflecting commonly reported resistance patterns for these agents. In contrast, nitrofurantoin and fosfomycin remained highly effective, with resistance detected in only a small number of isolates and no strain exhibiting resistance to both drugs simultaneously. These findings are clinically significant, as nitrofurantoin and fosfomycin are widely recommended for the treatment of uncomplicated urinary tract infections. Their preserved activity against UPEC isolates in Georgia supports their continued use as first-line therapeutic options.

Conclusion.

Overall, this study provides valuable insight into the molecular epidemiology and antimicrobial susceptibility of UPEC strains circulating in Georgia. The results emphasize the importance of region-specific surveillance data to inform empiric treatment decisions and reinforce the need for sustained antimicrobial stewardship efforts. Continued investigation into the genetic and phenotypic characteristics of UPEC will be essential for anticipating emerging resistance trends and optimizing the management of urinary tract infections.

Funding.

This work was supported by a grant from the Eliava foundation. Project N.2450/1.

Declaration of Competing Interests.

All authors declare that they have no relevant financial or non-financial interests to disclose.

Author's contribution.

All authors contributed to the study conception and design. The study was designed, directed and coordinated by S.R., I.K.,

All tasks and methodology were performed by S.R., I.K., Sh.K., M.G.,

The main text of the paper was written by S.R and improved and revised by S.R., I.K.; visualization and revision were done by S. R. and I.K., N.K

Investigation was performed by S.R., N.K., I. Tch., N.T.

Writing-editing was done by S.R., M.G., I.K.

Sequence analysis and interpretation of data by I.K., N.K.

All authors have read and agreed to the given version the manuscript.

Ethics approval.

This is an observational study. Ethical Approval- not applicable.

Consent to publish.

All authors have read and confirm their agreement for the publication of the provided version of the manuscript.

REFERENCES

1. Mancuso G, Midiri A, Gerace E, et al. Urinary Tract Infections: The Current Scenario and Future Prospects. Pathog Basel Switz. 2023;12.

2. Vila J, Sáez-López E, Johnson JR, et al. *Escherichia coli*: an old friend with new tidings. FEMS Microbiol Rev. 2016;40:437-463.

3. Brons JK, Vink SN, de Vos MGJ, et al. Fast identification of *Escherichia coli* in urinary tract infections using a virulence gene based PCR approach in a novel thermal cycler. J Microbiol Methods. 2020;169:105799.

4. Terlizzi ME, Gribaudo G, Maffei ME. UroPathogenic *Escherichia coli* (UPEC) Infections: Virulence Factors, Bladder Responses, Antibiotic, and Non-antibiotic Antimicrobial Strategies. Front Microbiol. 2017;8:1566.

5. Muriuki CW, Ogonda LA, Kyanya C, et al. Phenotypic and Genotypic Characteristics of Uropathogenic *Escherichia coli* Isolates from Kenya. Microb Drug Resist Larchmt N. 2022;28:31-38.

6. van Driel AA, Notermans DW, Meima A, et al. Antibiotic resistance of *Escherichia coli* isolated from uncomplicated UTI in general practice patients over a 10-year period. Eur J Clin Microbiol Infect Dis Off Publ Eur Soc Clin Microbiol. 2019;38:2151-8.

7. Lee DS, Lee SJ, Choe HS. Community-Acquired Urinary Tract Infection by *Escherichia coli* in the Era of Antibiotic Resistance. BioMed Res Int. 2018;2018:7656752.

