UNITED ARAB EMIRATES
MINISTRY OF HEALTH & PREVENTION

NATIONAL AMR SURVEILLANCE REPORT

in collaboration with:

هيئة الصحة بدبي
DUBAI HEALTH AUTHORITY

دائرة الصحة
DEPARTMENT OF HEALTH

مركز أبوظبي للصحة العامة
ABU DHABI PUBLIC HEALTH CENTRE

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Annual Report 2019

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- **Abu Dhabi Public Health Center (ADPHC)**
- **Mohammed Bin Rashid University, Dubai**
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Foreword

Antimicrobial resistance (AMR) has become a major threat to public health worldwide, including the Middle East and the Gulf Region. AMR impacts on human health due to increased length of stay, treatment failures, and significant human suffering and deaths, and is increasing healthcare costs as well as indirect costs.

The United Arab Emirates Ministry of Health and Prevention, in collaboration with the Ministry of Presidential Affairs (MOPA), Dubai Health Authority (DHA), Department of Health-Abu Dhabi (DoH), Abu Dhabi Public Health Center (ADPHC), and other entities, has in 2015 launched an initiative to combat antimicrobial resistance and established the UAE Higher Committee for AMR. Under the AMR Higher Committee, several technical Sub-Committees have been established, including a National Sub-Committee for Antimicrobial Resistance Surveillance.

The work of the UAE National Sub-Committee for AMR Surveillance has led to the creation of a network of currently 39 microbiology laboratories and 248 clinical surveillance sites across the country. These laboratories and surveillance sites are key to generating, collecting, and reporting AMR surveillance data to the central unit, and the AMR data from these hospitals, centers and clinics across all seven Emirates of the UAE form the basis of this report.

The United Arab Emirates are since 2018 also contributing data to the global AMR Surveillance System (GLASS), established in 2015 by the World Health Organization (WHO).

AMR surveillance data serves as local evidence and benchmark data for the antimicrobial resistance situation in participating countries. Sharing such surveillance data enables an open dialogue about challenges, differences, and communalities, and it allows tracking progress and effectiveness of antimicrobial stewardship programs, and policy and action over time, as the surveillance system and antibiotic stewardship initiatives mature.

Significant efforts have been made by the Higher Committee for AMR, the AMR Technical Sub-Committee for AMR Surveillance, the AMR focal points in participating surveillance sites and laboratories, and other experts, to strengthen the UAE national AMR surveillance system, to increase awareness for AMR, and to enhance the technical capacities for AMR surveillance.

It remains our goal to monitor the levels and trends of AMR surveillance in the UAE, and to guide UAE national AMR control policies based on the evidence generated.

We would like to thank all colleagues and focal points in the network of participating laboratories and surveillance sites, the AMR Surveillance Sub-Committee, and the pool of experts, for their efforts, support and dedication to the UAE National AMR surveillance network and contributions to this report.

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The Ministry of Health and Prevention wishes to thank all participating and collaborating entities and individuals for participating in the UAE National AMR Surveillance program and development of this Annual Report.

1. Executive Summary

The **UAE National AMR Surveillance System** has been established in 2015 by the Ministry of Health and Prevention. It is a lab-based surveillance system and relies on a network of currently 39 clinical microbiology laboratories across all seven Emirates, providing microbiology services for 248 surveillance sites, including 78 hospitals and 170 centers/clinics (**Figure 1.1, Figure 2.32, Table 2.3.1, and Annex 5.5/5.6**).

This is the first report of the UAE National AMR surveillance program, presenting AMR data on 482,312 patients from 248 surveillance sites (public and private sector), for the reporting period 2010-2019. Data for the reporting year 2019 is presented in form of cumulative antibiograms (**Section 4.2**), as well as more detailed statistics and annual trends for several AMR priority pathogens (**Section 4.3**).

This UAE National AMR surveillance data demonstrates that antibiotic resistance is widespread, and, overall, increasing in the United Arab Emirates. This surveillance data provides a basis for taking action to control AMR in UAE.

The data in this report presents a good estimate of current levels and trends of antimicrobial susceptibility and resistance in the UAE. Based on the large number of surveillance sites and reported isolates from all regions, sectors, and facility types in the UAE, and the distribution of pathogens, there is no indication of selective sampling. As such, the data is considered sufficiently representative for the UAE patient population; however, it should still be interpreted with caution.

Table 1.1 provides a summary overview of current antimicrobial resistance levels (percent resistant isolates, %R) in the UAE (2019):

Table 1.1 AMR Priority Pathogens – Percentage resistant isolates (%R), United Arab Emirates, 2019

Priority[a]	Organism	Antibiotic or antibiotic class	N (patients)	% resistant isolates
Priority 1: Critical	*Acinetobacter* spp.	Imipenem or meropenem	1,675	**25.0**
	Pseudomonas aeruginosa	Imipenem or meropenem	6,735	**14.4**
	Enterobacterales	Imipenem or meropenem	46,347	**4.3**
	Klebsiella pneumoniae	Imipenem or meropenem	10,456	**4.5**
	Enterobacterales	ESBL (ceftriaxone/cefotaxime)[b]	34,841	**27.6/27.0**
	Escherichia coli	ESBL (ceftriaxone/cefotaxime)[b]	20,425	**32.5/31.9**
	Klebsiella pneumoniae	ESBL (ceftriaxone/cefotaxime)[b]	7,580	**26.5/24.7**
Priority 2: High	*Enterococcus faecium*	VRE[c] (vancomycin)	320	**10.0**
	Staphylococcus aureus	MRSA[d] (oxacillin)	16,484	**35.3**
	Salmonella spp. (non-typhoid)	Fluoroquinolones (ciprofloxacin)	92	**18.5**
	Neisseria gonorrhoeae	3rd-generation cephalosporins	58	**0**
	Neisseria gonorrhoeae	Fluoroquinolones (ciprofloxacin)	58	**91.4**
Priority 3: Medium	*Streptococcus pneumoniae*	Penicillin (oral)	1,148	**11.8**
	Streptococcus pneumoniae	Penicillin (meningitis)	1,148	**42.7**
	Streptococcus pneumoniae	Penicillin (non-meningitis)	1,148	**3.1**
	Haemophilus influenzae	Ampicillin	1,132	**27.3**
	Shigella spp.	Fluoroquinolones (ciprofloxacin)	95	**42.1**

[a]WHO, 2017[1]/Tacconelli 2017[2]. [b]ESBL: Extended-spectrum beta-lactamase producer (based on resistance to ceftriaxone and/or cefotaxime), [c]VRE: Vancomycin-resistant *Enterococcus faecium*, [d]MRSA: Methicillin (oxacillin)-resistant *S. aureus*.

In conclusion, the information contained in this report provides evidence that antimicrobial resistance is widespread and, overall, increasing in clinical settings in the United Arab Emirates. This data provide a basis for taking action to control AMR in the United Arab Emirates.

Tables 1.2 to 1.4 provide a summary overview of antimicrobial resistance trends observed for Gram-negative bacteria, Gram-positive bacteria, *Candida albicans* and *Mycobacterium tuberculosis* in the UAE during the period 2010-2019:

Table 1.2 Antimicrobial resistance trends, United Arab Emirates, 2010-2019 – Gram-negative bacteria

Antibiotic class/substance	*Escherichia coli*	*Klebsiella pneumoniae*	*Salmonella* spp.	*Pseudomonas aeruginosa*	*Acinetobacter* spp.
Aminopenicillins	↓	**n/a**	↑↑	**R**	**R**
Beta-lactam/beta-lactamase inhibitor combination (AMC/TZP)	↑/↓	↑↑/→	**n.s.**	**R/↓**	**R/↓↓**
3rd-/4th-generation cephalosporins	↑↑/↑		↑/→	→/→	↓↓/↓↓
Carbapenems	↑	↑	→	↓	↓↓
Fluoroquinolones	↑↑	↑↑	↑	↑	↓↓
Aminoglycosides	↓	→	**n/a**	↓	↓↓
Trimethoprim/sulfamethoxazole	↓	**n.s.**	↓	**R**	↓↓
Multidrug resistance (≥ 3 classes)	**(↑)**	↑↑	↑↑	↓	↓↓

↓/↑/→: decreasing/increasing/horizontal trend of percentage resistant isolates (%R), R: intrinsically resistant, n/a: not applicable, n.s.: not significant, AMC: amoxicillin/clavulanic acid, TZP: piperacillin/tazobactam.

Table 1.3 Antimicrobial resistance trends, United Arab Emirates, 2010-2019 – Gram-positive bacteria

Antibiotic class/substance	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Enterococcus faecalis*	*Enterococcus faecium*
Beta-lactam antibiotics	↑↑ (OXA)	↓ (PEN)	→ (AMP)	→ (AMP)
Macrolides (erythromycin)	↑↑	↑↑	**n/a**	**n/a**
Lincosamides (clindamycin)	↑↑	→	**n/a**	**n/a**
Aminoglycosides	↑	**n/a**	↑↑ (GEN HL)	→
Fluoroquinolones	↑↑	↑	**↑ (MFX)**	→
Glycopeptides	**→ (0 %R)**	**→ (0 %R)**	**→ (<1 %R)**	**↓↓ (VRE)**
Trimethoprim/sulfamethoxazole	↑↑	↑	**R**	**R**
Multidrug resistance (≥ 3 classes)	↑↑	↑↑	↑	↑↑

↓/↑/→: decreasing/increasing/horizontal trend of percentage resistant isolates (%R), R: intrinsically resistant, n/a: not applicable, n.s.: not significant, OXA: oxacillin, PEN: penicillin, AMP: ampicillin, MFX: Moxifloxacin, VRE: Vancomycin-resistant *Enterococcus faecium*.

Table 1.4 Antimicrobial resistance trends, United Arab Emirates, 2010-2019 – *Candida albicans* and *Mycobacterium tuberculosis*

Antibiotic class/substance	*Candida albicans*
Triazoles	↑/↑↑
Fluconazole	↑
Voriconazole	↑↑
Polyenes	→
Amphotericin B	→
Echinocandins	↓
Caspofungin	↓
Micafungin	↓

Antibiotic class/substance	*M. tuberculosis*
Rifampin	↑
Ethambutol	→
Isoniazid	→
Pyrazinamide	→
Streptomycin	↑
Multidrug resistance (RIF+INH)	↑

↓/↑/→: decreasing/increasing/horizontal trend of percentage resistant isolates (%R)

2. Introduction

2.1. Antimicrobial resistance

Antimicrobial resistance (AMR) has become a major threat to public health worldwide, including the Middle East and the Gulf Region. AMR impacts on human health due to increased length of stay, treatment failures, and significant human suffering and deaths, as well as leading to increased healthcare costs and indirect costs. Globally, an estimated 700,000 deaths annually are currently attributable to antimicrobial resistance, and this number is expected to increase to 10,000,000 deaths by 2050, with an associated estimated loss to global gross domestic product of up to 100 trillion US dollar per year[3]. Without effective antibiotics, the success of major surgery and cancer chemotherapy would be compromised[4].

Antimicrobial resistance (AMR) is the ability of a microorganism to resist the action of one or more antimicrobial agents. The consequences can be severe, as prompt treatment with effective antimicrobials is the most important intervention to reduce the risk of poor outcome of serious infections. Development of AMR is a natural phenomenon caused by mutations in bacterial genes, or by acquisition of exogenous resistance genes carried by mobile genetic elements that can spread horizontally between bacteria. Bacteria can acquire multiple resistance mechanisms and hence become resistant to several, or even all, antimicrobial agents used to treat them, which is particularly problematic as it may severely limit the available treatment alternatives for the infection.

The major drivers behind the occurrence and spread of AMR are the use of antimicrobial agents and the transmission of antimicrobial-resistant microorganisms between humans; between animals; and between humans, animals and the environment. While antimicrobial use exerts ecological pressure on bacteria and contributes to the emergence and selection of AMR, poor infection prevention and control practices favour the further spread of these bacteria.

2.2 Surveillance of antimicrobial resistance

Public health surveillance is the continuous and systematic collection, analysis, interpretation and dissemination of health-related data needed for the planning, implementation, and evaluation of public health practice.

Such surveillance can serve as an early warning system for impending public health emergencies; it can document the impact of an intervention, or track progress towards specified goals; and monitor and clarify the epidemiology of health problems, to allow priorities to be set and to inform public health policy and strategies. Surveillance of antimicrobial resistance enables the concerned public health and health authorities to monitor, document and report on levels and trends of antibiotic resistance.

AMR Surveillance is not only important to better understand the epidemiology of antimicrobial resistance; this data can also be utilized to

- analyse and predict trends of resistance
- generate cumulative antibiograms (routine and enhanced antibiograms)
- detect and identify clusters and potential outbreaks of community-associated (CA) and healthcare-acquired infections (HAI)
- inform and guide, and monitor the effectiveness of antimicrobial stewardship programs,
- develop antibiotic usage guidelines for common infections, and
- assist health professionals with empiric antimicrobial treatment choices, tailored to the antibiotic resistance epidemiology in the patient's geographic region and setting.

2.3 UAE AMR surveillance system

The United Arab Emirates AMR surveillance system was first established in 2010 on a subnational level (Abu Dhabi Emirate, HAAD/DoH). In 2015, the system was expanded and established nationwide by the Ministry of Health and Prevention (MOHAP), in collaboration with the UAE Ministry of Presidential

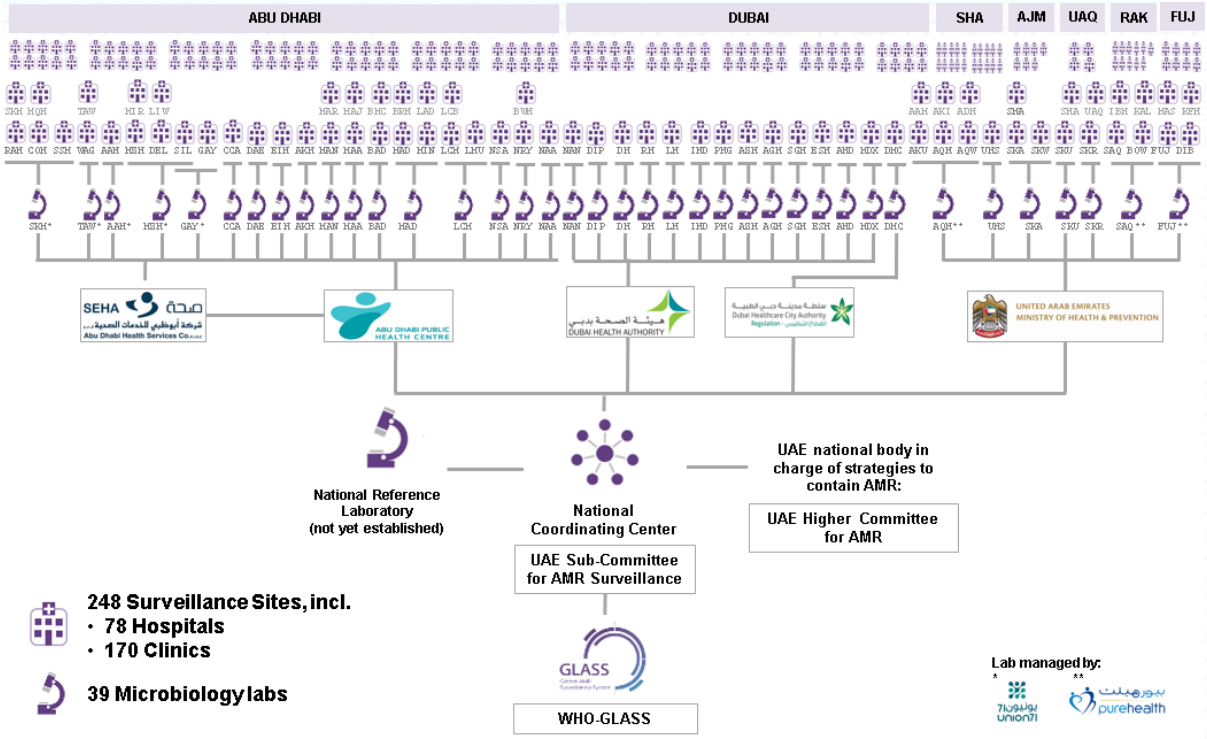
Affairs (MOPA), Dubai Health Authority (DHA), Dept. of Health Abu Dhabi (DoH), and Abu Dhabi Public Health Center (ADPHC).

The UAE National AMR surveillance system also participates in and provides AMR data to the Global AMR Surveillance System (GLASS), established by the World Health Organization (WHO) in 2015[5].

As of Oct 2020, the UAE AMR surveillance system relies on a network of 248 surveillance sites (78 hospitals and 170 centers/clinics), that are served by 39 clinical microbiology laboratories in all seven Emirates of the United Arab Emirates (**Figure 2.3.1**, **Table 2.3.1**, and **Annex 5.5/5.6**).

These surveillance sites and laboratories are key to generating and collecting AMR surveillance data and reporting it to the UAE Sub-Committee for AMR Surveillance, and the AMR clinical and microbiology data collected from these surveillance sites and laboratories form the basis of this surveillance report.

Figure 2.3.1 UAE National Network of AMR Surveillance Sites (NAMRS)



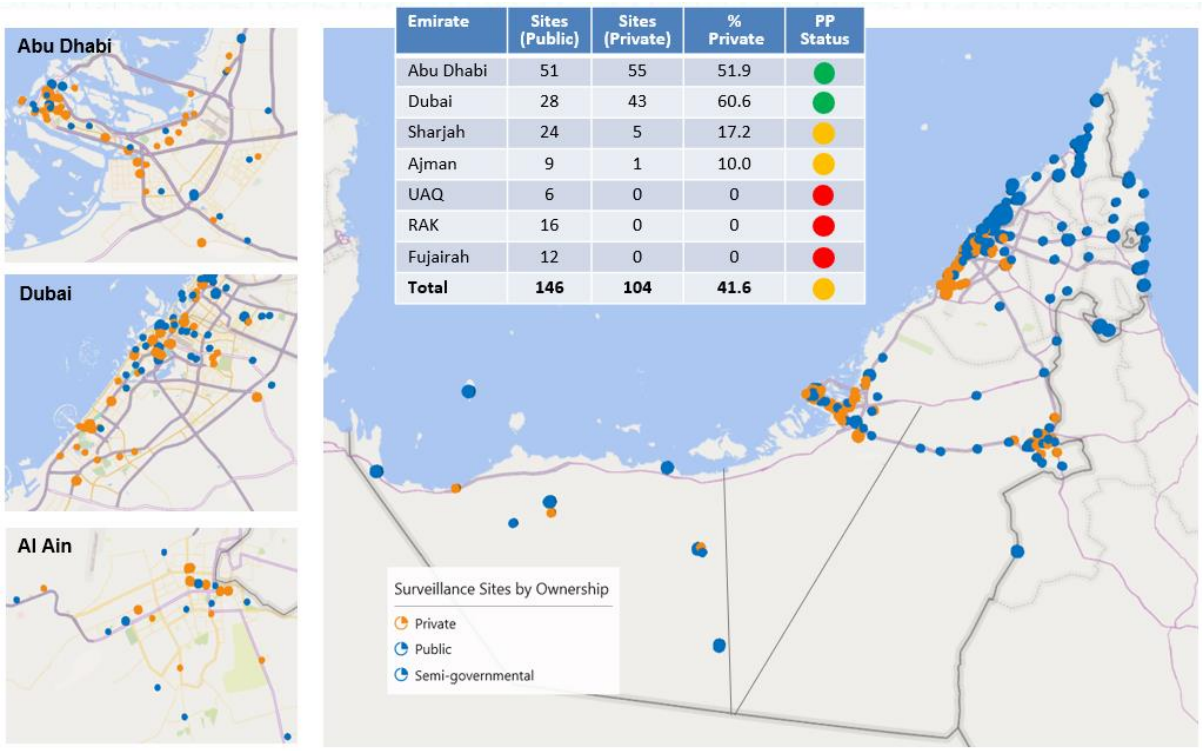
The AMR data submitted includes routine clinical and antibiotic susceptibility testing data from both, governmental as well as private healthcare facilities. There is no central confirmatory testing or central repository of isolates as there is no UAE national reference lab for antimicrobial resistance (NRL-AMR).

Surveillance sites and microbiology laboratories are sited in all seven Emirates of the UAE (**Figure 2.3.2, Table 2.3.1**). Since the start of the UAE AMR surveillance, the number of public and private healthcare facilities participating in AMR surveillance has increased significantly. **Figure 2.3.3** shows the number of public hospitals, private hospitals, and outpatient facilities (centers/clinics) reporting AMR data.

Table 2.3.1 AMR surveillance sites and labs – by Emirate (2019)

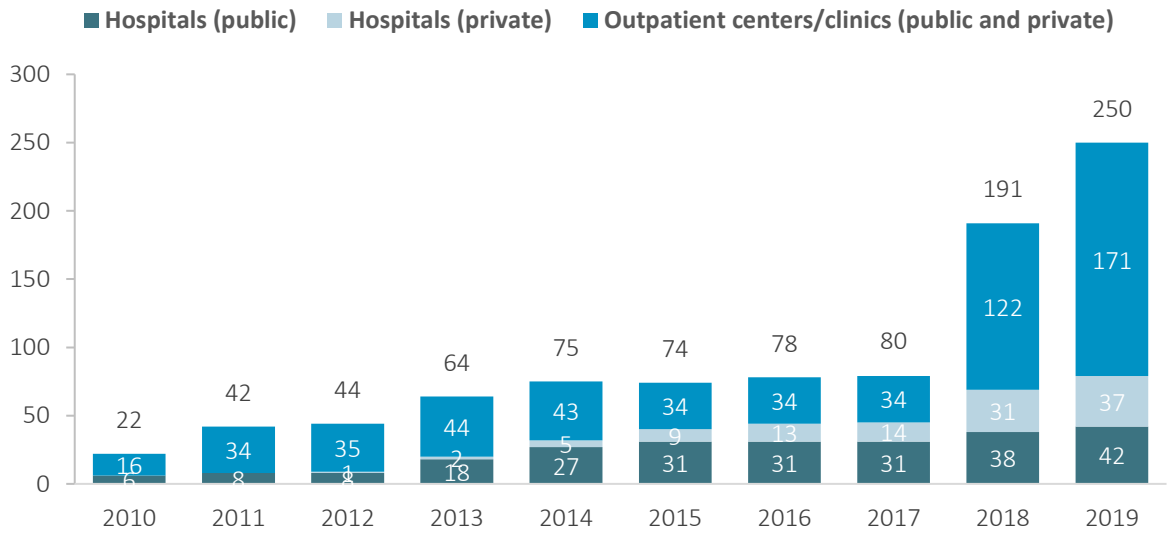
Facility Type	Abu Dhabi	Dubai	Sharjah	Ajman	UAQ	RAK	Fujairah	Total
Hospital	36	21	7	3	2	5	4	**78**
Center/clinic	70	50	20	7	4	11	8	**170**
Sites (total)	**106**	**71**	**27**	**10**	**6**	**16**	**12**	**248**
Laboratories	17	15	2	1	1	2	1	**39**

Figure 2.3.2 AMR surveillance sites[a] – by location, and ownership (public/private)



Emirate	Sites (Public)	Sites (Private)	% Private	PP Status
Abu Dhabi	51	55	51.9	
Dubai	28	43	60.6	
Sharjah	24	5	17.2	
Ajman	9	1	10.0	
UAQ	6	0	0	
RAK	16	0	0	
Fujairah	12	0	0	
Total	**146**	**104**	**41.6**	

Figure 2.3.3 Number of surveillance sites reporting AMR data - by year, facility type and sector



3. Methods

Hospitals, centers, clinics, and clinical microbiology labs are generating and collecting many clinical and AMR data as part of their routine patient care. This data can also be utilised for generating cumulative antibiograms and local monitoring of antimicrobial resistance (at the facility level), as well as for public health surveillance of antimicrobial resistance (at the Emirate- and/or country level).

3.1 Data generation

Identification of organisms: Thirty-eight out of 39 (97%) participating microbiology laboratories use at least one commercial automated system for identification of bacteria and/or yeast, including VITEK-2[6] (n=28, 72%), and BD Phoenix[7] (n=10, 26%), and MicroScan (n=1, 3%). Only one lab (n=1, 3%) relies on manual (API) systems only for identification[8]. Unusual test results are confirmed locally.

Antimicrobial susceptibility testing: Thirty-seven out of thirty-nine (n=37, 95%) microbiology laboratories use at least one commercial, automated system for routine antimicrobial susceptibility testing, the remaining two laboratories (n=2, 5%), use manual testing methods only (disc diffusion/Kirby Bauer). Selected organisms (*H. influenzae*, *S. pneumoniae*) are routinely tested by manual methods (disc diffusion), as per CLSI guideline recommendations. All labs follow CLSI guidelines for antimicrobial susceptibility testing[9]. Unusual antibiotic susceptibility testing results are confirmed locally.

Interpretation of susceptibility testing results: There are no Abu Dhabi or UAE national antibiotic susceptibility testing guidelines. For interpretation of susceptibility testing results for fungi and yeast, all participating laboratories apply the CLSI[10] guidelines as well as other guidelines, e.g. EUCAST[11], or CDC[12] (for Candida auris), where CLSI breakpoints are not available.

AST data submitted to DoH includes metadata (e.g. specimen type, specimen date, organism name, antibiotic name, AST test method used), as well as the measured and/or interpreted AST test results. Wherever available and technically feasible, the measured, numerical AST result is collected (MIC/IZD values, n=28 labs, 74%), otherwise the interpreted AST result is collected (S/I/R, n=10 labs, 26%).

Clinical and demographic data for each isolate is extracted from hospital/laboratory information systems (HIS/LIS) wherever available and technically feasible (59%, 23/39 labs). This includes information on e.g., patient date of birth, age, gender, nationality, location, location type, clinical specialty/department, date of encounter or admission, date of discharge, length of stay, health outcome, or other information, as available.

Quality control: All participating microbiology laboratories

- are operated by a healthcare provider that is licensed by the concerned Health Authority (MOHAP, DoH, DHA, DHCA, MOPA)
- are either lab-accredited, or in the final steps of lab-accreditation
- are headed by a licensed clinical pathologist or clinical microbiologist
- must comply with quality standards for clinical laboratories (e.g.: Abu Dhabi, ref.: (13))
- conduct routine internal quality control testing (e.g., ATCC); and
- are successfully participating since several years in at least one internationally recognised, external quality assurance programme (EQAS), i.e., CAP Pt, ACP-MLE, or REQAS.

Only final and validated antimicrobial susceptibility testing results are reported for AMR surveillance. As of Dec 2020, 31 out of 39 (80%) of participating microbiology labs are lab-accredited, by either CAP, or ISO 15189, or both. The remaining 8 labs (20%) are in the process of CAP and/or ISO accreditation (most of them expecting accreditation by summer 2021). Fifty-four of 80 (68%) participating hospitals are accredited by Joint Commission International (JCI).

