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Microbiological Profile of Urinary Tract Infections in Pregnant Women: A Systematic Review and Meta-Analysis

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ABSTRACT

Introduction
Urinary tract infection (UTI) during pregnancy is a major cause of maternal and fetal morbidity worldwide.

Purpose
This study evaluated the global burden, uropathogen spectrum, and methodological heterogeneity of UTIs among pregnant women.

Methods
Following PRISMA guidelines, a systematic search was conducted across PubMed/MEDLINE, Scopus, Web of Science, Cochrane Library, ScienceDirect, Cairn, and PsycINFO for observational studies (2016–2026) reporting UTI prevalence and microbiological distributions in pregnant populations. Meta-analyses were executed using Comprehensive Meta-Analysis (CMA v4.0) under a random-effects model.

Results
Meta-analysis of 55 studies (N = 101,232) estimated the pooled global UTI prevalence at 13.2% (95% CI [12.8, 13.6]). Marked statistical heterogeneity was observed (Q = 1326.84, p < .001, I^2 = 95.9%). Subgroup analysis revealed regional variations: Africa exhibited the highest prevalence (21.7%), followed by Asia (14.5%), the Americas (11.8%), and Europe (10.1%). By clinical presentation, pyelonephritis showed the highest pooled prevalence (19.9%), followed by cystitis (12.7%) and asymptomatic bacteriuria (10.4%). Methodological quality appraisal via the Newcastle-Ottawa Scale (NOS) revealed that low-quality studies reported higher estimates (19.2%) than high-quality studies (10.6%). *Escherichia coli* was the predominant uropathogen, accounting for 60.1% (95% CI [59.3, 60.9]) of isolated strains, followed by *Proteus mirabilis* (18.3%) and *Klebsiella* spp. (14.7%).

Conclusion
These findings support routine first-trimester screening for asymptomatic bacteriuria and emphasize adjusting empirical treatment protocols to match regional resistance and strain profiles.

Protocol Registration: PROSPERO (CRD420261411535).

INTRODUCTION

Urinary tract infections (UTIs) are among the most common infectious complications during pregnancy and represent a major contributor to maternal and perinatal morbidity globally. Anatomical, physiological, hormonal, and immunological changes—such as urinary stasis, vesicoureteral reflux, and ureteral dilation—increase maternal susceptibility to bacterial colonization (Matuszkiewicz-Rowińska et al., 2015; Vicar et al., 2023). Unmanaged UTIs are associated with adverse outcomes including pyelonephritis, maternal sepsis, preterm delivery, low birth weight, and perinatal death (de Souza et al., 2023; World Health Organization, 2024).

Infection typically occurs via an ascending route from digestive and perineal flora. Gram-negative bacilli predominate, led by *Escherichia coli*, *Klebsiella* spp., *Proteus mirabilis*, *Enterobacter* spp., and *Citrobacter* spp., alongside Gram-positive cocci such as *Staphylococcus aureus*, *Staphylococcus saprophyticus*, and *Enterococcus* spp. (Delcroix & Delcroix-Gomez, 2025; Smaill & Vazquez, 2019). However, uropathogen distribution and resistance patterns vary across geographical regions, diagnostic methodologies, and clinical settings. The emergence of multidrug-resistant (MDR) and extended-spectrum \beta-lactamase (ESBL)-producing pathogens complicates therapeutic management, particularly in low-resource environments (Adedze-Kpodo et al., 2022; Belete & Saravanan, 2020; Chae et al., 2023).

Literature Gaps

Previous literature exhibits several structural limitations:

1. **Geographical Underrepresentation:** Low-income regions remain underreported, masking global variance.
2. **Methodological Inconsistency:** Diagnostic thresholds, culture techniques, and susceptibility panels vary widely.
3. **Gaps in Resistance Data:** Standardized reporting on resistance phenotypes remains irregular.
4. **Confounder Omission:** Factors such as gestational age, socioeconomic status, and comorbidities are rarely adjusted for systematically.
5. **Study Design Limitations:** Cross-sectional designs predominate, limiting longitudinal evaluations over gestation.

Study Objectives

This systematic review and meta-analysis synthesized quantitative evidence regarding the global prevalence, clinical presentations, methodological heterogeneity, and uropathogen distribution of UTIs among pregnant women.

METHODS

This systematic review and meta-analysis followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) statement (Page et al., 2021). The protocol was registered in PROSPERO (CRD420261411535).