8. Rodrigues IC, Rodrigues SC, Duarte FV, et al. The Role of Outer Membrane Proteins in UPEC Antimicrobial Resistance: A Systematic Review. Membranes. 2022;12.
9. Bunduki GK, Heinz E, Phiri VS, et al. Virulence factors and antimicrobial resistance of uropathogenic *Escherichia coli* (UPEC) isolated from urinary tract infections: a systematic review and meta-analysis. BMC Infect Dis. 2021;21:753.
10. Clermont O, Christenson JK, Denamur E, et al. The Clermont *Escherichia coli* phylo-typing method revisited: improvement of specificity and detection of new phylo-groups. Environ Microbiol Rep. 2013;5:58-65.
11. Abellan-Schneyder I, Matchado MS, Reitmeier S, et al. Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing. mSphere. 2021;6.
12. Coura FM, Diniz S de A, Silva MX, et al. Phylogenetic Group Determination of *Escherichia coli* Isolated from Animals Samples. Scientific World Journal. 2015;2015:258424.
13. Sy BM, Tree JJ. The Small RNA CyaR Activates Translation of the Outer Membrane Haem Receptor chuA in Enterohemorrhagic *Escherichia coli*. Front Microbiol. 2022;13:821196.
14. Iranpour D, Hassanpour M, Ansari H, et al. Phylogenetic groups of *Escherichia coli* strains from patients with urinary tract infection in Iran based on the new Clermont phylotyping method. BioMed Res Int. 2015;2015:846219.
15. Shah C, Baral R, Bartaula B, et al. Virulence factors of uropathogenic *Escherichia coli* (UPEC) and correlation with antimicrobial resistance. BMC Microbiol. 2019;19:204.
16. Zhao X, Lv Y, Adam FEA, et al. Comparison of Antimicrobial Resistance, Virulence Genes, Phylogroups, and Biofilm Formation of *Escherichia coli* Isolated from Intensive Farming and Free-Range Sheep. Front Microbiol. 2021;12:699927.
17. Halaji M, Fayyazi A, Rajabnia M, et al. Phylogenetic Group Distribution of Uropathogenic *Escherichia coli* and Related Antimicrobial Resistance Pattern: A Meta-Analysis and Systematic Review. Front Cell Infect Microbiol. 2022;12:790184.
18. Cave R, Ter-Stepanyan MM, Kotsinyan N, et al. An Emerging Lineage of Uropathogenic Extended Spectrum β-Lactamase *Escherichia coli* ST127. Microbiol Spectr. 2022;10:e0251122.
19. Yazdanpour Z, Tadjrobehkar O, Shahkhah M. Significant association between genes encoding virulence factors with antibiotic resistance and phylogenetic groups in community acquired uropathogenic *Escherichia coli* isolates. BMC Microbiol. 2020;20:241.

Table 2. *Percentages related to virulence gene presence are calculated using 81 UPEC strains.*