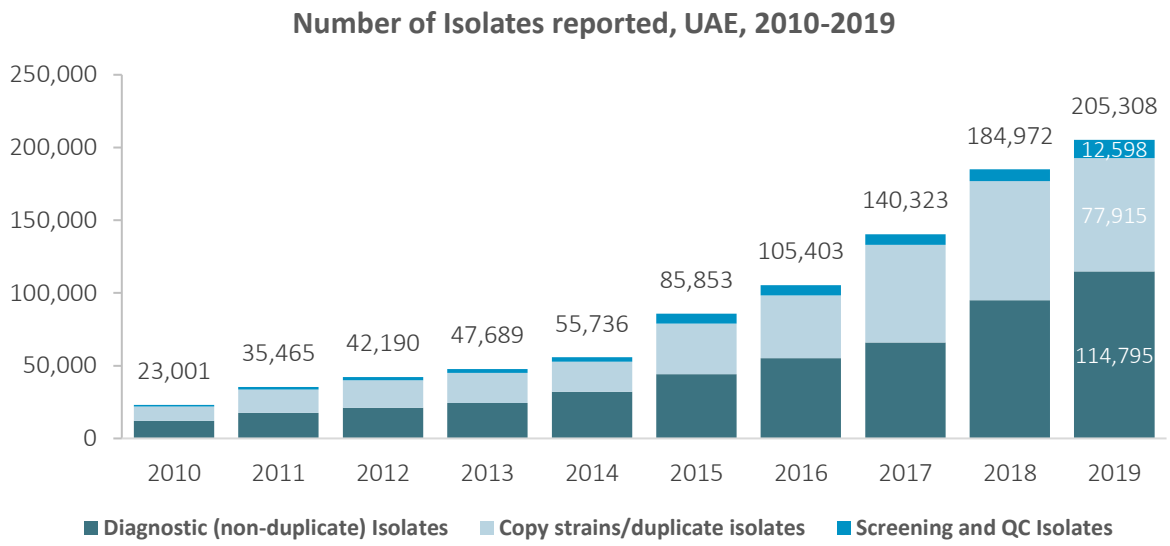
3.2 Data collection

Nominated focal points at participating surveillance sites are submitting AMR data on monthly, quarterly, or annual basis to the national AMR Surveillance Center. AMR data submitted includes microbiology data and, where available and technically feasible, clinical, and demographic data. The reporting

protocol is in line with UAE national AMR surveillance protocol and has adopted the global reporting protocols for AMR surveillance (WHO-GLASS)[14].

Since the start of the UAE AMR surveillance system in 2010, the number of bacterial and fungal isolates reported by participating surveillance sites has increased significantly (**Figure 3.1.1**).

Figure 3.1.1 Number of isolates reported by national surveillance sites, by year (2010-2019)



Screening isolates and quality control isolates accounted for 6% of reported isolates in 2019 and are routinely excluded from analysis. Copy strains (duplicate isolates) accounted for 38% of reported isolates in 2019 and are routinely excluded from analysis. Only diagnostic, non-duplicate isolates (~60% of all reported isolates) are included in the analysis (see **section 3.3** for details on inclusion, exclusion, and deduplication criteria).

The UAE National AMR surveillance system collects information on all bacteria and yeast grown by cultural methods and tested for antimicrobial susceptibility as part of daily patient routine in participating facilities. For analysis and public health reporting, it focuses then on the following nine bacterial pathogens of public health and clinical importance (enhanced surveillance for AMR priority pathogens):

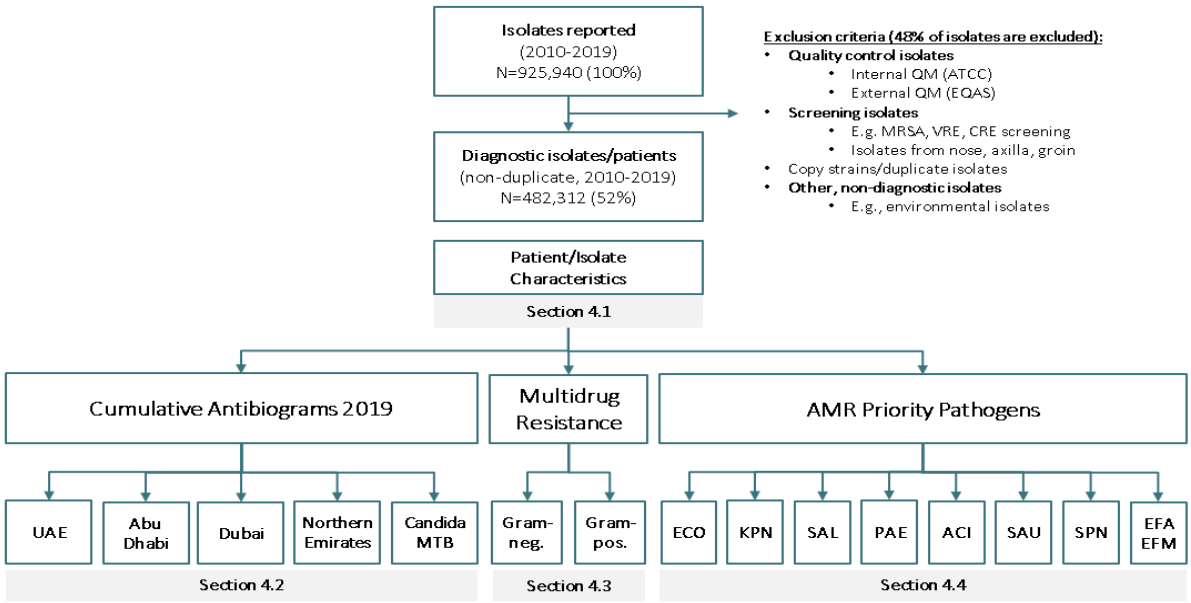
- *Escherichia coli* (*E. coli*)
- *Klebsiella pneumoniae* (*K. pneumoniae*)
- *Salmonella* spp. (non-typhoidal)
- *Pseudomonas aeruginosa* (*P. aeruginosa*)
- *Acinetobacter* spp.
- *Staphylococcus aureus* (*S. aureus*)
- *Streptococcus pneumoniae* (*S. pneumoniae*)
- *Enterococcus faecalis* (*E. faecalis*)
- *Enterococcus faecium* (*E. faecium*).

Annex 5.1 describes the AMR priority pathogens under enhanced AMR Surveillance and the main infections caused by these pathogens.

AMR data is collected and exported from laboratory- or hospital-information systems (LIS/HIS) wherever possible, or from semi-automated, commercial AST systems otherwise. After submission of AMR data to the national AMR Surveillance Center, the data is checked for plausibility, completeness and quality, and feedback is communicated to the AMR focal point at the surveillance site. If needed,

AMR focal points are asked to verify, update, and resubmit the data, as applicable. After conversion of AMR raw data to WHONET format, using the BacLink tool, the AMR data is added to the UAE AMR surveillance database (WHONET)[15]. **Figure 3.1.2** presents details on isolates reported and AMR surveillance reports available.

Figure 3.1.2 Number of isolates reported, and AMR surveillance reports available, 2010-2019



For the reporting period 2010-2019 the laboratory network submitted AMR data on 925,940 isolates. After applying exclusion criteria (**Figure 3.1.2**, and section 3.2), a total of 482,312 (52%) diagnostic, non-duplicate patient isolates remained for analysis. Data is presented in this report in Chapter four:

Section 4.1 (patient/isolate characteristics) presents the patient characteristics of isolates reported from all surveillance sites in the UAE during the 2019 reporting period.

Section 4.2 (cumulative antibiograms) presents the national cumulative antibiogram 2019, sub-national cumulative antibiograms for Abu Dhabi Emirate, Dubai Emirate, and the five Northern Emirates, plus cumulative antibiograms and annual trends for *Candida* spp., and *Mycobacterium tuberculosis*.

Section 4.3 (multidrug resistance) presents annual trends of multidrug resistance (%MDR) for Gram-negative and Gram-positive bacteria.

Section 4.4 (AMR priority pathogens) presents percent resistant/intermediate/susceptible (%RIS) statistics, and long-term AMR trends for the UAE (2010-2019) for the AMR priority pathogens. For selected pathogens detailed breakdowns are provided as percent resistant isolates (%R) – by Emirate, nationality status, age group, gender, location type, isolate source, department, and facility.

3.3 Data analysis

Data analysis was conducted with the WHONET 2020 Software for Antimicrobial Resistance Surveillance (version 20.9.25)[16].

Exclusion criteria: The following data was excluded from analysis, if technically possible:

- Internal quality control isolates (e.g., weekly ATCC QC strains)
- External quality control isolates (EQAS, i.e., CAP-Pt, ACP-MLE, RCPA, REQAS)
- Isolates labelled as 'screening', as well as isolates from nose, axilla, and groin
- Duplicate isolates (copy strains), i.e., only the first isolate per patient, specimen type and species during the reporting period was included
- Other non-diagnostic isolates (e.g., environmental, infection control)
- Species for which less than 10 isolates are available for analysis
- Antimicrobial agents that are not routinely tested

De-duplication: As per CLSI recommendation, multiple isolates (copy strains) are routinely excluded from the analysis, considering only the first isolate with antibiotic results of a given species per patient, specimen type, and analysis period (e.g., one year), irrespective of body site, antimicrobial susceptibility profile, or other phenotypical characteristics (e.g., biotype)[17].

Antimicrobial susceptibility testing results are presented as the proportion of isolates of a specific microorganism that are susceptible (S), intermediate (I), resistant (R), or non-susceptible (NS, i.e. I+R) to a specific antimicrobial agent. For example, the number of *E. coli* isolates resistant to ciprofloxacin is divided by the total number of *E. coli* isolates in which susceptibility to this antibiotic was tested.

The percentage resistant, intermediate, and susceptible (%RIS) isolates were either interpreted at the national AMR Surveillance Center (n=28/39 labs, 72%), or obtained from labs in form of already locally interpreted results (n=10/39 labs, 26%). Percent RIS interpretations were based on the CLSI interpretation standard CLSI M100 (ED30: 2020) for bacterial isolates and CLSI interpretation standard M60 ED1:2017 for yeast. For amphotericin B (AMB) EUCAST v9.0:2019 was used. For Candida auris tentative breakpoints from U.S. CDC were used[18]. Presentation standard for cumulative antibiograms is CLSI M39-A4:2014[19].

MRSA was defined as *Staphylococcus aureus*, resistant to oxacillin (OXA).

VRE was defined as *Enterococcus faecalis* or *Enterococcus faecium*, resistant to vancomycin (VAN).

CRE was defined as Enterobacteriaceae, non-susceptible to any carbapenem (imipenem, meropenem, or ertapenem).

MDR (multidrug resistance) was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial classes, as suggested by Magiorakos et al. (2012)[20].

MDR-TB was defined as combined resistance of M. tuberculosis to both, isoniazid (INH) and rifampin (RIF).

XDR/PDR: Magiorakos' et al. definitions for extensively drug-resistant (XDR) and pandrug-resistant (PDR) organisms could not be strictly applied as only a limited number of antibiotic classes were routinely tested by clinical labs, and MDR isolates were not routinely sent to a reference lab. As such, the following modified definitions were used for 'possible XDR' and 'possible MDR' isolates (modifications highlighted in *italics*):

- **'Possible XDR'**: Non-susceptibility to at least one agent *routinely tested by clinical labs* in all but two or fewer antimicrobial categories, (i.e. bacterial isolates remain susceptible to only one or two categories).

- **'Possible PDR'**: Non-susceptibility to all agents *routinely tested by clinical labs* in all antimicrobial categories (i.e. no agents tested as susceptible for that organism).

Antibiotics shown in this report are important for antimicrobial resistance surveillance purposes. They may or may not be first-line options for testing or treatment and should not be interpreted as such.

Statistical considerations:

Statistical analysis is conducted with WHONET (version 2020), or an online calculation tool[21] for Wilson confidence intervals, and with Epi Info™ for Windows (version 7.2)[22] for statistical significance of proportion trends over time.

If fewer than 30 AST results for a specific pathogen-antibiotic combination were available for analysis, then the table data are presented, but marked with a footnote, indicating that results should be interpreted with caution. If fewer than 10 AST results for a specific pathogen-antibiotic combination were submitted, then percentage SIR results are not presented.

Statistical significance of proportion trends over time: Statistical significance of temporal trends for antimicrobial resistance percentages was calculated if data from at least five years was available. If fewer than 30 isolates per year were reported, or data is not available for all years within the considered period, trend analysis was not conducted. Statistical significance of trends is expressed as a p-value, calculated by a Chi-square for trend test (extended Mantel-Haenszel), using Epi Info™ for Windows (version 7.2). A p-value of <0.05 was considered statistically significant.

Confidence intervals: For %RIS analyses, a 95% confidence interval is determined for the percentage of resistance (%R) and percentage of susceptibility (%S), based on the Wilson Score Interval with or without continuity correction method for calculating confidence intervals for a sample proportion (normal approximation to a binomial distribution)[23]. Confidence interval calculations were obtained either from WHONET (which uses the Wilson Score Interval with continuity correction method), or calculated using an online calculator tool, using the Wilson Score Interval (without continuity correction) method[24]. Error bars represent 95% confidence intervals.

4. Results

4.1 Patient/isolate characteristics

For the reporting period 2010 to 2019 (ten years), 925,940 isolates were reported by participating surveillance sites. After removal of non-diagnostic (i.e., screening, and quality control) isolates, and copy strains, 482,312 (52%) non-duplicate patients/isolates remained for analysis. For the reporting period 2019 (one year), n=144,894 diagnostic, non-duplicate isolates from n=248 surveillance sites are available for analysis. For 2019, most frequent reported pathogens were *E. coli* (26%), followed by *S. aureus* (15%), *K. pneumoniae* (10%), and *P. aeruginosa* (6%) (**Figure 4.1.1**).

Figure 4.1.1 Distribution of reported pathogens, UAE, 2019, by pathogen (n=144,894)

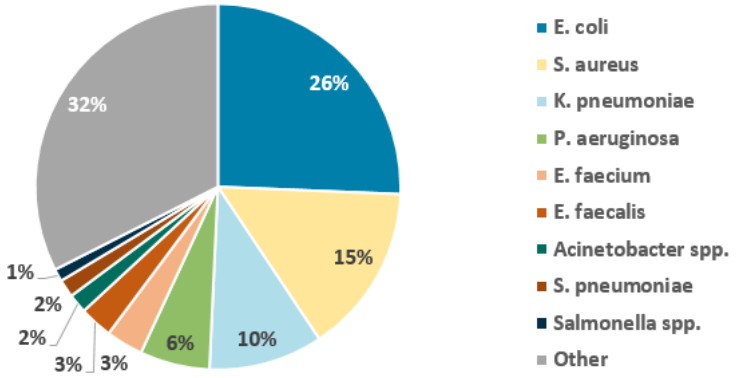


Figure 4.1.2 presents the distribution of reported patients/isolates by age category, gender, nationality status, isolate source, location type, department/specialty, and Emirate.

The data shows a typical **age group** distribution, with *Salmonella* and pneumococci as expected being more prevalent in the children age group. All age groups (adults, children, new-borns) are included.

Distribution by **gender** is largely balanced, with the exception of *E. coli* and *K. pneumoniae* being more prevalent in the female gender, which can be explained by the higher prevalence of urinary tract infections in females (*E. coli* and *K. pneumoniae* are the leading pathogens isolated from urinary tract).

Distribution by **nationality** status shows a balanced distribution between UAE nationals and expatriates, however, UAE nationals represent a significantly higher proportion in the reported data (about 20%) than in the general UAE population (about 12%), which could be explained by the higher rate of healthcare utilization by UAE nationals. Internal analysis of expatriates by nationality show that most nationalities (n>164) are represented in the data and reflecting the typical distribution of nationalities found in the UAE (data not shown).

Distribution by **Emirate** shows that patients from all seven Emirates are represented in the sample. The data are slightly skewed towards Abu Dhabi Emirate, whereas patients from the northern Emirates are slightly underrepresented, especially from the private sector.

Distribution by **isolate source** shows the typical and expected patterns of specimen sources: *E. coli*, *K. pneumoniae* and Enterococci are predominantly isolated from urine, *Salmonella* spp. from stool, pneumococci from respiratory tract, *S. aureus* from wound or pus, whereas *P. aeruginosa* and *Acinetobacter* spp. are mostly found in urine, pus, and the respiratory tract.

Distribution by **location type** shows that the data is balanced between outpatient and inpatients, and that all relevant location types are included in good numbers (outpatients, emergency, inpatient, intensive care).

Distribution by **department/clinical** specialty shows a good mix of all relevant clinical specialties, including internal medicine, surgery, emergency, paediatrics/neonatology, obstetrics/gynaecology, and other specialties.

Figure 4.1.2 Distribution of reported pathogens, UAE, 2019, by age category, gender, nationality status, isolate source, location type, department/clinical specialty, and Emirate

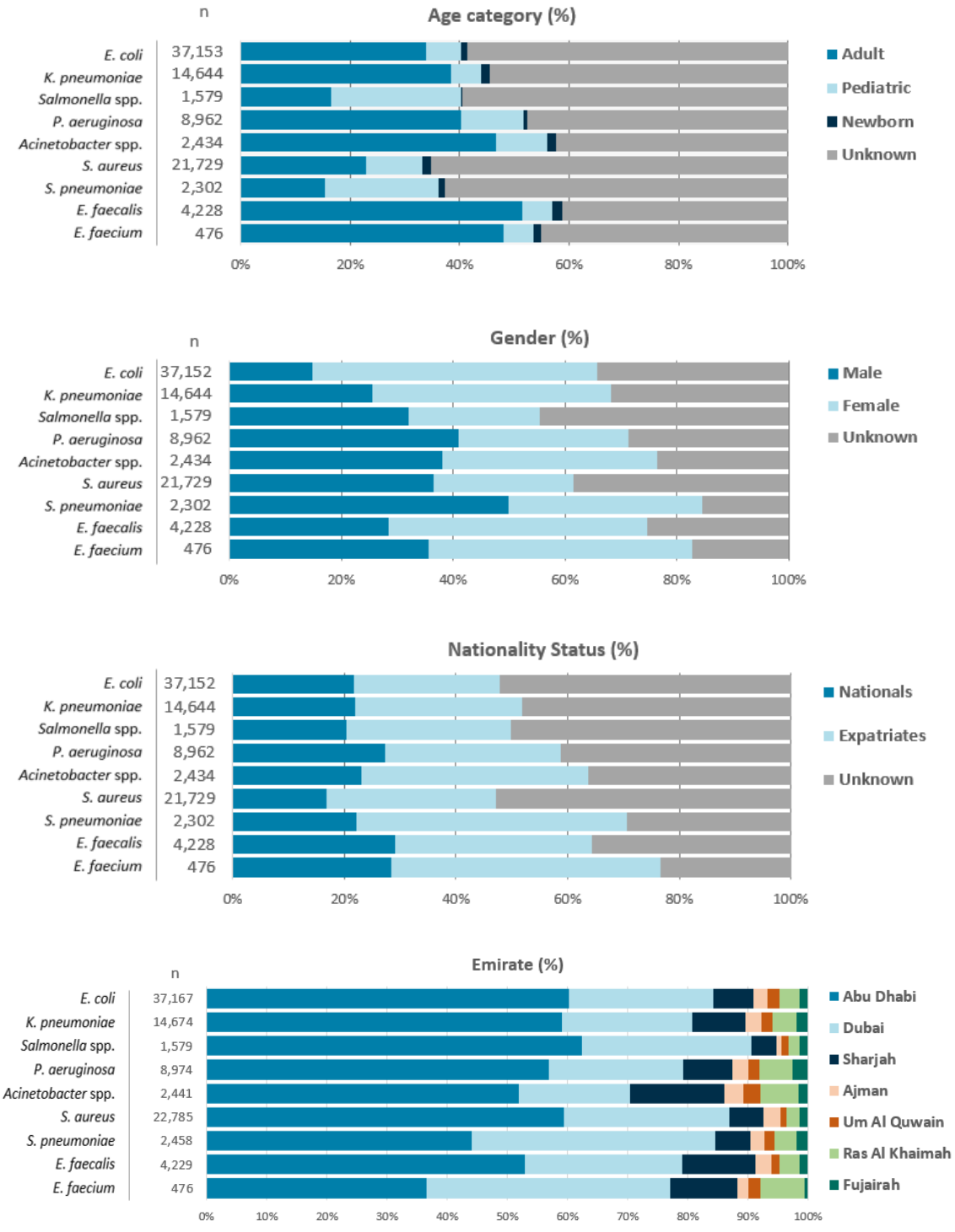
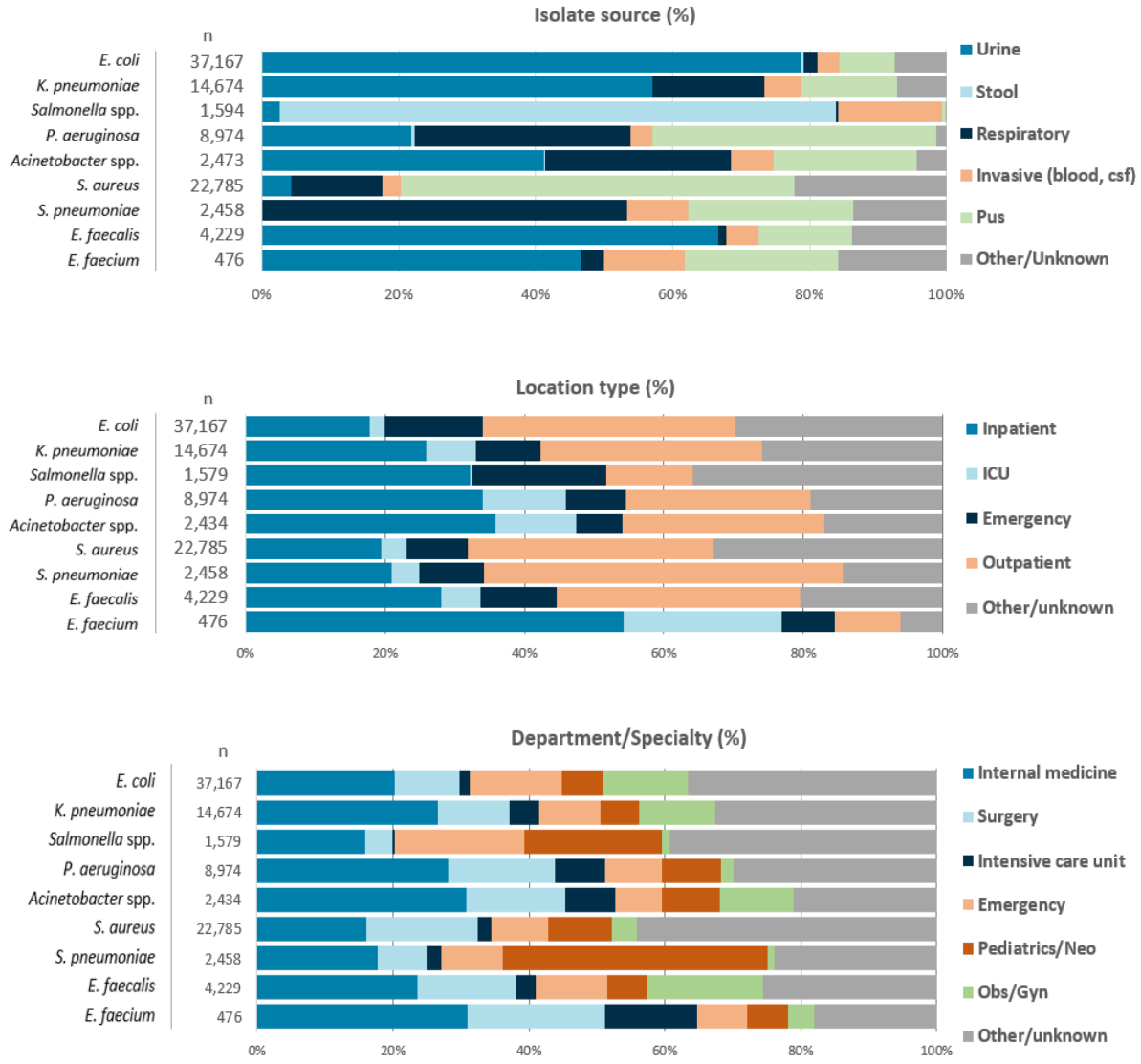


Figure 4.1.2 Distribution of reported pathogens, UAE, 2019, by age category, gender, nationality status, isolate source, location type, department/clinical specialty, and Emirate (continued)



Representativeness of the data for UAE population:

The data is largely representative of the whole UAE population, with a few important limitations. This report presents the largest data set and best currently available AMR data on a very large number of patients from all seven Emirates. The data includes all relevant regions, healthcare facility types, location types, age groups, and nationalities typically found in the UAE and representing a wide range of medical conditions and specialties.

The data is fully representative for public sector facilities in the UAE (100% sample size). The data is highly representative for inpatients and ICU patients, with 78 out of an estimated 150 hospitals participating in the system (52%). The data includes a large body of data from outpatients, however, results for outpatients need to be interpreted with some caution as still only a relatively small fraction of the many outpatient clinics/centers in the UAE are participating. The data is representative for both, the public and the private sector, except for the Emirates UAQ, RAK, and Fujairah, for which private facilities are not yet participating. The data is still slightly skewed towards Abu Dhabi because the surveillance system has been established there five years earlier than in the other Emirates.

The balancing of data will improve over time, as new surveillance sites are now preferably and increasingly selected from Dubai and the northern Emirates, private providers, and OP centers/clinics.

The surveillance sites included in this report were usually identified based on an assessment of their accessibility, suitability, location, facility type/size, availability of data in the required quality and format, and readiness and willingness to participate. Once identified, strict criteria for participation were applied, including the ability of generating and reporting high quality AMR data, having qualified staff, quality management, participation in external quality control, and lab accreditation. Not all data reported is utilized for analysis and reporting, some data or some surveillance sites are excluded from analysis if and when data quality issues are detected. See **section 3.1** for further details on quality control.

The possibility of selecting surveillance sites by utilizing an epidemiological model including random selection will be explored, to further improve the representativeness of the data. However, to our knowledge there is currently no country in the world that would have selected the AMR surveillance sites using an epidemiological model strictly based on random selection. Most, if not all national AMR surveillance systems have started with few entities only and have grown organically over time in size and by quality and quantity of data reported, with the data over time automatically being more and more representative of the whole population, as more and more sites are joining the system. For example, Germany started in 2002 with only six university hospitals; as of now (2021) the German ARS has 18,500 participating facilities and is considered highly representative of the population. This could be a model for the UAE.

Selecting surveillance sites by random using an epidemiological model does in theory, but not necessarily in practice and reality result in better, or more representative data. It would, however, certainly result in a smaller sample size and thus less statistical power, as obviously not all of the currently many participating facilities would be (randomly) selected for reporting, i.e., a significant amount of historic and currently available high quality AMR data would no longer be utilized for analysis and reporting, and as such would be lost.

