

Study	Year	Study design	Sample size	Population	Definition of recurrent UTI	Control/comparison group	Urine collection method	Microbiome technique	Principal findings	Major limitations
Adebayo et al.	2020	Cross-sectional community cohort	1,600 women	Community-dwelling older women in the TwinsUK cohort	Not an rUTI cohort; prior UTI captured as a clinical exposure	Women with versus without prior UTI and other host exposures	Clean-catch midstream urine	16S rRNA gene amplicon sequencing	Identified a diverse core urinary microbiome; age, prior UTI, host genetics, and environmental factors contributed to compositional variation.	Cross-sectional design; prior UTI partly history-based; limited clinical characterization of active infection.
Adu-Oppong et al.	2022	Mixed cross-sectional and longitudinal observational study	132 participants; 152 specimens (122 symptomatic specimens plus 30 serial specimens from 10 controls)	Adults with suspected UTI plus asymptomatic female volunteers	Not an rUTI-specific study; symptomatic specimens classified using standard clinical culture/urinalysis	10 asymptomatic women sampled at three time points	Mixed catheterized and midstream clinical specimens; clean-catch midstream controls	Shotgun metagenomic sequencing plus standard urine culture	Symptomatic and asymptomatic microbiota states substantially overlapped; routine culture preferentially recovered traditional uropathogens and missed broader community composition.	Convenience remnant specimens, heterogeneous collection methods, and limited control of clinical confounding.
Anglin et al.	2022	Prospective nonrandomized pre/post cohort	37 women (17 rUTI; 20 controls)	Postmenopausal women receiving local estrogen therapy	At least 2 culture-confirmed UTIs in 6 months or 3 in 12 months	Postmenopausal women without rUTI	Aseptic transurethral catheterization at baseline and 3–6 months	16S rRNA V1–V2 sequencing and fungal ITS sequencing	Local estrogen altered the urinary community; <i>Prevotella</i> magna decreased, but <i>Lactobacillus</i> abundance did not significantly increase.	Small cohort, incomplete follow-up, and no untreated concurrent control.
Bradley et al.	2022	Prospective longitudinal cohort	26 adults; 6 had serial samples	Adults aged >65 years residing in one nursing home	Not an rUTI cohort; UTI symptoms and antibiotic treatment were prospectively recorded	Comparisons by duration of residence, frailty, exposures, and serial sampling	Clean-catch midstream urine	16S rRNA gene sequencing	Urinary microbiome composition varied with length of residence and frailty; <i>Aerococcus</i> urinae increased with longer residence.	Single-center small cohort; serial sampling limited to six participants; attrition not analytically addressed.
Burnett et al.	2021	Cross-sectional study	43 women	Predominantly postmenopausal women with established rUTI	Established clinical rUTI diagnosis; precise frequency threshold not reported in the article	No non-rUTI control; clinical symptom clusters compared within cohort	Paired catheterized and midstream voided urine	Expanded quantitative urine culture (EQUC) and standard urine culture	Clinical symptom profiles were associated with distinct culture-based urobionome patterns, although individual symptoms were not linked to single organisms.	Small single cohort, no healthy comparator, and limited confounder adjustment.
Cepnja et al.	2021	Cross-sectional case series with longitudinal modeling	28 patients; one patient sampled longitudinally	Adults with suspected bacterial cystitis	Cystitis based on symptoms and culture; not an rUTI-specific enrollment definition	No healthy control; comparisons across cystitis microbiota and within one treated patient	First-void midstream urine	16S rDNA Illumina sequencing with generalized Lotka–Volterra modeling	Cystitis was associated with community-level dysbiosis; modeling suggested dynamic microbial interactions during antimicrobial treatment.	Small heterogeneous series; no external control; longitudinal inference largely based on one patient.
Chen et al.	2018	Longitudinal case series	39 women; 9 severe cases followed for 2 years (102 specimens)	Women with refractory urge incontinence and coexisting rUTI	Recurrent clinically diagnosed symptomatic UTIs; exact frequency threshold not clearly specified	No healthy control; within-person comparisons over recurrent episodes	Midstream urine	Standard culture, 16S rRNA profiling, and <i>E. coli</i> limit strain typing	A diverse urinary microbiota was present; recurrent episodes reflected both persistence of the same <i>E. coli</i> strain and acquisition of new strains.	Selected severe subgroup, small sample, and no comparator group.