#	Strain	source of Isolation	Antibiotic susceptibility							Phylogenetic grouping						Phylogenetic group	UPEC marker genes			UPEC
			ceftriaxone (30 µg)	ciprofloxacin (5 µg)	trimethoprim (5 µg)	nitrofuranthion (100 µg)	norfloxacin (10 µg)	fosfomycin (200 µg)	gentamicin (10 µg)	QP-11-chuA	QP-12-yjaA	QP-13-TspE4.C2	QP-14-arpA	GE-15-arpA	GF-16-trpA		c3509	c3686	chuA	
15	E. coli	Urine	6(R))	6(R)	6(R)	20	6(R)	6(R)	24	N (no)	Y (yes)	Y	Y			unclassifed	Y	N	N	UPEC
17	E. coli	Urine	6(R)	6(R)	6(R)	20	6(R)	29	24	N	Y	Y	Y			unclassifed	Y	N	N	UPEC
19	E. coli	Urine	6(R)	35	23	24	30	29	6(R)	N	N	Y	Y			B1	Y	N	N	UPEC
20	E. coli	Urine	11(R)	6(R)	28	29	6(R)	13(R)	24	Y	Y	Y	Y			B2	Y	Y	Y	UPEC
21	E. coli	Urine	29	30	25	23	29	30	24	N	Y	Y	N			B1	Y	N	N	UPEC
25	E. coli	Urine	33	30	6(R)	25	26	30	25	N	N	Y	Y			B1	Y	N	N	UPEC
26	E. coli	Urine	29	30	34	25	30	29	23	N	Y	Y	Y			unclassifed	Y	N	N	UPEC
27	E. coli	Urine	32	6(R)	6(R)	22	6(R)	11(R)	6(R)	Y	N	Y	N			B2	Y	Y	Y	UPEC
28	E. coli	Urine	32	32	24	24	30	30	20	Y	Y	Y	N			B2	Y	Y	Y	UPEC
29	E. coli	Urine	32	34	6(R)	23	30	25	23	Y	Y	Y	N			B2	Y	Y	Y	UPEC
30	E. coli	Urine	30	30	24	25	29	30	24	N	N	Y	N			B2	Y	N	N	UPEC
31	E. coli	Urine	30	12(R)	6(R)	25	8(R)	28	23	N	Y	N	N			clade I or II	Y	N	N	UPEC
32	E. coli	Urine	34	32	25	22	32	30	22	Y	Y	Y	N			B2	N	Y	Y	UPEC
33	E. coli	Urine	32	30	6(R)	24	32	30	23	Y	N	Y	N			B2	Y	N	Y	UPEC
34	E. coli	Urine	34	40	25	25	40	30	25	N	Y	Y	N			unclassifed	N	N	N	
35	E. coli	Urine	32	26	27	26	23	28	24	Y	Y	Y	N			B2	Y	Y	Y	UPEC
36	E. coli	Urine	10 (R)	6(R)	6(R)	25	6(R)	29	26	Y	Y	Y	N			B2	Y	Y	Y	UPEC
38	E. coli	Urine	30	29	24	25	30	29	23	Y	Y	Y	N			B2	Y	Y	Y	UPEC
39	E. coli	Urine	30	28	24	25	30	29	23	Y	Y	Y	N			B2	Y	Y	Y	UPEC
40	E. coli	Urine	34	26	6(R)	24	21(R)	26	23	Y	Y	N	N			B2	Y	N	Y	UPEC
41	E. coli	Urine	30	32	26	25	32	27	24	Y	Y	N	N			B2	N	N	Y	UPEC
43	E. coli	Urine	15(R)	12(R)	6(R)	26	10(R)	6(R)	14(R)	N	Y	N	Y		N	A	N	N	N	
44	E. coli	Urine	28	6(R)	6(R)	24	6(R)	29	8(R)	Y	Y	Y	N			B2	N	Y	Y	UPEC
45	E. coli	Urine	30	30	26	22	26	25	22	Y	Y	N	N			B2	N	Y	Y	UPEC
46	E. coli	Urine	32	34	24	25	28	26	22	Y	Y	Y	N			B2	N	Y	Y	UPEC
47	E. coli	Urine	32	40	25	20	32	26	20	Y	Y	Y	N			B2	N	Y	Y	UPEC
48	E. coli	Urine	30	30	6(R)	20	25	26	20	N	Y	Y	Y			unclassifed	Y	N	N	UPEC
52	E. coli	Urine	6(R)	30	26	26	25	26	10(R)	N	Y	N	N			clade I or II	N	N	N	
53	E. coli	Urine	6(R)	21(R)	6(R)	25	18(R)	25	24	Y	Y	N	N			B2	Y	Y	Y	UPEC
54	E. coli	Urine	35	38	25	26	26	26	21	Y	Y	N	N			B2	Y	Y	Y	UPEC
55	E. coli	Urine	30	38	24	25	32	26	20	Y	Y	Y	N			B2	Y	Y	Y	UPEC