It would also mean to identify and select new facilities (based on the epidemiological model), who may or may not be able and ready to report the data in the quality, quantity and format expected, or who perhaps do not meet other important criteria (QM/EQA, accreditation, qualified staff, patient mix, ..). Furthermore, no historical data will be available for these new sites, which limits the reporting of annual trends to future trends only, again losing ten years of valuable historic surveillance data and trends.

Currently already 52% (n=78) of an estimated 150 hospitals in the UAE are participating. Even if some hospitals would be excluded and others included to make the system more balanced, given the large number of facilities already in the system the results are expected to change only slightly, e.g., after the decimal point. For practical purposes it does not make a difference if a resistance rate is, for example, 31.0 %R or 31.2 %R. Even if sites were chosen purely by random, the actual effect on %RIS statistics is expected to be negligible, given the large sample size. Still, significant efforts are made include facilities from currently underrepresented sectors, to make the system more and more balanced over time.

Based on the large number of surveillance sites and reported isolates, and the distribution of pathogens, there is no indication of selective sampling of patients/isolates or sampling bias.

The reported percentages of susceptibility/resistance are therefore expected to be generalizable to the overall patient population in the UAE, within the few limitations as described above.

4.2 Cumulative Antibiograms (2019)

4.2.1 United Arab Emirates (National Cumulative Antibiogram)

Table 4.2.1.1 United Arab Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=83,378)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins				Cephalosporins				Carbapenems									
	N	AMP	AMC	TZP	CZO[b]	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	83,378	-	67	90	-	-	70	-	82	90	95	93	97	88	86	66	69	69	75[b]
Haemophilus influenzae[c]	2,289	71	77	-	-	90	-	-	-	-	-	-	-	-	-	98	-	74	-
Moraxella (Branh.) catarrhalis[d]	463	-	94	-	-	100	-	-	-	-	-	-	-	-	-	94	-	89	-
Enterobacteriaceae	64,988	28	69	92	53	-	72	-	82	93	98	97	98	89	87	54	75	68	-
Citrobacter koseri (diversus)	1,395	R	95	96	86	47/75[i]	92	-	94	97	99	97	99	99	97	95	91	98	74[b]
Enterobacter cloacae	1,893	R	R	85	R	17/29[i]	74	-	90	88	97	92	99	94	93	85	82	88	40[b]
Enterobacter aerogenes (*K. aer.*)	1,323	R	R	86	R	R	81	-	93	62	97	96	100	96	94	89	83	92	22[b]
Escherichia coli [e]	37,153	37	74	94	31	50/64[i]	68	-	78	98	99	98	99	88	86	58	71	61	94[b]
Klebsiella pneumoniae	14,644	R	77	88	42	57/68[i]	74	-	83	94	96	95	96	92	87	69	76	77	35[b]
Klebsiella oxytoca	491	R	85	93	60	70/73[i]	89	-	89	96	97	95	99	95	90	86	77[f]	86	76[b]
Morganella morganii	725	R	R	97	R	R	68	-	92	40	98	98	100	80	76	47	80	63	R
Proteus mirabilis	2,041	61	87	99	79	88/89[i]	91	-	92	13	97	96	98	78	83	64	88	61	R
Proteus vulgaris	52	R	88	100	R	R	86[g]	-	92	37	95	94	95	92	-	73	71[f]	65	R
Providencia spp.	217	R	R	98	R	-	93	-	98	42	96	91	98	82	82	68	-	83	R
Salmonella spp. (non-typhoid)	1,399	76	93	98	-	-	95	-	99	-	-	-	-	-	-	77[g]	-	96	-
Salmonella Typhi/Paratyphi	197	64	86	93	-	56/75[i]	81	-	79	-	-	-	-	-	-	15[g]	-	73	-
Serratia marcescens	1,363	R	R	94	R	R	90	-	96	78	98	95	99	97	88	89	95	97	R
Shigella spp.	165	24	69	98	-	-	58	-	90	-	-	-	-	-	-	41	-	32	-
Non-fermenting Gram-neg. rods	14,484	R	R	81	-	-	-	82	82	80	82	R	89	83	85	76	50	62	-
Acinetobacter baumannii	1,951	R	R	70	-	-	-	68	71	74	75	R	88	75	68	70	R	82	-
Pseudomonas aeruginosa	8,962	R	R	88	-	R	R	87	90	85	86	R	95	91	95	83	67	R	R
Stenotrophomonas maltophilia[h]	880	R	R	R	-	-	R	58	-	R	R	R	R	R	R	-	R	91	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2019 (de-duplicated data). [c] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: disc diffusion data (KB): LVX 96 %S, CRO 86 %S, AZM 98 %S, CLR 43 %S. [d] *M. catarrhalis*: CLR 96%, ERY 100 %S, AZM 99%, LVX 88 %S, TCY 78 %S. [e] *E. coli* (urinary tract isolates): FOS 99 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. refer to extra-intestinal (non-stool) isolates only. [h] *S. maltophilia*: MNO 99 %S, TCC 80 %S. [i] Cefuroxime: oral/parenteral breakpoints.

AMC=Amoxicillin/Clavulanic acid, **AMK**=Amikacin, **AMP**=Ampicillin, **ATM**=Aztreonam, **AZM**=Azithromycin, **CAZ**=Ceftazidime, **CIP**=Ciprofloxacin, **CLR**=Clarithromycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **CXM**=Cefuroxime, **CZO**=Cefazolin, **ETP**=Ertapenem, **ERY**=Erythromycin, **FEP**=Cefepime, **FOS**=Fosfomycin, **GEN**=Gentamicin, **IPM**=Imipenem, **LVX**=Levofloxacin, **MEM**=Meropenem, **MNO**=Minocycline, **NIT**=Nitrofurantoin, **SXT**=Trimethoprim/Sulfamethoxazole, **TCC**=Ticarcillin/Clavulanic acid, **TCY**=Tetracycline, **TOB**=Tobramycin, **TZP**=Piperacillin/Tazobactam.

%S=Percent of isolates susceptible, FQ=Fluoroquinolones, MIC=Minimal inhibitory concentration data only, unless mentioned otherwise (usually derived by antibiotic susceptibility testing platforms), except for *H. influenzae* and *M. catarrhalis* (disc diffusion data), N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

Table 4.2.1.2 United Arab Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=53,768)

Gram-positive Bacteria	Isolates	β-Lactams						Macrolides		Aminoglycosides			FQ		Glycopept.		Other					
	N	AMP	PEN	AMC	OXA	CRO	CTX	ERY	CLI	GEN	GEH	STH	LVX	MFX	VAN	TEC	SXT	NIT[b]	LNZ	TCY	RIF	QDA
Gram-positive organisms (all)	53,768	-	-	-	-	-	-	55	79	-	-	-	76	60	99	98	69	97	99	-	-	-
Enterococcus spp.	5,370	93	-	-	-	R	R	-	R	R	84	97	69	70	98	98	R	93	94	-	-	-
Enterococcus faecalis	4,228	99	-	-	-	R	R	-	R	R	84	97	69	70	99	99	R	97	93	-	-	R
Enterococcus faecium	476	27	-	-	-	R	R	-	R	R	79	95	29	23	90	91	R	21	94	-	-	83
Staphylococcus aureus	21,729	-	-	65[c]	65	-	-	70	86	90	-	-	66	74	100	100	74	99	100	87	100	88
MSSA	12,037	-	-	100	100	-	-	77	90	97	-	-	71	78	100	100	76	99	100	89	100	92
MRSA	5,688	-	-	-	-	-	-	58	80	77	-	-	55	63	100	100	67	99	100	84	99	78
Coagulase-neg. staphylococci (CNS)	5,293	-	-	30[c]	30	-	-	33	69	78	-	-	66	65	99	92	80	99	98	81	95	91
Staphylococcus epidermidis	1,914	-	-	25[c]	25	-	-	28	63	69	-	-	56	52	99	86	71	99	98	81	95	92
Staphylococcus saprophyticus [g]	729	-	-	16[c]	16	-	-	35	76	99	-	-	98	98	99	99	94	100	99	90	99	95
Staphylococcus lugdunensis	295	-	-	79[c]	79	-	-	80	84	94	-	-	96	95	99	99	98	100	100	92	99	98
Streptococcus pneumoniae	2,302	-	93[d]	-	-	96[e]	95[e]	46	71	-	-	-	94	97	99	100	60	-	100	58	100	99
Streptococcus pyogenes [h]	4,562	100[f]	100	-	-	96	92	67	90	-	-	-	87	-	100	99	-	-	100	79	-	-
Streptococcus agalactiae [i]	10,139	99	97	-	-	99	97	48	64	-	-	-	87	-	99	99	-	95	100	14	-	99
Streptococcus spp. (viridans group)	1,241	-	58	-	-	87	88	52	78	-	-	-	89	-	98	-	-	-	99	60	-	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2019 (de-duplicated data). [b] NIT: Nitrofurantoin data from testing urine isolates only. [c] Extrapolated, based on Oxacillin. [d] Data shown is based on non-meningitis breakpoints for Pen G. Pen G (meningitis breakpoints/oral breakpoints): 57 %S. [e] CRO/CTX: Data shown is based on non-meningitis breakpoints. [f] Extrapolated, based on Penicillin G. [g] includes ss bovis and ss saprophyticus. [h] includes *Streptococcus*, beta-haemolytic group A (GAS). [i] includes *Streptococcus*, group B (GBS).

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **GEH**=Gentamicin, high-level, **GEN**=Gentamicin, **LNZ**=Linezolid, **LVX**=Levofloxacin, **MFX**=Moxifloxacin, **NIT**=Nitrofurantoin, **OXA**=Oxacillin, **PEN**=Penicillin G, **QDA**=Quinupristin/Dalfopristin, **RIF**=Rifampin, **STH**=Streptomycin, high-level, **SXT**=Trimethoprim/Sulfamethoxazole, **TEC**=Teicoplanin, **TCY**=Tetracycline, **VAN**=Vancomycin.
%S=Percent of isolates susceptible, FQ=Fluoroquinolones, GAS=Group A streptococci, GBS=Group B streptococci, Glycopept.=Glycopeptides, MIC=Minimal inhibitory concentration data only, unless mentioned otherwise (usually derived by antibiotic susceptibility testing platforms), MRSA=Oxacillin-resistant *S. aureus*, MSSA=Oxacillin-susceptible *S. aureus*, N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, or small number of isolates tested (N<30), or antimicrobial agent is not indicated or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

4.2.2 Abu Dhabi Emirate

Table 4.2.2.1 Abu Dhabi Emirate Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=49,093)

Gram-negative Bacteria	Isolates	β-Lactams: Penicillins			β-Lactams: Cephalosporins				β-Lactams: Carbapenems				Aminoglycosides			FQ	Other		
	N	AMP	AMC	TZP	CZO	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	49,093	-	69	91	-	-	73	-	83	91	96	96	97	89	87	65	68	70	76[b]
Haemophilus influenzae[c]	1,327	84	90	-	-	95	96	-	-	-	-	-	-	-	-	92	-	76	-
Moraxella (Bran.) catarrhalis[d]	397	-	94	-	-	100	-	-	-	-	-	-	-	-	-	93	-	89	-
Enterobacteriaceae	38,531	29	70	93	30	-	75	-	83	94	99	98	98	90	88	63	80	70	76[b]
Citrobacter koseri (diversus)	744	R	95	96	89	30/76[i]	93	-	96	99	99	98	99	99	98	95	95	99	81[b]
Enterobacter cloacae	995	R	R	83	R	24/40[i]	75	-	91	89	98	95	99	94	94	86	84	88	43[b]
Enterobacter aerogenes (*K. aer.*)	714	R	R	85	R	R	81	-	95	65	99	97	100	96	95	90	88	94	20[b]
Escherichia coli [e]	22,410	37	75	94	29	46/66[i]	70	-	79	99	99	99	99	89	87	57	77	62	94[b]
Klebsiella pneumoniae	8,645	R	79	89	40	54/70[i]	77	-	84	97	97	97	98	92	88	68	79	80	37[b]
Klebsiella oxytoca	240	R	88	94	-	80/85[i]	94	-	98	99	99	99	99	97	94	90	83[f]	92	78[b]
Morganella morganii	406	R	R	97	R	R	70	-	92	42	99	100	100	80	76	49	89	62	R
Proteus mirabilis	1,193	62	92	99	81	92/93[i]	91	-	95	15	98	97	98	78	83	66	93	59	R
Proteus vulgaris	24	R	80[f]	100[f]	R	R	100[f]	-	100[f]	24[f]	100[f]	100[f]	100[f]	94[f]	-	77[f]	-	65[f]	R
Providencia spp.	98	R	R	99	R	-	92	-	100	51	98	94	97	79	86	62	-	84	R
Salmonella spp. (non-typhoid)	907	77	94	98	-	-	95	-	99	-	-	-	-	-	-	79[g]	-	96	-
Salmonella Typhi/Paratyphi	86	71[f]	91[f]	97[f]	-	-	91[f]	-	92 [f]	-	-	-	-	-	-	24[g]	-	79[f]	-
Serratia marcescens	778	R	R	97	R	R	90	-	97	81	99	98	99	96	91	88	95	97	R
Shigella spp.	90	16	67	98	-	-	50	-	83	-	-	-	-	-	-	38	-	30	-
Non-fermenting Gram-neg. rods	8,354	R	R	81	-	-	-	82	81	79	80	R	88	83	84	75	46	74	-
Acinetobacter baumannii	986	R	R	71	-	-	-	68	70	75	74	R	85	75	73	70	R	82	-
Pseudomonas aeruginosa	5,095	R	R	91	-	R	R	87	89	84	84	R	95	91	95	83	64	R	R
Stenotrophomonas maltophilia[h]	493	R	R	R	-	-	R	60	-	R	R	R	R	R	R	-	R	90	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2019 (de-duplicated data). [c] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 98 %S, CRO 96 %S, AZM 98%S, CLR 63 %S. [d] *M. catarrhalis*: CLR 95 %S, ERY 100 %S, AZM 99%, LVX 87 %S, TCY 78 %S. [e] *E. coli* (urinary tract isolates): FOS 99 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. refer to extra-intestinal (non-stool) isolates only. [h] *S. maltophilia*: MNO: 99 %S, TCC: 80 %S. [i] Cefuroxime: oral/parenteral breakpoint.

AMC=Amoxicillin/Clavulanic acid, **AMK**=Amikacin, **AMP**=Ampicillin, **ATM**=Aztreonam, **AZM**=Azithromycin, **CAZ**=Ceftazidime, **CIP**=Ciprofloxacin, **CLR**=Clarithromycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **CXM**=Cefuroxime, **CZO**=Cefazolin, **ETP**=Ertapenem, **ERY**=Erythromycin, **FEP**=Cefepime, **FOS**=Fosfomycin, **GEN**=Gentamicin, **IPM**=Imipenem, **LVX**=Levofloxacin, **MEM**=Meropenem, **MNO**=Minocycline, **NIT**=Nitrofurantoin, **SXT**=Trimethoprim/Sulfamethoxazole, **TCC**=Ticarcillin/Clavulanic acid, **TCY**=Tetracycline, **TOB**=Tobramycin, **TZP**=Piperacillin/Tazobactam.

%S=Percent of isolates susceptible, FQ=Fluoroquinolones, MIC=Minimal inhibitory concentration data only, except for *H. influenzae* and *M. catarrhalis* (disc diffusion data), N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

Table 4.2.2.2 Abu Dhabi Emirate Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=31,751)

Gram-positive Bacteria	Isolates	β-Lactams						Macrolides		Aminoglycosides			FQ		Glycopept.		Other					
	N	AMP	PEN	AMC	OXA	CRO	CTX	ERY	CLI	GEN	GEH	STH	LVX	MFX	VAN	TEC	SXT	NIT[b]	LNZ	TCY	RIF	QDA
Gram-positive organisms (all)	31,751	-	-	-	-	-	-	56	79	-	-	-	79	59	99	98	68	98	99	-	-	-
Enterococcus spp.	2,928	94	-	-	-	R	R	-	R	R	87	95	78	75	98	98	R	95	98	-	-	-
Enterococcus faecalis	2,233	100	-	-	-	R	R	-	R	R	87	95	76	72	99	99	R	97	98	-	-	R
Enterococcus faecium	174	24	-	-	-	R	R	-	R	R	83	90	32	-	87	89	R	35	98	-	-	95
Staphylococcus aureus	12,745	-	-	63[3]	63	-	-	70	86	91	-	-	68	71	100	100	73	99	100	87	100	89
MSSA	5,965	-	-	100	100	-	-	76	90	97	-	-	73	77	100	100	75	100	100	89	100	93
MRSA	3,092	-	-	-	-	-	-	56	78	80	-	-	57	57	100	100	67	99	100	84	99	78
Coagulase-neg. staphylococci (CNS)	2,408	-	-	34[c]	34	-	-	35	73	78	-	-	73	69	99	92	81	99	99	82	95	95
Staphylococcus epidermidis	887	-	-	25[c]	26	-	-	27	68	68	-	-	47	60	99	88	71	100	98	81	95	94
Staphylococcus saprophyticus [g]	306	-	-	32[c]	32	-	-	42	79	98	-	-	100	99	99	100	95	99	98	90	96	97
Staphylococcus lugdunensis	169	-	-	75[c]	75	-	-	79	82	94	-	-	99	96	100	100	95	100	100	93	100	99
Streptococcus pneumoniae	996	-	93[d]	-	-	97[e]	95[e]	51	73	-	-	-	95	99	100	100	63	-	100	61	100	99
Streptococcus pyogenes [h]	3,395	100[f]	100	-	-	96	97	68	87	-	-	-	88	-	100	-	-	-	100	78	-	-
Streptococcus agalactiae [i]	6,176	100	96	-	-	99	96	45	51	-	-	-	88	-	99	-	-	98	100	15	-	99
Streptococcus spp. (viridans group)	652	56	58	-	-	89	88	51	79	-	-	-	88	-	99	-	-	-	99	61	-	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2019 (de-duplicated data). [b] NIT: Nitrofurantoin data from testing urine isolates only. [c] Extrapolated, based on Oxacillin. [d] Data shown is based on non-meningitis breakpoints for Pen G. Pen G (meningitis breakpoints/oral breakpoints): 46 %S. [e] CRO/CTX: Data shown is based on non-meningitis breakpoints [f] Extrapolated, based on Penicillin G [g] includes subspecies bovis and saprophyticus [h] includes *Streptococcus*, beta-haemolytic group A (GAS) [i] includes *Streptococcus*, group B (GBS)

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **GEH**=Gentamicin, high-level, **GEN**=Gentamicin, **LNZ**=Linezolid, **LVX**=Levofloxacin, **MFX**=Moxifloxacin, **NIT**=Nitrofurantoin, **OXA**=Oxacillin, **PEN**=Penicillin G, **QDA**=Quinupristin/Dalfopristin, **RIF**=Rifampin, **STH**=Streptomycin, high-level, **SXT**=Trimethoprim/Sulfamethoxazole, **TEC**=Teicoplanin, **TCY**=Tetracycline, **VAN**=Vancomycin.
%S=Percent of isolates susceptible, FQ=Fluoroquinolones, GAS=Group A streptococci, GBS=Group B streptococci, Glycopept.=Glycopeptides, MIC=Minimal inhibitory concentration data only, MRSA=Oxacillin-resistant *S. aureus*, MSSA=Oxacillin-susceptible *S. aureus*, N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, or small number of isolates tested (N<30), or antimicrobial agent is not indicated or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

4.2.3 Dubai Emirate

Table 4.2.3.1 Dubai Emirate Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=19,492)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins			Cephalosporins					Carbapenems									
	N	AMP	AMC	TZP	CZO[b]	CXM[i]	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	19,492	-	62	93	-	-	63	-	80	91	96	88	98	88	92	71	74	66	78[b]
Haemophilus influenzae[c]	638	56	58	-	-	71	-	-	-	-	-	-	-	-	-	95	-	57	-
Moraxella (Branh.) catarrhalis[d]	54	-	94	-	-	100[f]	-	-	-	-	-	-	-	-	-	100[f]	-	90	-
Enterobacteriaceae	15,320	27	67	93	45	56/58[i]	65	-	79	92	96	94	98	89	94	69	76	68	79[b]
Citrobacter koseri (diversus)	369	R	93	98	80	67/73[i]	89	-	88	93	97	93	100	99	-	96	92	96	57[b]
Enterobacter cloacae	480	R	R	92	R	6/10[i]	83	-	85	87	96	89	100	95	-	88	86	89	41[b]
Enterobacter aerogenes (*K. aer.*)	334	R	R	92	R	R	88	-	91	52	95	94	100	97	-	92	86	92	34[b]
Escherichia coli[e]	8,872	37	70	94	45	61/62[i]	59	-	75	97	97	97	100	87	96	62	70	59	95[b]
Klebsiella pneumoniae	3,169	R	75	89	55	66/67[i]	65	-	81	92	94	91	97	92	91	77	80	77	40[b]
Klebsiella oxytoca	150	R	80	93	-	69/69[i]	79	-	82	93	94	90	99	94	-	90	80[f]	82	77[b]
Morganella morganii	166	R	R	98	R	R	73	-	97	38	96	95	100	87	-	62	86	75	R
Proteus mirabilis	455	65	85	99	67	81/81[i]	92	-	93	16	99	94	97	83	81	70	86	68	R
Proteus vulgaris	18	R	100[f]	100[f]	R	R	-	-	92[f]	64[f]	92[f]	91[f]	92[f]	92[f]	-	77[f]	-	62[f]	R
Providencia spp.	53	R	R	100[f]	R	-	80[f]	-	91[f]	32[f]	86[f]	74[f]	100[f]	77[f]	-	75[f]	-	75[f]	R
Salmonella spp. (non-typhoid)		76	94	98	-	-	95	-	99	-	-	-	-	-	-	80[g]	-	96	-
Salmonella Typhi/Paratyphi		71	88	96	-	-	89	-	92	-	-	-	-	-	-	16[g]	-	79	-
Serratia marcescens	319	R	R	99	R	R	90	-	93	71	98	84	99	99	-	96	100	99	R
Shigella spp.	56	38[f]	78[f]	100[f]	-	-	86[f]	-	100[f]	-	-	-	-	-	-	29[f]	-	17[f]	-
Non-fermenting Gram-neg. rods	3,047	R	R	88	-	-	-	90	89	87	90	R	91	86	91	82	59	50	-
Acinetobacter baumannii	333	R	R	91	-	-	-	88	92	95	94	R	92	88	75[f]	89	R	94	-
Pseudomonas aeruginosa	2,006	R	R	90	-	R	R	92	93	87	90	R	97	92	93	86	78	R	R
Stenotrophomonas maltophilia[h]	208	R	R	R	-	-	R	57	-	R	R	R	R	R	R	-	R	80	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2018 (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 95 %S, CRO 72 %S, AZM: no data, CLR: no data. [d] *M. catarrhalis*: CLR: no data, ERY 100 %S, AZM 91%, LVX: no data, TCY: no data. [e] *E. coli* (urinary tract isolates): FOS 99 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. refer to extra-intestinal (non-stool) isolates only. [h] *S. maltophilia*: MNO: 100 %S, TCC: no data. [i] Cefuroxime: oral/parenteral breakpoint.

AMC=Amoxicillin/Clavulanic acid, **AMK**=Amikacin, **AMP**=Ampicillin, **ATM**=Aztreonam, **AZM**=Azithromycin, **CAZ**=Ceftazidime, **CIP**=Ciprofloxacin, **CLR**=Clarithromycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **CXM**=Cefuroxime, **CZO**=Cefazolin, **ETP**=Ertapenem, **ERY**=Erythromycin, **FEP**=Cefepime, **FOS**=Fosfomycin, **GEN**=Gentamicin, **IPM**=Imipenem, **LVX**=Levofloxacin, **MEM**=Meropenem, **MNO**=Minocycline, **NIT**=Nitrofurantoin, **SXT**=Trimethoprim/Sulfamethoxazole, **TCC**=Ticarcillin/Clavulanic acid, **TCY**=Tetracycline, **TOB**=Tobramycin, **TZP**=Piperacillin/Tazobactam.

%S=Percent of isolates susceptible, FQ=Fluoroquinolones, MIC=Minimal inhibitory concentration data only, except for *H. influenzae* and *M. catarrhalis* (disc diffusion data), N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

Table 4.2.3.2 Dubai Emirate Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=13,710)

Gram-positive Bacteria	Isolates	β-Lactams						Macrolides		Aminoglycosides			FQ		Glycopept.		Other					
	N	AMP	PEN	AMC	OXA	CRO	CTX	ERY	CLI	GEN	GEH	STH	LVX	MFX	VAN	TEC	SXT	NIT[b]	LNZ	TCY	RIF	QDA
Gram-positive organisms (all)	13,710	-	-	-	-	-	-	58	78	-	-	-	74	73	99	98	73	97	99	-	-	-
Enterococcus spp.	1,399	94	-	-	-	R	R	-	R	R	76	100	61	71	98	98	R	95	91	-	-	-
Enterococcus faecalis	1,112	99	-	-	-	R	R	-	R	R	76	100	62	71	99	99	R	99	92	-	-	R
Enterococcus faecium	193	42	-	-	-	R	R	-	R	R	74[h]	100[h]	47	-	95	95	R	29	83	-	-	67[h]
Staphylococcus aureus	6,084	-	-	68[3]	68	-	-	71	84	89	-	-	65	83	100	100	77	99	100	89	100	83
MSSA	4,159	-	-	100	100	-	-	76	89	97	-	-	69	82	100	100	78	99	100	91	100	88
MRSA	1,618	-	-	-	-	-	-	59	81	72	-	-	54	71	100	100	67	100	100	83	99	72
Coagulase-neg. staphylococci (CNS)	1,645	-	-	26[c]	26	-	-	33	70	80	-	-	77	66	99	92	83	99	98	79	96	87
Staphylococcus epidermidis	522	-	-	29[c]	29	-	-	28	62	72	-	-	63	53	99	80	71	100	96	78	95	91
Staphylococcus saprophyticus [g]	320	-	-	4[c]	4	-	-	34	77	98	-	-	99	99	100	99	94	100	99	89	100	87
Staphylococcus lugdunensis	87	-	-	80[c]	80	-	-	80	83	95	-	-	89[h]	91	98	97	96	100	100	87	97	93[h]
Streptococcus pneumoniae	973	-	93[d]	-	-	100[e]	96[e]	38	67	-	-	-	94	94	100	-	55	-	100	54	100	100[h]
Streptococcus pyogenes [h]	686	100[f]	100	-	-	98	97	72	89	-	-	-	83	-	100	-	-	-	100	81	-	-
Streptococcus agalactiae [i]	2,174	99	96	-	-	99	96	44	65	-	-	-	84	-	97	-	-	93	99	13	-	99
Streptococcus spp. (viridans group)	362	77	74	-	-	88	94	63	78	-	-	-	94	-	99	-	-	-	99	63	-	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2019 (de-duplicated data). [b] NIT: Nitrofurantoin data from testing urine isolates only. [c] Extrapolated, based on Oxacillin. [d] Data shown is based on non-meningitis breakpoints for Pen G. Pen G (meningitis breakpoints/oral breakpoints): 86 %S. [e] CRO/CTX: Data shown is based on non-meningitis breakpoints [f] Extrapolated, based on Penicillin G [g] includes subspecies bovis and saprophyticus [h] includes *Streptococcus*, beta-haemolytic group A (GAS) [i] includes *Streptococcus*, group B (GBS). [h]A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution.