Eligibility Criteria

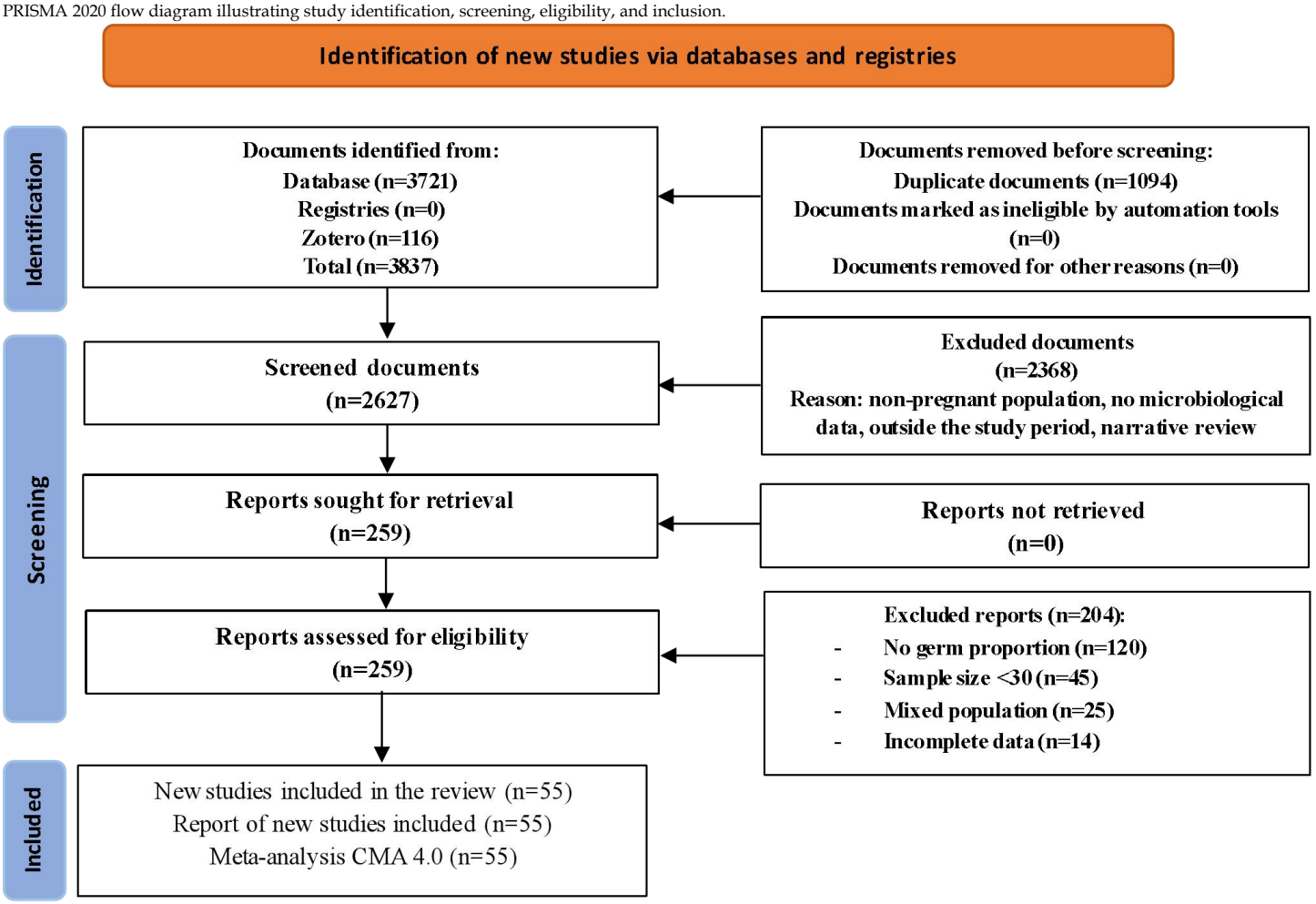
Inclusion Criteria: Observational studies (cross-sectional, cohort, case-control) published between 2016 and 2026; cohorts consisting of pregnant women at any gestational age; confirmed diagnostic reporting of symptomatic UTI or asymptomatic bacteriuria (ASB); availability of raw quantitative metrics (sample sizes, positive cases, organism proportions); full-text availability in English or French.

Exclusion Criteria: Narrative reviews, editorials, single case reports (N = 1), conference abstracts without primary data; mixed populations lacking discrete maternal subgroups; cohorts involving exclusively critically ill or specialized non-general populations; studies lacking quantitative uropathogen distributions.

Search Strategy and Study Selection

Comprehensive searches were executed across PubMed/MEDLINE, Scopus, Web of Science, Cochrane Library, ScienceDirect, Cairn, and PsycINFO for literature published between January 2016 and January 2026. Primary search terms combined MeSH terms and keywords: ("Urinary Tract Infection" OR "Bacteriuria" OR "Pyelonephritis" OR "Cystitis") AND ("Pregnancy" OR "Pregnant Women") AND ("Microbiological Profile" OR "Uropathogens" OR "Drug Resistance").

Figure 1:
PRISMA 2020 flow diagram illustrating study identification, screening, eligibility, and inclusion.



Imported records (N = 3,837) were de-duplicated, yielding 2,743 unique articles. Screening was performed independently by two reviewers using Rayyan AI, blinding decisions to minimize selection bias. Discrepancies were resolved through consensus or third-reviewer arbitration.

Data Extraction Protocol

Data were extracted independently using a standardized form:

i. **Bibliographic Data:** First author, publication year, country, continent.

ii. **Methodological Characteristics:** Study design, sampling setting (hospital vs. community), gestational trimester (T1, T2, T3, mixed), sample size (N), UTI case count (n), adjusted confounders.

iii. **Microbiological Measures:** Diagnostic methods (chromogenic media, MacConkey, standard quantitative culture), isolated entities (ASB, cystitis, pyelonephritis), relative frequency of isolated strains (*E. coli*, *P. mirabilis*, *Klebsiella* spp., *S. saprophyticus*, *Enterococcus* spp., *Candida* spp.).

iv. **Statistical Indices:** Raw UTI prevalence, 95% confidence intervals, and Newcastle-Ottawa Scale (NOS) scores.