56	E. coli	Urine	31	6(R)	6(R)	25	6(R)	25	23	N	Y	N	N			clade I or II	N	N	N	
57	E. coli	Urine	30	40	25	22	32	26	22	N	Y	Y	N			unclassifed	Y	N	N	UPEC
58	E. coli	Urine	35	38	6(R)	10(R)	33	24	8(R)	Y	Y	N	N			B2	Y	Y	Y	UPEC
59	E. coli	Urine	32	36	6(R)	24	30	25	24	Y	Y	Y	N			B2	Y	Y	Y	UPEC
65	E. coli	Urine	35	32	27	25	26	30	22	N	N	Y	Y			B1	Y	N	N	UPEC
66	E. coli	Urine	32	30	22	23	30	34	22	Y	Y	Y	N			B2	Y	Y	Y	UPEC
67	E. coli	Urine	6(R)	6(R)	6(R)	25	6(R)	26	21	Y	Y	Y	N			B2	Y	Y	Y	UPEC
68	E. coli	Urine	31	30	25	23	30	28	22	Y	Y	N	N			B2	N	N	Y	UPEC
69	E. coli	Urine	28	30	25	24	26	28	20	Y	Y	Y	N			B2	Y	Y	Y	UPEC
70	E. coli	Urine	30	6(R)	6(R)	28	6(R)	30	6(R)	N	Y	N	N			clade I or II	N	N	N	
71	E. coli	Urine	30	6(R)	6(R)	22	6(R)	20(R)	10(R)	Y	Y	Y	N			B2	N	N	Y	UPEC
72	E. coli	Urine	30	32	6(R)	24	28	26	20	N	Y	N	Y		N	A	y	N	N	UPEC
73	E. coli	Urine	32	32	25	24	32	26	21	Y	Y	Y	N			B2	Y	N	Y	UPEC
74	E. coli	Urine	30	30	24	20	28	28	22	Y	Y	Y	N			B2	Y	Y	Y	UPEC
75	E. coli	Urine	6(R)	6(R)	6(R)	24	6(R)	12(R)	6(R)	Y	Y	Y	N			B2	Y	N	Y	UPEC
76	E. coli	Urine	28	30	20	22	30	24	20	N	Y	Y	Y			unclassifed	Y	N	N	UPEC
77	E. coli	Urine	26	32	22	22	26	26	23	Y	Y	N	Y	N		clade I	Y	Y	Y	UPEC
78	E. coli	Urine	30	30	26	23	27	26	22	Y	Y	Y	N			B2	Y	Y	Y	UPEC
79	E. coli	Urine	28	28	20	24	26	26	20	Y	Y	Y	N			B2	Y	N	Y	UPEC
80	E. coli	Urine	32	28	20	23	28	28	22	Y	Y	Y	N			B2	Y	Y	Y	UPEC
81	E. coli	Urine	30	32	6(R)	20	32	30	27	Y	Y	Y	N			B2	Y	Y	Y	UPEC
82	E. coli	Urine	28	30	6(R)	18	30	30	22	Y	Y	Y	N			B2	Y	Y	Y	UPEC
83	E. coli	Urine	28	30	26	22	32	30	28	Y	Y	Y	N			B2	Y	N	Y	UPEC
84	E. coli	Urine	26	28	26	20	30	27	22	Y	Y	Y	Y			unclassifed	Y	N	Y	UPEC
85	E. coli	Urine	30	28	21	19	30	28	24	Y	N	Y	N			B2	Y	Y	Y	UPEC
86	E. coli	Urine	30	28	6(R)	18	28	25	23	Y	Y	N	N			B2	Y	Y	Y	UPEC
87	E. coli	Urine	30	6(R)	6(R)	20	6(R)	28	22	Y	Y	N	N			B2	Y	N	Y	UPEC
88	E. coli	Urine	30	32	24	20	28	28	22	N	Y	Y	N			B2	Y	Y	N	UPEC
89	E. coli	Urine	30	30	30	22	28	28	20	Y	Y	Y	N			B2	Y	Y	Y	UPEC
90	E. coli	Urine	30	30	28	20	32	30	20	Y	Y	Y	N			B2	Y	N	Y	UPEC
91	E. coli	Urine	32	6(R)	6(R)	24	6(R)	28	6(R)	Y	Y	N	N			B2	Y	Y	Y	UPEC
92	E. coli	Urine	10(R)	26	26	22	25	26	22	Y	Y	N	N			B2	N	Y	Y	UPEC
93	E. coli	Urine	28	30	22	16	26	26	24	N	N	N	Y			A	Y	N	N	UPEC
94	E. coli	Urine	6(R)	6(R)	6(R)	8(R)	6(R)	28	22	N	Y	N	Y		N	A	N	N	N	
95	E. coli	Urine	28	30	28	18	28	26	24	Y	Y	Y	N			B2	N	Y	Y	UPEC

