UNITED ARAB EMIRATES
MINISTRY OF HEALTH & PREVENTION

NATIONAL **AMR SURVEILLANCE** REPORT

In collaboration with:

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دائرة الصحة DEPARTMENT OF HEALTH
مركز أبوظبي للصحة العامة ABU DHABI PUBLIC HEALTH CENTRE

United Arab Emirates
Surveillance of Antimicrobial Resistance
Annual Report 2022

September 2022

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- **Emirates Health Services Establishment (EHS)**
- **Department of Health, Abu Dhabi (DoH)**
- **Dubai Health Authority (DHA)**
- **H.H. The President Initiatives Hospitals**
- **Ministry of Health and Prevention (MOHAP)**
- **Mohammed Bin Rashid University, Dubai**
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- **Public and private clinical microbiology laboratories (see Annex 5.6)**
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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 44 microbiology laboratories and 318 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, clinics and laboratories 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), which was 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 44 clinical microbiology laboratories across all seven Emirates, providing microbiology services for 318 surveillance sites, including 87 hospitals and 231 centers/clinics (**Figure 2.3.2, Table 2.3.1, Annex 5.5, Annex 5.6**).

This is the second report of the UAE National AMR surveillance program, presenting AMR data on 658,662 patients from 318 surveillance sites (public and private sector), over a 11-year reporting period (2010-2020). Data for the reporting year 2020 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**).

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 (2020) levels of antimicrobial resistance (AMR) among relevant and priority pathogens in the United Arab Emirates (percent resistant isolates, %R):

Table 1.1 Current levels of antimicrobial resistance (AMR) among relevant and priority pathogens in the UAE, Percentage resistant isolates (%R), United Arab Emirates, 2020

Priority[a]	Organism	Antibiotic or antibiotic class	N (isolates)	% Resistant isolates
Priority 1: Critical	*Acinetobacter* spp.	Carbapenems (IPM or MEM)	1,772	**21.9**
	Pseudomonas aeruginosa	Carbapenems (IPM or MEM)	7,322	**14.5**
	Enterobacterales (all)	Carbapenems (IPM or MEM)	43,085	**4.0**
	Escherichia coli	Carbapenems (IPM or MEM)	26,335	**1.0**
	Klebsiella pneumoniae	Carbapenems (IPM or MEM)	10,760	**4.8**
	Enterobacterales (all)	Ceftriaxone/Cefotaxime (ESBL)[b]	33,273	**27.6/25.0**
	Escherichia coli	Ceftriaxone/Cefotaxime (ESBL)[b]	19,103	**33.0/30.3**
	Klebsiella pneumoniae	Ceftriaxone/Cefotaxime (ESBL)[b]	7,544	**29.0/23.0**
Priority 2: High	*Enterococcus faecium*	Vancomycin (VRE)[c]	338	**8.9**
	Staphylococcus aureus	Oxacillin (MRSA)[d]	14,103	**35.1**
	Salmonella spp. (non-typh.)	Fluoroquinolones (ciprofloxacin)	149	**5.4**
	Neisseria gonorrhoeae	3rd-generation cephalosporins	245	**1.2**
	Neisseria gonorrhoeae	Fluoroquinolones (ciprofloxacin)	272	**90.0**
Priority 3: Medium	*Streptococcus pneumoniae*	Penicillin (oral)	442	**13.8**
	Streptococcus pneumoniae	Penicillin (meningitis)	442	**45.5**
	Streptococcus pneumoniae	Penicillin (non-meningitis)	442	**3.2**
	Haemophilus influenzae	Ampicillin	723	**30.7**
	Shigella spp.	Fluoroquinolones (ciprofloxacin)	45	**20.0**

[a] Based on: (WHO, 2017), (Tacconelli, et al., 2018). [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 AMR surveillance data provides evidence and serves as a basis for acting 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 2010-2020:

Table 1.2 Antimicrobial resistance trends, United Arab Emirates, 2010-2020 – Gram-negative bacteria