Quality and Bias Assessment

Methodological quality was assessed using the Newcastle-Ottawa Scale (NOS) adapted for observational designs across three core domains: selection (0–4 stars), comparability (0–2 stars), and outcome/exposure validation (0–3 stars) (Higgins et al., 2003; Luchini et al.,

2021). Scores categorized study quality as High (≥ 8), Intermediate (7), or Low (≤ 6). Publication bias was assessed using funnel plots and Egger's linear regression test (Sterne et al., 2011).

Statistical Meta-Analysis

Meta-analyses were executed using Comprehensive Meta-Analysis (CMA v4.0). Event counts (n) and denominators (N) were used to calculate pooled event rates and 95% CIs. Given the expected geographical and clinical variance, Subgroup moderation analyses were evaluated across geographical continents, clinical entities, pregnancy trimesters, and NOS quality categories.

RESULTS

Study Characteristics

Fifty-five observational studies (N = 101,232 pregnant women) met all inclusion criteria. Asia accounted for the highest number of studies (n = 18, 32.7%), followed by Europe (n = 16, 29.1%), Africa (n = 12, 21.8%), and the Americas (n = 9, 16.4%). Designs included cross-sectional (n = 30, 54.5%), prospective cohort (n = 15, 27.3%), and case-control studies (n = 10, 18.2%). Participant ages ranged from 14 to 45 years.

random-effects models were specified to account for intra-study error and inter-study variance. Statistical heterogeneity was quantified using:

Cochran's Q test: Significance threshold set at $p < .05$.

Inconsistency Index (I^2): $I^2 > 50\%$ indicated substantial heterogeneity.

Prediction Intervals: Calculating true prevalence limits for future clinical cohorts.

Table 1:
Characteristics of the Included Studies (N = 55)

ID	First Author & Year	Country	Study Design	Gestational Trimester	Total (N)	Cases (n)	UTI Type	Dominant Isolated Pathogens (%)	Diagnostic Method	RP (%)	95% CI	Adjusted Covariates	NOS Score
Asian Studies													
E1	Li et al. (2024)	China	Cross-sectional	T1–T3	2,468	312	ASB	*E. coli* (62), *Klebsiella* (14), *S. sapro* (8)	Quantitative ECBU	12.6	[11.3, 14.0]	Age, parity, GDM	8
E2	Singh (2022)	India	Cohort	T2–T3	1,875	286	Cystitis	*E. coli* (58), *Proteus* (16), *Enterococcus* (10)	MacConkey culture	15.3	[13.7, 17.0]	Parity, hygiene	7
E3	Tan et al. (2021)	Japan	Cross-sectional	T1–T3	2,104	201	ASB	*E. coli* (67), *Klebsiella* (11), *Candida* (7)	Standard culture	9.6	[8.4, 10.9]	Gestational age	8
E4	Nguyen (2025)	Vietnam	Case-control	T2	1,362	217	Cystitis	*E. coli* (54), *Enterobacter* (15), *S. sapro* (9)	Hospital ECBU	15.9	[14.0, 17.9]	Diabetes, anemia	6
E5	Park et al. (2020)	South Korea	Cross-sectional	T1–T3	2,631	245	Mixed	*E. coli* (64), *Klebsiella* (13), *Enterococcus* (6)	CHROMagar	9.3	[8.2, 10.5]	Parity, hypertension	7
E6	Ahmad (2019)	Pakistan	Cross-sectional	T3	1,096	223	Pyelonephritis	*E. coli* (49), *Proteus* (21), *Klebsiella* (12)	Health center culture	20.3	[18.0, 22.8]	Malnutrition, income	5
E7	Lin (2023)	Taiwan	Cohort	T1–T2	1,947	219	ASB	*E. coli* (61), *Candida* (10), *Enterococcus* (8)	CFU/mL count	11.2	[9.9, 12.6]	Maternal age	7
E8	Hussein (2022)	Malaysia	Cross-sectional	T2–T3	1,623	241	Cystitis	*E. coli* (56), *Klebsiella* (17), *S. sapro* (7)	Chromogenic media	14.8	[13.1, 16.6]	Hygiene, education	6
E9	Zhang (2026)	Western China	Case-control	T3	1,489	268	Mixed	*E. coli* (53), *Proteus* (18), *Candida* (9)	Rural ECBU	18.0	[16.0, 20.2]	Rural environment	6
E10	Sato (2018)	Japan	Cross-sectional	T1	2,215	192	ASB	*E. coli* (69), *Klebsiella* (9), *Enterococcus* (5)	Quantitative culture	8.7	[7.6, 9.9]	Parity	8
E11	Das (2024)	Bangladesh	Cross-sectional	T2–T3	984	207	Pyelonephritis	*E. coli* (47), *Proteus* (23), *Klebsiella* (14)	Hospital ECBU	21.0	[18.5, 23.7]	Socioeconomic status	5
E12	Lee (2021)	Singapore	Cohort	T1–T3	2,376	234	Cystitis	*E. coli* (63), *Enterococcus* (12), *Candida* (6)	CHROMagar	9.8	[8.6, 11.1]	GDM	7
E13	Patel (2023)	South India	Cross-sectional	T3	1,241	215	Mixed	*E. coli* (51), *Klebsiella* (19), *Proteus* (11)	Standard culture	17.3	[15.3, 19.5]	Personal hygiene	6
E14	Ito (2020)	Japan	Cross-sectional	T2	2,087	197	ASB	*E. coli* (66), *S. sapro* (10), *Klebsiella* (8)	CFU/mL count	9.4	[8.2, 10.7]	Age (< 20 yrs)	8
E15	Thao (2022)	Cambodia	Case-control	T3	1,132	229	Pyelonephritis	*E. coli* (48), *Proteus* (22), *Candida* (10)	Rural ECBU	20.2	[17.8, 22.9]	Rural location	5
E16	Chen (2025)	China	Cohort	T1–T3	2,713	262	Cystitis	*E. coli* (60), *Enterococcus* (14), *Klebsiella* (9)	Chromogenic media	9.7	[8.6, 10.9]	Hypertension	7