96	E. coli	Urine	33	40	24	17	30	30	24	Y	Y	Y	N			B2	N	Y	Y	UPEC
97	E. coli	Urine	6(R)	6(R)	25	18	6(R)	28	22	Y	N	N	N			F	N	Y	Y	UPEC
98	E. coli	Urine	30	15(R)	26	22	18(R)	28	25	Y	Y	Y	N			B2	N	Y	Y	UPEC
99	E. coli	Urine	6(R)	6(R)	6(R)	20	6(R)	30	24	N	Y	N	N			clade I or II	Y	N	N	UPEC
100	E. coli	Urine	28	32	22	20	32	28	22	Y	Y	Y	N			B2	N	Y	Y	UPEC
101	E. coli	Urine	32	40	28	25	30	28	30	Y	N	N	N			F	Y	Y	Y	UPEC
102	E. coli	Urine	15(R)	6(R)	6(R)	20	6(R)	26	27	N	Y	N	N			clade I or II	N	N	N	
103	E. coli	Urine	14(R)	6(R)	6(R)	18	6(R)	30	30	N	Y	N	Y		N	A	N	Y	N	UPEC
104	E. coli	Urine	6(R)	6(R)	6(R)	22	6(R)	28	6(R)	Y	Y	Y	N			B2	N	Y	Y	UPEC
105	E. coli	Urine	28	30	30	22	32	30	26	Y	Y	N	N			B2	N	Y	Y	UPEC
108	E. coli	Urine	30	6(R)	24	22	6(R)	26	21	Y	Y	Y	N			B2	N	Y	Y	UPEC
109	E. coli	Urine	6(R)	6(R)	6(R)	20	6(R)	18(R)	20	Y	Y	Y	N			B2	N	Y	Y	UPEC
110	E. coli	Urine	30	28	30	18	28	30	22	N	Y	N	Y			A	N	N	N	
111	E. coli	Urine	32	30	6(R)	18	26	28	20	N	Y	Y	N			unclassifed	N	N	N	
112	E. coli	Urine	30	32	22	18	26	28	22	N	Y	Y	N			unclassifed	Y	N	N	UPEC
113	E. coli	Urine	6(R)	6(R)	26	20	6(R)	26	22	N	Y	Y	N			unclassifed	Y	N	N	UPEC
114	E. coli	Urine	30	32	28	22	30	28	6	N	N	N	N			unclassifed	Y	N	N	UPEC
115	E. coli	Urine	6(R)	6(R)	20	26	6(R)	26	22	Y	Y	Y	N			B2	N	N	Y	UPEC
116	E. coli	Urine	36	40	6(R)	30	32	28	26	Y	Y	Y	N			B2	N	Y	Y	UPEC
117	E. coli	Urine	36	38	28	22	30	28	21	Y	Y	Y	N			B2	N	Y	Y	UPEC
118	E. coli	Urine	38	40	30	30	36	30	22	Y	Y	Y	N			B2	N	Y	Y	UPEC
119	E. coli	Urine	36	40	6(R)	30	30	28	26	Y	N	N	N			F	N	Y	Y	UPEC
120	E. coli	Urine	6(R)	6(R)	6(R)	26	6(R)	26	24	Y	Y	N	N			B2	N	Y	Y	UPEC
121	E. coli	Urine	36	40	32	26	32	30	28	Y	Y	Y	N			B2	N	Y	Y	UPEC