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **GEH**=Gentamicin, high-level, **GEN**=Gentamicin, **LNZ**=Linezolid, **LVX**=Levofloxacin, **MFX**=Moxifloxacin, **NIT**=Nitrofurantoin, **OXA**=Oxacillin, **PEN**=Penicillin G, **QDA**=Quinupristin/Dalfopristin, **RIF**=Rifampin, **STH**=Streptomycin, high-level, **SXT**=Trimethoprim/Sulfamethoxazole, **TEC**=Teicoplanin, **TCY**=Tetracycline, **VAN**=Vancomycin.
%S=Percent of isolates susceptible, FQ=Fluoroquinolones, GAS=Group A streptococci, GBS=Group B streptococci, Glycopept.=Glycopeptides, MIC=Minimal inhibitory concentration data only, MRSA=Oxacillin-resistant *S. aureus*, MSSA=Oxacillin-susceptible *S. aureus*, N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, or small number of isolates tested (N<30), or antimicrobial agent is not indicated or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

4.2.4 Northern Emirates

Table 4.2.4.1 Northern Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=14,803)

Gram-negative Bacteria	Isolates	β-Lactams: Penicillins				β-Lactams: Cephalosporins				Carbapenems			Aminoglycosides			FQ	Other		
	N	AMP	AMC	TZP	CZO[b]	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	14,803	-	65	87	-	-	60	-	82	88	93	89	96	87	84	64	63	65	68[b]
Haemophilus influenzae[c]	324	60	63	-	-	86[f]	-	-	-	-	-	-	-	-	-	96[f]	-	-	-
Moraxella (Branh.) catarrhalis[d]	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Enterobacteriaceae	11,147	25	67	90	-	29/50[j]	66	-	82	90	96	94	97	88	81	62	66	67	69[b]
Citrobacter koseri (diversus)	282	R	96	96	-	75/75[j]	89	-	96	98	99	98	99	100	92	94	87	97	72[b]
Enterobacter cloacae	418	R	R	85	R	11/11[j]	66	-	90	87	94	84	99	93	87	82	72	87	35[b]
Enterobacter aerogenes (*K. aer.*)	275	R	R	82	R	R	75	-	89	66	96	93	98	95	89	84	70	88	17[b]
Escherichia coli [e]	5,880	35	73	93	-	53/53[j]	62	-	80	99	99	97	99	87	80	55	60	59	93[b]
Klebsiella pneumoniae	2,831	R	72	84	-	56/56[j]	66	-	82	91	92	90	93	90	76	66	65	71	25[b]
Klebsiella oxytoca	101	R	84	91	-	41/41[j]	73	-	85	92	95	90	99	91	72	74	66[f]	78	71[b]
Morganella morganii	153	R	R	97	R	R	50	-	89	38	97	94	100	76	76	40	61[f]	58	R
Proteus mirabilis	393	57	76	99	-	72/72[j]	91	-	85	7	95	94	97	76	80	53	85	56	R
Proteus vulgaris	10	R	88[f]	100[f]	R	R	60[f]	-	80[f]	30[f]	90[f]	-	90[f]	90[f]	-	60[f]	-	70[f]	R
Providencia spp.	66	R	R	97	R	-	97	-	97	33	96	94	97	88	75	74	-	85	R
Salmonella spp. (non-typhoid)	127	75	87	95	-	-	100[f]	-	100	-	-	-	-	-	-	86[f,g]	-	98	-
Salmonella Typhi/Paratyphi	26	52[f]	76[f]	83[f]	-	-	-	-	74[f]	-	-	-	-	-	-	10[f, g]	-	57[f]	-
Serratia marcescens	266	R	R	82	R	R	87	-	94	83	97	95	99	97	80	85	90	95	R
Shigella spp.	19	31[f]	63[f]	93[f]	-	-	-	-	94[f]	-	-	-	-	-	-	44[f]	-	60[f]	-
Non-fermenting Gram-neg. rods	3,083	R	R	75	-	-	-	78	81	80	81	R	91	81	86	74	54	56	-
Acinetobacter baumannii	632	R	R	62	-	-	-	60	66	66	67	R	90	69	45	63	R	75	-
Pseudomonas aeruginosa	1,861	R	R	81	-	R	R	85	89	86	86	R	96	89	94	81	67	R	R
Stenotrophomonas maltophilia[i]	179	R	R	R	-	-	R	27	-	R	R	R	R	R	R	-	R	90	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2018 (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 98 %S, CRO 77 %S, AZM 100 %S, CLR no data. [d] *M. catarrhalis*: CLR, ERY, AZM, LVX, TCY: no data. [e] *E. coli* (urinary tract isolates): FOS 99 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. refer to extra-intestinal (non-stool) isolates only. [i] *S. maltophilia*: MNO, TCC: no data. [i] Cefuroxime: oral/parenteral breakpoint.

AMC=Amoxicillin/Clavulanic acid, **AMK**=Amikacin, **AMP**=Ampicillin, **ATM**=Aztreonam, **AZM**=Azithromycin, **CAZ**=Ceftazidime, **CIP**=Ciprofloxacin, **CLR**=Clarithromycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **CXM**=Cefuroxime, **CZO**=Cefazolin, **ETP**=Ertapenem, **ERY**=Erythromycin, **FEP**=Cefepime, **FOS**=Fosfomycin, **GEN**=Gentamicin, **IPM**=Imipenem, **LVX**=Levofloxacin, **MEM**=Meropenem, **MNO**=Minocycline, **NIT**=Nitrofurantoin, **SXT**=Trimethoprim/Sulfamethoxazole, **TCC**=Ticarcillin/Clavulanic acid, **TCY**=Tetracycline, **TOB**=Tobramycin, **TZP**=Piperacillin/Tazobactam.

%S=Percent of isolates susceptible, FQ=Fluoroquinolones, MIC=Minimal inhibitory concentration data only, except for *H. influenzae* and *M. catarrhalis* (disc diffusion data), N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

Table 4.2.4.2 Northern Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=8,311)

Gram-positive Bacteria	Isolates	β-Lactams						Macrolides		Aminoglycosides			FQ		Glycopept.		Other					
	N	AMP	PEN	AMC	OXA	CRO	CTX	ERY	CLI	GEN	GEH	STH	LVX	MFX	VAN	TEC	SXT	NIT[b]	LNZ	TCY	RIF	QDA
Gram-positive organisms (all)	8,311	-	-	-	-	-	-	50	80	-	-	-	72	48	99	98	68	92	98	-	-	-
Enterococcus spp.	1,043	90	-	-	-	R	R	-	R	R	79	98	62	51	98	97	R	87	87	-	-	-
Enterococcus faecalis	883	99	-	-	-	R	R	-	R	R	79	98	67	61	99	97	R	96	86	-	-	R
Enterococcus faecium	109	23	-	-	-	R	R	-	R	R	64	98	20	18[j]	91	96[j]	R	9	94	-	-	72[j]
Staphylococcus aureus	2,903	-	-	64[3]	64	-	-	72	88	90	-	-	64	71	100	100	76	100	100	86	99	98
MSSA	1,913	-	-	100	100	-	-	78	90	97	-	-	68	74	100	100	80	100	100	88	100	99
MRSA	980	-	-	-	-	-	-	71	85	75	-	-	54	64	100	100	68	100	100	83	99	96
Coagulase-neg. staphylococci (CNS)	1,240	-	-	26[c]	26	-	-	30	63	76	-	-	57	59	98	93	75	100	98	82	95	72
Staphylococcus epidermidis	505	-	-	21[c]	21	-	-	28	57	68	-	-	52	52	99	90	68	96	99	82	94	91
Staphylococcus saprophyticus [g]	103	-	-	12[c]	12	-	-	26	71	100	-	-	91	96	99	100	91	100	99	94	100	-
Staphylococcus lugdunensis	39	-	-	89[c]	89	-	-	81	92	92	-	-	94	97	95	100	100	-	100	95	100	-
Streptococcus pneumoniae	334	-	94[d]	-	-	90[e]	93[e]	47	78	-	-	-	92	97	97	-	60	-	100	60	99	-
Streptococcus pyogenes [h]	481	100[f]	100	-	-	94	81	59	96	-	-	-	85	-	99	-	-	-	100	79	-	-
Streptococcus agalactiae [i]	1,789	99	99	-	-	99	99	52	79	-	-	-	87	-	100	-	-	96	100	15	-	100[j]
Streptococcus spp. (viridans group)	227	58	46	-	-	83	84	44	76	-	-	-	88	-	98	-	-	-	99	54	-	-

[a] The %S for each organism/antimicrobial combination was generated by including the first isolate only of that organism encountered on a given patient during 2018 (de-duplicated data). [b] NIT: Nitrofurantoin data from testing urine isolates only. [c] Extrapolated, based on Oxacillin. [d] Data shown is based on non-meningitis breakpoints for Pen G. Pen G (meningitis breakpoints/oral breakpoints): 48 %S. [e] CRO/CTX: Data shown is based on non-meningitis breakpoints [f] Extrapolated, based on Penicillin G [g] includes subspecies bovis and saprophyticus [h] includes *Streptococcus*, beta-haemolytic group A (GAS) [i] includes *Streptococcus*, group B (GBS). [j] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution.

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **GEH**=Gentamicin, high-level, **GEN**=Gentamicin, **LNZ**=Linezolid, **LVX**=Levofloxacin, **MFX**=Moxifloxacin, **NIT**=Nitrofurantoin, **OXA**=Oxacillin, **PEN**=Penicillin G, **QDA**=Quinupristin/Dalfopristin, **RIF**=Rifampin, **STH**=Streptomycin, high-level, **SXT**=Trimethoprim/Sulfamethoxazole, **TEC**=Teicoplanin, **TCY**=Tetracycline, **VAN**=Vancomycin.
%S=Percent of isolates susceptible, FQ=Fluoroquinolones, GAS=Group A streptococci, GBS=Group B streptococci, Glycopept.=Glycopeptides, MIC=Minimal inhibitory concentration data only, MRSA=Oxacillin-resistant *S. aureus*, MSSA=Oxacillin-susceptible *S. aureus*, N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, or small number of isolates tested (N<30), or antimicrobial agent is not indicated or not effective clinically. Interpretation standard: CLSI M100 ED29:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020. Version 1.3 (17 Nov 2020).

4.2.5. Candida spp.

Table 4.2.5.1 United Arab Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – *Candida* spp. (isolates from all sources, N=3,336)

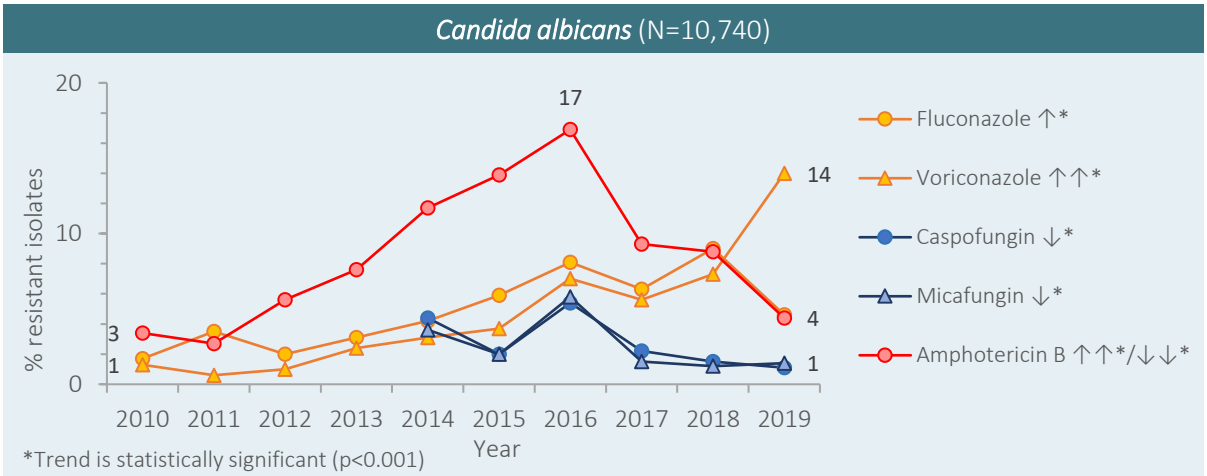
	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU	VOR	AMB[b]	CAS[c]	MIF
***Candida* spp.**	3,336	100	85	73	-	94	98
Candida albicans	1,652	50	93	83	96	99	98
Candida spp. (non-albicans)	1,956	50	69	56	-	85	94
Candida tropicalis	479	14	93	96	99	97	98
Candida parapsilosis	273	8	75	79	97	100	100
Candida glabrata	256	8	7	-[d]	99	70	98
Candida auris [e]	91	3	28	-	6	96	100
Candida lusitaniae	60	2	100	-	-	-	-
Candida krusei	63	2	-	-	85	68	100
Other (non-albicans)	734	38	-	-	-	-	-

[a]The %S for each organism/antimicrobial combination was generated by including the first isolate of that organism encountered on a given patient (de-duplicated data). [b]AMB: based on EUCAST and CDC breakpoints (S≤1, R≥2) for C. albicans, C. glabrata, C. krusei, C. parapsilosis, C. tropicalis, and C. auris. [c]CAS: Caspofungin susceptibility testing *in vitro* has been associated with significant inter-laboratory variability. [d]For *C. glabrata* and Voriconazole, current data are insufficient to demonstrate a correlation between in vitro susceptibility testing and clinical outcome. [e]*Candida auris* breakpoints based on U.S. CDC tentative MIC breakpoints for *Candida auris*.

AMB=Amphotericin B, **CAS**=Caspofungin, **FLU**=Fluconazole, **MIF**=Micafungin, **VOR**=Voriconazole.

%S=Percent of isolates susceptible, MIC=Minimal inhibitory concentration data only (usually derived by antibiotic susceptibility testing platforms), N=Number, spp.=species, R=intrinsically resistant, (-) =No data available, or very small number of isolates tested (N<10), or antimicrobial agent is not indicated or not effective clinically. Interpretation standard: CLSI M60 ED1:2017. For AMB: EUCAST v9.0:2019. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2020 (20.9.25). Version 1.3 (17 Nov 2020).

Figure 4.2.5.1 Trend for percentage of isolates resistant (%R) for *Candida albicans*, United Arab Emirates, 2010-2019



- In 2019, resistance of *C. albicans* to antifungals ranged from 1% for Caspofungin and micafungin to 14% for voriconazole.
- Resistance of *C. albicans* to polyenes (amphotericin B) increased from 3 %R (2010) to 17 %R in 2016, and then decreased to 4 %R in 2019.
- Resistance of *C. albicans* to triazoles is increasing. Resistance to fluconazole increased from 1.7 %R (2010) to 4.6 %R (2019); resistance to voriconazole increased from 1.3 %R (2010) to 14.0 %R (2019).
- Resistance of *C. albicans* to echinocandins is decreasing. Resistance to caspofungin decreased from 4.4 %R (2014) to 1.1 %R (2019); resistance to micafungin decreased from 3.6 %R (2014) to 1.4 %R (2019).

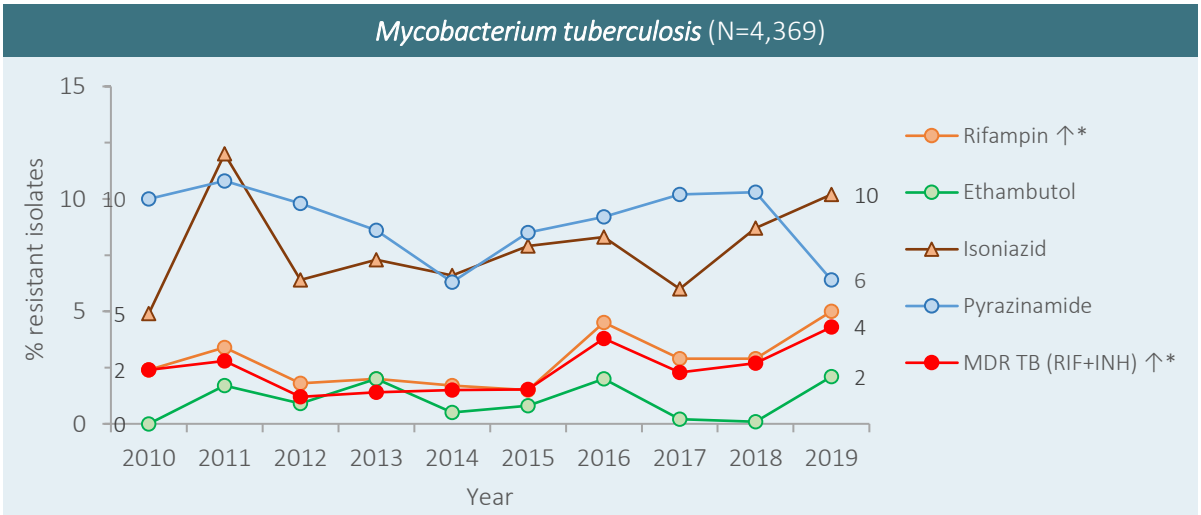
4.2.6. Mycobacterium tuberculosis

Table 4.2.6.1 United Arab Emirates Cumulative Antibiogram (2019): Percent susceptible isolates (%S[a]) – *Mycobacterium tuberculosis* (isolates from all sources, N=800)

	Isolates (N)	Rifampin	Ethambutol	Isoniazid	Pyrazinamide	Streptomycin
Mycobacterium tuberculosis	800	95	98	88	94	92
Abu Dhabi Emirate	529	96	98	88	94	90 [b]
Dubai Emirate	271	93	98	88	92	93

[a]The %S for each organism/antimicrobial combination was generated by including the first isolate of that organism encountered on a given patient during the reporting period (de-duplicated data). [b] n=98 isolates only were tested for streptomycin. %S=Percent of isolates susceptible, N=Number.

Figure 4.2.6.1 Trend for percentage of isolates resistant (%R) for *Mycobacterium tuberculosis*, United Arab Emirates, 2010-2019



- In 2019, resistance of *M. tuberculosis* to first-line antibiotics ranged from 2% for ethambutol to 10% for isoniazid.
- Rifampin showed an increasing trend of resistance, from 2.4 %R (2010) to 5.0 %R (2019).
- Multidrug-resistant (MDR) TB, defined as non-susceptibility to isoniazid and rifampin, increased from 2.4 % MDR-TB (2010) to 4.3 %MDR-TB (2019).
- Second-line antibiotics: no data / not routinely tested.

4.3 Multidrug resistance (MDR)

Multidrug resistance (MDR) is defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes as per (Magiorakos et al., 2011).

Between 2019 and 2019, multidrug resistance has increased significantly in the United Arab Emirates, in particular for Enterobacteriaceae, Gram-positive pathogens, and *Mycobacterium tuberculosis*, whereas multidrug resistance decreased for non-lactose fermenting bacteria.

4.3.1 Gram-negative Bacteria (%MDR)

For 2019, prevalence of multidrug resistance (%MDR) in Gram-negative bacteria was 45% (*E. coli*), 35% (*K. pneumoniae*), 25% (*Acinetobacter* spp.), 17% (*P. aeruginosa*), and 14% (*Salmonella* spp.) (**Fig. 4.3.1**).

Between 2010 and 2019, multidrug resistance (%MDR) increased for Enterobacterales:

- *K. pneumoniae* from 20% to 35%
- *Salmonella* spp. from 14% to 14%
- *E. coli* from 44% to 45%.

Between 2019 and 2019, multidrug resistance (%MDR) decreased for lactose non-fermenting Gram-negative bacteria ("Non-fermenters"):

- *Acinetobacter* spp.: from 49% to 25%
- *P. aeruginosa:* from 22 % to 17%.

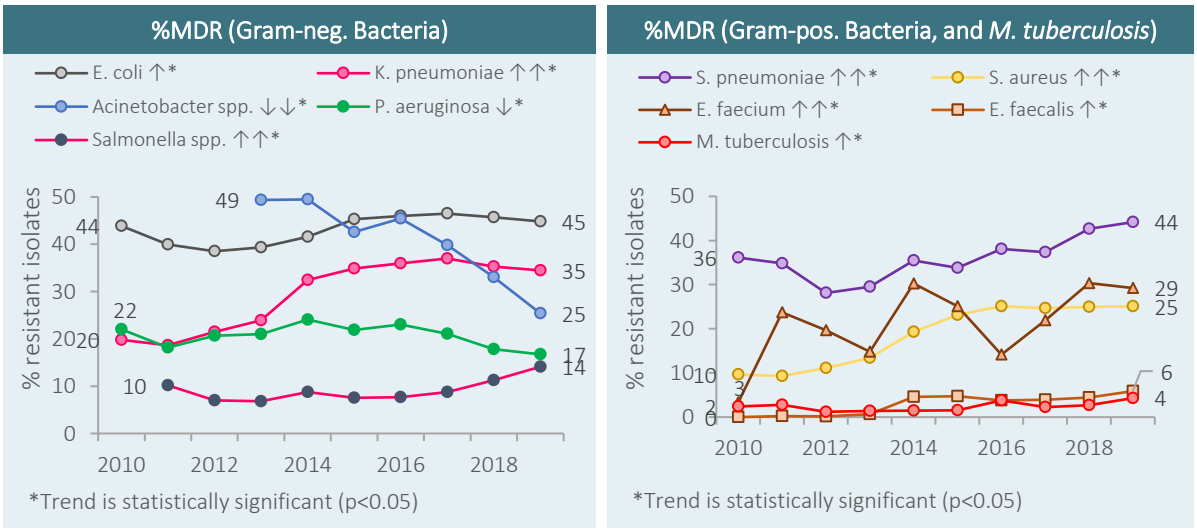
4.3.2 Gram-positive Bacteria (%MDR), and *M. tuberculosis*

For 2019, prevalence of multidrug resistance (%MDR) in Gram-positive bacteria was 44% (*S. pneumoniae*), 29% (*E. faecium*), 25% (*S. aureus*), 6% (*E. faecalis*), and 4% (*M. tuberculosis*) (**Figure 4.3.1**).

Between 2010 and 2019, multidrug resistance (%MDR) increased for:

- *S. pneumoniae* from 36% to 44%
- *S. aureus*: from 10% to 25%
- *E. faecium*: from 3% to 29%
- *E. faecalis*: from 0% to 6%
- *M. tuberculosis*: from 0% to 4%.

Figure 4.3.1 Annual trends for percentage of isolates multidrug resistant (%MDR) for Gram-negative bacteria, Gram-positive bacteria, and *M. tuberculosis*, United Arab Emirates, 2010-2019



4.4 AMR priority pathogens

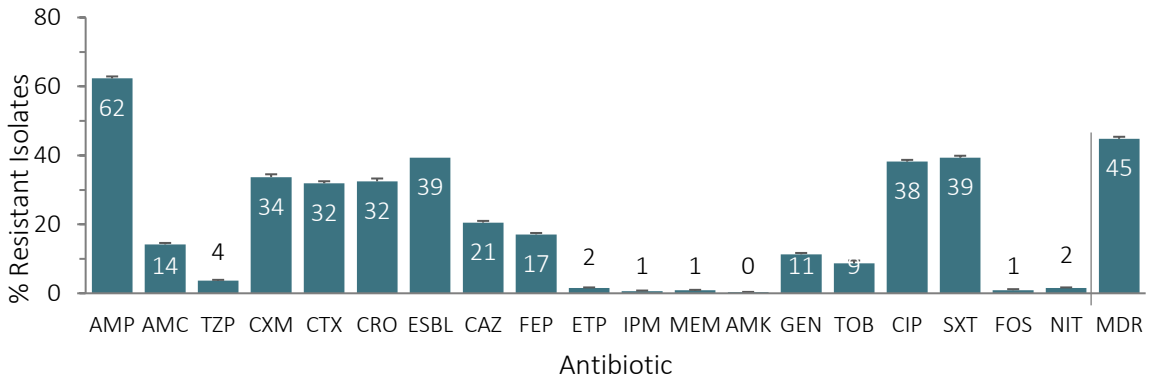
4.4.1 Escherichia coli

Table 4.4.1.1 Percentages of resistant, intermediate, and susceptible isolates for *Escherichia coli* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Escherichia coli* (N=37,153)			
		Isolates (N)	% R	% I	% S
Ampicillin	AMP	30,324	62.3	1.1	36.6
Amoxicillin/clavulanic acid	AMC	29,777	14.2	12.3	73.5
Piperacillin/tazobactam	TZP	30,393	3.7	2.5	93.9
Cefuroxime (oral)	CXM	12,257	33.7	16.5	48.3
Ceftriaxone	CRO	11,736	32.5	0.2	67.3
Cefotaxime	CTX	20,425	31.9	0.5	67.6
Extended-spectrum β-lactamase	ESBL	16,647	39.3	16.5	62.3
Ceftazidime	CAZ	30,489	20.5	1.5	78.0
Cefepime	FEP	26,219	17.1	4.5	78.4
Ertapenem	ETP	22,720	1.5	0.2	98.2
Imipenem	IPM	27,467	0.7	1.0	98.4
Meropenem	MEM	30,072	0.9	0.4	98.7
Gentamicin	GEN	30,520	11.3	0.4	88.3
Tobramycin	TOB	5,206	8.7	5.1	86.2
Amikacin	AMK	26,076	0.3	0.4	99.3
Ciprofloxacin	CIP	30,622	38.2	4.1	57.7
Trimethoprim/sulfamethoxazole	SXT	30,622	39.3	0	60.7
Nitrofurantoin	NIT	25,273	1.5[a]	4.4[a]	94.1[a]
Multidrug-resistance (≥3 classes NS)[b]	MDR	13,733/30,653	44.8	–	–

[a] Nitrofurantoin: Isolates from urinary tract only.
[b] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

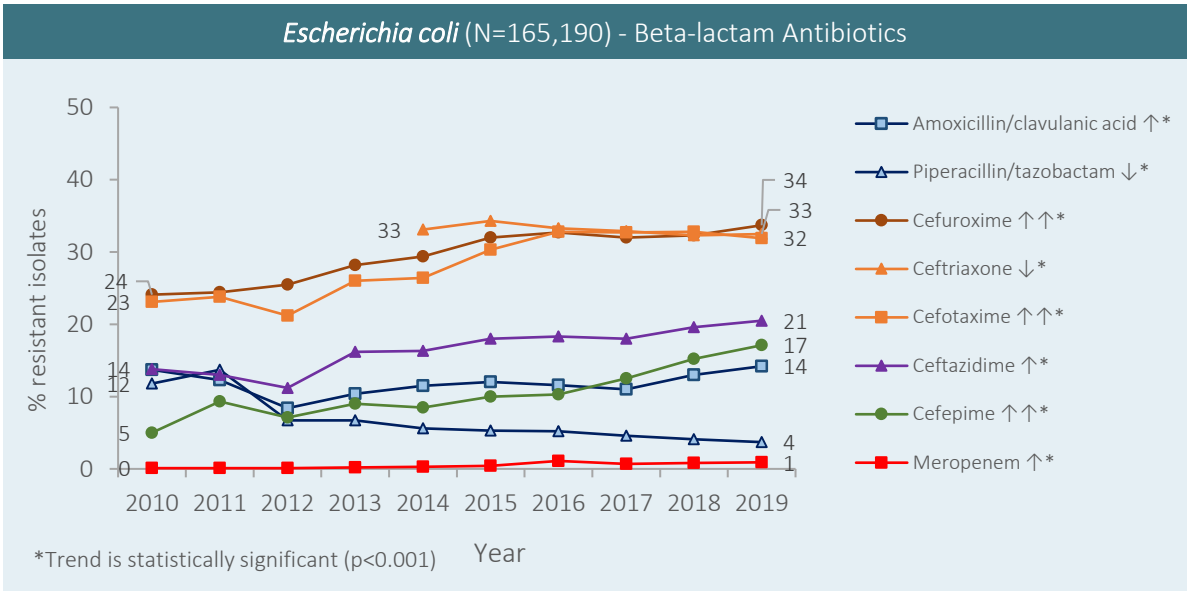
Figure 4.4.1.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Escherichia coli* among isolates from all sources, United Arab Emirates, 2019



For 2019, resistance in *Escherichia coli* ranged from 0.3% for aminoglycosides (amikacin) to 62% for aminopenicillins (ampicillin).