Antibiotic class/substance	*Escherichia coli*	*Klebsiella pneumoniae*	*Salmonella* spp. (non-typhoid) [a]	*Pseudomonas aeruginosa*	*Acinetobacter* spp. [a]
Aminopenicillins (Ampicillin)	↓	n/a	↑↑	R	R
Amoxicillin/Clavulanic acid	↑	↑↑	→	R	R
Piperacillin/Tazobactam	↓	↓	→	↓	↓↓
3rd-/4th-gen. cephalosporins	↑↑/↑↑	↑↑/↑↑	→	→/→	↓↓/↓↓
Carbapenems (IPM/MEM)	**<1 %R**	→/↑	→ **(<1%R)**	→/→	↓↓/↓↓
Fluoroquinolones (Ciprofloxacin)	↑	↑↑	→	→	↓↓
Aminoglycosides (Gentamicin)	↓	↑	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

[a] Salmonella spp. (non-typhoid), and Acinetobacter spp.: Trend is for 2014-2020 only.

Table 1.3 Antimicrobial resistance trends, United Arab Emirates, 2010-2020 – Gram-positive bacteria

Antibiotic class/substance	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Enterococcus faecalis*	*Enterococcus faecium*
Beta-lactam antibiotics	↑↑ (OXA)	↓ (PEN)/↑ (CTX)	→ (AMP)	→ (AMP)
Macrolides (Erythromycin)	↑↑	↑↑	n/a	n/a
Lincosamides (Clindamycin)	↑↑	→ **(33%R)**	n/a	n/a
Aminoglycosides (Gentamicin)	↑	n/a	↑↑	↑↑
Fluoroquinolones (Levo/Moxi))	↑↑/↑↑	↑/↑	↑ (LVX)	→
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, AMP: Ampicillin, CTX: Cefotaxime (non-meningitis breakpoints), LVX: Levofloxacin, OXA: oxacillin, PEN: penicillin, VRE: Vancomycin-resistant *Enterococcus faecium*.

Table 1.4 Antimicrobial resistance trends, United Arab Emirates, 2010-2020 – *Candida albicans* and *Mycobacterium tuberculosis*

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

Antibiotic class/substance	*M. tuberculosis*
Rifampin	↑
Ethambutol	→ **(<2%R)**
Isoniazid	→
Pyrazinamide	↓
Streptomycin	No data
Multidrug resistance (RIF+INH)	↑ **(3.2%)**

↓/↑/→: 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 (Jim O'Neill, 2014). Without effective antibiotics, the success of major surgery and cancer chemotherapy would be compromised (WHO, 2021).

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, guide, and monitor the effectiveness of antimicrobial stewardship programs,
- develop antibiotic usage guidelines for common infections, and
- assist healthcare 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

