Li et al. One Health Advances (2024) 2:16
https://doi.org/10.1186/s44280-024-00045-z

One Health Advances

ARTICLE

Open Access

Trend of distribution and antimicrobial resistance in uropathogens in China from the CHINET antimicrobial resistance surveillance program, a 7-year retrospective study

Yanming Li[1], Mingxiang Zou[1], Qun Yan[1], Jingzhong Liao[1*], Wenen Liu[1,2*] and on behalf of the China Antimicrobial Surveillance Network (CHINET) Study Group

Abstract

Urinary tract infections (UTIs) are common urological diseases that easily relapse and have led to an increasing economic and health burdens. The China Antimicrobial Surveillance Network (CHINET) system is one of the most influential antimicrobial resistance surveillance networks in China. This study analyzed antimicrobial resistance and distribution trends of uropathogens from 2015 to 2021 using the CHINET system. A total of 261,893 non-duplicate strains were collected; Gram-positive bacteria accounted for 23.8% while Gram-negative bacteria accounted for 76.2%. *Escherichia coli*, *Enterococcus faecium*, *Klebsiella pneumoniae,* and *Enterococcus faecalis* were the most common species. The resistance to vancomycin, linezolid, and teicoplanin in *E. faecalis* and *E. faecium* was less than 3%. The prevalence of carbapenem-resistant strains of *E. coli, K. pneumoniae*, *Pseudomonas aeruginosa,* and *Acinetobacter baumannii* was 1.7%, 18.5%, 16.4%, and 40.3%, respectively. The prevalence of carbapenem-resistant *A. baumannii* increased from 27.6% in 2015 to 43.4% in 2021. The prevalence of methicillin-resistant *Staphylococcus aureus* decreased from 40.6% in 2015 to 22.9% in 2021. The resistance rates to most β-lactam antimicrobials, aminoglycosides and fluoroquinolones in *E. coli*, *K. pneumoniae*, *P. aeruginosa* and *A. baumannii* isolated from ICU inpatients were significantly higher than in those isolated from outpatients and non-ICU inpatients. This study indicates that *E. coli*, *Enterococcus*, and *K. pneumoniae* were the most commonly isolated uropathogens in China. The bacterial species isolated and their antimicrobial resistance patterns differed in different patient populations. More attention must be paid uropathogen resistance surveillance to provide data for the rational use of antimicrobial agents.

Keywords Urine specimen, Bacterial resistance surveillance, Antimicrobial susceptibility testing, *Escherichia coli*, Multi-drug resistant bacteria

*Correspondence:
Jingzhong Liao
liaojingzhong0808@163.com
Wenen Liu
wenenliu@163.com
[1] Department of Clinical Laboratory, Xiangya Hospital, Central South University, Hunan Province, Changsha 410008, China
[2] National Clinical Research Center for Geriatric Disorders, Xiangya Hospital, Hunan Province, Changsha, China

Introduction

Urinary tract infections (UTIs) are among the most common bacterial infections. Approximately 150 million people worldwide experience UTIs every year, causing severe health problems and socioeconomic burdens [1]. Regular monitoring of the antimicrobial resistance in bacteria isolated from urine specimens is necessary to guide the rational use of antibiotics and reduce bacterial resistance. The China Antimicrobial Surveillance Network (CHINET) was founded in 2004; a total of 21 hospitals (including 19 general hospitals and 2 specialized children's hospitals) participated in the network as of 2015. As of 2021, there are 51 hospitals (including 45 general hospitals and 6 specialized children's hospitals) involved from 29 provinces, municipalities, and autonomous regions across the country. In this study, we analyzed the antimicrobial resistance of bacteria isolated from urine using data from CHINET system from 2015 to 2021. Bacterial species and antimicrobial resistance over seven years were summarized to guide antimicrobial therapy.

Results

Distribution of clinical isolates

A total of 261,893 non-duplicate bacterial strains were isolated from urine, including 62,219 (23.8%) Gram-positive bacteria and 199,674 (76.2%) Gram-negative bacteria (Table 1). The number of isolates continously grew over 7 years as increasing numbers of hospitals participated in the system, but the proportion remained largely consistent. The top ten bacteria isolated were *E. coli* (46.7%), *Klebsiella* spp. (11.5%), *E. faecium* (10.4%), *E. faecalis* (8.7%), *P. mirabilis* (3.5%), *P. aeruginosa* (3.4%), *S. agalactiae* (2.6%), *E. cloacae* (2.1%), *A. baumannii* (1.7%), and *S. aureus* (1.1%).

Among the 261,893 non-duplicate bacterial strains, 161,063 strains (61.5%) were obtained from females, and 100,830 strains (38.5%) were obtained from males. In terms of age distribution, 36,894 strains (14.1%) were collected from patients ≤ 18 years old, 37,819 strains (14.4%) were from patients aged 18–44, 57,705 strains (22.0%) were from patients aged 45–59, and 129,475 strains (49.4%) were from patients ≥ 60 years old.

There were significant differences in the dominant bacteria among populations of various ages and genders. The proportions of *E. coli*, *E. faecium*, *K. pneumoniae*, *P. mirabilis*, and *S. agalactis* isolated from female patients were higher than those isolated from male patients, while the proportions of *E. faecalis*, *P. aeruginosa*, *E. cloacae*, *A. baumannii*, and *S. aureus* isolated from female patients were lower. Almost half of the isolates were isolated from people aged ≥ 60 years. Among 6910 strains of *S. agalactiae*, only 2.8% were isolated from individuals ≤ 18 years, which was significantly different from the distribution trend of other bacteria (Fig. 1).

The majority of the isolates were from non-ICU inpatients (74.6%), 18.4% were from outpatients, 2.4% were from emergency patients, and 4.6% were from ICU