- Susceptibility of urinary tract isolates of *E. coli* to fluoroquinolones (ciprofloxacin) was 59%.
- Prevalence of multidrug resistance (%MDR) in *E. coli* was 45 %.

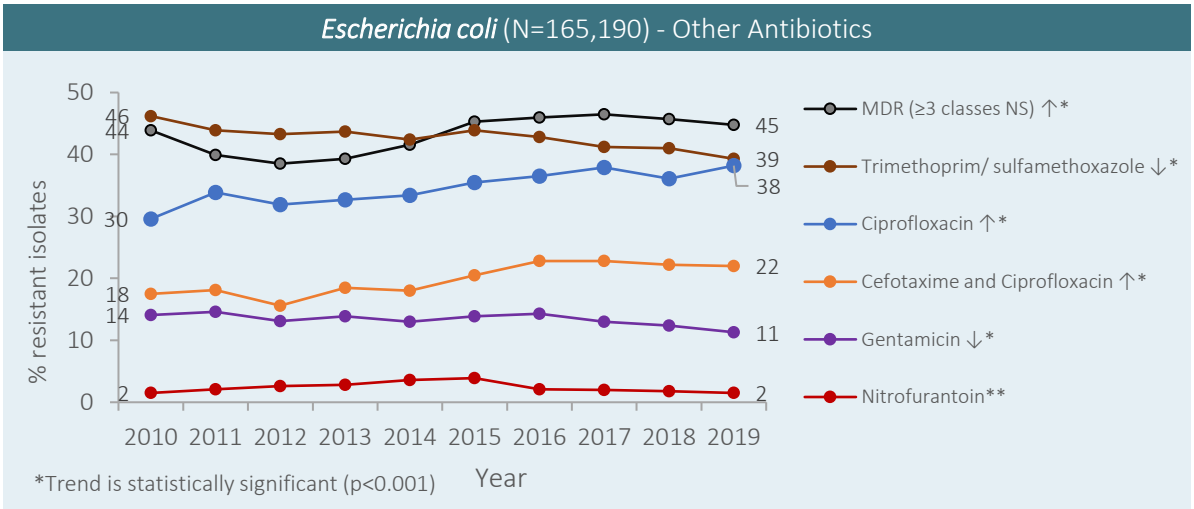
Figure 4.4.1.2 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, United Arab Emirates, 2010-2019 – Beta-lactam Antibiotics



For beta-lactam antibiotics, *Escherichia coli* shows increasing trends of resistance for

- Broad-spectrum penicillins (amoxicillin/clavulanic acid (↑), but not piperacillin/tazobactam (↓)),
- Second- (cefuroxime ↑↑), third- (cefotaxime ↑↑, ceftazidime ↑), and fourth-generation cephalosporins (cefepime ↑↑), but not ceftriaxone (↓).
- Resistance to carbapenems (imipenem, meropenem) is low (<1%), but slowly increasing (↑).

Figure 4.4.1.3 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, United Arab Emirates, 2010-2019 – Other Antibiotics



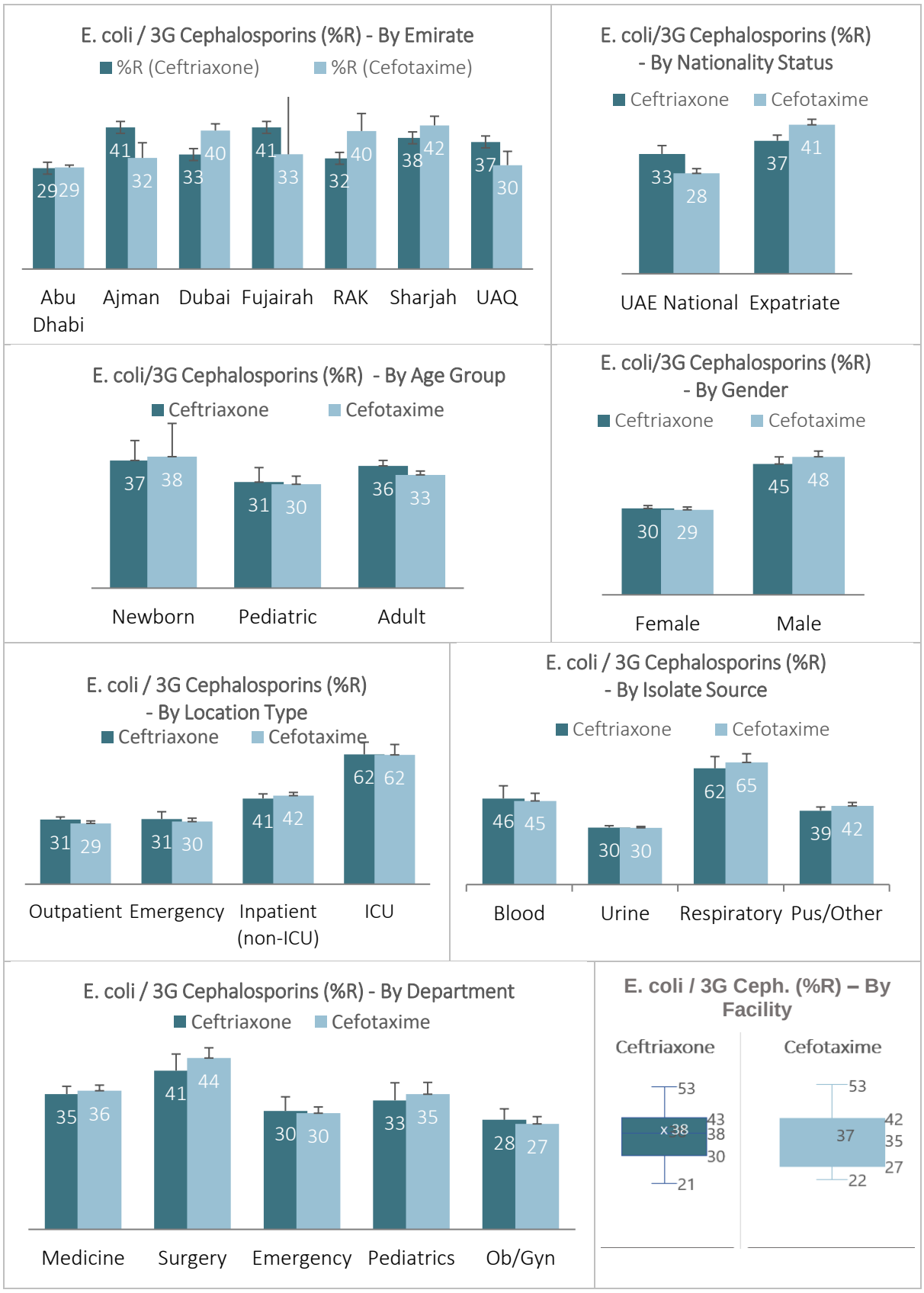
E. coli shows increasing trends of resistance for

- Fluoroquinolones (ciprofloxacin ↑),
- Third generation cephalosporins and fluoroquinolones combined (↑), and
- Multi-drug resistance (%MDR, ≥3 antimicrobial classes, ↑).

E. coli shows decreasing or horizontal trends of resistance for

- Trimethoprim/ sulfamethoxazole (↓),
- Aminoglycosides (gentamicin ↓, amikacin →), and
- Nitrofurantoin (→).

Figure 4.4.1.4 Percentage of isolates resistant (%R) to third generation cephalosporins (ceftriaxone, cefotaxime) for *Escherichia coli*, United Arab Emirates, 2019 – By emirate, nationality status, age group, gender, patient location, isolate source, department, and facility



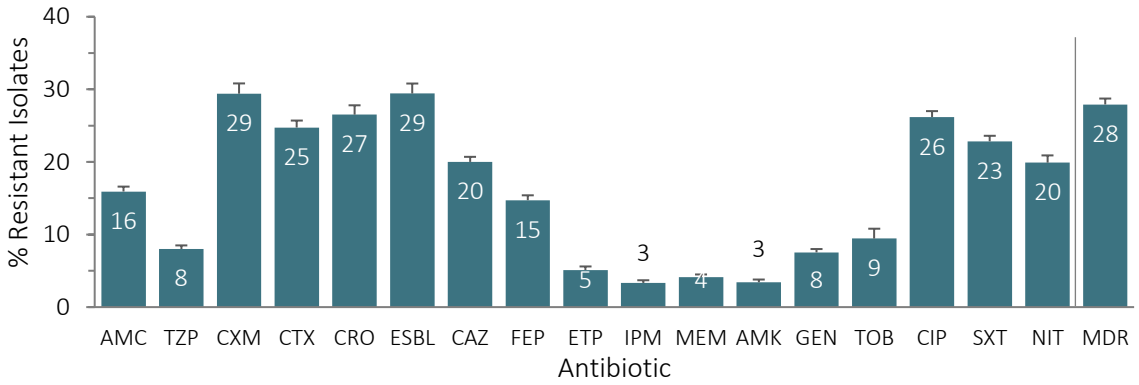
4.4.2 Klebsiella pneumoniae

Table 4.4.2.1 Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Klebsiella pneumoniae* (N=14,644)			
		Isolates (N)	% R	% I	% S
Amoxicillin/clavulanic acid	AMC	11,412	15.9	7.3	76.8
Piperacillin/tazobactam	TZP	11,725	8.0	4.2	87.8
Cefuroxime (oral)	CXM	4,400	29.4	13.6	55.0
Ceftriaxone	CRO	4,764	26.5	0.8	72.7
Cefotaxime	CTX	7,580	24.7	1.2	74.1
Extended-spectrum β-lactamase	ESBL	5,955	29.4	13.6	72.7
Ceftazidime	CAZ	11,748	20.0	3.2	76.8
Cefepime	FEP	10,077	14.7	2.6	82.6
Ertapenem	ETP	8,241	5.1	0.4	94.5
Imipenem	IPM	10,553	3.3	2.3	94.3
Meropenem	MEM	11,508	4.1	0.4	95.5
Gentamicin	GEN	11,750	7.5	0.8	91.6
Tobramycin	TOB	2,097	9.4	3.7	86.6
Amikacin	AMK	10,059	3.4	0.4	96.1
Ciprofloxacin	CIP	11,778	26.2	4.5	69.4
Trimethoprim/sulfamethoxazole	SXT	5,352	23.3	0	76.7
Nitrofurantoin	NIT	7,177	19.9[a]	45.3[a]	34.8[a]
Multidrug-resistance (≥3 classes NS)[b]	MDR	3,303/11,833	27.9	–	–

[a] Nitrofurantoin: Isolates from urinary tract only.
[b] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

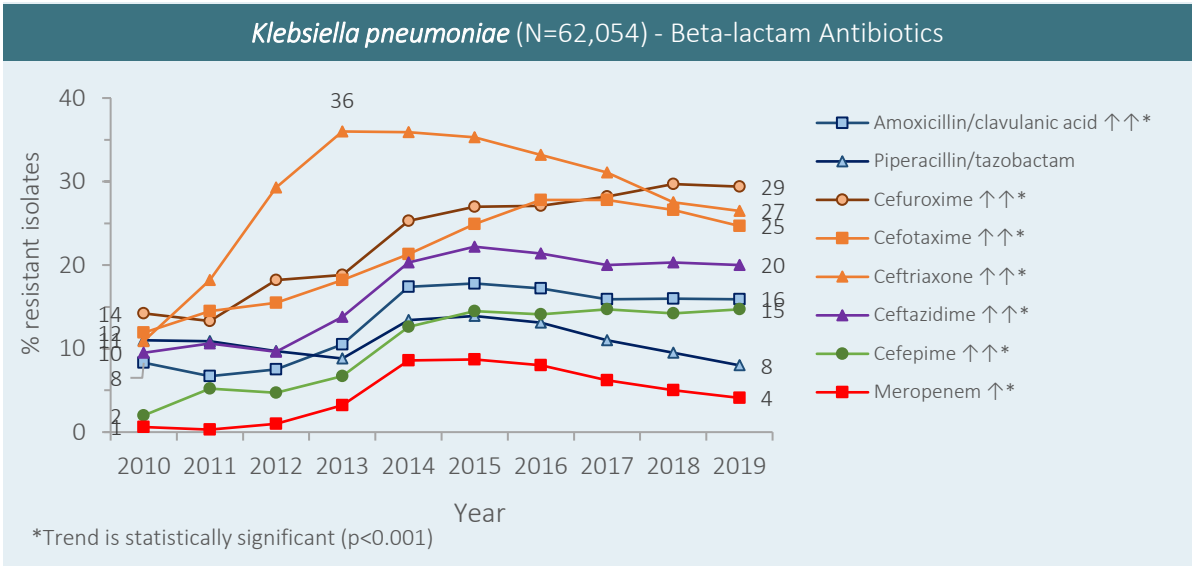
Figure 4.4.2.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Klebsiella pneumoniae* among isolates from all sources, United Arab Emirates, 2019



For 2019, resistance in *Klebsiella pneumoniae* ranged from 3.4 %R for amikacin (aminoglycosides), to 29 %R for ESBL (extended-spectrum beta-lactamases).

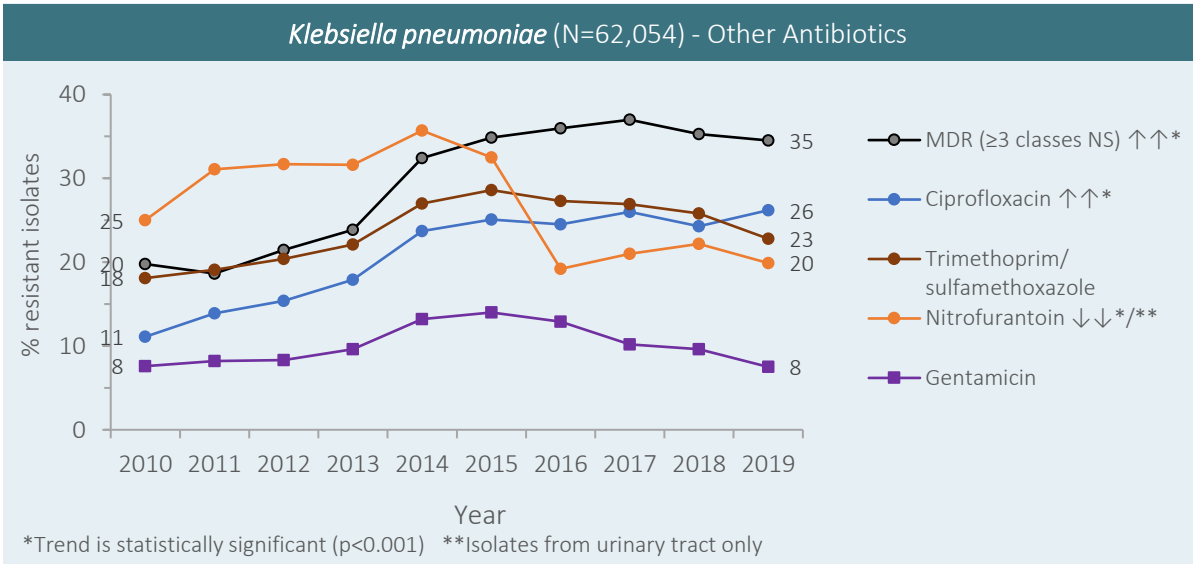
- Non-susceptibility (%R+%I) to carbapenems was 5.7%, 4.5%, and 5.7 %NS for imipenem, meropenem and ertapenem, respectively.
- Susceptibility of urinary tract isolates of *K. pneumoniae* to fluoroquinolones (ciprofloxacin) was 58 %S.
- Prevalence of multidrug resistance in *K. pneumoniae* was 28 %.

Figure 4.4.2.2 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, United Arab Emirates, 2010-2019 – Beta-lactam Antibiotics



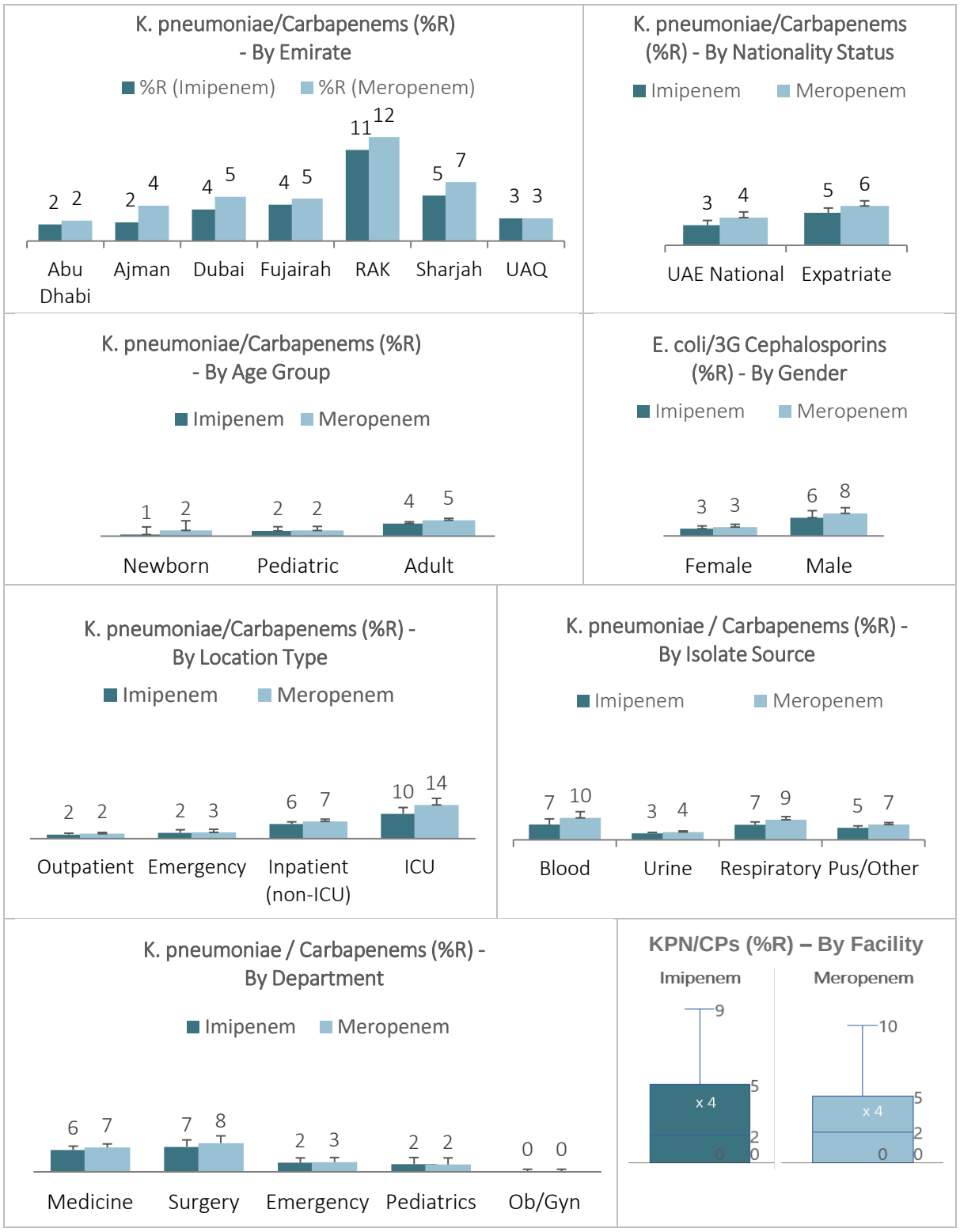
- *Klebsiella pneumoniae* shows overall increasing trends of resistance for most beta-lactam antibiotics, including
    - Broad-spectrum penicillins (amoxicillin/clavulanic acid ↑↑) – but not piperacillin/ tazobactam),
    - second- (cefuroxime ↑↑), third- (ceftazidime ↑↑, cefotaxime ↑↑), and fourth-generation (cefepime ↑↑) cephalosporins, and
    - carbapenems (imipenem ↑, meropenem ↑).
- After peaking between 2013-2016, some previously increasing resistance rates (%R) have either levelled off, or are slightly decreasing.

Figure 4.4.2.3 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, United Arab Emirates, 2010-2019 – Other Antibiotics



- *Klebsiella pneumoniae* shows increasing trends of resistance to fluoroquinolones (ciprofloxacin ↑↑), as well as for multidrug resistance (MDR ↑↑).
- *Klebsiella pneumoniae* shows an overall decreasing trend of resistance to nitrofurantoin (↓).

Figure 4.4.2.4 Percentage of isolates resistant (%R) to carbapenems for *Klebsiella pneumoniae*, United Arab Emirates, 2019 – By emirate, nationality status, age group, gender, patient location, isolate source, department, and facility



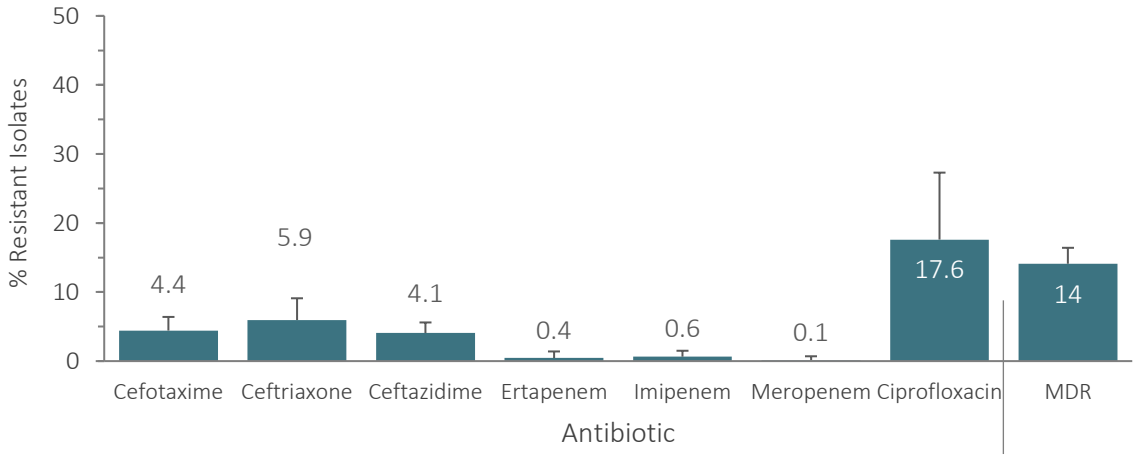
4.4.3 *Salmonella* spp. (non-typhoidal)

Table 4.4.3.1 Percentages of resistant, intermediate, and susceptible isolates for *Salmonella* spp. (non-typhoidal) among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Salmonella* spp. (non-typhoid) (N=1,397)			
		Isolates (N)	% R	% I	% S
Cefotaxime	CTX	633	4.4	0.2	95.4
Ceftriaxone	CRO	353	5.9	0.3	93.8
Ceftazidime	CAZ	959	4.1	0.8	95.1
Ertapenem	ETP	667	0.4	0	99.6
Imipenem	IPM	936	0.6	0.9	98.5
Meropenem	MEM	936	0.1	0.1	99.8
Ciprofloxacin	CIP	91	17.6[a]	5.5[a]	76.9[a]
Multidrug-resistance (≥3 classes NS)[b]	MDR	143/1,013	14.1	–	–

[a] Ciprofloxacin results refer to extra-intestinal (non-stool) isolates only.
[b] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

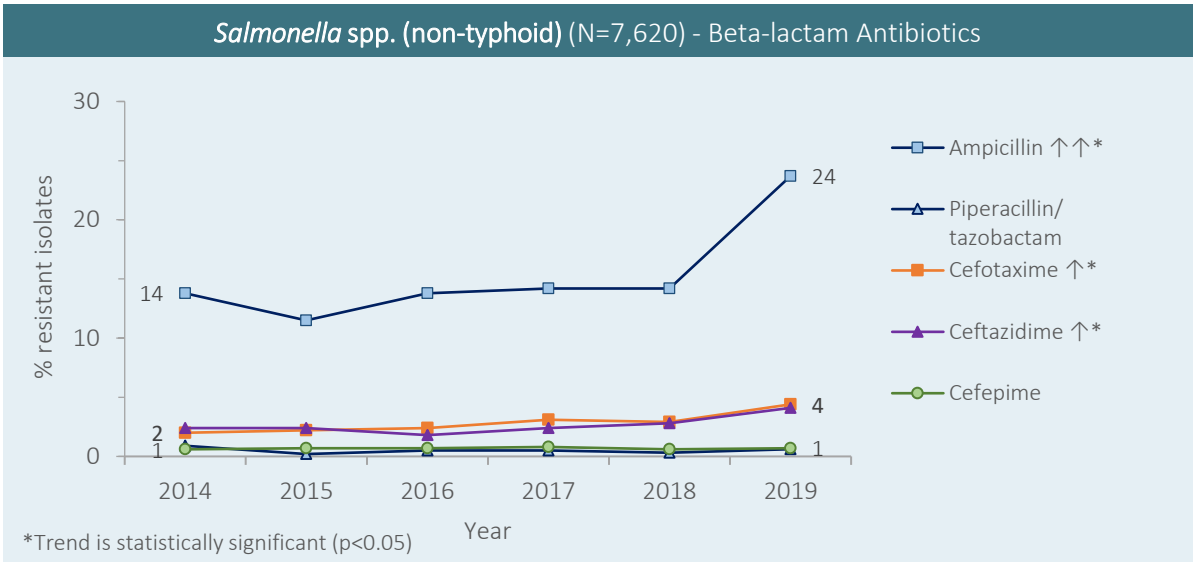
Figure 4.4.3.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Salmonella* spp. (non-typhoidal) among isolates from all sources, United Arab Emirates, 2019



For 2019, resistance in *Salmonella* spp. (non-typhoidal) ranged from 0 %R for carbapenems (imipenem, meropenem, ertapenem), to 18 %R for fluoroquinolones (ciprofloxacin).

