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Uropathogenic Escherichia coli in China: antibiotic resistance, virulence genes, and phylogenetic characteristics – a systematic review and meta-analysis: a protocol for systematic review and meta-analysis

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ADMINISTRATIVE INFORMATION

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Review Stage at time of this submission - Completed but not published.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 12 August 2026 and was last updated on 12 August 2026.

INTRODUCTION

Review question / Objective Population (P): Clinical isolates of uropathogenic Escherichia coli (UPEC) from Chinese patients with urinary tract infections (UTIs). Intervention (I): Not applicable (observational study). Comparator (C): Not applicable. Outcome (O): (1) Prevalence of antibiotic resistance to commonly used antimicrobial agents; (2) Prevalence of virulence-associated genes; (3) Distribution of phylogenetic groups; (4) Prevalence of multidrug resistance (MDR) and extended-spectrum beta-lactamase (ESBL) production. Study design (S): Observational studies (cross-sectional, cohort, case-control).

Objective: To systematically evaluate the antibiotic resistance profiles, virulence gene prevalence, and

phylogenetic group distribution of UPEC clinical isolates from the Chinese population.

Rationale Urinary tract infections (UTIs) are among the most prevalent infectious diseases globally, affecting an estimated 150 million individuals annually. Uropathogenic Escherichia coli (UPEC) is the leading cause of UTIs, accounting for approximately 65% of cases. In China, the rising prevalence of antimicrobial resistance, particularly extended-spectrum beta-lactamase (ESBL) production and multidrug resistance (MDR), has significantly complicated clinical management. Additionally, UPEC harbors a diverse array of virulence factors that facilitate adhesion, invasion, iron acquisition, and immune evasion, contributing to infection severity and recurrence. The distribution of these resistance phenotypes and virulence determinants varies geographically. However, a comprehensive national-level synthesis of UPEC characteristics in China is lacking.

Therefore, this systematic review and meta-analysis aims to consolidate available evidence on antibiotic resistance, virulence gene prevalence, and phylogenetic group distribution of UPEC clinical isolates from Chinese populations, providing critical data to inform empirical treatment strategies and public health surveillance.

Condition being studied Urinary tract infection (UTI) is an infection affecting any part of the urinary system, including the urethra, bladder, ureters, and kidneys. Lower UTIs (cystitis and urethritis) present with symptoms such as dysuria, urinary frequency, and urgency, while upper UTIs (pyelonephritis) manifest with fever, chills, and flank pain and can progress to urosepsis if untreated. UTIs impose a significant disease burden across all age groups, with particularly high incidence in female populations, male infants, and elderly males. Uropathogenic *Escherichia coli* (UPEC) is the predominant etiological agent, and its increasing antimicrobial resistance poses a major challenge to effective treatment.

METHODS

Search strategy A comprehensive literature search was conducted in PubMed, ScienceDirect, Scopus, Web of Science, and Google Scholar for publications from 2002 to 2024. The following search terms were used:

((UPEC) AND ((China) OR (Taiwan))

((UPEC) OR (Uropathogenic *E. coli*) OR (Uropathogenic *Escherichia coli*)) AND ((China) OR (Taiwan)) AND (UTI)

((Uropathogenic *Escherichia coli*) OR (UPEC)) AND ((Virulence Genes) OR (Virulence Factors) OR (Virulence Determinants)) AND ((China) OR (Taiwan))

((UTI) OR (Urinary Tract Infections)) AND ((UPEC) OR (*Escherichia coli*) OR (*E. coli*)) AND ((China) OR (Taiwan))

(UPEC) AND (Characterization) AND ((China) OR (Taiwan))

((UPEC) OR (Uropathogenic *E. coli*) OR (Uropathogenic *Escherichia coli*)) AND ((Resistance Profile) OR (Antibiotic Resistance)) AND ((China) OR (Taiwan))

((*Escherichia coli*) OR (*E. coli*) OR (UPEC)) AND (Urine) AND ((China) OR (Taiwan))

(Uropathogens) AND ((Antibiotic Resistant) OR (Antibiotic Resistance)) AND ((China) OR (Taiwan))

(Virulence Factors) AND ((Urinary Tract Infections) OR (UTI)) AND ((*Escherichia coli*) OR (*E. coli*) OR (UPEC)) AND ((China) OR (Taiwan))

All search outputs were documented in Microsoft Excel prior to screening.

Participant or population Clinical isolates of uropathogenic *Escherichia coli* (UPEC) obtained from human urine samples of patients with urinary tract infections (UTIs) in China, across all age groups and both genders.

Intervention Not applicable (observational study).

Comparator Not applicable.