Cheng et al.	2025	Cross-sectional comparative study	51 adults (18 healthy; 14 chronic UTI pretreatment; 19 on treatment)	Adults with chronic lower urinary tract symptoms and healthy controls	Chronic UTI defined clinically by persistent UTIs and pyuria; not the conventional episodic rUTI definition	Healthy controls and treated versus untreated chronic UTI groups	Midstream urine	Culture and 16S rRNA amplicon sequencing; targeted ecological analyses	Chronic UTI was associated with restructuring of the urinary community rather than a single causative organism.	Cross-sectional, modest sample, and chronic UTI phenotype differs from standard UTI definitions.
Hochstetler et al.	2022	Cross-sectional paired-specimen study	43 women	Symptomatic adult women with established rUTI	Established clinical rUTI diagnosis; exact episode threshold not reported	Within-participant comparison of specimen and culture methods	Paired catheterized and midstream voided urine	Standard culture and EQUC	EQUC detected more uropathogens than standard culture; voided and catheterized specimens produced meaningfully different organism profiles.	Small single-center cohort; no non-rUTI comparator; culture-based rather than sequencing-based community characterization.
Huang et al.	2022	Cross-sectional case-control study	152 enrolled; 111 successfully amplified (67 rUTI; 44 controls)	Adult women with culture-negative rUTI and age-matched asymptomatic controls	At least 2 symptomatic UTIs in 6 months or at least 3 in 12 months	Age-matched asymptomatic women with normal urinalysis	Standard clean-catch midstream urine	16S rRNA V3–V4 Illumina sequencing	Culture-negative rUTI showed distinct urinary microbiota and differential taxa compared with controls.	Single center; amplification failures; midstream contamination risk; cross-sectional design.
Jiang et al.	2024	Secondary cross-sectional metagenomic analysis and diagnostic-model study	75 women (25 rUTI relapse; 25 remission; 25 healthy controls)	Women represented in a previously published metagenomic dataset	At least 2 symptomatic UTIs in 6 months or 3 in 12 months	Healthy women and rUTI remission group	Clean-catch midstream urine in source cohort	Shotgun metagenomics with virulence-factor annotation; machine-learning models	Virulence-factor gene profiles differed by rUTI state; exploratory models distinguished healthy versus rUTI and relapse versus remission.	Secondary dataset analysis, limited confounder control, and no independent external model validation.
Johnson et al.	2022	Human isolate study with ex vivo mechanistic experiments	64 urinary isolates representing 24 bacterial and 2 fungal species	Postmenopausal women with no rUTI, rUTI, or rUTI receiving antibiotic prophylaxis	Clinical rUTI history from parent cohort; exact frequency threshold not restated	Isolates from women without rUTI and from rUTI groups	Catheterized urine in parent cohort	EQUC, MALDI-TOF/Sanger identification, and ex vivo inhibition assays	Many urinary <i>Lactobacillus</i> isolates inhibited uropathogens, supporting potential protective antimicrobial interactions.	Isolate-level ex vivo findings may not reflect in vivo effects; selected culturable organisms; limited participant-level inference.
Kelly et al.	2024	Cross-sectional study	54 children	Children aged 3 months–11 years undergoing clinically indicated VCUG	History categorized as 1, 2, or at least 3 UTIs; recurrent group represented by at least 3 prior UTIs	Comparisons by sex, age, and number of prior UTIs	Catheterized urine during VCUG	Synthetic long-read 16S rRNA gene sequencing	Urobionome composition varied by sex and age; diversity was lower among children with at least 3 prior UTIs.	Small convenience sample, prophylactic antibiotic exposure, and limited infant representation.
Neugent et al.	2023	Cross-sectional comparative study	75 women (25 per group)	Postmenopausal women with no UTI history, rUTI without active UTI, or rUTI with active UTI	Recent clinical history of rUTI; exact episode threshold referenced to parent study	No lifetime-UTI controls and inactive versus active rUTI groups	Clean-catch midstream urine	Whole-genome shotgun metagenomics plus targeted LC-MS/MS glycosaminoglycan profiling	Urinary glycosaminoglycan patterns were associated with rUTI status and urobionome ecology.	Cross-sectional biomarker association; selected postmenopausal cohort; requires external validation.