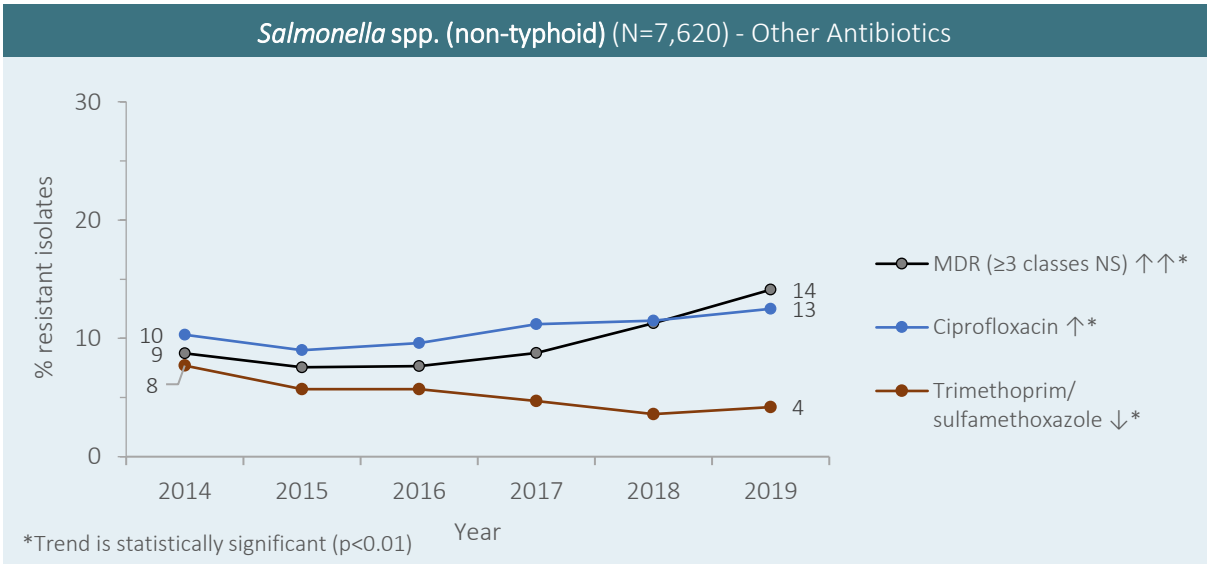
- Susceptibility of non-typhoidal *Salmonella* spp. (extra-intestinal isolates) to ciprofloxacin was 77%.
- Prevalence of multidrug resistance (%MDR) in *Salmonella* spp. (non-typhoidal) was 14 %.

Figure 4.4.3.2. Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp. (non-typhoidal), United Arab Emirates, 2014-2019 – Beta-lactam Antibiotics



- For *Salmonella* spp. (non-typhoidal), an increasing trend of resistance was observed for aminopenicillins (ampicillin ↑↑), but not for broad-spectrum penicillins (piperacillin-tazobactam).
- Resistance to third generation cephalosporins (cefotaxime ↑, ceftazidime ↑) is low (< 5% R), but slowly increasing.
- Resistance to carbapenems was very low (<1 %R) during the observation period 2014-2019.

Figure 4.4.3.3 Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp. (non-typhoidal), United Arab Emirates, 2014-2019 – Other Antibiotics



- For trimethoprim/sulfamethoxazole a decreasing trend of resistance (↓) was observed, from 8 %R (2014) to 4 %R (2019).
- Resistance to fluoroquinolones (ciprofloxacin ↑) increased from 10 %R (2014) to 13 %R (2019).
- Multidrug resistance (≥ 3 classes) increased from 9 %MDR (2014) to 14 %MDR (2019).

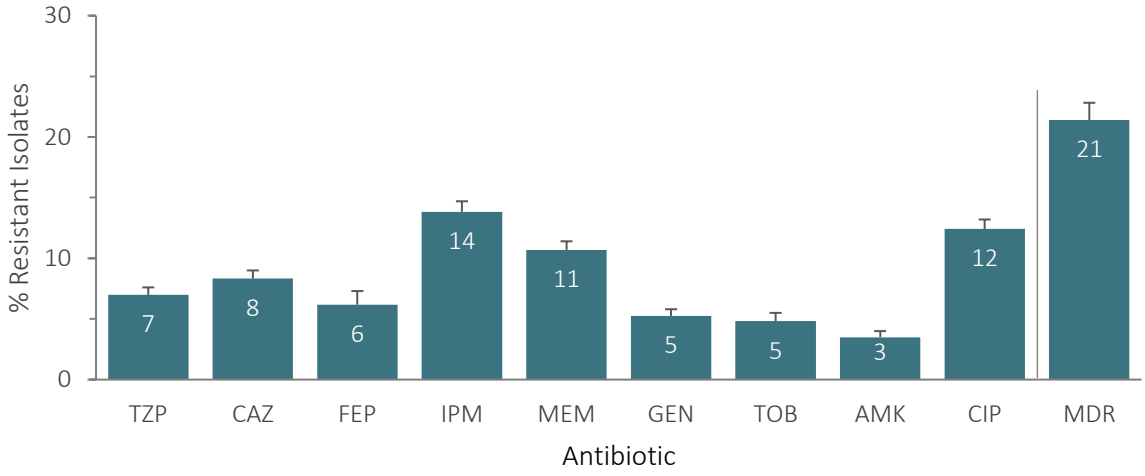
4.4.4 Pseudomonas aeruginosa

Table 4.4.4.1 Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Pseudomonas aeruginosa* (N=8,962)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	6,563	7.0	5.3	87.7
Ceftazidime	CAZ	7,000	8.3	4.5	87.1
Cefepime	FEP	6,719	6.2	3.9	89.5
Imipenem	IPM	6,780	13.8	0.9	85.3
Meropenem	MEM	6,951	10.7	3.8	85.5
Gentamicin	GEN	6,994	5.2	4.1	90.7
Tobramycin	TOB	5,043	4.8	0.6	94.6
Amikacin	AMK	6,703	3.5	1.2	95.3
Ciprofloxacin	CIP	6,996	12.4	4.7	82.8
Multidrug-resistance (≥3 classes NS)[a]	MDR	1,170/6,997	16.7	–	–

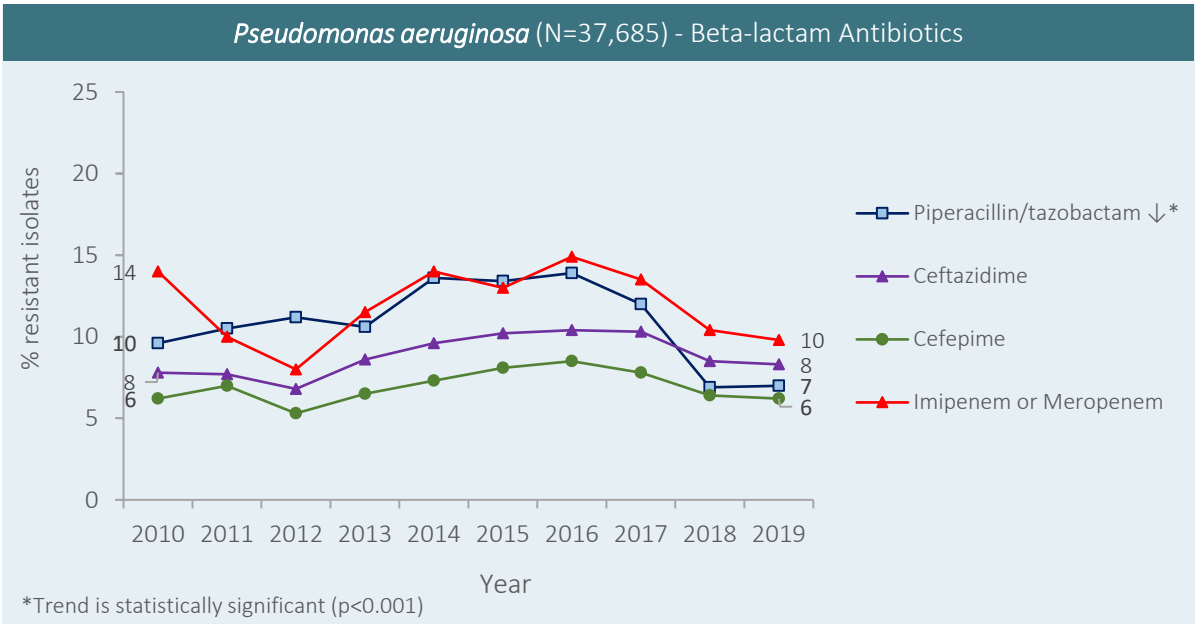
[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

Figure 4.4.4.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Pseudomonas aeruginosa* among isolates from all sources, United Arab Emirates, 2019



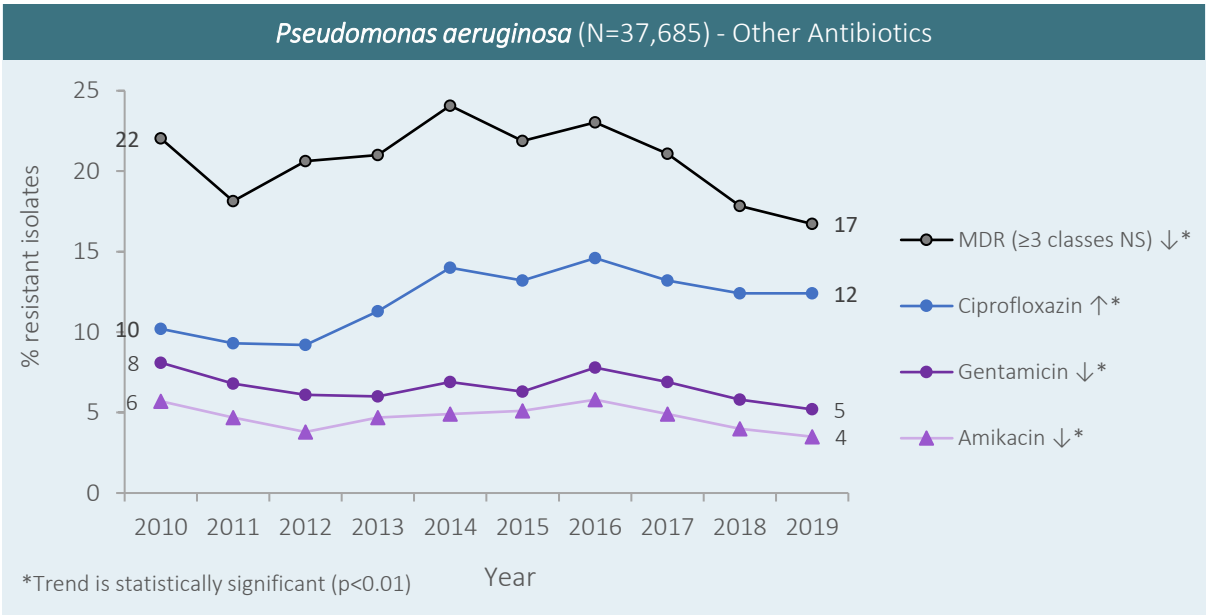
- For 2019, resistance in *Pseudomonas aeruginosa* ranged from 4-5 %R for aminoglycosides (amikacin: 3.5 %R, tobramycin: 4.8 %R, gentamicin: 5.2 %R), to 12-16 %R for fluoroquinolones (ciprofloxacin, 12 %R) and carbapenems (meropenem: 12 %R, imipenem: 14 %R).
- Prevalence of multidrug resistance (%MDR) in *Pseudomonas aeruginosa* was 17 %.

Figure 4.4.4.2 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, United Arab Emirates, 2010-2019 – Beta-lactam Antibiotics



- *Pseudomonas aeruginosa* shows decreasing resistance to broad-spectrum penicillins (piperacilllin-tazobactam (↓).
- Horizontal trends for resistance to cephalosporins (ceftazidime →, cefepime →).
- Resistance to carbapenems (IMP or MEM) is fluctuating around 12 ± 2.3 %R, no clear trend.

Figure 4.4.4.3 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, United Arab Emirates, 2010-2019 – Other Antibiotics



- Multidrug resistance in *P. aeruginosa* (%MDR) decreased from 22% (2010) to 17% (2019).
- *Pseudomonas aeruginosa* shows an increasing trend of resistance for fluoroquinolones (ciprofloxacin ↑).
- Decreasing trends of resistance for aminoglycosides (gentamicin ↓, amikacin ↓).

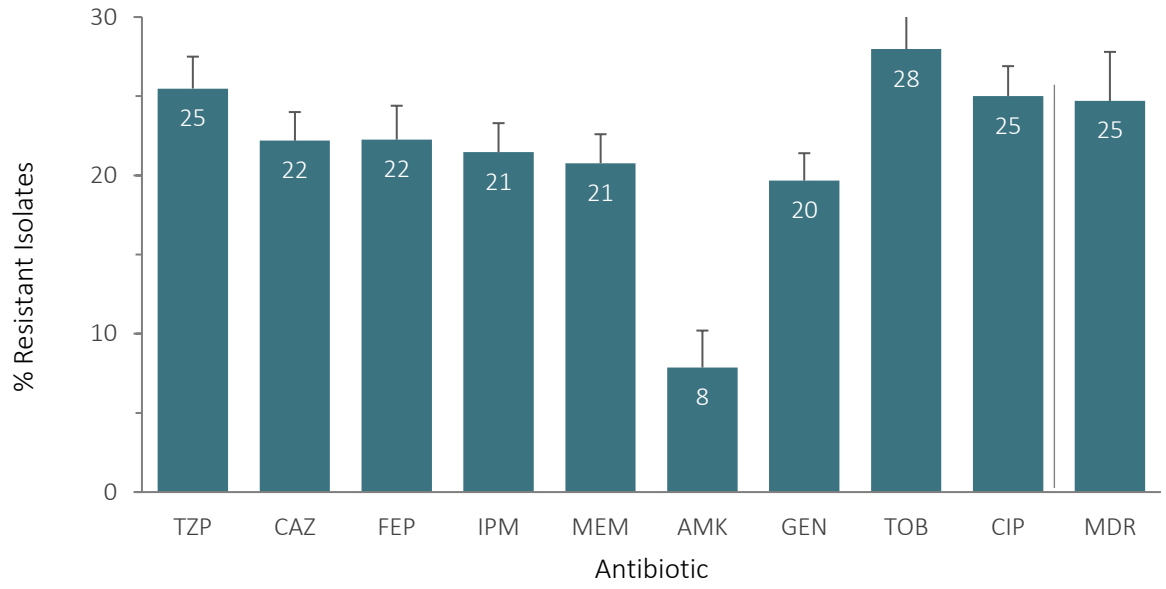
4.4.5 Acinetobacter spp.

Table 4.4.5.1 Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp. among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Acinetobacter* spp. (N=2,466)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	2,013	25.5	1.9	72.6
Ceftazidime	CAZ	2,163	22.2	7.0	70.8
Cefepime	FEP	1,896	22.3	2.3	75.3
Imipenem	IPM	2,101	21.5	0.2	78.3
Meropenem	MEM	2,133	20.8	0.8	78.5
Gentamicin	GEN	2,171	19.7	2.9	77.4
Tobramycin	TOB	940	28.0	1.8	70.2
Amikacin	AMK	155	7.7	1.3	91.0
Ciprofloxacin	CIP	2,132	25.0	2.0	73.0
Multidrug-resistance (≥3 classes NS)[a]	MDR	554/2,178	25.4	–	–

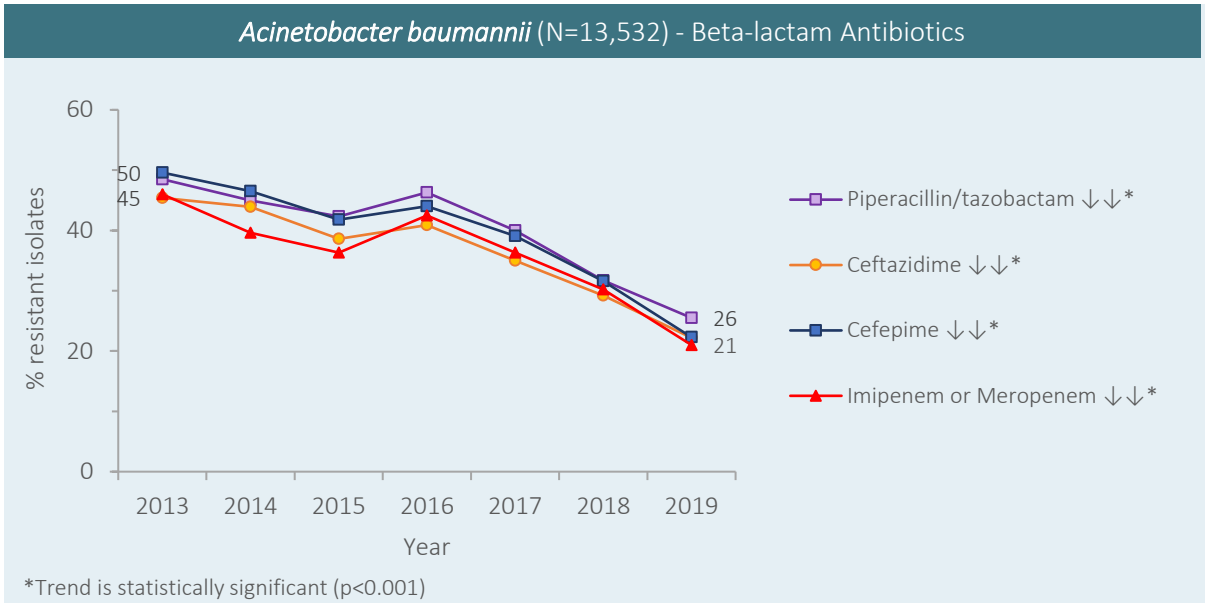
[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

Figure 4.4.5.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Acinetobacter* spp. among isolates from all sources, United Arab Emirates, 2019



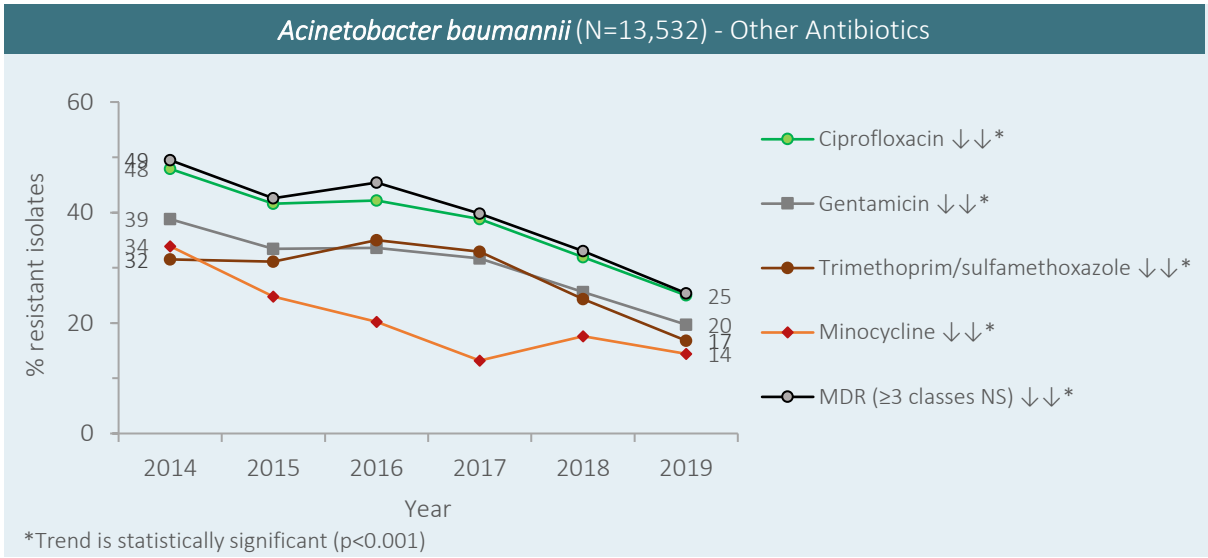
- For 2019, resistance in *Acinetobacter* spp. ranged from 8 %R for amikacin (aminoglycosides) to 28 %R for cefepime (fourth generation cephalosporins).
- Prevalence of multidrug resistance (%MDR) in *Acinetobacter* spp. was 25 %.

Figure 4.4.5.2 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., United Arab Emirates, 2011-2019 – Beta-lactam antibiotics



- *Acinetobacter* spp. shows decreasing trends of resistance for all beta-lactam antibiotics, including
  - Broad-spectrum penicillins (piperacillin-tazobactam ↓↓),
  - Third- (ceftazidime ↓↓), and fourth generation (cefepime ↓↓) cephalosporins, and
  - Carbapenems (imipenem or meropenem ↓↓).

Figure 4.4.5.3 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., United Arab Emirates, 2011-2019 – Other Antibiotics



- *Acinetobacter* spp. shows decreasing trends of resistance for
  - Aminoglycosides (gentamicin ↓↓),
  - Fluoroquinolones (ciprofloxacin ↓↓),
  - Trimethoprim/sulfamethoxazole ↓↓,
  - Minocycline ↓↓, and
  - Tetracycline ↓↓.
- Multidrug resistance (%MDR) decreased from 35% (2011) to 25% (2019).

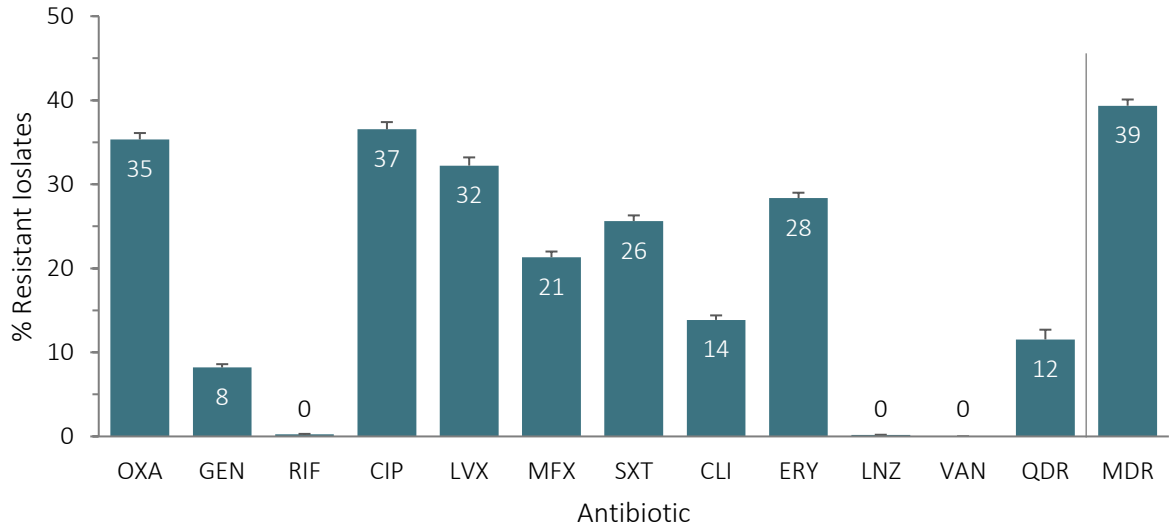
4.4.6 Staphylococcus aureus

Table 4.4.6.1 Percentages of resistant, intermediate, and susceptible isolates for *Staphylococcus aureus* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Staphylococcus aureus* (n=21,729)			
		Isolates (N)	% R	% I	% S
Oxacillin	OXA	16,484	35.3[a]	–	64.7[a]
Gentamicin	GEN	16,776	8.2	1.4	90.4
Rifampicin	RIF	14,666	0.2	0.1	99.7
Ciprofloxacin	CIP	11,298	36.5	1.0	62.5
Levofloxacin	LVX	8,890	32.2	1.9	65.9
Moxifloxacin	MFX	15,017	21.3	4.3	74.4
Trimethoprim/sulfamethoxazole	SXT	16,585	25.6	0	74.3
Clindamycin	CLI	16,753	13.9	0.2	86.0
Erythromycin	ERY	16,755	28.4	1.4	70.3
Linezolid	LNZ	16,242	0.2	0	99.8
Vancomycin	VAN	16,532	0	0	100.0
Quinupristin/Dalfopristin	QDA	3,172	11.5	0	88.4
Multidrug-resistance (≥3 classes NS)[b]	MDR	6,633/16,856	39.4	–	–

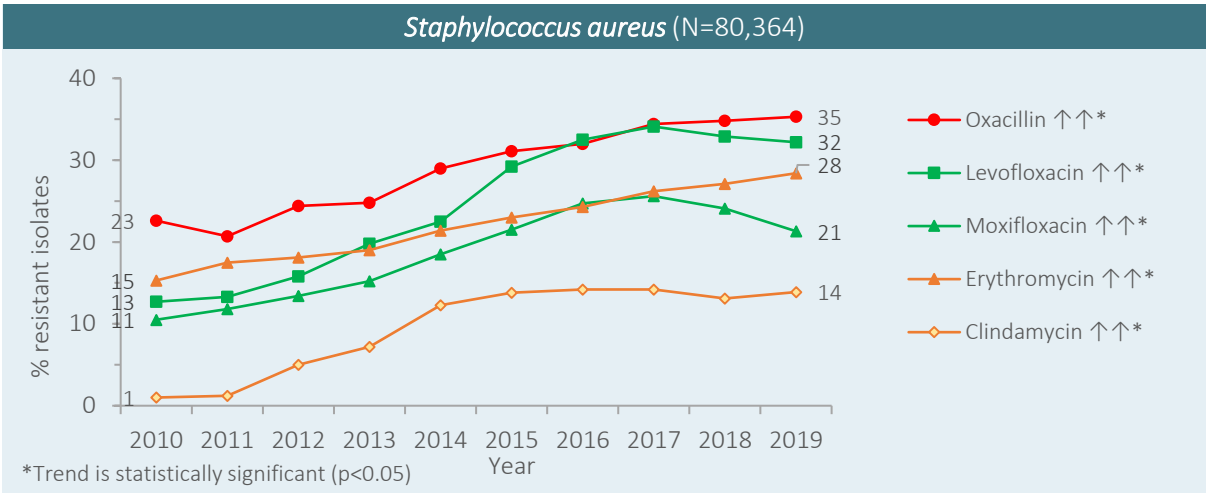
[a] MRSA/MSSA is calculated as resistance/susceptibility to oxacillin: %MRSA = 35.3% and %MSSA = 64.7%.
[b] Multidrug resistance (MDR) was defined as a) isolate being a MRSA, or b) acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

Figure 4.4.6.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Staphylococcus aureus* among isolates from all sources, United Arab Emirates, 2019



- For 2019, resistance in *Staphylococcus aureus* ranged from 0% for vancomycin and linezolid, to 37% for ciprofloxacin
- Percentage MRSA was 35% for all isolates and 38% for blood culture isolates only.
- Percentage MRSA was 31% for outpatients and 48% for inpatients (ICU: 50%).
- Prevalence of multidrug resistance (%MDR) in *S. aureus* was 39%.