Table 1 Distribution of 261,893 bacteria in urine specimens over 7 years

Organism	2015		2016		2017		2018		2019		2020		2021		Total	
	No	%	No	%	No	%	No	%	No	%	No	%	No	%	No	%
E. coli	7907	45.9	12,332	47.3	14,016	47.0	18,018	47.9	22,055	49.0	22,004	45.1	26,052	45.5	122,384	46.7
Klebsiella spp.	1880	10.9	2862	11.0	3384	11.4	4391	11.6	5021	11.1	5853	12.0	6763	11.8	30,154	11.5
E. faecium	1856	10.8	2764	10.6	3210	10.8	3812	10.1	4525	10.1	5121	10.5	6055	10.6	27,343	10.4
E. faecalis	1669	9.7	2215	8.5	2613	8.8	3009	8.0	3576	7.9	4299	8.8	5360	9.4	22,741	8.7
P. mirabilis	627	3.6	862	3.3	1013	3.4	1351	3.6	1510	3.4	1731	3.5	2019	3.5	9113	3.5
P. aeruginosa	572	3.3	949	3.6	1053	3.5	1325	3.5	1440	3.2	1811	3.7	1866	3.3	9016	3.4
S. agalactiae	421	2.4	608	2.3	781	2.6	950	2.5	1156	2.6	1372	2.8	1622	2.8	6910	2.6
E. cloacae	389	2.3	552	2.1	645	2.2	761	2.0	868	1.9	1096	2.2	1208	2.1	5519	2.1
A. baumannii	308	1.8	414	1.6	541	1.8	600	1.6	670	1.5	877	1.8	987	1.7	4397	1.7
S. aureus	183	1.1	389	1.5	308	1.0	444	1.2	470	1.0	535	1.1	635	1.1	2964	1.1
C. freundii	160	0.9	260	1.0	325	1.1	349	0.9	465	1.0	469	1.0	572	1.0	2600	1.0
M. morganii	132	0.8	203	0.8	278	0.9	352	0.9	413	0.9	517	1.1	669	1.2	2564	1.0
S. maltophilia	87	0.5	154	0.6	167	0.6	180	0.5	193	0.4	274	0.6	274	0.5	1329	0.5
S.marcescens	70	0.4	131	0.5	142	0.5	216	0.6	198	0.4	231	0.5	272	0.5	1260	0.5
B. cepacia	242	1.4	230	0.9	84	0.3	209	0.6	110	0.2	77	0.2	45	0.1	997	0.4
P. vulgaris	91	0.5	100	0.4	74	0.2	135	0.4	160	0.4	155	0.3	165	0.3	880	0.3
others	637	3.7	1071	4.0	1177	3.9	1548	4.1	2191	5.0	2369	4.8	2754	4.6	11,722	4.6
total	17,231	100	26,096	100	29,811	100	37,650	100	45,021	100	48,791	100	57,318	100	261,893	100

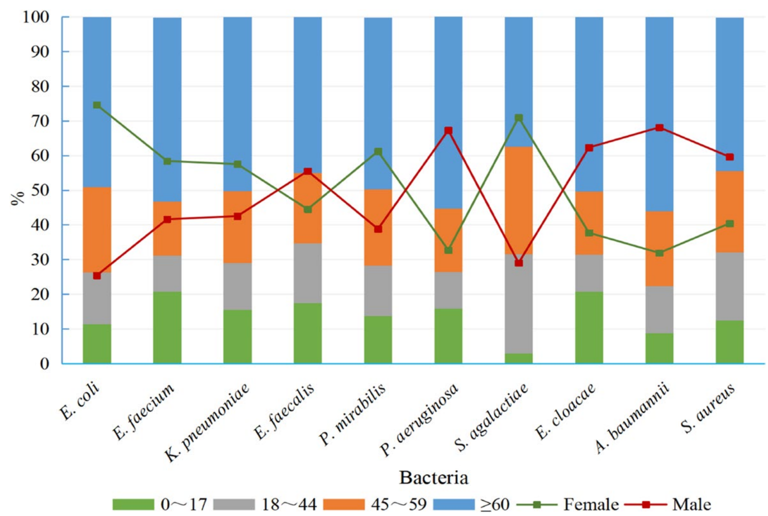

Fig. 1 Distribution of the most common isolates across different ages and genders. Gender distribution is shown as a line chart and age distribution is shown as a stacked bar chart

patients. The dominant strains varied among patients from different departments. As shown in Supplementary Table 1, the top five bacteria isolated from outpatients were *E. coli*, *K. pneumoniae*, *E. faecalis*, *P. mirabilis,* and *S. agalactiae*; the top five bacteria isolated from emergency patients and non-ICU inpatients were *E. coli*, *E. faecium*, *K. pneumoniae*, *E. faecalis*, and *P. aeruginosa*, while they were *E. faecium*, *E. coli*, *K. pneumoniae*, *E. faecalis,* and *P. aeruginosa* in ICU inpatients. *E. faecium* was the most common in ICU inpatients, but it ranked 6th in outpatients.

Antimicrobial resistance in Gram-positive cocci

Enterococcus spp.

A total of 51,436 *Enterococcus* strains were isolated from urine specimens from 2015 to 2021; *E. faecium* accounted for 53.2% (27,343), *E. faecalis* accounted for 44.2% (22,741) and other *Enterococcus* accounted for 2.6% (1352). Compared with *E. faecalis*, *E. faecium* showed higher resistance rates to ampicillin, levofloxacin, high concentrations of gentamicin (GEH), and nitrofurantoin ($P < 0.05$) (Fig. 2). Less than 2.2% of *E. faecalis* and *E. faecium* were resistant to vancomycin, linezolid, and teicoplanin in our study.

Staphylococcus spp.

A total of 3248 strains of *Staphylococcus* were isolated, including 2964 strains of *S. aureus* (91.3%) and 284 strains of *S. saprophytic* (8.7%). No *Staphylococcus* were found to be resistant to vancomycin and linezolid. The prevalences of methicillin-resistant *S. aureus* (MRSA) and methicillin-resistant *S. saprophyticus (*MRSAP) were

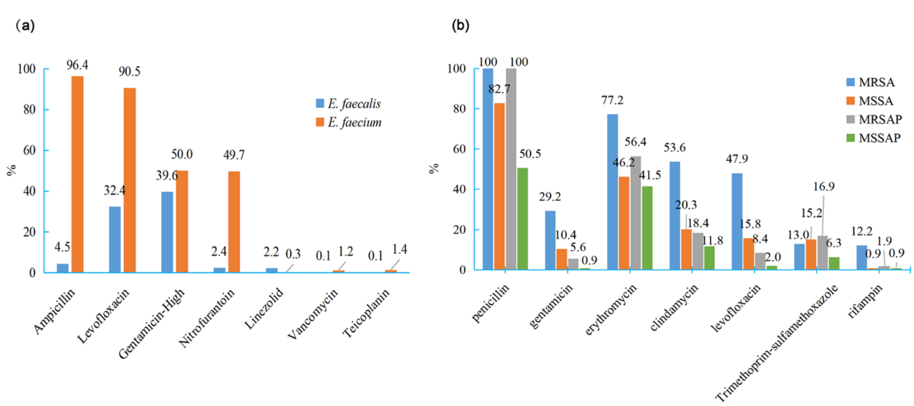

Fig. 2 Resistance profiles of *Enterococcus* and *Staphylococcus* isolated from urine towards common antimicrobial agents. **a** Resistance rates of *E. faecalis* and *E. faecium* for antimicrobial agents; **b** Resistance rates of *S. aureus* and *S. saprophyticus* to antimicrobial agents. MRSA: methicillin-resistant *S. aureus*; MSSA: methicillin-sensitive *S. aureus*; MRSAP: methicillin-resistant *S. saprophyticus*; MSSAP: methicillin-sensitive *S. saprophyticus*

27.8% (819/2947) and 59.3% (162/273), respectively. As shown in Fig. 2, the resistance rates of MRSA to gentamicin, erythromycin, clindamycin, levofloxacin and rifampicin were much higher than those of methicillin-sensitive *S. aureus* (MSSA) ($P<0.05$). The resistance rates to gentamicin, erythromycin, levofloxacin, and trimethoprim-sulfamethoxazole (SMZ-TMP) were much higher than that of methicillin-sensitive *S. saprophyticus* (MSSAP) ($P<0.05$).