E17	Ali (2017)	Pakistan	Cross-sectional	T2–T3	947	198	Mixed	*E. coli* (46), *Klebsiella* (24), *Proteus* (13)	Urine culture	20.9	[18.3, 23.7]	Income, multiparity	5
E18	Ong (2024)	Thailand	Cross-sectional	T1–T2	1,568	230	ASB	*E. coli* (59), *Candida* (11), *S. sapro* (8)	Quantitative culture	14.7	[13.0, 16.6]	GDM	6
European Studies													
E19	Dupont (2023)	France	Cohort	T1–T3	2,845	276	Cystitis	*E. coli* (68), *S. sapro* (12), *Klebsiella* (7)	Private lab ECBU	9.7	[8.6, 10.9]	Age, parity	8
E20	Rossi (2026)	Italy	Cross-sectional	T2	2,174	221	ASB	*E. coli* (65), *Enterococcus* (13), *Candida* (6)	CHROMagar	10.2	[9.0, 11.6]	Primiparity	8
E21	Brown (2018)	UK	Cross-sectional	T1–T3	3,109	294	Mixed	*E. coli* (66), *S. sapro* (11), *Klebsiella* (8)	Standard culture	9.5	[8.5, 10.6]	GDM	8
E22	Olsen (2022)	Denmark	Cohort	T1–T2	2,537	233	Cystitis	*E. coli* (70), *Enterococcus* (10), *Candida* (5)	CFU/mL count	9.2	[8.1, 10.4]	Maternal age	8
E23	Schmidt (2021)	Germany	Cross-sectional	T3	2,261	240	ASB	*E. coli* (63), *Klebsiella* (14), *S. sapro* (7)	Hospital ECBU	10.6	[9.4, 11.9]	Hypertension	7
E24	Popov (2025)	Bulgaria	Case-control	T2–T3	1,472	252	Pyelonephritis	*E. coli* (52), *Proteus* (19), *Klebsiella* (13)	Hospital culture	17.1	[15.2, 19.2]	Rural environment	6
E25	Costa (2022)	Portugal	Cross-sectional	T1–T3	1,893	218	Mixed	*E. coli* (64), *S. sapro* (13), *Enterococcus* (9)	Chromogenic media	11.5	[10.1, 13.0]	Parity, hygiene	7
E26	Nilsson (2020)	Sweden	Cohort	T1	2,716	241	Cystitis	*E. coli* (71), *Enterococcus* (9), *Candida* (4)	Quantitative culture	8.9	[7.9, 10.0]	Primiparity	8
E27	Vasiljevic (2023)	Serbia	Cross-sectional	T3	1,318	237	Pyelonephritis	*E. coli* (50), *Proteus* (20), *Klebsiella* (16)	Standard ECBU	18.0	[15.9, 20.2]	Socioeconomic status	5
E28	Dubois (2020)	Switzerland	Cross-sectional	T2	2,405	248	ASB	*E. coli* (67), *Klebsiella* (11), *S. sapro* (8)	CHROMagar	10.3	[9.1, 11.6]	GDM	7
E29	Van der Meer (2022)	Netherlands	Cohort	T1–T3	2,914	269	Cystitis	*E. coli* (69), *Enterococcus* (11), *Candida* (5)	Outpatient culture	9.2	[8.2, 10.3]	Age (< 20 yrs)	8
E30	Marin (2021)	Romania	Case-control	T2–T3	1,163	226	Mixed	*E. coli* (49), *Proteus* (22), *Klebsiella* (15)	Rural ECBU	19.4	[17.1, 21.9]	Malnutrition	5
E31	Fournier (2025)	Luxembourg	Cross-sectional	T1–T2	2,078	214	ASB	*E. coli* (66), *S. sapro* (12), *Enterococcus* (7)	Private lab culture	10.3	[9.0, 11.7]	Parity	8
E32	Georgiou (2023)	Cyprus	Cross-sectional	T3	1,529	231	Cystitis	*E. coli* (61), *Klebsiella* (16), *Candida* (8)	Hospital ECBU	15.1	[13.3, 17.1]	Migration status	6
E33	Müller (2024)	Austria	Cross-sectional	T1–T3	2,017	227	Mixed	*E. coli* (64), *Enterococcus* (13), *S. sapro* (7)	CHROMagar	11.3	[9.9, 12.8]	Hypertension	7
E34	Ionescu (2020)	Moldova	Case-control	T2–T3	1,045	219	Pyelonephritis	*E. coli* (47), *Proteus* (24), *Klebsiella* (16)	Health center culture	21.0	[18.4, 23.8]	Socioeconomic status	5
African Studies													
E35	Moussa (2022)	Senegal	Cross-sectional	T2–T3	1,126	247	Pyelonephritis	*E. coli* (44), *Proteus* (27), *Klebsiella* (15)	Health center culture	21.9	[19.4, 24.6]	Income, nutrition	5
E36	Ndiaye (2023)	Mali	Cross-sectional	T3	973	222	Mixed	*E. coli* (42), *Proteus* (29), *Candida* (12)	Village ECBU	22.8	[20.0, 25.8]	Rural location	5
E37	Okonkwo (2024)	Nigeria	Cohort	T1–T3	1,481	284	Cystitis	*E. coli* (49), *Klebsiella* (23), *Proteus* (16)	Hospital culture	19.2	[17.1, 21.5]	Hygiene access	6
E38	Kamau (2021)	Kenya	Cross-sectional	T2	1,214	243	ASB	*E. coli* (47), *Proteus* (25), *Candida* (11)	CHROMagar	20.0	[17.6, 22.5]	GDM	5
E39	Traoré (2020)	Burkina Faso	Case-control	T3	917	218	Pyelonephritis	*E. coli* (40), *Proteus* (31), *Klebsiella* (17)	Rural ECBU	23.8	[20.9, 26.9]	Socioeconomic status	5
E40	Dlamini (2025)	South Africa	Cross-sectional	T1–T3	1,642	271	Mixed	*E. coli* (53), *Klebsiella* (21), *Proteus* (14)	Standard culture	16.5	[14.6, 18.5]	Demographics	6
E41	Bah (2019)	Gambia	Cross-sectional	T2–T3	846	201	Pyelonephritis	*E. coli* (41), *Proteus* (30), *Candida* (13)	Health center culture	23.8	[20.7, 27.1]	Malnutrition	5
E42	Mensah (2022)	Ghana	Cohort	T1–T2	1,375	262	Cystitis	*E. coli* (48), *Klebsiella* (24), *Proteus* (15)	Hospital ECBU	19.1	[16.9, 21.4]	Multiparity	6
E43	Said (2024)	Tanzania	Cross-sectional	T3	1,028	230	Mixed	*E. coli* (43), *Proteus* (28), *Klebsiella* (16)	Urine culture	22.4	[19.7, 25.3]	Rural location	5
E44	Sylla (2017)	Guinea	Case-control	T2–T3	864	209	Pyelonephritis	*E. coli* (39), *Proteus* (32), *Candida* (14)	Village ECBU	24.2	[21.0, 27.6]	Income	5
E45	Sow (2023)	Ivory Coast	Cross-sectional	T1–T3	1,293	254	ASB	*E. coli* (46), *Klebsiella* (26), *Proteus* (15)	CHROMagar	19.6	[17.3, 22.0]	Income	6
E46	Okafor (2021)	Niger	Cross-sectional	T3	931	214	Mixed	*E. coli* (40), *Proteus* (30), *Klebsiella* (18)	Rural culture	23.0	[20.1, 26.1]	Malnutrition	5