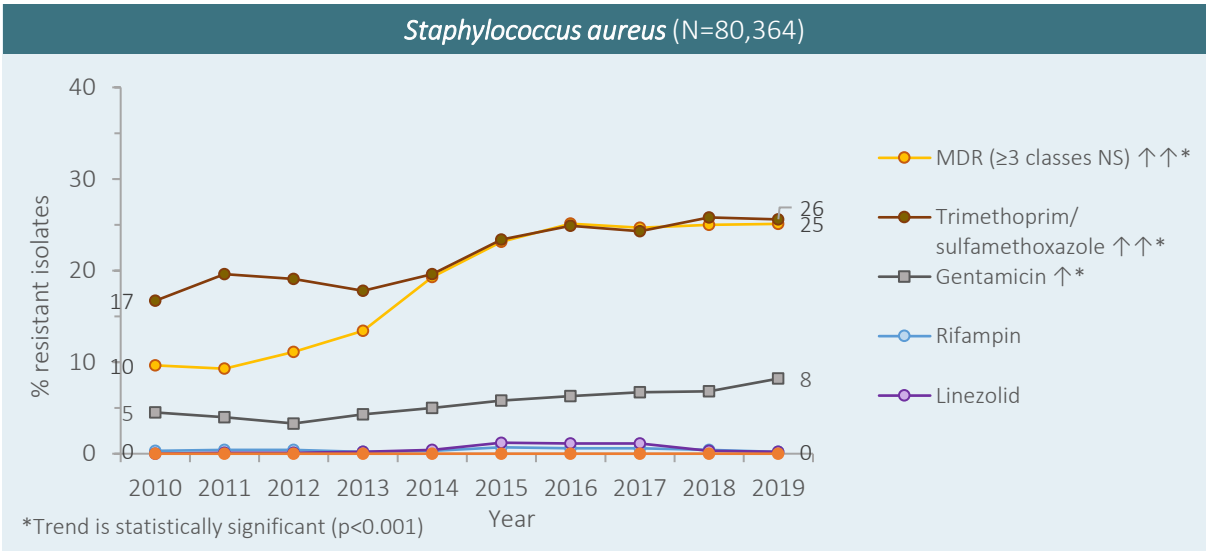
Figure 4.4.6.2 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, United Arab Emirates, 2010-2019 – Beta-lactams, fluoroquinolones, macrolides and lincosamides



Staphylococcus aureus shows increasing trends of resistance for beta-lactams, fluoroquinolones, macrolides, and lincosamides:

- Beta-lactams: %MRSA (↑↑) increased from 23% (2010) to 35% (2019).
- Fluoroquinolones: resistance to levofloxacin (↑↑) and moxifloxacin (↑↑) increased from 13%/11% (2010) to 32%/21% (2019), respectively.
- Macrolides: resistance to erythromycin (↑↑) increased from 15% (2010) to 28% (2019).
- Lincosamides: resistance to clindamycin (↑↑) increased from 1% (2010) to 14 % (2019).

Figure 4.4.6.3 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, United Arab Emirates, 2010-2019 – Other Antibiotics



Staphylococcus aureus shows increasing trends of resistance for:

- Trimethoprim/sulfamethoxazole (↑↑): resistance increased from 17% (2010) to 26% (2019).
- Aminoglycosides (gentamicin ↑): resistance increased from 5 % (2010) to 8% (2019).
- Resistance to rifampin and linezolid remains very low (< 1%).
- Resistance to glycopeptides (vancomycin, teicoplanin) was not observed.

Multidrug resistance (MDR) increased from 10 %MDR (2010) to 25 %MDR (2019).

Figure 4.4.6.4 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2019 –By emirate, nationality status, age group, gender, patient location, isolate source, department, and facility

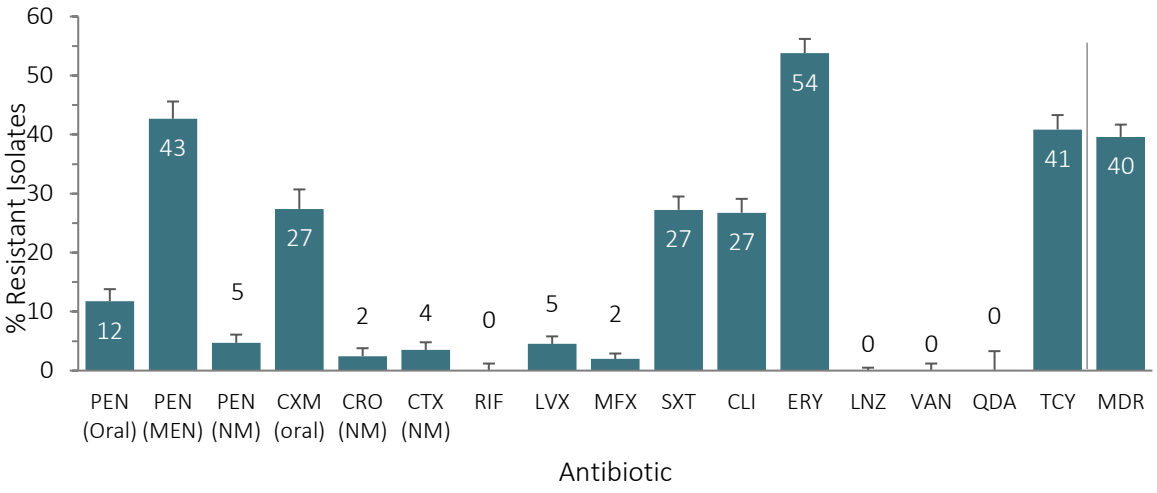
4.4.7 Streptococcus pneumoniae

Table 4.4.7.1 Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Streptococcus pneumoniae* (N=2,302)			
		Isolates (N)	% R	% I	% S
Penicillin G (oral Breakpoints)	PEN (Oral)	1,148	11.8	31.3	57.0
Penicillin G (non-meningitis breakpoints)	PEN (NM)	1,148	4.7	2.3	93.0
Penicillin G (meningitis breakpoints)	PEN (MEN)	1,148	42.7	0.3	57.0
Cefuroxime (oral breakpoints)	CXM	770	27.4	4.2	68.4
Cefotaxime (non-meningitis breakpoints)	CTX (NM)	1,142	3.5	1.4	95.1
Ceftriaxone (non-meningitis breakpoints)	CRO (NM)	817	2.4	1.8	95.7
Rifampin	RIF	404	0	0.5	99.5
Levofloxacin	LVX	1,350	4.5	1.7	93.8
Moxifloxacin	MFX	1,417	2.0	1.2	96.8
Trimethoprim/Sulfamethoxazole	SXT	1,582	27.2	12.5	60.1
Clindamycin	CLI	1,454	26.8	2.1	71.2
Erythromycin	ERY	1,654	53.8	0.2	45.9
Linezolid	LNZ	1,602	0	0	99.9
Vancomycin	VAN	1,527	0	0	99.3
Quinupristin/Dalfopristin	QDA	140	0	0.7	99.3
Tetracycline	TCY	1,655	40.8	1.1	58.1
Multidrug-resistance (≥3 classes)[a]	MDR	868/2,192	39.6	–	–

[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

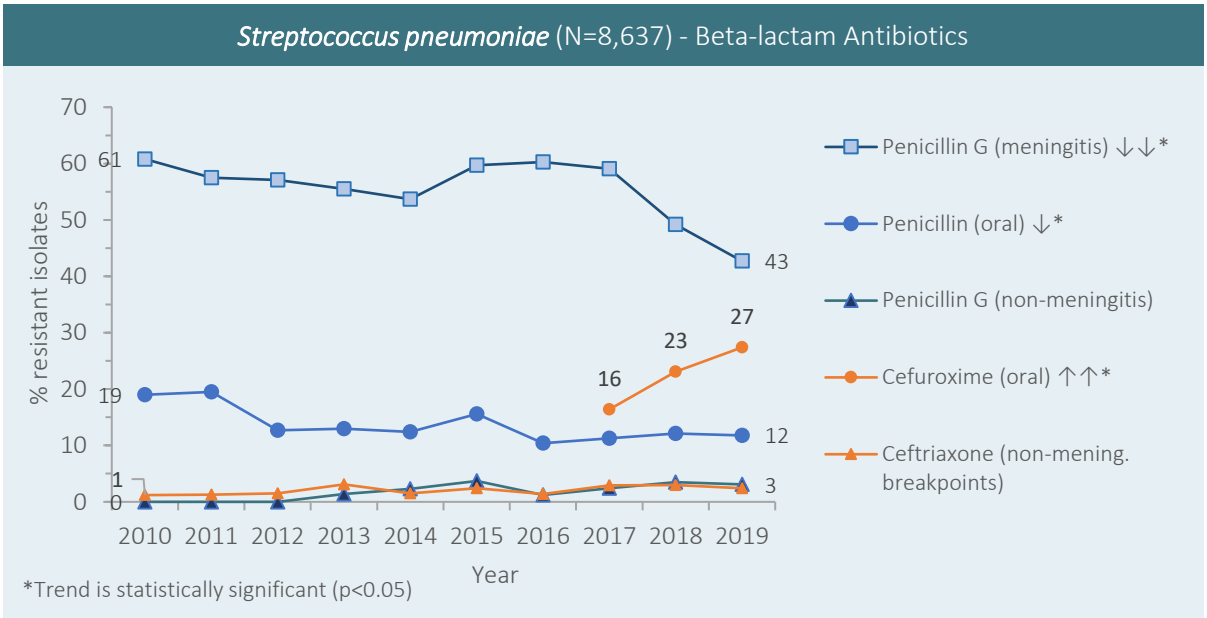
Figure 4.4.7.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Streptococcus pneumoniae* among isolates from all sources, United Arab Emirates, 2019



For 2019, resistance in *Streptococcus pneumoniae* ranged from 0% for rifampin, linezolid, vancomycin, and QDA, to 54% for erythromycin.

- Prevalence of multidrug resistance (%MDR) in *S. pneumoniae* was 40%.

Figure 4.4.7.2 Annual trends for percentage of isolates resistant (%R) for *Streptococcus pneumoniae*, United Arab Emirates, 2010-2019 – Beta-lactam Antibiotics

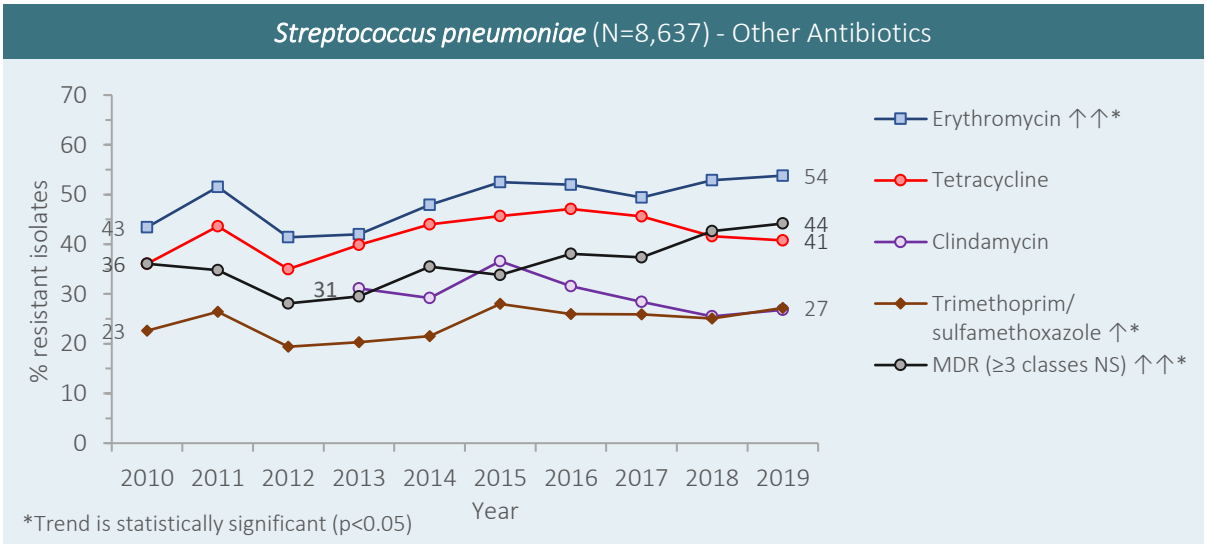


Streptococcus pneumoniae shows increasing trends of resistance for

- Second-generation cephalosporins: resistance to cefuroxime (↑↑) increased from 16% (2017) to 27% (2019).

Resistance decreased for penicillin G (↓, oral breakpoints) and penicillin G (↓↓, meningitis breakpoints).

Figure 4.4.7.3 Annual trends for percentage of isolates resistant (%R) for *Streptococcus pneumoniae*, United Arab Emirates, 2010-2019 – Other Antibiotics



Streptococcus pneumoniae shows increasing trends of resistance for

- Macrolides: resistance to erythromycin (↑↑) increased from 43 % (2010) to 54 % (2019).
- Trimethoprim/sulfamethoxazole (↑): resistance increased from 23 % (2010) to 27 % (2019).

Multidrug resistance (MDR) increased from 36 %MDR (2010) to 44 %MDR (2019).

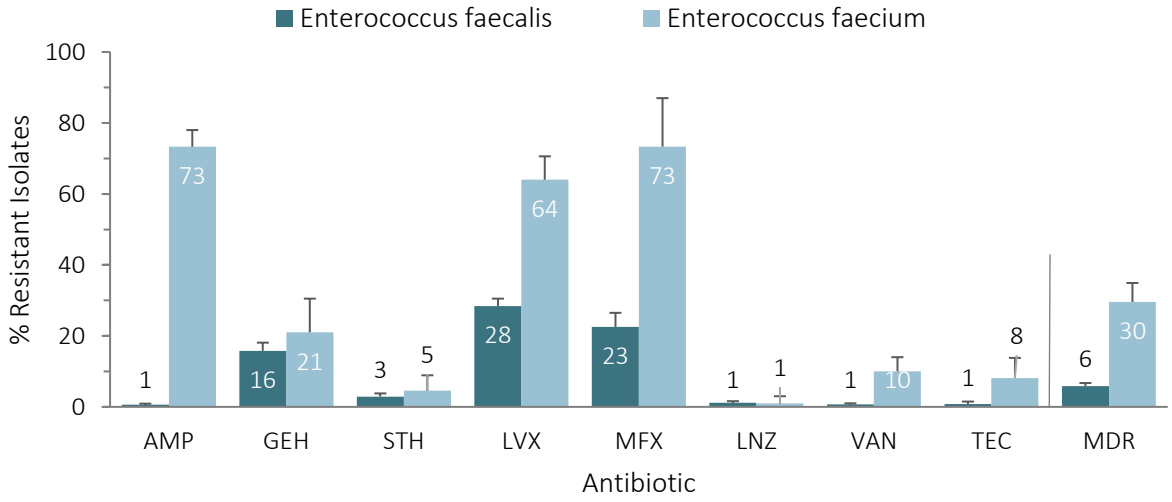
4.4.8 Enterococcus faecalis and Enterococcus faecium

Table 4.4.8.1 Percentages of resistant, intermediate, and susceptible isolates for *Enterococcus faecalis* and *Enterococcus faecium* among isolates from all sources, United Arab Emirates, 2019

Antibiotic	Code	*Enterococcus faecalis* (N=4,228)				*Enterococcus faecium* (N=476)			
		N	% R	% I	% S	N	% R	% I	% S
Ampicillin	AMP	3,457	0.5	0	99.4	322	73.3	0	26.7
Gentamicin (high level)	GEH	1,076	15.8	0	84.2	100	21.0	0	79.0
Streptomycin (high level)	STH	1,758	2.9	0	97.1	195	4.6	0	95.4
Levofloxacin	LVX	2,047	28.4	2.4	69.1	200	64.0	7.0	29.0
Moxifloxacin	MFX	497	22.5	7.8	69.6	30	73.3	3.3	23.3
Linezolid	LNZ	3,311	1.1	5.4	93.4	319	0.9	5.0	94.0
Vancomycin	VAN	3,401	0.6[b]	0.2	99.1	320	10.0[b]	0.3	89.7
Teicoplanin	TEC	1,567	0.8	0.1	99.0	160	8.1	0.6	91.3
Multidrug-resistance (≥3)[c]	MDR	205	5.9	–	–	94	29.6	–	–

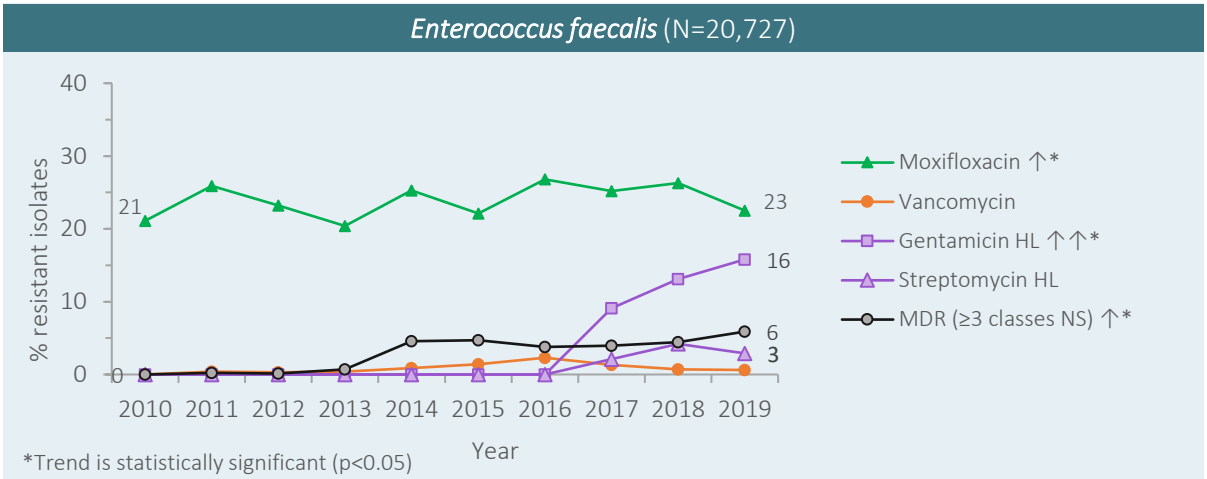
[a] A small number of isolates were tested (N<30): percentage resistance should be interpreted with caution.
[b] VRE is calculated as resistance to vancomycin: %VRE (E. faecalis) = 1.0%, %VRE (E. faecium) = 12.9%.
[c] Multidrug resistance (MDR) was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2011).

Figure 4.4.8.1 Percentages of resistant (%R), and multidrug-resistant (%MDR) isolates for *Enterococcus faecalis* and *Enterococcus faecium* among isolates from all sources, United Arab Emirates, 2019



- For 2019, resistance in *Enterococcus faecalis* ranged from 1% for aminopenicillins (ampicillin), oxazolidinones (linezolid), and glycopeptides (vancomycin, teicoplanin), to 28% for fluoroquinolones (levofloxacin, moxifloxacin).
- For *Enterococcus faecium*, resistance ranged from 1% for oxazolidinones (linezolid), to 73% for fluoroquinolones (moxifloxacin) and aminopenicillins (ampicillin).
- Vancomycin-resistant Enterococci (VRE) were observed in 1% of *E. faecalis*, and 13% of *E. faecium* isolates, respectively, and in 2% of all *Enterococcus* spp. isolates combined.
- Prevalence of multidrug resistance (%MDR) was 6% in *E. faecalis* and 30% in *E. faecium*.

Figure 4.4.8.2 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecalis*, United Arab Emirates, 2010-2019

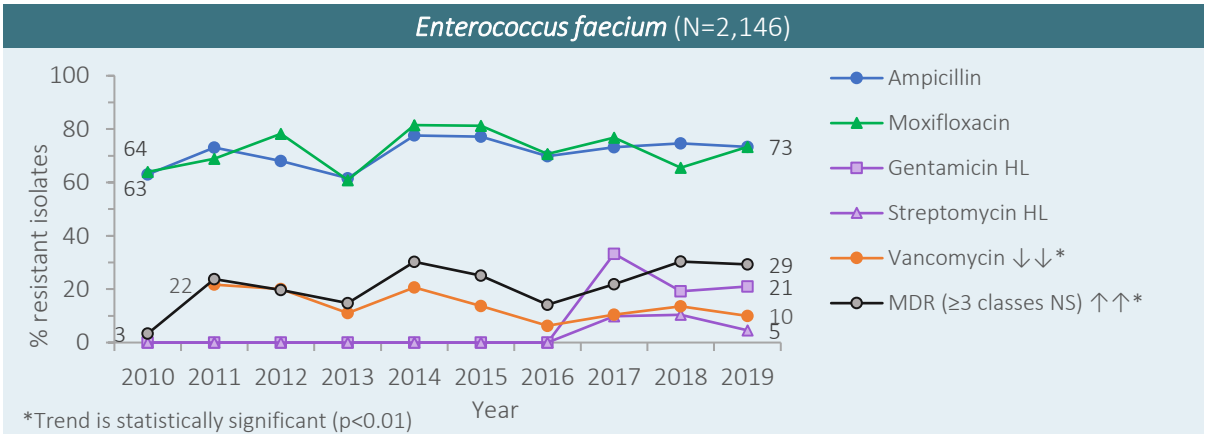


Enterococcus faecalis shows an increasing trend of resistance for

- Fluoroquinolones: resistance to moxifloxacin (↑) increased from 21% (2010) to 23% (2019).
- Aminoglycosides: resistance to gentamicin-HL (↑↑, high level) increased since 2016 (0%) to 16 %R (2019).

Multidrug resistance (MDR) increased from 0 %MDR (2010) to 6 %MDR (2019).
Resistance to vancomycin (%VRE) was very low (≤3%) during the reporting period.

Figure 4.4.8.3 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecium*, United Arab Emirates, 2010-2019



Enterococcus faecium shows a decreasing trend of resistance for glycopeptides:

- Resistance to vancomycin (%VRE) decreased (↓↓) from 22 %VRE (2011) to 10 %VRE (2019).

Enterococcus faecium shows high resistance levels for aminopenicillins (ampicillin, fluctuating between 62% and 78%) and fluoroquinolones (moxifloxacin, fluctuating between 64% and 82%), but no statistically significant trend was observed.

Since 2017, elevated levels of resistance to high level gentamicin/streptomycin are observed, however these trends are statistically not significant (p>0.05).

Multidrug resistance (%MDR) increased (↑↑) from 3 %MDR (2010) to 29 %MDR (2019).

5. Annex

Annex 5.1 AMR priority pathogens

The following text on pathogens under UAE AMR Surveillance was adopted from the Antimicrobial Resistance global report on surveillance 2014 published by WHO[25] and the annual report of the EARS-Net published by the ECDC in 2015[26].

E. coli

Escherichia coli is part of the normal intestinal flora of both humans and animals. Nevertheless, it:

- is the most frequent cause of both community-acquired and hospital-acquired urinary tract infections (including pyelonephritis)
- is the most frequent cause of blood stream infection among people of all ages
- is associated with intra-abdominal infections such as spontaneous and post-surgical peritonitis, and with skin and soft tissue infections
- causes meningitis in neonates; and
- is one of the leading causes of food-borne infections worldwide.

Infections with *E. coli* usually originate from the person affected (autoinfection), but strains with a particular resistance or disease-causing properties can also be transmitted from direct contact with animals; through consumption of contaminated food or person-to-person contact.

K. pneumoniae

Like *E. coli*, bacteria of the species *Klebsiella pneumoniae* are frequent colonizers of the gut in humans and may often be found on skin, in the oropharynx and upper airways, particularly in individuals with a history of hospitalization, as well as in other vertebrates. Infections with *K. pneumoniae*:

- are particularly common in hospitals among vulnerable individuals such as preterm infants and patients with impaired immune systems, diabetes or alcohol-use disorders and those receiving advanced medical care
- are usually urinary and respiratory tract infections and, among neonates, bloodstream infections
- are the second a common cause of Gram-negative bloodstream infections including sepsis and septic shock; and
- can spread readily between patients, leading to nosocomial outbreaks, which frequently occur in intensive care units and neonatal care facilities.

Many of these infections are hospital-acquired and can be life-threatening, especially if the strains are resistant to antimicrobial agents. The presence of invasive devices, contamination of respiratory support equipment, use of urinary tract catheters, and use of antibiotics are factors that increase the likelihood of nosocomial infections with *K. pneumoniae*. The mortality rates for hospital-acquired *K. pneumoniae* infections depend on the severity of the underlying condition, even when people are treated with appropriate antibacterial drugs.

Salmonella

Salmonella:

- is a major cause of foodborne illness throughout the world,
- is a zoonotic pathogen and can thus be found in the intestines of many food-producing animals such as poultry and pigs, and infection is usually acquired by consumption of contaminated water or food of animal origin such as undercooked meat, poultry, eggs and milk;
- can also contaminate the surface of fruits and vegetables through contact with human or animal faeces, which can lead to foodborne outbreaks; and
- mostly causes gastroenteritis, while some strains, particularly *Salmonella enterica* serotypes Typhi and Paratyphi, are more invasive and typically cause enteric fever – a more serious infection that poses problems for treatment due to antibiotic-resistant strains in many parts of the world.

UAE AMR surveillance focuses on non-typhoidal *Salmonella* because these are the main diarrhoeal pathogens transmitted via the food chain. In many countries, the incidence of non-typhoidal *Salmonella* infections has increased markedly in recent years, for reasons that are unclear. One estimate suggests that there are around 94 million cases, resulting in 155 000 deaths, of non-typhoidal *Salmonella* gastroenteritis each year. The majority of the disease burden, according to this study, is in the WHO South-East Asian Region and the WHO Western Pacific Region[27].

P. aeruginosa

Pseudomonas aeruginosa:

- is a non-fermenting Gram-negative bacterium that is ubiquitous in aquatic environments in nature;
- is an opportunistic pathogen for plants, animals and humans and is a major cause of infections in hospitalized patients with localised or systemic impairments of immune defences;
- commonly causes hospital-acquired infections (diffuse bronchopneumonia, including ventilator-associated pneumonia), bloodstream infections (including septic shock), and urinary tract infections, and may also cause gastrointestinal (necrotizing enterocolitis), haemorrhagic and necrotizing skin and soft tissue infections;
- is difficult to control in hospitals and institutional environments, because of its ubiquity, enormous versatility and intrinsic tolerance to many detergents, disinfectants and antimicrobial compounds;
- may chronically colonize patients with cystic fibrosis, causing severe intermittent exacerbation of the condition with, for example, bronchiolitis and acute respiratory distress syndrome; and
- is commonly found in burn units where it is almost impossible to eradicate colonizing strains with classic infection control procedures.

Acinetobacter spp.