β-hemolytic Streptococcus

A total of 7412 strains of β-hemolytic *Streptococcus* were isolated, 93.2% of which were *S. agalactiae*. All *S. agalactiae* strains were sensitive to penicillin, ceftriaxone, vancomycin and linezolid. The resistance rates to erythromycin, clindamycin, and levofloxacin were more than 50%.

Antimicrobial resistance in Gram-negative bacilli

Enterobacteriaceae

A total of 178,979 strains of Enterobacteriaceae were isolated, including 122,384 strains of *E. coli* (68.4%), 30,316 strains of *Klebsiella* spp. (16.9%), and 10,271 strains of *Proteus* spp. (5.7%). The resistance rates of *E. coli* to imipenem, piperacillin-tazobactam and tigecycline remained lower than 4% while resistance rates to cefazolin, cefuroxime, and ciprofloxacin were higher (Fig. 3). The resistance rates of *E. coli* to cefazolin, cefuroxime, cefepime and gentamicin decreased gradually over seven years. Similarly, *K. pneumoniae* showed relatively high resistance rates to cefazolin, cefuroxime and ciprofloxacin, with resistance rates of 40%–60%. The average resistance frequencies of *K. pneumoniae* to tigecycline and polymyxin B were 6.9% (1027/14,890) and 3.2% (118/3708), respectively. In the early years of 2015–2021, susceptibility test for polymyxin B were conducted only when carbapenem resistance was identified in some hospitals; because of this, the results of polymyxin B are present for informational purposes only.

Nonfermenting Gram-negative Bacilli

Low average resistance rates were observed toward polymyxin B (0.8%, 15/1899) and amikacin (5.4%, 480/8890) in *P. aeruginosa*. The resistance rates of *P. aeruginosa* to imipenem, ceftazidime, cefepime, cefoperazone-sulbactam, and piperacillin-tazobactam ranged from 8 to 17%. In addition, *A. baumannii* maintained a lower resistance rate to polymyxin B (0.7%, 7/934) and tigecycline (4.4%, 14/3234). More than 40% of the strains were resistant to

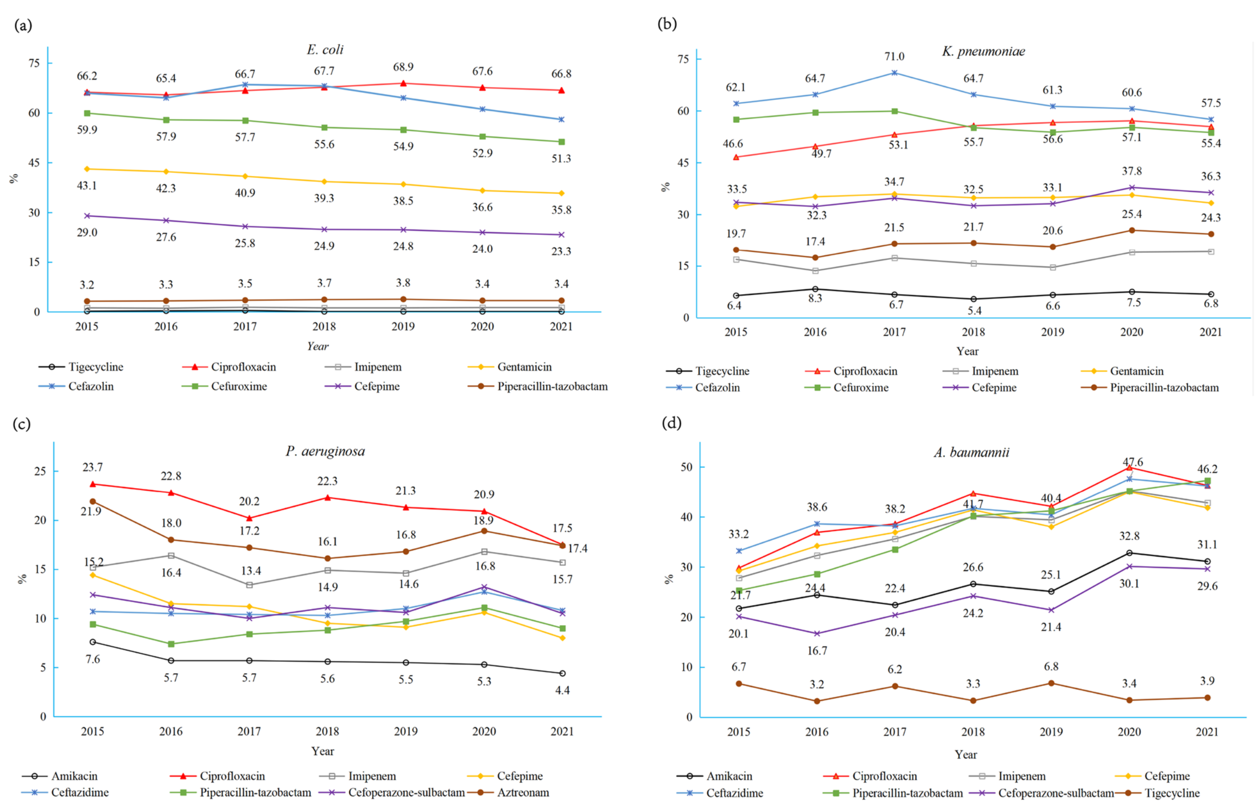

Fig. 3 Resistance profiles of *E. coli*, *K. pneumoniae*, *P. aeruginosa,* and *A. baumannii* isolated from urine towards common antimicrobial agents over seven years. **a** Resistance rates of *E. coli* for antimicrobial agents; **b** Resistance rates of *K. pneumoniae* for antimicrobial agents; **c** Resistance rates of *P. aeruginosa* for antimicrobial agents; **d** Resistance rates of *A. baumannii* for antimicrobial agents

ceftazidime and ciprofloxacin. Increasing trends were observed in the resistance rates of *A. baumannii* to amikacin, imipenem, cefepime, ceftazidime, piperacillin-tazobactam, cefoperazone-sulbactam and ciprofloxacin over the 7 years examined (Fig. 3).