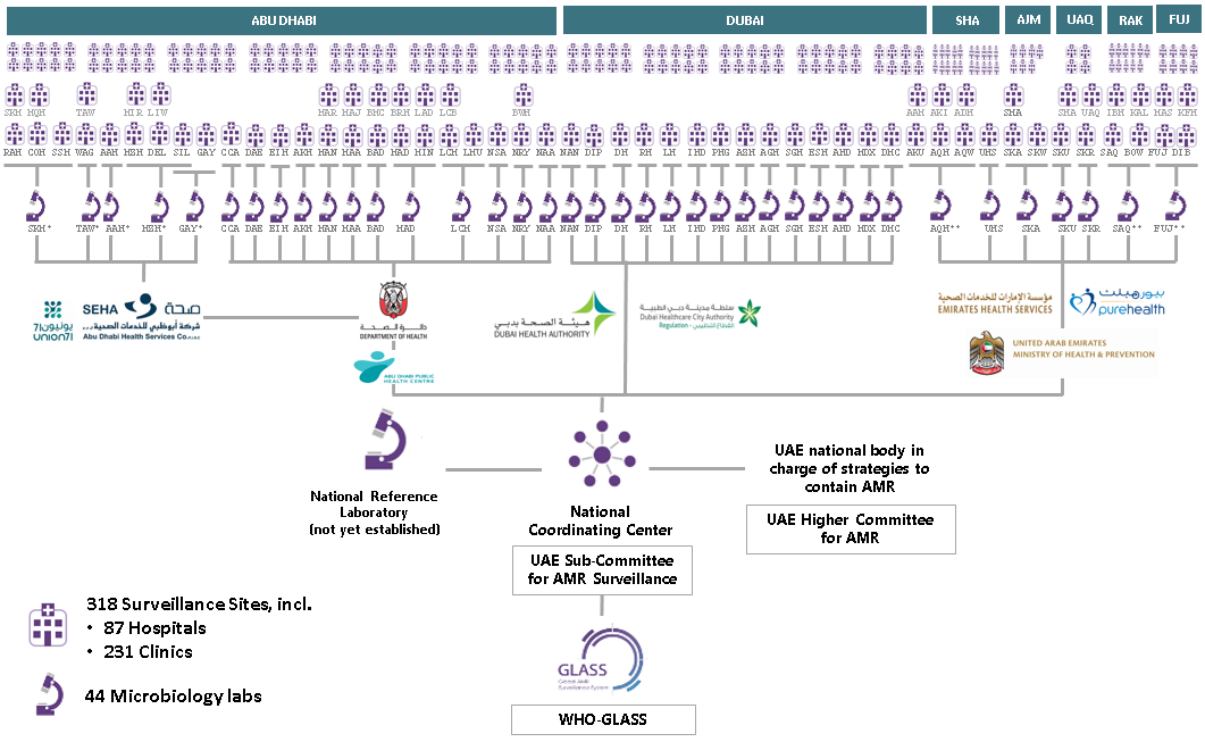
The United Arab Emirates AMR surveillance system was first established in 2010 on a subnational level (Abu Dhabi Emirate, HAAD/DoH). In 2015, the system was expanded and established nationwide by the Ministry of Health and Prevention (MOHAP), in collaboration with the UAE Ministry of Presidential Affairs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

As of July 2022, the UAE AMR surveillance system relies on a network of **318 surveillance sites** (87 hospitals and 231 centers/clinics), that are served by **44 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 and Labs



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 participating public hospitals, private hospitals, and outpatient facilities (centers/clinics).

Table 2.3.1 AMR surveillance sites and labs – by Emirate (as of July 2022)

Facility Type	Abu Dhabi	Dubai	Sharjah	Ajman	Um Al Quwain	Ras Al Khaimah	Fujairah	Total
Surveillance sites	**140**	**92**	**28**	**10**	**6**	**28**	**14**	**318**
Hospitals	36	28	7	3	2	7	4	**87**
Centers/Clinics	104	64	21	7	4	21	10	**231**
Laboratories	**17**	**19**	**2**	**1**	**1**	**3**	**1**	**44**

Figure 2.3.2 AMR surveillance sites – by location and ownership (public/private)