Study designs to be included Observational studies including cross-sectional, prospective cohort, retrospective cohort, and case-control studies that reported antibiotic resistance rates, virulence gene prevalence, or phylogenetic group distributions of UPEC clinical isolates.

Eligibility criteria Inclusion criteria: (1) Observational studies (cross-sectional, cohort, or case-control); (2) Human-derived UPEC clinical isolates; (3) Reported antimicrobial resistance profiles, virulence determinants, or phylogenetic groupings; (4) Studies conducted in China; (5) Publications from 2002 to 2024; (6) English language.

Exclusion criteria: (1) Non-human or environmental samples; (2) Non-UPEC bacterial species; (3) Sample size <10 isolates; (4) Publications before 2002; (5) Non-English articles; (6) Duplicates; (7) Review articles; (8) Unavailable full texts.

Information sources Electronic databases: PubMed, ScienceDirect, Scopus, Web of Science, and Google Scholar. All searches were performed for publications from 2002 to 2024. Search outputs were managed using Microsoft Excel and EndNote.

Main outcome(s) (1) Pooled prevalence of antibiotic resistance to individual antimicrobial agents (e.g., penicillins, cephalosporins, quinolones, carbapenems, tetracyclines, etc.) among UPEC clinical isolates in China. (2) Pooled prevalence of multidrug resistance (MDR) and extended-spectrum beta-lactamase (ESBL) production.

(3) Pooled prevalence of each virulence-associated gene (e.g., fimH, papGII, feoB, kpsMTII, hlyA, cnf1, etc.).

(4) Distribution and pooled prevalence of phylogenetic groups (A, B1, B2, C, D, E, F, and clade I).

Additional outcome(s) (1) Association between multidrug resistance and virulence factor modulation.

(2) Regional variation in resistance rates, virulence gene prevalence, and phylogenetic group distribution across Chinese provinces.

Data management All identified records were exported to EndNote for duplicate removal. Screening (title/abstract and full-text) and data extraction were performed independently by two authors (Ting Yu and Meng Yu) using standardized Microsoft Excel spreadsheets. Any disagreements were resolved through discussion and consensus. A third author was consulted if consensus could not be reached. Quality assessment was independently performed by Xiaona Xu and Lili Wang using a modified Newcastle-Ottawa Scale (NOS).

Quality assessment / Risk of bias analysis Risk of bias was independently assessed by two authors (Xiaona Xu and Lili Wang) using a modified Newcastle-Ottawa Scale (NOS) tailored for cross-sectional studies. The NOS includes three components: Selection (up to 5 points), Comparability (up to 2 points), and Outcome (up to 3 points), with a maximum total score of 10 points. Studies were categorized as: Low quality (score <4), Moderate quality (score 4-6), and High quality (score 7-10). Disagreements were resolved through discussion with a third author.

Strategy of data synthesis All statistical analyses were performed using Stata 15. Pooled prevalence rates of antibiotic resistance, virulence genes, and phylogenetic groups, along with their 95% confidence intervals (CIs), were calculated using the metaprop and metaprop_one commands. A random-effects model was applied due to anticipated between-study heterogeneity. Heterogeneity was assessed using the I^2 statistic, with $I^2 > 40\%$ indicating moderate to high heterogeneity. Publication bias was evaluated using Egger's test, with $p < 0.05$ indicating significant bias. Subgroup analyses were planned by geographic region if sufficient data were available.

Subgroup analysis Subgroup analyses were planned by geographic region (Chinese provinces

and administrative regions) to explore sources of heterogeneity in antibiotic resistance rates, virulence gene prevalence, and phylogenetic group distribution. However, due to limited data from certain regions, not all planned subgroup analyses could be performed.

Sensitivity analysis Sensitivity analyses were performed to assess the robustness of pooled estimates by sequentially excluding studies with small sample sizes ($n < 30$) or studies of moderate quality (NOS score <7) to evaluate their impact on the overall prevalence estimates.

Language restriction Only English-language articles were included.

Country(ies) involved China (including Mainland China, Taiwan, and Hong Kong).

Other relevant information This protocol is being registered retrospectively as the review has already been completed. The registration was prompted by the journal's peer review process to enhance research transparency.

Keywords Uropathogenic *Escherichia coli*; UPEC; urinary tract infection; antibiotic resistance; virulence factors; phylogenetic groups; meta-analysis; China.

Dissemination plans The results of this systematic review and meta-analysis will be submitted for publication in a peer-reviewed scientific journal and presented at relevant academic conferences. The full dataset and analysis code will be made available upon reasonable request.

Contributions of each author

Author 1 - Ting Yu - Drafted the manuscript and performed data extraction. Co-first author.

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