Minocycline was the most effective antimicrobial agent in *S. maltophilia* strains, which had a resistance rate of only 2.2% (23/1050). The resistance rates to levofloxacin and TMP-SMZ of *S. maltophilia* were 14.4% (178/1234) and 12.9% (155/1202), respectively. Lower resistance rates in *B. cepacia* were observed against ceftazidime (3.3%, 32/967), meropenem (4.5%, 43/953) and TMP-SMZ (6.9%, 68/981).

Antimicrobial resistance within different populations

As shown in Fig. 4, the resistance rates to ampicillin and GEH in *E. faecalis* and *E. faecium* from ICU inpatients were significantly higher than in those from outpatients and other inpatients ($P < 0.05$).

The resistance rates to most β-lactam antimicrobials, aminoglycosides, and fluoroquinolones in *E. coli* and *Klebsiella* spp. from ICU inpatients were significantly higher than those from outpatients and other inpatients ($P < 0.05$). The resistance rates to most β-lactam antimicrobials in *E. coli* and *Klebsiella* spp. from pediatric outpatients and inpatients aged < 18 years were higher than those from inpatients aged ≥ 18 years, while the opposite was observed for resistance to aminoglycosides and fluoroquinolones.

Except for tigecycline and polymyxin, the resistance rates to other antimicrobial agents in *P. aeruginosa* and *Acinetobacter* spp. from ICU inpatients were significantly higher than those from outpatients and non-ICU inpatients ($P < 0.05$). Among non-ICU inpatients, the resistance rates to most antimicrobials in isolated from medical inpatients aged ≥ 18 years were higher than in those from surgical inpatients aged ≥ 18 years and

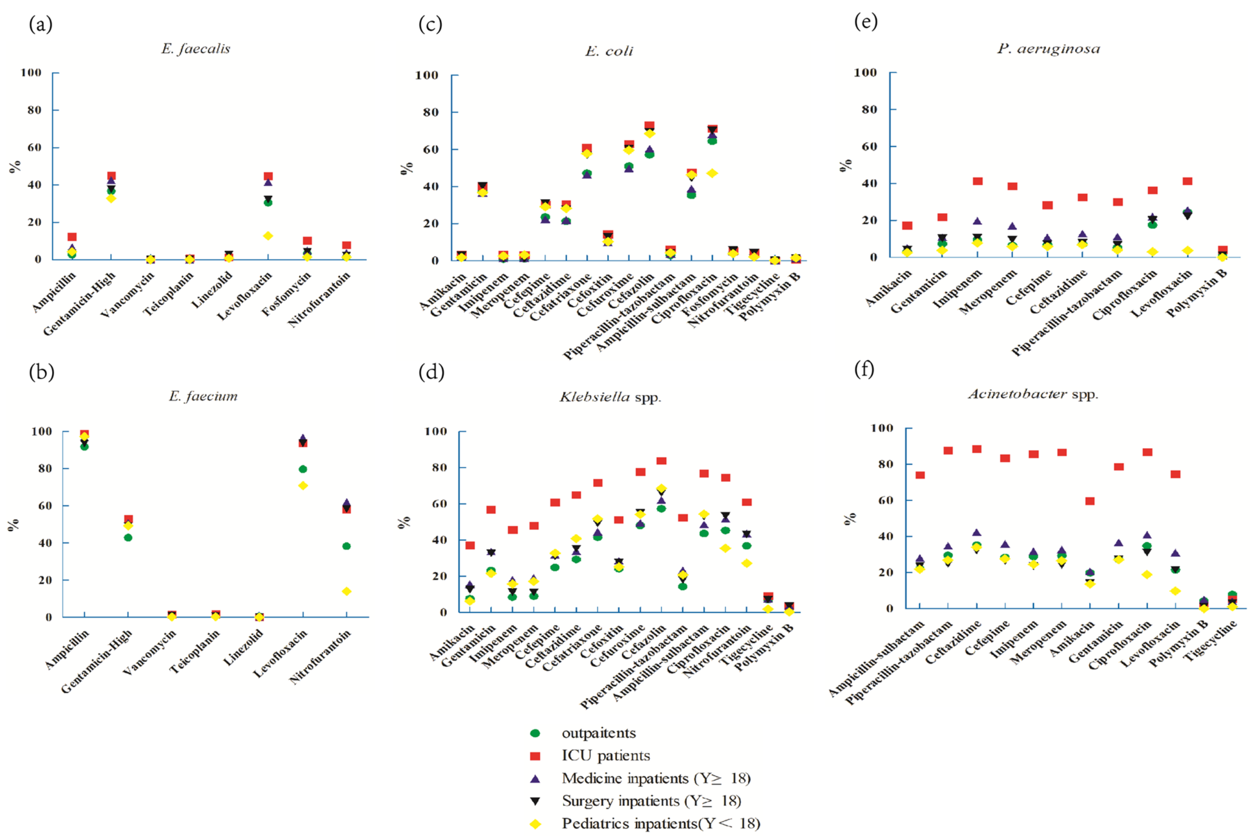

Fig. 4 Comparison of antibiotic resistance of *E. faecalis*, *E. faecium*, *E. coli*, *Klebsiella* spp., *P. aeruginosa*, and *Acinetobacter* spp. between the different populations. **a** Antibiotic resistance of *E. faecalis* between different populations; **b** Antibiotic resistance of *E. faecium* between different populations; **c** Antibiotic resistance of *E. coli* between different populations; **d** Antibiotic resistance of *Klebsiella* spp. between different populations; **e** Antibiotic resistance of *P. aeruginosa* between different populations; **f** Antibiotic resistance of *Acinetobacter* spp. between different populations

inpatients aged < 18 years ($P < 0.05$). Detailed results are shown in Supplementary Tables 2–4.