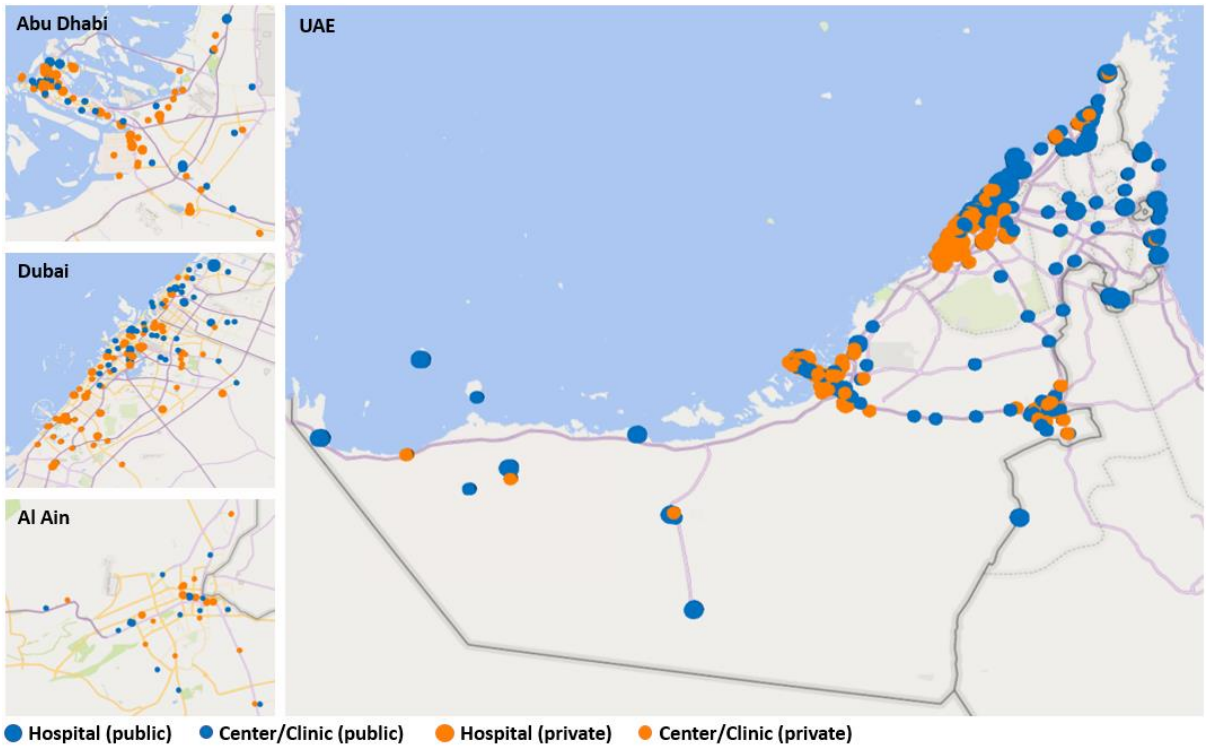
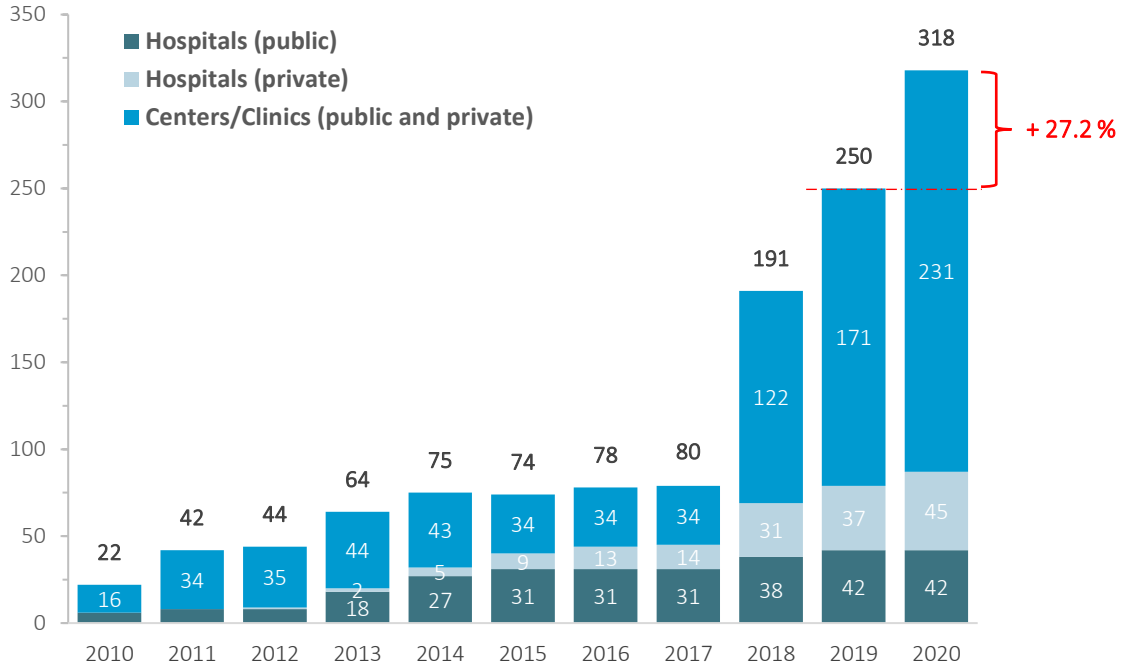