The *Acinetobacter* genus comprises many species that can be roughly divided between the *Acinetobacter baumannii* group (consisting of the species *A. baumannii*, *A. pittii* and *A. nosocomialis*) and the *Acinetobacter* non-baumannii group (consisting of many environmental species with low pathogenicity). Species belonging to the *A. baumannii* group:

- have been identified as pathogens in nosocomial pneumonia (particularly ventilator-associated pneumonia), central line-associated bloodstream infections, urinary tract infections, surgical site infections and other types of wound infection;
- are not considered ubiquitous in nature, in contrast to many species of the *Acinetobacter* genus; and
- have low carrying rates on the skin and in the faeces.

Risk factors for infection with the *A. baumannii* group include advanced age, the presence of serious underlying diseases, immune suppression, major trauma or burn injuries, invasive procedures, presence of indwelling catheters, mechanical ventilation, extended hospital stay and previous administration of antimicrobial agents. The risks for acquiring a multidrug-resistant strain of the *A. baumannii* group are similar and also include prolonged mechanical ventilation, prolonged intensive care unit or hospital stay, exposure to infected or colonized patients, increased frequency of interventions, increased disease severity and receiving broad-spectrum antimicrobial agents, especially third-generation cephalosporins, fluoroquinolones and carbapenems.

S. aureus

Staphylococcus aureus:

- is a gram-positive bacterium that can be part of the normal microbiota on the skin and in the nose, but is also one of the most important human pathogens;
- can cause a variety of infections – most notably skin, soft tissue, bone and bloodstream infections - and is also the most common cause of postoperative wound infections; and
- produces toxic factors (some strains) that can cause a variety of specific symptoms, including toxic shock syndrome and food poisoning.

Several successful *S. aureus* clones are responsible for most of the international spread and outbreaks in health care and community settings. A recent structured survey showed that the most prevalent clones among methicillin-resistant *S. aureus* (MRSA) in EU countries are ST22 (EMRSA15), ST225 (New York/Japan), ST8 (US300), ST5 (New York/Japan), and ST8 (South German)[28]. Among methicillin-susceptible *S. aureus*, the most prevalent clones are ST7, ST15, ST5, ST45 and ST8.

The clonal structure of MRSA and methicillin-susceptible *S. aureus* in the UAE has been assessed by Sonnevend et al., who reported a change in predominance of certain MRSA clones over a 5-year period (2003-2008). In 2003, typical healthcare-associated (HA-MRSA) genotypes (ST239-MRSA-III, ST22-MRSA-IV and ST5-MRSA-II) represented the majority (61.5%) of the isolates. By 2008, this pattern had changed and clonal types considered as community-associated (CA) MRSA comprised 73.1% of the strains, with ST80-MRSA-IV, ST5-MRSA-IV and ST1-MRSA with non-typable SCCmec types being the most frequent[29].

S. pneumoniae

Streptococcus pneumoniae:

- is the leading cause of community-acquired pneumonia worldwide, which is among the leading causes of death of children younger than five years;
- causes other common, mild, self-limiting infections such as acute otitis media but also extends to cases of invasive disease with high mortality such as meningitis; and
- is associated with the highest case-fatality rate among the bacterial causes of meningitis and is the most likely infection to leave survivors with permanent residual symptoms.

The clinical burden of pneumococcal infection is concentrated among the oldest and youngest sections of the population. It caused about 826,000 deaths (582,000–926,000) among children 1–59 months old. For HIV-negative children, pneumococcal infection corresponds to 11% of all deaths in this age group[30].

It is commonly found as asymptomatic nasopharyngeal carriage, where the prevalence varies by age and region. The asymptomatic carriage state is responsible for much of the transmission within populations, such as in childcare centres.

E. faecium and *E. faecalis*

Enterococci:

- belong to the normal bacterial microbiota of the gastrointestinal tract of both humans and other animals, are usually low-pathogenic but can cause invasive disease under certain circumstances,
- can act as true pathogens and not only as opportunistic commensals, as high-risk clones were recently recognized,
- can cause a variety of infections, including endocarditis, bloodstream and urinary tract infections, and are associated with peritonitis and intra-abdominal abscesses,
- contribute to increasing mortality as well as additional hospital stay,
- emerge as important nosocomial pathogens, as documented in epidemiological data collected over the last two decades and exemplified by the expansion of a major hospital-adapted polyclonal subcluster clonal complex 17 (CC17) in *E. faecium* and by CC2 and CC9 in *E. faecalis*, with the latter clones isolated from farm animals; and
- are highly tenacious and thus easily disseminate in the hospital setting and infections caused by resistant strains are difficult to treat.

E. faecalis and *E. faecium* cause the vast majority of clinical enterococci infections in humans. The emergence of particular clones and clonal complexes of *E. faecalis* and *E. faecium* was paralleled by increases in resistance to glycopeptides and high-level resistance to aminoglycosides. These two antimicrobial classes represent the few remaining therapeutic options for treating human infections caused by *E. faecium* when resistance has emerged against penicillins.

Annex 5.2 Abbreviations

%I	Percent intermediate
%MDR	Percent multidrug-resistant
%NS	Percent non-susceptible
%R	Percent resistant
%S	Percent susceptible
ACP-MLE	American College of Physicians - Medical Laboratory Evaluation
ADPHC	Abu Dhabi Public Health Center
AMR	Antimicrobial resistance
API	Analytical Profile Index
AST	Antimicrobial susceptibility test
ATCC	American Type Culture Collection
BLI	Beta-lactamase inhibitor
CA	Community-associated
CAESAR	Central Asian and Eastern European Surveillance of AMR
CAP	College of American Pathologists
CAP-Pt	CAP proficiency testing
CC	Clonal complex
CLSI	Clinical and Laboratory Standards Institute
CSF	Cerebrospinal fluid
DOH	Department of Health Abu Dhabi
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
EUCAST	European Committee for Antimicrobial Susceptibility Testing
ESBL	Extended spectrum beta-lactamase
DoH	Abu Dhabi Dept. of Health
E. coli	*Escherichia coli*
E. faecalis	*Enterococcus faecalis*
E. faecium	*Enterococcus faecium*
EQAS	External quality assurance system
GAS	Group A streptococci (*Streptococcus pyogenes*)
GBS	Group B streptococci (*Streptococcus agalactiae*)
GCC	Gulf Cooperation Council
GLASS	Global AMR Surveillance System (WHO)
HAAD	Health Authority Abu Dhabi
HAI	Healthcare-associated infections
HIS	Hospital information system
HL	High level
ICU	Intensive care unit
JCI	Joint Commission International
K. pneumoniae	*Klebsiella pneumoniae*
LIS	Laboratory information system
MDR	Multidrug resistance
MIC	Minimal inhibitory concentration
MRGN	Multi-resistant gram negative
MSSA	Methicillin- (oxacillin-) susceptible *Staph. aureus*
MRSA	Methicillin- (oxacillin-) resistant *Staph. aureus*
M. tuberculosis	*Mycobacterium tuberculosis*
NA	Not applicable
N. gonorrhoeae	*Neisseria gonorrhoeae*
N	Number
NM	Non-meningitis
NRL	National Reference Lab
NS	Non-susceptible
P. aeruginosa	*Pseudomonas aeruginosa*
PHC	Primary Healthcare Center
PDR	Pandrug-resistant
R	Intrinsically resistant
RCPAQAP	Royal College of Pathologists of Australasia Quality Assurance Program
REQAS	Regional External Quality Assurance Services (Muscat)
Resp.	Respiratory
S./Staph. aureus	*Staphylococcus aureus*
S. pneumoniae	*Streptococcus pneumoniae*
SEHA	Abu Dhabi Health Services Company (PJSC)
sp.. spp.	Species
UAE	United Arab Emirates
U.S.A.	United States of America
VRE	Vancomycin-resistant Enterococci
WHO	World Health Organization
XDR	Extensively drug resistant

Annex 5.2.1 Abbreviations (antibiotics)

AG	Aminoglycosides
AMB	Amphotericin B
AMC	Amoxicillin/clavulanic acid
AMK	Amikacin
AMP	Ampicillin
AZM	Azithromycin
ATM	Aztreonam
CAS	Caspofungin
CAZ	Ceftazidime
CIP	Ciprofloxacin
CLI	Clindamycin
CLR	Clarithromycin
CRO	Ceftriaxone
CTX	Cefotaxime
CXM	Cefuroxime
CZO	Cefazolin
DAP	Daptomycin
ETH	Ethambutol
ETP	Ertapenem
ERY	Erythromycin
FCT	5-Fluorocytosine
FEP	Cefepime
FLU	Fluconazole
FOS	Fosfomycin
FOX	Cefoxitin
FQ	Fluoroquinolones
GEH	Gentamicin (high level)
GEN	Gentamicin
INH	Isoniazid
IPM	Imipenem
LNZ	Linezolid
LVX	Levofloxacin
MIF	Micafungin
MFX	Moxifloxacin
MEM	Meropenem
MNO	Minocycline
MUP	Mupirocin
NIT	Nitrofurantoin
NOR	Norfloxacin
OXA	Oxacillin
PEN	Penicillin G
PTH	Prothionamide
PZA	Pyrazinamide
QDA	Quinupristin/dalfopristin
RIF	Rifampin, rifampicin
SAM	Ampicillin/sulbactam
STH	Streptomycin (high level)
SXT	Trimethoprim/sulfamethoxazole
TCC	Ticarcillin/clavulanic acid
TEC	Teicoplanin
TCY	Tetracycline
TOB	Tobramycin
TZP	Piperacillin/tazobactam
VAN	Vancomycin
VOR	Voriconazole

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Annex 5.4 AMR surveillance sites

Annex 5.4.1 AMR surveillance sites – Hospitals:

Nr.	Code	Hospital name	Emirate	Ownership
1	SKM	Sheikh Khalifa Medical City	Abu Dhabi	Public
2	MQH	Mafraq hospital	Abu Dhabi	Public
3	RAH	Al Rahba hospital	Abu Dhabi	Public
4	COH	Corniche hospital	Abu Dhabi	Public
5	SSM	Sheikh Shakhbout Medical City	Abu Dhabi	Public
6	AAH	Al Ain hospital	Abu Dhabi	Public
7	TAW	Tawam hospital	Abu Dhabi	Public
8	WAG	Tawam Al Wagan hospital	Abu Dhabi	Public
9	MZH	Al Dhafra hospitals – Madinat Zayed hospital	Abu Dhabi	Public
10	LIW	Al Dhafra hospitals – Liwa hospital	Abu Dhabi	Public
11	MIR	Al Dhafra hospitals – Mirfa hospital	Abu Dhabi	Public
12	SIL	Al Dhafra hospitals – Silla hospital	Abu Dhabi	Public
13	DEL	Al Dhafra hospitals – Delma island hospital	Abu Dhabi	Public
14	GYH	Al Dhafra hospitals – Gayathi hospital	Abu Dhabi	Public
15	CCA	Cleveland Clinic Abu Dhabi hospital	Abu Dhabi	Semi-governmental
16	DAE	Danat Al Emarat hospital	Abu Dhabi	Private
17	UAD	Universal hospital Abu Dhabi (closed since 2019)	Abu Dhabi	Private
18	UAA	Universal hospital Al Ain (closed since 2019)	Abu Dhabi	Private
19	EIH	Emirates International Hospital Al Ain	Abu Dhabi	Private
20	AKH	Ain Al Khaleej Hospital Al Ain	Abu Dhabi	Private
21	MAN	Mediclinic Al Noor hospital Abu Dhabi	Abu Dhabi	Private
22	MAR	Mediclinic Al Noor hospital Airport Road	Abu Dhabi	Private
23	MAA	Mediclinic Al Ain hospital	Abu Dhabi	Private
24	MAJ	Mediclinic Al Jowhara hospital	Abu Dhabi	Private
25	BAD	Burjeel hospital Abu Dhabi	Abu Dhabi	Private
26	BRH	Burjeel Royal hospital Al Ain	Abu Dhabi	Private
27	LCB	Lifecare hospital Baniyas	Abu Dhabi	Private
28	LCM	Lifecare hospital Mussafah	Abu Dhabi	Private
29	LAD	LLH hospital Abu Dhabi	Abu Dhabi	Private
30	LMU	LLH hospital Musaffah	Abu Dhabi	Private
31	MAD	Medeor 24x7 hospital Abu Dhabi	Abu Dhabi	Private
32	MIN	Medeor 24x7 International hospital Al Ain	Abu Dhabi	Private
33	NSA	NMC Specialty hospital Abu Dhabi	Abu Dhabi	Private
34	NRY	NMC Royal hospital Khalifa City A	Abu Dhabi	Private
35	BWH	NMC Royal Women's hospital Abu Dhabi	Abu Dhabi	Private
36	NAA	NMC Specialty hospital Al Ain	Abu Dhabi	Private
37	NAN	NMC Specialty hospital Al Nahda	Dubai	Private
38	DIP	NMC Royal hospital, DIP	Dubai	Private
39	DH	Dubai hospital	Dubai	Public
40	RH	Rashid hospital	Dubai	Public
41	LH	Latifa hospital	Dubai	Public
42	HAT	Hatta hospital	Dubai	Public
43	NHD	Neurospinal hospital Dubai	Dubai	Private
44	IHD	Iranian hospital	Dubai	Private
45	PHG	Prime Health hospital	Dubai	Private
46	AZH	Al Zahra hospital Dubai	Dubai	Private

Annex 5.4.1 AMR Surveillance Sites – Hospitals (continued):

Nr.	Code	Hospital name	Emirate	Ownership
47	AGH	Al Garhoud hospital	Dubai	Private
48	SGH	Saudi German hospital	Dubai	Private
49	ESH	Emirates Specialty hospital	Dubai	Private
50	AHD	American hospital Dubai	Dubai	Private
51	AKU	Al Kuwait hospital (previously: Al Baraha hospital)	Dubai	Public
52	AAM	Al Amal Psychiatric hospital	Dubai	Public
53	BAS	Burjeel hospital for Advanced Surgery	Dubai	Private
54	MDX	Medeor 24x7 hospital Dubai	Dubai	Private
55	MCIT	Mediclinic City hospital Dubai	Dubai	Private
56	MWEL	Mediclinic Welcare hospital	Dubai	Private
57	MPAR	Mediclinic Parkview hospital	Dubai	Private
58	AQH	Al Qassimi hospital	Sharjah	Public
59	AQW	Al Qassimi Women's and Children's hospital	Sharjah	Public
60	AKI	Al Kuwaiti hospital	Sharjah	Public
61	KFH	Khor Fakkan hospital	Sharjah	Public
62	ADH	Al Dhaid hospital	Sharjah	Public
63	UHS	University hospital Sharjah	Sharjah	Public
64	BSS	Burjeel Specialty hospital Sharjah	Sharjah	Public
65	SKA	Sheikh Khalifa Medical City Ajman (SKMCA)	Ajman	Public
66	SKW	Sheikh Khalifa Women's and Children's hospital	Ajman	Public
67	SMA	Sheikh Khalifa hospital - Masfout	Ajman	Public
68	SKU	Sheikh Khalifa General hospital (SKGH) UAQ	Um Al Quwain	Public
69	UAQ	Um Al Quwain hospital	Um Al Quwain	Public
70	SKRAK	Sheikh Khalifa Specialty hospital (SKSH) RAK	Ras Al Khaimah	Public
71	IBHO	Ibrahim Bin Hamad Obaidullah hospital/RAK Psych.	Ras Al Khaimah	Public
72	SAQR	Saqr hospital	Ras Al Khaimah	Public
73	BOW	Abdullah Bin Omran hospital for Obstetrics and Gyn.	Ras Al Khaimah	Public
74	SHA	Shaam hospital	Ras Al Khaimah	Public
75	FUJ	Fujairah hospital	Fujairah	Public
76	DIB	Dibba hospital	Fujairah	Public
77	KAL	Al Kalba hospital	Fujairah	Public
78	MAS	Masafi hospital	Fujairah	Public

Annex 5.4 AMR surveillance sites (continued)

Annex 5.4.2. AMR Surveillance Sites – Center/Clinics

Nr.	Center/Clinic name	Region	Ownership
1	Al Bahia Healthcare Center	Abu Dhabi	Public
2	Al Bateen Healthcare Center	Abu Dhabi	Public
3	Al Falah Healthcare Center	Abu Dhabi	Public
4	Al Khatim Healthcare Center	Abu Dhabi	Public
5	Al Khazna Healthcare Center	Abu Dhabi	Public
6	Al Madina Occupational Health Center	Abu Dhabi	Public
7	Al Maqtaa Healthcare Center	Abu Dhabi	Public
8	Al Mushrif Children's Speciality Center	Abu Dhabi	Public
9	Al Nahda Healthcare Center	Abu Dhabi	Public
10	Al Rowdha Healthcare Center	Abu Dhabi	Public
11	Al Samha Healthcare Center	Abu Dhabi	Public
12	Al Shamkha Healthcare Center	Abu Dhabi	Public
13	Al Zafrana Healthcare Center	Abu Dhabi	Public
14	Baniyas Healthcare Center	Abu Dhabi	Public
15	HMS Abu Dhabi Center	Abu Dhabi	Public
16	Madinat Khalifa Healthcare Center	Abu Dhabi	Public
17	Madinat Mohamed Bin Zayed Healthcare Center	Abu Dhabi	Public
18	Sweihan Healthcare Center	Abu Dhabi	Public
19	Al Hayar Healthcare Center	Abu Dhabi	Public
20	Al Hili Healthcare Center	Abu Dhabi	Public
21	Al Jahili Healthcare Center	Abu Dhabi	Public
22	Al Maqam Healthcare Center	Abu Dhabi	Public
23	Al Muwaeji Healthcare Center	Abu Dhabi	Public
24	Al Niyadat Healthcare Center	Abu Dhabi	Public
25	Al Quaa Healthcare Center	Abu Dhabi	Public
26	Al Shwaib Healthcare Center	Abu Dhabi	Public
27	Al Towayya Healthcare Center	Abu Dhabi	Public
28	Al Yahar Healthcare Center	Abu Dhabi	Public
29	Health Management System (HMS) Al Ain Center (DPSC)	Abu Dhabi	Public
30	Mezyad Healthcare Center	Abu Dhabi	Public
31	Neima Healthcare Center	Abu Dhabi	Public
32	Oud Al Touba Healthcare Center	Abu Dhabi	Public
33	Remah Healthcare Center	Abu Dhabi	Public
34	Zhaker Healthcare Center	Abu Dhabi	Public
35	Al Dhafra Family Medicine Center	Abu Dhabi	Public
36	Bida Mutawa Clinics	Abu Dhabi	Public
37	Health Plus Fertility Clinic – Al Karama area	Abu Dhabi	Private
38	Health Plus Family Health Center - Al Bandar	Abu Dhabi	Private
39	Health Plus Women's Health Center – Al Karama area	Abu Dhabi	Private
40	Health Plus Diabetes and Endocrinology Center	Abu Dhabi	Private
41	Health Plus Family Health Center - Al Forsan	Abu Dhabi	Private
42	Danat Al Emarat Clinic for Women and Children	Abu Dhabi	Private
43	Moorfields Eye Hospital Center – Al Marina	Abu Dhabi	Private
44	Mediclinic Al Bateen	Abu Dhabi	Private
45	Mediclinic Al Marmoura	Abu Dhabi	Private
46	Mediclinic Khalifa City A	Abu Dhabi	Private
47	Mediclinic Baniyas	Abu Dhabi	Private
48	Mediclinic Al Mussafah	Abu Dhabi	Private
49	Mediclinic Madinat Zayed	Abu Dhabi	Private
50	Mediclinic ENEC	Abu Dhabi	Private
51	Mediclinic Gayathi	Abu Dhabi	Private
52	Mediclinic Al Madar	Abu Dhabi	Private
53	Mediclinic Al Yahar	Abu Dhabi	Private
54	Mediclinic Al Bawadi	Abu Dhabi	Private
55	Mediclinic Zakher	Abu Dhabi	Private

Annex 5.4.2 AMR Surveillance Sites – Centers/Clinics (continued)

Nr.	Center/Clinic name	Region	Ownership
56	Burjeel Day Surgery Center, Al Reem island	Abu Dhabi	Private
57	Burjeel Medical Center, Shamkha	Abu Dhabi	Private
58	Burjeel Medical Center, Shahama	Abu Dhabi	Private
59	Burjeel MHPC Marina Medical Center	Abu Dhabi	Private
60	Burjeel Tajmeel Kid's Park Medical Center	Abu Dhabi	Private
61	Burjeel Medical Center, Yas Mall	Abu Dhabi	Private
62	Burjeel Medical Center, Al Zeina	Abu Dhabi	Private
63	NMC Royal Family Medical Center, Al Musaffah	Abu Dhabi	Private
64	NMC Family Medical Center, Al Bateen	Abu Dhabi	Private
65	NMC ADNOC OHC	Abu Dhabi	Private
66	NMC Provita International Medical Center, Abu Dhabi	Abu Dhabi	Private
67	NMC Medical Centre Mohammed Bin Zayed	Abu Dhabi	Private
68	NMC Medical Center Al Wadi	Abu Dhabi	Private
69	NMC UAE University Clinics	Abu Dhabi	Private
70	NMC Provita International Medical Center, Al Ain	Abu Dhabi	Private
71	NMC Medical Center, Deira	Dubai	Private
72	NMC BR Medical Suites	Dubai	Private
73	Al Muhaisnah Medical Fitness Center	Dubai	Public
74	Al Rashidya Medical Fitness Center	Dubai	Public
75	Abu Hail Clinic	Dubai	Public
76	Al Mamzar Health Center	Dubai	Public
77	Al Khawaneej Clinic	Dubai	Public
78	Al Towar Clinic	Dubai	Public
79	Al Qusais 2 Clinic	Dubai	Public
80	Police Clinics	Dubai	Public
81	Private Clinics	Dubai	Private
82	Al Badaa Health Center	Dubai	Public
83	Al Mankhool Health Center	Dubai	Public
84	Zabeel Health Center	Dubai	Public
85	Al Lussily Health Center	Dubai	Public
86	Dubai Diabetic Centre	Dubai	Public
87	Prime Medical Center, Reef Mall	Dubai	Private
88	Prime Medical Center, Deira	Dubai	Private
89	Premier Diagnostics and Medical Center, Deira	Dubai	Private
90	Prime Medical Center, Mizhar	Dubai	Private
91	Prime Medical Center, Bur Dubai	Dubai	Private
92	Prime Medical Center, Motor city	Dubai	Private
93	Prime Medical Center, Jumeirah	Dubai	Private
94	Prime Medical Center, Barsha Heights	Dubai	Private
95	Prime Medical Center, Al Qusais	Dubai	Private
96	Premier Diagnostics and Medical Center, Ajman	Ajman	Private
97	Prime Medical Center, Al Nahda	Sharjah	Private
98	Prime Medical Center, Al Qasimia	Sharjah	Private
99	Prime Medical Specialist Center, King Faisal Road/Safeer Mall	Sharjah	Private
100	Prime Medical Center, Zero-6 mall	Sharjah	Private
101	Al Garhoud Private hospital Clinic, Shorouq	Dubai	Private
102	Al Garhoud Private hospital, FIFA Centre of Excellence	Dubai	Private
103	American hospital clinic, Al Barsha	Dubai	Private
104	American hospital clinic, Media city	Dubai	Private
105	Hor Al Anz Health Center	Dubai	Public
106	Al Ittihad Health Center	Dubai	Public
107	Al Muhaisnah Health Center	Dubai	Public
108	Al Qusais Health Center	Dubai	Public
109	Al Quoz Health Center	Dubai	Public
110	Al Refaa Health Center	Dubai	Public
111	Al Aweer Health Center	Dubai	Public
112	Al Rashidiya Health Center	Dubai	Public

Annex 5.4.2 AMR Surveillance Sites – Centers/Clinics (continued)

113	Mediclinic Dubai Mall Clinic	Dubai	Private
114	Mediclinic Ibn Battuta Clinic	Dubai	Private
115	Mediclinic Al Sufouh Clinic	Dubai	Private
116	Mediclinic Arabian Ranches Clinic	Dubai	Private
117	Mediclinic Meadows Clinic	Dubai	Private
118	Mediclinic Springs Clinic	Dubai	Private
119	Mediclinic Deira City Center Clinic	Dubai	Private
120	Mediclinic Mirdif Clinic	Dubai	Private
121	Mediclinic Qusais Clinic	Dubai	Private
122	Mediclinic Me'aisem Clinic	Dubai	Private
123	Safa Polyclinic	Dubai	Private
124	Day Surgery Center (Karama)	Dubai	Private
125	Unilabs (SCL)	Dubai	Private
126	Al Batayeh Health Center	Sharjah	Public
127	Dhaid Medical Center	Sharjah	Public
128	Dibba Al Hisn Clinic	Sharjah	Public
129	Al Hamriya Health Center	Sharjah	Public
130	Khalidiya Health Center	Sharjah	Public
131	Lualuea Health Center	Sharjah	Public
132	Madam Health Center	Sharjah	Public
133	Qarain Health Center	Sharjah	Public
134	Al Rafa Medical Center	Sharjah	Public
135	Al Riqqa Health Center	Sharjah	Public
136	Sabkha Health Center	Sharjah	Public
137	Sharjah Health Center	Sharjah	Public
138	Thameed Health Center	Sharjah	Public
139	Wasit Health Center	Sharjah	Public
140	Family Health Promotion Center	Sharjah	Public
141	Al Maliha Medical Center	Sharjah	Public
142	Rashid Centre for Diabetes and Research	Ajman	Public
143	LAIQ Medical Screening Center	Ajman	Public
144	Al Dhait Health Center	RAK	Public
145	Al Digdagga Health Center	RAK	Public
146	Julphar Clinic	RAK	Public
147	Al Jazeera Medical Clinic	RAK	Public
148	Kadra Health Center	RAK	Public
149	Al Mamourah Health Center	RAK	Public
150	Ras Al Khaimah Health Center	RAK	Public
151	Al Rams Clinic	RAK	Public
152	Saif Bin Ali Health Center	RAK	Public
153	Al Nakheel Health Center	RAK	Public
154	Shamal Health Center	RAK	Public
155	Falaj Clinic	Um Al Quwain	Public
156	Al Khazan Health Center	Um Al Quwain	Public
157	Al Raffa Health Center	Um Al Quwain	Public
158	Al Salamah Health Center	Um Al Quwain	Public
159	Al Hamidiyah Health Center	Ajman	Public
160	Al Madina Clinic	Ajman	Public
161	Manama Medical Center	Ajman	Public
162	Mushairef Health Center	Ajman	Public
163	Murishid Primary Health Clinic	Fujairah	Public
164	Madina Medical Center	Fujairah	Public
165	Al Faseel Family Health	Fujairah	Public
166	Al Qurrayah Health Center	Fujairah	Public
167	Dhadna Health Center	Fujairah	Public
168	Al Halah Health Center	Fujairah	Public
169	Al Khulaibia Health Center	Fujairah	Public
170	Murbah Health Center	Fujairah	Public

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