Multidrug resistance (MDR) and special antimicrobial resistance

MDR was defined as resistantance to at least one antimicrobial agents from three or more different antimicrobial classes. The prevalence of MDR in *E. coli*, *K. pneumoniae*, *E. faecium* and *E. faecalis* was 72.0% (88,105/122,384), 62.1% (15,929/25,642), 77.0% (21,063/27,343), and 23.4% (5312/22,741), respectively. The prevalence of MDR *E. coli* and *K. pneumoniae* in male patients was higher than that in female patients while the prevalence of MDR *E. faecalis* in male patients was lower than that in female patients ($P < 0.05$). The prevalence of MDR was significantly higher in isolates from ICU inpatients than in non-ICU inpatients, emergency patients, and outpatients ($P < 0.05$). Further details are available in the Supplementary Table 5.

The prevalence of carbapenem-resistant *A. baumannii* (CRABA) increased from 27.6% in 2015 to 43.4% in 2021. The prevalence of carbapenem-resistant *E. coli* (CRECO) was relatively stable from 1.4% to 2.9% during the same period, while the prevalences of carbapenem-resistant *K. pneumoniae* (CRKPN) and carbapenem-resistant *P. aeruginosa* (CRPAE) fluctuated between 14.7% and 20.5%. A significant decrease in the prevalence of methicillin-resistant *S. aureus* (MRSA) was observed, from 40.6% in 2015 to 22.9% in 2021. The average prevalence of vancomycin-resistant *E. faecalis* and *E. faecium* were 0.1% and 1.3%, respectively, and those of linezolid-resistant *E. faecalis* and *E. faecium* were 2.2% and 0.3%, respectively (Fig. 5).

Compared with female patients, the prevalence of CRECO, CRKPN and CRABA in male patients was significantly higher; the prevalence of CRECO and CRKPN was nearly two times greater in man than in women. The prevalence of CRECO, CRKPN, CRPAE and CRABA in ICU inpatients was higher than other patients (Supplementary Table 6).

Discussion

This is the first summary of antimicrobial resistance trends in uropathogens from CHINET system. The surveillance results showed that 76.2% of the bacteria isolated from urinary tract specimens were Gram-negative bacteria; *E. coli*, *E. faecalis*, *E. faecium* and *K. pneumoniae* were predominantly identified isolates. The dominant bacteria differed among populations of various ages and genders. The resistance patterns varied among different bacteria, and there were also differences in their changes over time.

Most of the strains were isolated from hospitalized patients. Uropathogens were more common in females and half were isolated from people > 60 years of age. *E. coli*, *E. faecium*, *K. pneumoniae*, *P. mirabilis* and *S. agalactis* were more frequently isolated from urine specimens from female patients, while *E. faecalis*, *P. aeruginosa*, *E.*

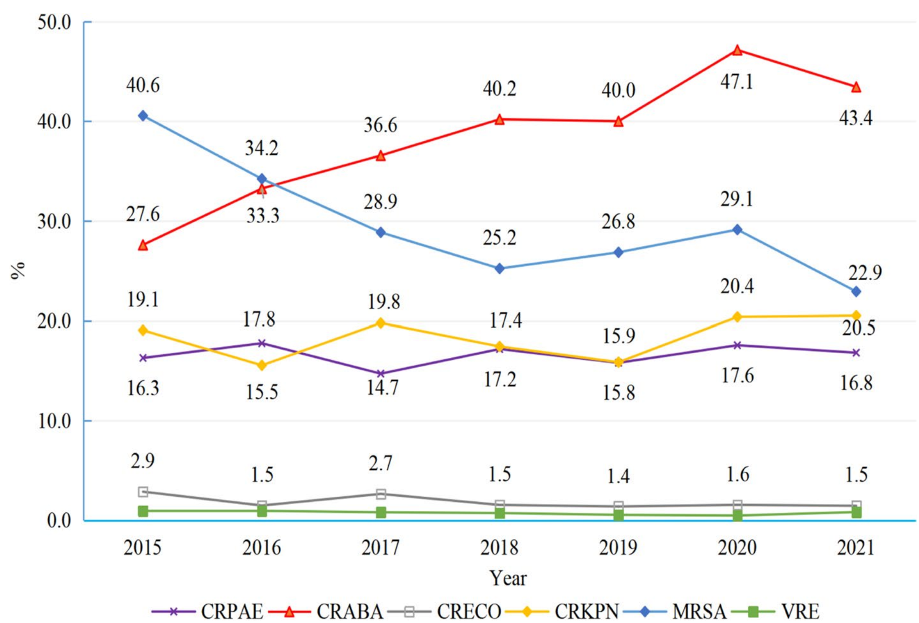

Fig. 5 Prevalence of MRSA, CRECO, CRKPN, CRPAE, CRABA and VRE. MRSA: methicillin-resistant *S. aureus*; CRECO: carbapenem-resistant *E. coli*; CRKPN: carbapenem-resistant *K. pneumoniae*; CRPAE: carbapenem-resistant *P. aeruginosa*; CRABA: carbapenem-resistant *A. baumannii*; VRE: vancomycin-resistant *Enterococcus*

cloacae, *A. baumannii* and *S. aureus* were more common in male patients. The proximity of the urethral orifice to the anus and short urethra in females may be the reason for a greater susceptibility to infection by intestinal bacteria [2, 3]. *P. aeruginosa* and *A. baumannii,* as common pathogens causing hospital-acquired infections [4, 5], were more common in male patients. It is worth further analysis to determine whether UTIs are hospital acquired or community acquired.

The most common Gram-negative bacilli isolated from urine samples were *E. coli* and *K. pneumoniae*, accounting for 46.7% and 9.8% of isolates, respectively, with high resistance rates to cefazolin, cefuroxime, and ciprofloxacin. The resistance rates to tigecycline, amikacin and imipenem were relatively low, which was consistent with the CHINET antimicrobial resistance monitoring results from other types of samples [6]. Fluoroquinolones cannot be easily catabolized in vivo and are mainly excreted in urine in a prototype form, so they are often used as empirical drugs for UTIs. Monitoring showed that the resistance rates to fluoroquinolones in *E. coli* and *K. pneumoniae* ranged from 50% to 70%. This is lower than that reported in the literature [7], where it was found that the resistance rate of *E. coli* from the urine of diabetes patients in Somalia to ciprofloxacin was 77.8%. Cai et al. reported that the resistance rates to ciprofloxacin were 29.9% and 52.4% in *E. coli* and *Klebsiella* spp. isolated from female outpatients affected by uncomplicated cystitis at three hospitals in Italy [8]. This indicates that the resistance rate varies among different populations in different regions. We found that the resistance rate to fluoroquinolones was lower in patients ≤ 18 years of age. In the analysis of the etiology of UTIs and antibiotic resistance of isolated strains at a pediatric hospital in Warsaw, the resistance rates of *E. coli* and *Klebsiella* spp. to ciprofloxacin were 11.9% and 31.1%, respectively. This suggests that the individualized treatment for UTIs should depend on host factors, severity of illness, and risk for multidrug resistance [3].