Figure 2.3.3 Number of participating surveillance sites - by year, facility type and ownership (public/private), UAE, 2010-2020



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 and selection of surveillance sites and labs: Surveillance sites and labs included in this report were usually identified based on epidemiological needs/gaps, followed by an initial assessment of their location, facility type and size, accessibility, 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, a quality management system, participation in external quality control, and lab accreditation.

Identification of organisms: 43 out of 44 (98%) participating microbiology laboratories use at least one commercial, automated system for identification of bacteria and/or yeast, including VITEK-2[1] (n=31, 71%), and BD Phoenix[2] (n=11, 25%), and MicroScan[3] (n=1, 3%). Only one lab (n=1, 3%) relies on manual (API) systems only for identification[4]. Unusual test results are confirmed locally.

Antimicrobial susceptibility testing: 42 out of 44 (96%) 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 (*Haemophilus, Neisseria*) are routinely tested by manual methods (disc diffusion), as per CLSI guideline recommendations. All labs follow CLSI guidelines for antimicrobial susceptibility testing of bacteria (CLSI-M100) and fungi (CLSI-M60) (CLSI, 2022). Unusual antibiotic susceptibility testing results are confirmed locally.

Interpretation of susceptibility testing results: There are no national antibiotic susceptibility testing guidelines in the UAE. For interpretation of susceptibility testing results for fungi and yeast, all participating laboratories routinely apply the CLSI guidelines. If CLSI has not set breakpoints for certain pathogen/antibiotic combinations, then other guidelines are applied, including EUCAST guidelines (EUCAST, 2022) (for tigecycline and amphotericin B), or CDC tentative guidelines (CDC C. auris, 2020), for *Candida auris*.

AST data submitted to the national AMR surveillance Center includes information on the specimen type, specimen collection date, organism name, antibiotic name, AST test method used etc.), as well as the measured and/or interpreted AST test results. Wherever available and technically feasible, the measured, numerical[5] AST result is collected and used for analysis (n=36 labs, 82%), otherwise the locally interpreted AST result (S/I/R[6]) is collected (n=8 labs, 18%).

Clinical and demographic data for each isolate is extracted from hospital/laboratory information systems (HIS/LIS) wherever available and technically feasible (66%, 29/44 labs). This includes information on e.g., patient date of birth, age, gender, nationality, location, location type, clinical specialty/department, date of admission/discharge, health outcome, etc.

Quality control: All participating microbiology laboratories

- are operated by a licensed healthcare provider, i.e. licensed by MOHAP, DoH, or DHA
- are either lab-accredited (n=43/44; 98%), or in the final steps of lab-accreditation (n=1/44; 2%))
- are headed by a licensed clinical pathologist or clinical microbiologist
- must comply with governmental quality standards for clinical laboratories, e.g.: (DOH, 2011)

[1] VITEK® 2. BioMérieux SA, Craponne, France. https://www.biomerieux.com/
[2] BD Phoenix™. Becton Dickinson, New Jersey, USA. https://www.bd.com
[3] MicroScan WalkAway. Beckman Coulter, Brea, CA, USA. https://www.beckmancoulter.com/
[4] API® test system. Analytical Profile Index. BioMérieux SA, Craponne, France. https://www.biomerieux.com/
[5] Minimal inhibitory concentration (MIC, in µg/ml), or the inhibition zone diameter (IZD, in mm)
[6] SIR, susceptible/intermediate/resistant

- are expected to conduct routine (e.g. weekly) internal quality control testing (ATCC); and
- are successfully participating in at least one internationally recognised, external quality assurance programme (EQAS), i.e., CAP Pt, ACP-MLE, or REQAS.