Neugent et al.	2025	Cross-sectional multi-omics and prognostic analysis	75 women (25 per group)	Postmenopausal women with no UTI history, inactive rUTI, or active rUTI	Recent clinical history of rUTI; exact episode threshold referenced to parent study	No lifetime-UTI controls and inactive versus active rUTI groups	Clean-catch midstream urine	Shotgun metagenomics plus targeted LC-MS/MS metabolomics	Defined microbiome–metabolite networks, an active-rUTI lipid signature, and deoxycholic acid as an exploratory recurrence marker.	Biomarker derivation and internal testing used the same cohort; no independent external validation.
Robino et al.	2024	Cross-sectional comparative study	141 adults (69 symptomatic; 72 asymptomatic)	Adult women and men with UTI symptoms or no symptoms	Not rUTI-specific; UTI required compatible symptoms/signs and >100,000 CFU/mL	Asymptomatic adults	Self-collected midstream urine	Intracellular culture assay, confocal microscopy, standard culture, and MALDI-TOF	Intracellular bacteria occurred in symptomatic and asymptomatic participants; intracellular <i>E. coli</i> was associated with symptoms.	Convenience recruitment, cross-sectional design, and limited adjustment for sex and other confounders.
Vaughan et al.	2021	Cross-sectional analysis of longitudinal cohort baseline	64 women	Postmenopausal women using vaginal estrogen; rUTI with prophylaxis, rUTI without prophylaxis, and controls	Clinical rUTI history; exact frequency threshold not restated	Age-matched postmenopausal women without rUTI	Catheterized urine collected without active infection	EQUC and 16S rRNA gene sequencing	Anaerobic taxa, particularly <i>Bacteroides</i> / <i>Prevotella</i> spp., differed among rUTI and control phenotypes despite similar overall species counts.	Small sample, cross-sectional baseline analysis, and antibiotic/vaginal-estrogen exposure.
Vilko et al.	2022	Cross-sectional case-control study	49 for 16S; 96 for metabolomics	Children with vesicoureteral reflux with or without renal scarring and surgical controls	Recurrent febrile UTI history; exact episode threshold not stated	Healthy pediatric surgical controls and VUR subgroups	Sterile catheterization or sterile voiding at surgery	16S rRNA sequencing and mass-spectrometry metabolomics	VUR and recurrent UTI were associated with distinct microbial profiles and broad metabolomic alterations.	Different analytic sample sizes, pilot design, multiple comparisons, and confounding by VUR severity/treatment.
Yoo et al.	2021	Retrospective cross-sectional study	42 women (11 acute uncomplicated cystitis; 31 recurrent cystitis)	Women undergoing urine culture and NGS for cystitis	Repeated cystitis episodes after prior treatment; exact numeric threshold not clearly specified	Acute uncomplicated cystitis group	Transurethral catheterization	16S rRNA gene amplification/NGS plus conventional culture	NGS was more sensitive than culture; recurrent and acute cystitis showed different diversity and taxonomic patterns.	Small retrospective cohort; prior antibiotic use, and no healthy control.
Yoo et al.	2022	Retrospective cross-sectional human study	96 women (79 rUTI; 18 controls)	Women with rUTI and normal controls	Clinical recurrent cystitis/rUTI history; exact numeric threshold not clearly specified	Normal control group	Transurethral catheterization	16S rRNA gene sequencing	<i>Gardnerella</i> detection alone did not distinguish groups; its association with rUTI depended on community context and other risk factors.	Small control and <i>Gardnerella</i> -positive subgroups; retrospective selection, and animal experiments excluded from this review.
Yoo et al.	2024	Retrospective cross-sectional study	564 women (42 controls; 34 sporadic cystitis; 488 recurrent cystitis)	Women with sporadic or recurrent uncomplicated cystitis and symptom-free controls	At least 2 cystitis episodes in 6 months or at least 3 in 12 months	Healthy controls and sporadic uncomplicated cystitis	Transurethral catheterization	16S rRNA NGS plus conventional culture	Control, sporadic, and recurrent cystitis groups had distinct microbiome profiles; NGS substantially increased organism detection.	Retrospective referral cohort; prior antibiotic/probiotic exposure and unequal group sizes.