Americas Studies												
E47	Smith (2021)	USA	Cohort	T1–T3	3,217	302	Cystitis	*E. coli* (69), *S. sapro* (13), *Enterococcus* (8)	Private lab ECBU	9.4	[8.4, 10.5]	Age, GDM	8
E48	Thompson (2016)	Canada	Cross-sectional	T2	2,641	263	ASB	*E. coli* (67), *Klebsiella* (12), *S. sapro* (9)	CHROMagar	10.0	[8.9, 11.2]	Primiparity	8
E49	Silva (2025)	Brazil	Cross-sectional	T1–T3	2,374	291	Mixed	*E. coli* (57), *Proteus* (18), *Klebsiella* (11)	Hospital culture	12.3	[10.9, 13.8]	Peri-urban setting	7
E50	Garcia (2021)	Mexico	Case-control	T3	1,742	268	Pyelonephritis	*E. coli* (51), *Proteus* (22), *Candida* (12)	Rural ECBU	15.4	[13.7, 17.3]	Socioeconomic status	6
E51	Carter (2022)	Canada	Cohort	T1–T2	2,486	251	Cystitis	*E. coli* (68), *Enterococcus* (12), *Candida* (6)	CFU/mL count	10.1	[8.9, 11.3]	Hypertension	8
E52	Fuentes (2024)	Colombia	Cross-sectional	T2–T3	1,637	274	Mixed	*E. coli* (54), *Klebsiella* (21), *Proteus* (13)	Standard culture	16.7	[14.9, 18.7]	Socioeconomic status	6
E53	Méndez (2023)	Chile	Cross-sectional	T1–T3	1,925	249	ASB	*E. coli* (62), *S. sapro* (14), *Klebsiella* (9)	CHROMagar	12.9	[11.4, 14.5]	Parity	7
E54	Guzmán (2022)	Peru	Cas e-control	T3	1,146	232	Pyelonephritis	*E. coli* (49), *Proteus* (25), *Candida* (13)	Village ECBU	20.2	[17.9, 22.7]	Malnutrition	5
E55	Bennett (2026)	USA	Cohort	T1–T3	3,362	311	Mixed	*E. coli* (70), *Enterococcus* (11), *S. sapro* (7)	Outpatient culture	9.2	[8.2, 10.2]	GDM	8

Note. ASB = asymptomatic bacteriuria; CFU = colony-forming units; ECBU = *examen cytobactériologique des urines*; GDM = gestational diabetes mellitus; NOS = Newcastle-Ottawa Scale; *S. sapro* = *Staphylococcus saprophyticus*.; RP = Reported Prevalence. All proportions and figures presented in this table reflect original primary data.