The prevalence of nosocomial infections caused by MDR pathogens is increasing and has attracted widespread attention, with complex treatment and high mortality rates [9]. In this 7-year retrospective study, the prevalence of MDR in *E. coli*, *K. pneumoniae*, *E. faecium*, and *E. faecalis* was 72.0%, 62.1%, 77.0%, and 23.4%, respectively, higher than that reported in the Jiaxing Region [10]. Although in this study, the prevalence of MRSA constantly decreased from 40.6% in 2015 to 22.9% in 2021, it was still relatively high compared with that in some European countries [11, 12]. MRSA bacteria often carries both aminoglycoside and quinolone resistantance genes and exhibits different degrees of resistance to β-lactams, aminoglycosides, quinolones, and other antibiotics [13]. Based on this study, in terms of medication selection for UTIs caused by MRSA, rifampicin, vancomycin or linezolid can be considered for UTIs caused by MRSA. The widespread use of carbapenems has led to a notable increase in the resistance rate, and carbapenem-resistance organisms (CROs) have emerged as a critical priority antibiotic-resistant pathogens worldwide [14, 15]. In this study we found a continuous increase in the prevalence of CRABA that was higher in male patients than in females; it even exceeded 80% in ICU inpatients. Clinicians should rationally select antibacterial drugs based on the results of bacterial culture and drug susceptibility testing, and closely monitor the treatment of CRO infection.

Carbapenem-resistant *Enterobacteriaceae* (CRE) have increased gradually and caused widespread concern and attention [16]. In this study, the prevalence of CRKPN isolated from urine was 18.5%, slowly increasing from 2015 to 2021; this trends was slightly lower than that from all specimens monitored in CHINET during the same period [17]. Tigecycline and polymyxin are relatively effective antimicrobials in in vitro drug sensitivity assays of CRE strains, but as their concentrations are low in urine and cannot reach effective therapeutic concentrations, they are not recommended for the treatment of UTIs caused by CRE. The Infectious Diseases Society of America [18] recommends ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, nitrofurantoin, or a single dose of an aminoglycoside are preferred treatment options; ceftazidime-avibactam, meropenem-vaborbactam, imipenem-cilastatin-relebactam, or cefiderocol are alternative options for UTIs caused by CRE.

The predominant Gram-positive cocci isolated from urine samples were *E. faecalis* and *E. faecium* (10.4% and 8.7%, respectively). According to monitoring results, *E. faecalis* was more prevalent than *E. faecium* in outpatients, *E. faecium* was more prevalent than *E. faecalis* in inpatients, and *E. faecium* accounted for nearly 80% of Gram-positive isolates in ICU inpatients. This is was consistent with the reports on antibiotic resistance patterns in uropathogens from selected hospitals in China and Poland [19, 20]. The resistance rates of *E. faecalis* to ampicillin and nitrofurantoin were less than 10%, while those of *E. faecium* to ampicillin and levofloxacin exceeded 90%. Empiric antibiotic therapy should be used with different priorities for UTIs caused by *Enterococcus* in different populations. *Enterococcus* is sensitive to vancomycin, linezolid, and teicoplanin, which are the most effective antimicrobial drugs against UTIs caused by this genera; however, some *Enterococcus* have developed resistance to vancomycin, linezolid, and teicoplanin in recent years, complicating the treatment of *Enterococcus* infections.

In this study, the prevalences of vancomycin-resistant *E. faecalis* and *E. faecium* were 0.1% and 1.3%, respectively, while the prevalences of linezolid-resistant *E. faecalis* and *E. faecium* were 2.2% and 0.3%, respectively. The prevalence of VRE was lower than that in Europe and America [21–23], however, it should still be monitored with greater vigilance.

The resistance rates of *Enterobacteriaceae* and other bacteria from inpatients to most antimicrobial drugs were higher than those of isolates from outpatients and emergency patients. The resistance rates to most antimicrobial agents in ICU inpatients were significantly higher than those in non-ICU inpatients, outpatients and emergency patients; this may be because hospitalized patients are more likely to have a history of antibacterial drug use, which has a screening effect on antibiotic-resistant bacteria. ICU patients usually have a longer length of hospitalization and a higher risk of exposure to immunosuppressants, chemotherapy drugs and antibiotics [24, 25]. The incidence of multidrug-resistant bacterial infections in ICU inpatients is rising [26], making it essential to implement antimicrobial stewardship interventions in the ICU setting.

In summary, we analyzed the distribution trend and antimicrobial resistance of uropathogens in China through a 7-year retrospective study using the CHINET antimicrobial resistance surveillance program. Data were collected from 51 hospitals in different provinces and cities in China from 2015 to 2021, making the results extensively representative, though there were some limitations in our analysis. Firstly, this study was retrospective, meaning selection bias and incomplete data (such as that for polymyxin B resistance) may have been present. Secondly, we did not distinguish the differences in bacterial species and drug sensitivity among different urine collection methods such as catheter urine, and midstream urine, cystocentesis urine, etc. Lastly, we did not obtain more detailed information to associate the severity and duration of UTIs with bacterial species and drug resistance to provide more reference value for clinical treatment. Despite this, the findings provide a valuable reference for empiric treatment of UTIs.

Conclusions

E. coli, *Enterococcus*, and *K. pneumoniae* were the most common pathogens causing UTIs in China. The bacterial species and antimicrobial resistance in different patient populations are different. Strengthening of monitoring and surveillance of bacterial resistance in urine samples is needed to minimize the further spread and evolution of multidrug-resistant superbugs such as CRE and VRE.

Materials and methods

Bacterial strains and species identification

All aerobic bacteria isolated from urine specimens of outpatients and inpatients were obtained from the CHINET surveillance system for seven years between 2015 and 2021. Duplicate strains from the same patient were eliminated. Species identification was performed by a commercialized automated system at each participating site and confirmed by matrix-assisted laser desorption ionization-time of flight mass spectrometry at the central laboratory. The quality control strains were *S. aureus* ATCC25923, *E. coli* ATCC25922, *P. aeruginosa* ATCC27853, and *E. faecalis* ATCC29212.

Antimicrobial susceptibility testing

According to a CHINET uniform protocol, the broth microdilution method was used for minimum inhibitory concentration (MIC) testing by an automated antimicrobial susceptibility system, and the Kirby-Bauer disk diffusion method was used to supplement some antimicrobial agents that were not available in automated systems. Throughout the seven-year sampling period, the methodology remained unchanged in every participating hospital.