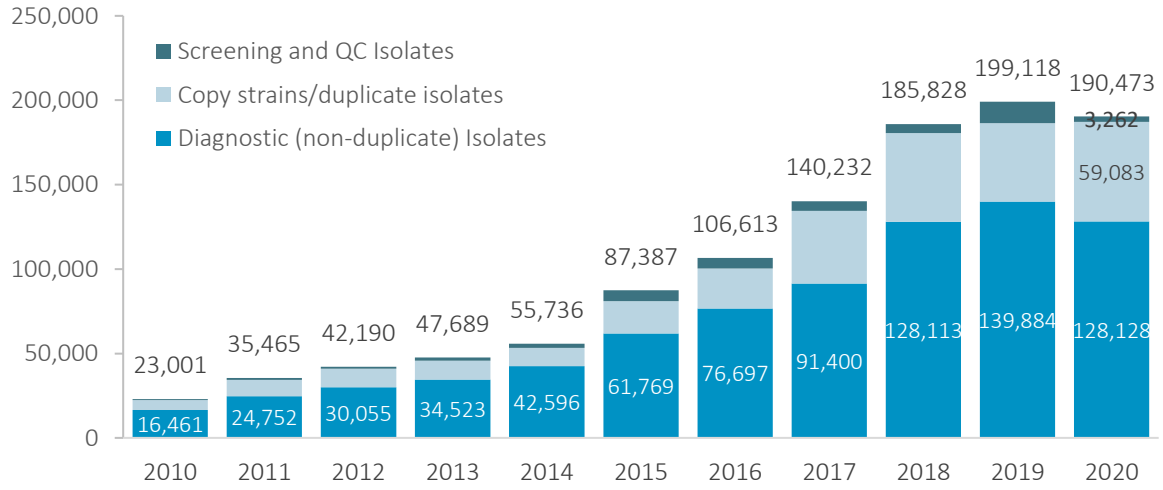
Only final and validated antimicrobial susceptibility testing results are reported for AMR surveillance. As of August 2022, 43 out of 44 (98%) of participating microbiology labs are lab-accredited, by either CAP, or ISO 15189, or both. The remaining one lab is in the process of ISO 15189 accreditation (expected by March 2023). At least 70 out of 87 (80.5%) of 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, 2015). See **Annex 5.7** for details on the data fields collected from surveillance sites and labs.

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 (2010-2020)



For reporting period 2020, a total of n=190,473 isolates were reported by surveillance sites/labs. Screening and quality control isolates (n=3,262; 1.7%), as well as copy strains (duplicate isolates, n=59,083; 31.0%) were routinely excluded from the analysis. Only the remaining diagnostic (non-duplicate) isolates (n=128,128; 67.3%) are included in the analysis and presented in this report (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 eleven bacterial and fungal 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)*
- *Candida* spp., and
- *Mycobacterium tuberculosis*.