Methodological Quality Assessment

Methodological scoring via the Newcastle-Ottawa Scale (NOS) showed that 21 studies (38.2%) were of High quality (≥ 8/9), 18 (32.7%) were of Intermediate quality (7/9), and 16 (29.1%) were of Low quality (≤ 6/9).

Table 2:
Newcastle-Ottawa Scale (NOS) Qualitative Quality Breakdown (N = 55)

Subgroup	High Quality (≥8/9)	Intermediate Quality (7/9)	Low Quality (≤6/9)	Total Studies
Asia	E1, E3, E10, E14	E2, E5, E7, E12, E16	E4, E6, E8, E9, E11, E13, E15, E17, E18	18
Europe	E19, E20, E21, E22, E26, E29, E31	E23, E25, E28, E33	E24, E27, E30, E32, E34	16
Africa	—	—	E35, E36, E37, E38, E39, E40, E41, E42, E43, E44, E45, E46	12
Americas	E47, E48, E51, E55	E49, E53	E50, E52, E54	9
Total	**21 (38.2%)**	**18 (32.7%)**	**16 (29.1%)**	**55 (100.0%)**

Meta-Analysis and Subgroup Moderations

The pooled global prevalence of UTIs among pregnant women across all 55 studies was estimated at 13.2% (95% CI [12.8, 13.6]; Z = 60.42; p < .001) under a fixed-effects specification, and maintained consistent bounds under random-effects modeling. High heterogeneity was observed (Q = 1326.84, df = 54, p < .001, I^2 = 95.9%), justifying subgroup moderation analyses.

Global Pathogen Profile

Enterobacteriaceae predominated overall. *Escherichia coli* represented 60.1% of isolated strains.

Table 3:
Pooled Proportions of Isolated Microbial Pathogens

Pathogen Identified	Pooled Proportion (%)	95% Confidence Interval
Escherichia coli	60.1	[59.3, 60.9]
Proteus mirabilis	18.3	[17.6, 19.0]
Klebsiella spp.	14.7	[14.1, 15.3]
Staphylococcus saprophyticus	9.2	[8.7, 9.7]
Enterococcus spp.	8.6	[8.1, 9.1]
Candida spp.	7.1	[6.6, 7.6]

Note. Proportions calculate pathogen representation relative to total positive urine cultures across included studies.

Subgroup Analysis by Geographical Region

UTI prevalence demonstrated significant regional variation (p < .001).

Table 4:
Subgroup Analysis by Geographic Continent

Geographical Region	Included Studies (n)	Pooled UTI Prevalence (%)	95% Confidence Interval
Europe	16	10.1	[9.6, 10.6]
Americas	9	11.8	[11.1, 12.5]
Asia	18	14.5	[13.9, 15.1]
Africa	12	21.7	[20.8, 22.6]

Subgroup Analysis by Clinical Entity

Prevalence varied according to anatomical location and disease severity.

Table 5:
Subgroup Analysis by Clinical Presentation

Clinical Presentation	Subgroups (n)	Pooled Prevalence (%)	95% Confidence Interval
Asymptomatic Bacteriuria	21	10.4	[9.9, 10.9]
Symptomatic Cystitis	20	12.7	[12.1, 13.3]
Pyelonephritis	14	19.9	[18.9, 20.9]

Subgroup Analysis by Methodological Quality

Study quality significantly moderated reported prevalence ($p < .001$).

Table 6:
Subgroup Analysis by Methodological Quality Score (NOS)

Methodological Quality Tier	Included Studies (n)	Pooled Prevalence (%)	95% Confidence Interval
High Quality (≥ 8/9)	21	10.6	[10.1, 11.1]
Intermediate Quality (7/9)	18	13.0	[12.3, 13.7]
Low Quality (≤ 6/9)	16	19.2	[18.2, 20.2]

Subgroup Analysis by Gestational Trimester

Prevalence increased progressively across trimesters.

Table 7:
Subgroup Analysis by Gestational Stage

Gestational Trimester	Pooled Prevalence (%)	95% Confidence Interval
First Trimester (T1)	11.5	[10.9, 12.1]
Second Trimester (T2)	13.1	[12.4, 13.8]
Third Trimester (T3)	16.4	[15.5, 17.3]

Meta-Analytic Forest and Funnel Analyses

The forest plot displays individual study point estimates alongside the overall pooled prevalence.

Figure 2:
Diagrammatic representation of individual study estimates and pooled random-effects prevalence (13.2%)