All results were interpreted by using breakpoints for susceptibility and resistance according to the Clinical and Laboratory Standards Institute (CLSI) 2022 M100-32 guidelines [27], except for tigecycline and polymyxin B. The MICs of tigecycline were interpreted following the breakpoint established by US Food and Drug Administration [28], while the The MICs of polymyxin B were interpreted following the European Committee on Antimicrobial Susceptibility Testing (EUCAST) MIC interpretive breakpoints for colistin [29].

Data analysis

Statistical analysis was conducted using WHONET5.6 software. Pearson's χ^2 test or Fisher's exact test were used for comparisons between two groups. Statistical significance was set at $P < 0.05$ (two-tailed).

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s44280-024-00045-z.

Supplementary Material 1.

Acknowledgements
We would like to express our thanks to members of CHINET for their contribution in the collection of the isolates in this study, including the following: Yang Yang, Fupin Hu, and Demei Zhu from the Institute of Antibiotics, Huashan Hospital, Fudan University; Yingchun Xu and Xiaojiang Zhang from Peking Union Medical College Hospital; Fengbo Zhang and Ping Ji from the First Afliated Hospital of Xinjiang Medical University; Yi Xie and Mei Kang from West China Hospital, Sichuan University; Chuanqing Wang and Pan Fu from Children's Hospital of Fudan University; Yuanhong Xu and Ying Huang from the First Afliated Hospital of Anhui Medical University; Zhongju Chen and Ziyong Sun from Tongji Hospital, Tongji Medical College, Huazhong University of Science & Technology; Yuxing Ni and Jingyong Sun from Ruijin Hospital, Shanghai Jiaotong University School of Medicine; Yunzhuo Chu and Sufei Tian from the First Afliated Hospital of China Medical University; Zhidong Hu and Jin Li from Tianjin Medical University General Hospital; Yunsong Yu and Jie Lin from Sir Run Run Shaw Hospital, Zhejiang University School of Medicine; Bin Shan and Yan Du from the First Afliated Hospital of Kunming Medical University; Sufang Guo and Yanyan Wang from the First Afliated Hospital of Inner Mongolia Medical University; Lianhua Wei and Fengmei Zou from Gansu Provincial Hospital; Hong Zhang and Chun Wang from Children's Hospital of Shanghai; Yunjian Hu and Xiaoman Ai from Beijing Hospital; Chao Zhuo and Danhong Su from the First Afliated Hospital of Guangzhou Medical University; Dawen Guo and Jinying Zhao from the First Afliated Hospital of Harbin Medical University; Xiangning Huang and Hua Yu from Sichuan Provincial People's Hospital; Yan Jin and Chunhong Shao from Shandong Provincial Hospital; Xuesong Xu and Chao Yan from China-Japan Union Hospital, Jilin University; Shanmei Wang and Yafei Chu from Henan Provincial People's Hospital; Lixia Zhang and Juan Ma from Shaanxi Provincial People's Hospital; Shuping Zhou and Yan Zhou from Jiangxi Provincial Children's Hospital; Lei Zhu and Jinhua Meng from Children's Hospital of Shanxi; Fang Dong and Zhiyong Lu from Beijing Children's Hospital affiliated to Capital Medical University; Fangfang Hu from Guizhou Provincial People's Hospital; Han Shen and Wanqing Zhou from Nanjing Drum Tower Hospital, Afliated Hospital of Nanjing; Gang Li and Wei Jia from General Hospital of Ningxia Medical University; Jinsong Wu and Yuemei Lu from Shenzhen People's Hospital; Jihong Li from the Second Hospital of Hebei Medical University; Jinju Duan and Jianbang Kang from the Second Hospital of Shanxi Medical University; Xiaobo Ma and Yanping Zheng from The First Afliated Hospital of Xiamen University; Ruyi Guo and Yan Zhu from Quanzhou First Hospital, Fujian; Yunsheng Chen and Qing Meng from Shenzhen Children's Hospital; Shifu Wang from Qilu Children's Hospital of Shandong University; Xuefei Hu from the First Affiliated Hospital of Nanchang University; Jilu Shen from the Fourth Affiliated Hospital of Anhui Medical University; Ruizhong Wang and Hua Fang from Pudong New Area People's Hospital; Bixia Yu from Zhejiang Ningbo Zhenhai Longsai Hospital; Ping Gong and Yong Zhao from the People's Hospital of Zigui, Hubei Province; Kaizhen Weng and Yirong Zhang from Jinjiang Municipal Hospital; Jiangshan Liu from Jinchang Hospital of Integrated Traditional Chinese and Western Medicine; Longfeng Liao from the People's Hospital of Ganxian; Hongqin Gu from Guangrao County People's Hospital; Lin Jiang from the People's Hospital of Huixian, Henan Province; Wen He from Central Hospital of Yingkou Development Zone, Liaoning Province; Shunhong Xue from Huzhu County People's Hospital, Qinghai Province; Jiao Feng from the People's Hospital of Linshui, Sichuan Province and Chunlei Yue from Jiutai People's Hospital.

Authors' contributions
All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Y.L. and J.L. The first draft of the manuscript was written by Y.L. and the final review was done by W.L. and Q.Y.. All authors contributed to the article and approved the submitted version.

Funding
This work was funded by the China Antimicrobial Surveillance Network (independent medical grants from Pfizer, 2020QD049) and the Innovative R&D Project Subsidy Program of the Hunan Provincial Development and Reform Commission (Project No. 2019875).

Availability of data and materials
The datasets used or analyzed during the current study are available in CHINET, www.chinets.com.

Declarations

Ethics approval and consent to participate
The study protocol was approved by the Institutional Review Board of Huashan Hospital, Fudan University (no. 2019–460).

Consent for publication
Not applicable.

Competing interests
The authors report no conflicts of interest in this work.