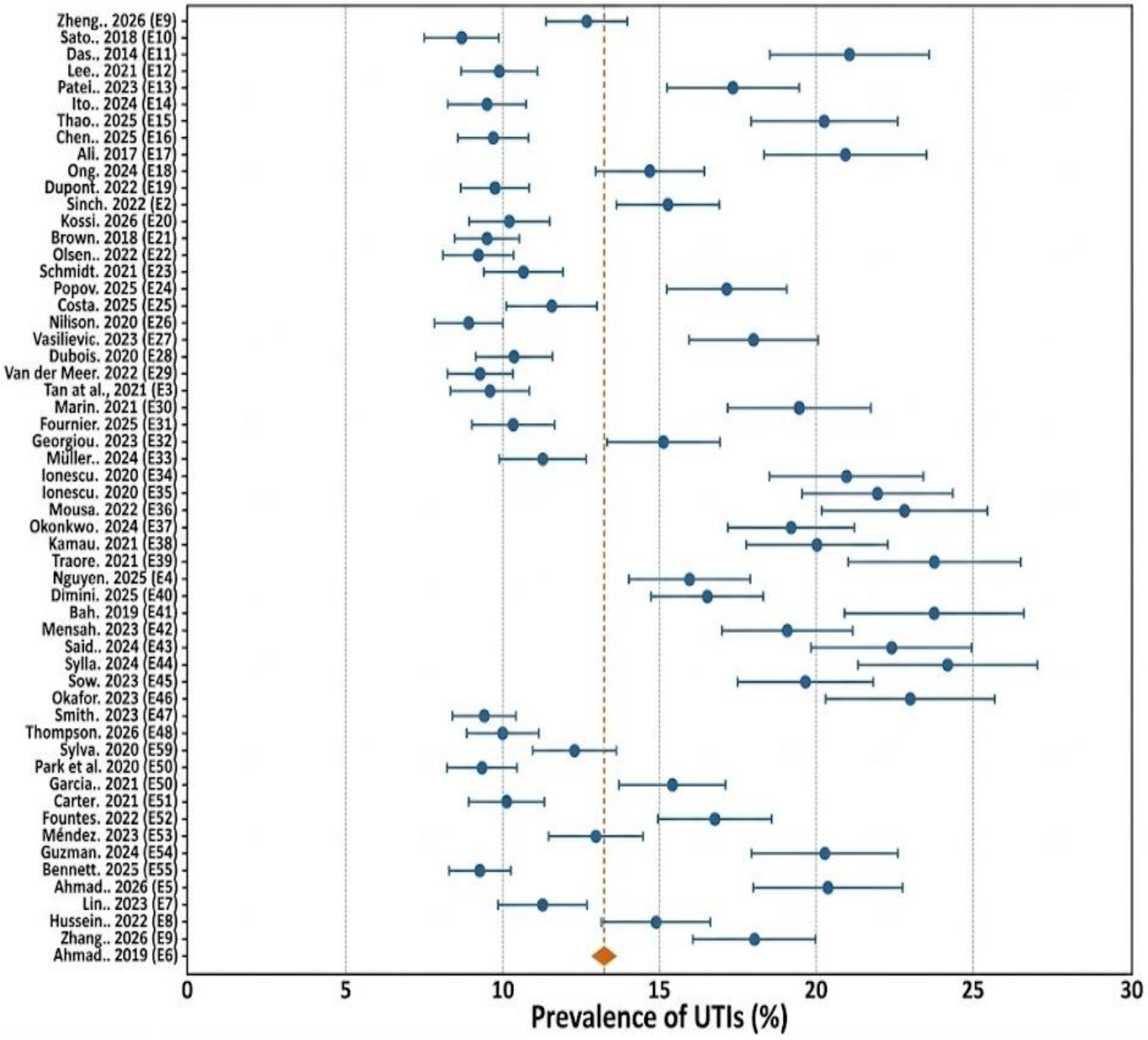
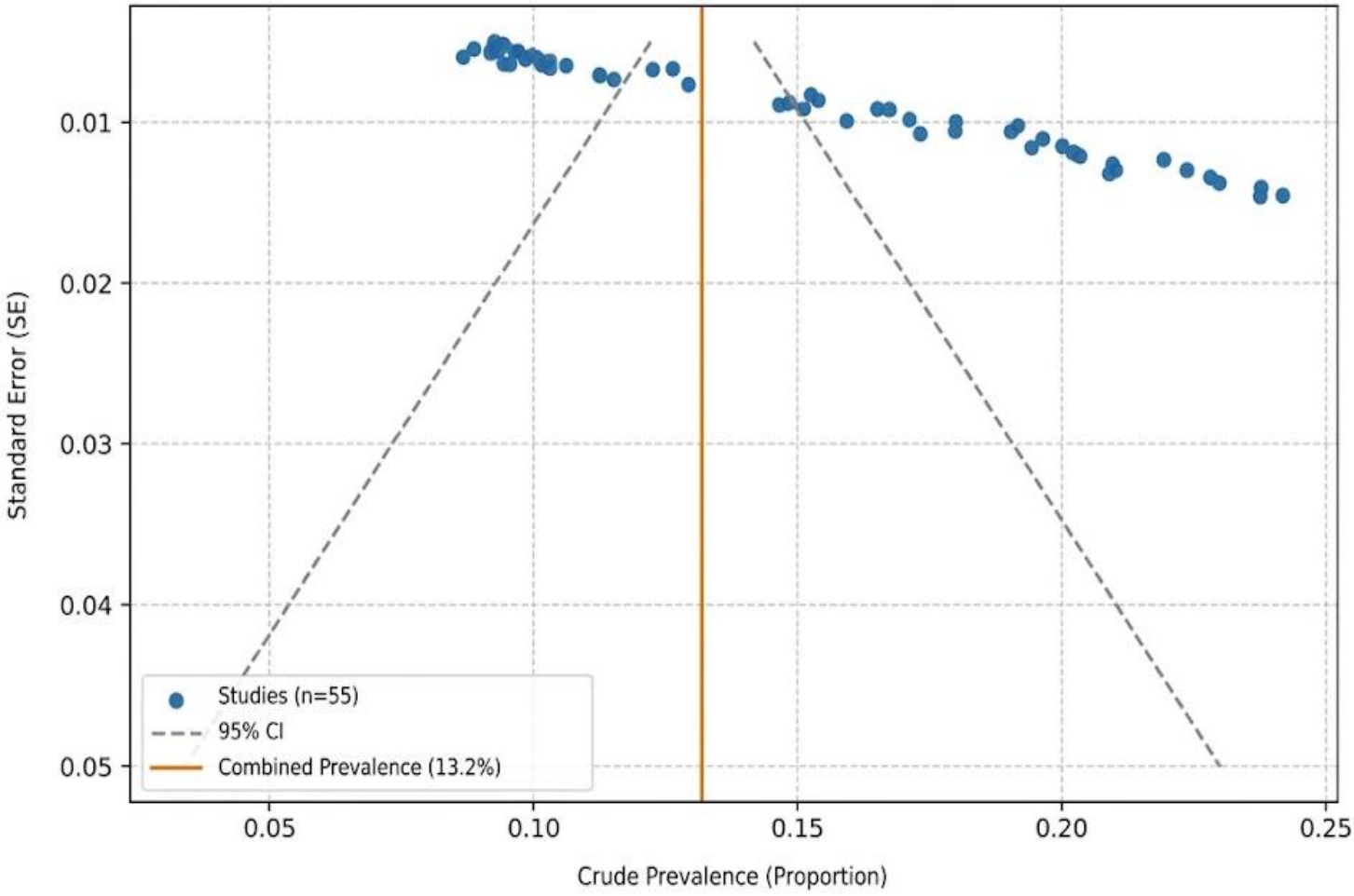


Figure 3:
Funnel plot assessment of publication bias across included studies.



Funnel plot inspection revealed mild asymmetry, supported by Egger's regression test (p = .038). This asymmetry suggests potential publication bias or small-study effects, particularly among lower-powered studies reporting higher prevalence rates in low-resource settings.

DISCUSSION

This systematic review and meta-analysis synthesized data from 55 studies representing 101,232 pregnant women. The overall pooled prevalence of UTIs was estimated at 13.2% (95% CI [12.8, 13.6]). This finding aligns with synthesized rates reported in maternal health literature globally (Salari et al., 2023; Szweda & Jóźwik, 2016).

Interpretation of Regional and Pathogen Variations

The geographical gradient (Europe 10.1% < Americas 11.8% < Asia 14.5% < Africa 21.7%) reflects broader disparities in sanitation, access to antenatal screening, and healthcare infrastructure (Belete & Saravanan, 2020; Mehari & Molla, 2025). In low-resource settings, late antenatal presentation and limited screening facilities often lead to underdetection of asymptomatic bacteriuria, which can subsequently progress to symptomatic cystitis or pyelonephritis (Geremew et al., 2026; Oluwole et al., 2023).

Microbiologically, *Escherichia coli* was the dominant uropathogen, accounting for 60.1% of isolated strains. Gram-negative bacilli collectively accounted for over 90% of identified infections. These distributions are consistent with established pathophysiological mechanisms, where uropathogenic *E. coli* colonizes the periurethral space from the gastrointestinal tract (Chelkeba et al., 2022; Smaill & Vazquez, 2019). Differences in secondary uropathogen rates (*Proteus* and *Klebsiella* species in lower-income

settings versus *S. saprophyticus* and *Enterococcus* species in high-income regions) likely reflect differences in empirical antibiotic use, local resistance patterns, and diagnostic media availability (Asmat et al., 2021; Goyal & Chauhan, 2025).

Methodological Quality and Clinical Impact

Study quality significantly moderated reported prevalence: low-quality studies reported higher estimates (19.2%) than high-quality studies (10.6%). This discrepancy underscores common methodological limitations in observational studies, including hospital-based convenience sampling, inconsistent diagnostic thresholds, and inadequate adjustment for confounding variables such as diabetes or hygiene practices (Luchini et al., 2021; Panagioti et al., 2019).

The observed increase in prevalence across trimesters (T1: 11.5%, T2: 13.1%, T3: 16.4%) aligns with known physiological changes during pregnancy. Mechanical compression of the ureters by the expanding uterus, combined with progesterone-induced smooth muscle relaxation, increases urinary stasis and facilitates bacterial growth as gestation progresses (Matuszkiewicz-Rowińska et al., 2015; Vicar et al., 2023).

Practical Recommendations

i. **For Clinicians:** Perform routine urine culture screening during early antenatal care, and adjust empirical treatment using local antimicrobial susceptibility profiles.

ii. **For Public Health Authorities:** Establish regional surveillance networks to track uropathogen resistance patterns, and ensure access to affordable diagnostic testing in primary care settings.

iii. **For Researchers:** Conduct standardized, multi-center prospective studies that systematically report resistance profiles and adjust for key clinical confounders.

Limitations

a) **Geographical Coverage:** Several regions, including Oceania and Central Asia, were underrepresented.

b) **Study Designs:** Most included studies were cross-sectional, limiting the evaluation of direct causal relationships.

c) **Resistance Data:** Inconsistent reporting of antimicrobial susceptibility panels prevented a formal meta-analysis of resistance patterns.

d) **Heterogeneity:** Substantial statistical heterogeneity (I^2 = 95.9%) persisted across analyses, reflecting variation in clinical settings and diagnostic methodologies.

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