Received: 9 August 2023 Revised: 20 March 2024 Accepted: 28 March 2024
Published online: 22 May 2024

References

1. Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. Nat Rev Microbiol. 2015;13(5):269–84.
2. Kunin CM, Evans C, Bartholomew D, Bates DG. The antimicrobial defense mechanism of the female urethra: a reassessment. J Urol. 2002;168(2):413–9.
3. Gupta K, Grigoryan L, Trautner B. Urinary tract infection. Ann Intern Med. 2017;167(7):ITC49–64.
4. Liu C, Chen K, Wu Y, Huang L, Fang Y, Lu J, et al. Epidemiological and genetic characteristics of clinical carbapenem-resistant *Acinetobacter baumannii* strains collected countrywide from hospital intensive care units (ICUs) in China. Emerg Microbes Infect. 2022;11(1):1730–41.
5. Zhang B, Xu X, Song X, Wen Y, Zhu Z, Lv J, et al. Emerging and re-emerging KPC-producing hypervirulent *Pseudomonas aeruginosa* ST697 and ST463 between 2010 and 2021. Emerging Microbes Infect. 2022;11(1):2735–45.
6. Hu F, Zhu D, Wang F, Wang M. Current status and trends of antibacterial resistance in China. Clin Infect Dis. 2018;67(suppl_2):S128–34.
7. Hassan SA, Ahmed Y, Hassan GD. Antimicrobial susceptibility of *Escherichia coli* isolated from diabetic patients in Mogadishu. Somalia Front Microbiol. 2023;14:1204052.
8. Cai T, Verze P, Arcaniolo D, Pandolfo SD, Smarrazzo F, Manfredi C, et al. Antibiotic resistance patterns among uropathogens in female outpatients affected by uncomplicated cystitis: focus on fosfomycin trometamol. Int J Antimicrob Agents. 2023;62(5):106974.
9. Whelan S, Lucey B, Finn K. Uropathogenic *Escherichia coli* (UPEC)-associated urinary tract infections: the molecular basis for challenges to effective treatment. Microorganisms. 2023;11(9):2169.
10. Niu X, Hou B, Yang L, Wang L, Yu Q, Mao M, et al. Patterns of drug resistance and bacterial pathogen distribution in patients with urinary tract infections in the Jiaxing region from 2020 to 2022. Infect Drug Resist. 2023;16:5911–21.
11. Rödenbeck M, Ayobami O, Eckmanns T, Pletz MW, Bleidorn Jutta, Markwart R, et al. Clinical epidemiology and case fatality due to antimicrobial resistance in Germany: a systematic review and meta-analysis, 1 January 2010 to 31 December 2021. Euro Surveill. 2023;28(20):2200672.
12. Möller V, Östholm-Balkhed A, Berild D, Fredriksson M, Gottfredsson M, Holmbom M, et al. Antibiotic resistance among major pathogens compared to hospital treatment guidelines and antibiotic use in Nordic hospitals 2010–2018. Infect Dis. 2021;53(8):607–618.
13. Jiang K, Chen X, Zhang W, Guo Y, Liu G. Nonribosomal antibacterial peptides isolated from *Streptomyces agglomeratus* 5-1-3 in the Qinghai-Tibet Plateau. Microb Cell Fact. 2023;22(1):5.
14. Satlin MJ, van Duin D, Tamma PD, Lodise TP, Van Tyne D, Rodvold KA, et al. Priorities and progress in Gram-negative bacterial infection research by the antibacterial resistance leadership group. Clin Infect Dis. 2023;77(Supplement_4):S305–13.
15. Castanheira M, Kimbrough JH, DeVries S, et al. Trends of β-Lactamase occurrence among *Escherichia coli* and *Klebsiella pneumoniae* in United States hospitals during a 5-Year period and activity of antimicrobial

agents against isolates stratified by β-Lactamase type. Open Forum Infect Dis. 2023;10(2):ofad38.
16. Perez F, Bonomo RA. Carbapenem-resistant *Enterobacteriaceae*: global action required. Lancet Infect Dis. 2019;19(6):561–2.
17. Yang W, Ding L, Han R, Yin D, Wu S, Yang Y, et al. Current status and trends of antimicrobial resistance among clinical isolates in China: a retrospective study of CHINET from 2018 to 2022. One Health Advances. 2023;1(1):8.
18. Tamma PD, Aitken SL, Bonomo RA, et al. Infectious diseases society of America 2022 guidance on the treatment of extended-spectrum β-lactamase producing *Enterobacterales* (ESBL-E), Carbapenem-Resistant *Enterobacterales* (CRE), and *Pseudomonas aeruginosa* with difficult-to-treat resistance (DTR-*P. aeruginosa*). Clin Infect Dis. 2022;75(2):187–212.
19. Huang L, Huang C, Yan Y, et al. Urinary tract infection etiological profiles and antibiotic resistance patterns varied among different age categories: a retrospective study from a tertiary general hospital during a 12-Year period. Front Microbiol. 2022;12:813145.
20. Kraszewska Z, Skowron K, Kwiecińska-Piróg J, Grudlewska-Buda K, Przekwas J, Wiktorczyk-Kapischke N, et al. Antibiotic resistance of *Enterococcus spp.* isolated from the urine of patients hospitalized in the university hospital in North-Central Poland, 2016–2021. Antibiotics. 2022;11(12):1749.
21. Ayobami O, Willrich N, Reuss A, Eckmanns T, Markwart R. The ongoing challenge of vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis* in Europe: an epidemiological analysis of bloodstream infections. Emerg Microbes Infect. 2020;9(1):1180–93.
22. Carvalhaes CG, Sader HS, Streit JM, Castanheira M, Mendes RE. Activity of oritavancin against Gram-positive pathogens causing bloodstream infections in the United States over 10 years: focus on drug-resistant enterococcal subsets (2010–2019). Antimicrob Agents Chemother. 2022;66(2):e166721.
23. Jernigan JA, Hatfield KM, Wolford H, Nelson RE, Olubajo B, Reddy SC, et al. Multidrug-resistant bacterial infections in U.S. hospitalized patients, 2012–2017. N Engl J Med. 2020;382(14):1309–19.
24. Medina-Polo J, Naber KG, Bjerklund Johansen TE. Healthcare-associated urinary tract infections in urology. GMS Infect Dis. 2021;9:Doc05.
25. Pasero D, Cossu AP, Terragni P. Multi-drug resistance bacterial infections in critically ill patients admitted with COVID-19. Microorganisms. 2021;9(8):1773.
26. Timsit J, Bassetti M, Cremer O, Daikos G, de Waele J, Kallil A, et al. Rationalizing antimicrobial therapy in the ICU: a narrative review. Intensive Care Med. 2019;45(2):172–89.
27. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. CLSI supplement M100. 32nd ed. Wayne: Clinical and Laboratory Standards Institute; 2022.
28. U.S. Food and Drug Administration. FDA-identified interpretive criteria. https://www.fda.gov/drugs/development-resources/tigecycline-injection-products. Accessed 2 Aug 2023.
29. The European Committee on Antimicrobial Susceptibility Testing (EUCAST). Clinical reakpoints tables for interpretation of MICs and zone diameters. https://eucast.org/fleadmin/src/media/PDFs/EUCAST_fles/Breakpoint_tables/v_12.0_Breakpoint_Tables.pdf. Accessed 2 Aug 2023.

Publisher's Note