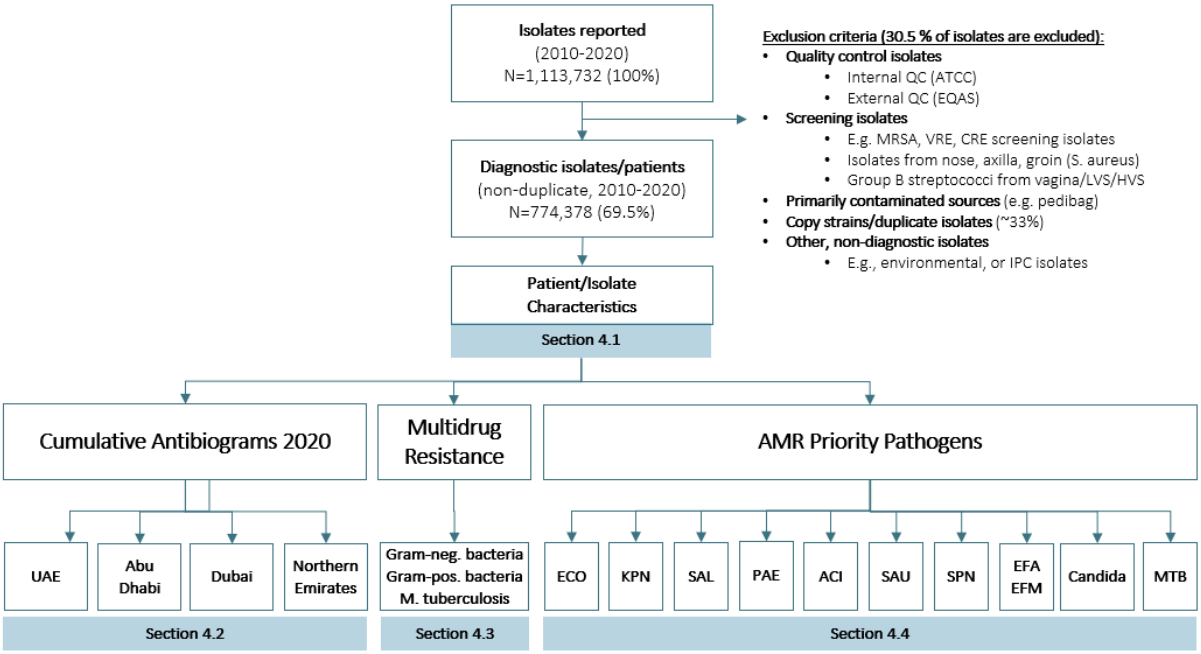
Annex 5.1 describes the AMR priority pathogens under enhanced AMR Surveillance and the main infections caused by these pathogens.

Data submission: At facility level, AMR data is collected and exported from laboratory- or hospital-information systems (LIS/HIS) wherever possible, or from semi-automated, commercial AST systems otherwise. Authorized AMR focal points are submitting the data through a secure file upload platform where available (Abu Dhabi Emirate), or by Email attachment otherwise.

Data cleaning: After submission of AMR data to the national AMR Surveillance Center, the raw data is initially checked and cleaned for plausibility, quality, and completeness; 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. At central level, any remaining identifiable QC and screening data is removed from the raw data before further processing and analysis. After conversion of AMR raw data to WHONET format, using the BacLink tool, each WHONET AMR data file is checked and cleaned again using a SQLite database browsing tool (DB Browser[7]).

Finally, all WHONET AMR data files are added to the national AMR surveillance database (WHONET, 2022). **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, 2010-2020



For the reporting period 2010-2020, the surveillance sites/labs submitted AMR data on 1,113,732 isolates. After data cleaning and applying exclusion criteria (**Figure 3.1.2**, and section 3.2), a total of n=774,378 (69.5%) diagnostic (non-duplicate) patient isolates remained for analysis.

Results are presented in this report in section four:

- **Section 4.1 (patient/isolate characteristics)** presents the patient characteristics of isolates reported from all surveillance sites in the UAE during the 2020 reporting period.
- **Section 4.2 (cumulative antibiograms)** presents the national cumulative antibiogram 2020, as well as sub-national cumulative antibiograms for Abu Dhabi Emirate, Dubai Emirate, and the five Northern Emirates (together), for Gram-negative and Gram-positive bacteria.

[7] DB Browser for SQ Lite, https://sqlitebrowser.org/

- **Section 4.3 (multidrug resistance)** presents annual trends of multidrug resistance (%MDR) for Gram-negative and Gram-positive bacteria, and *Mycobacterium tuberculosis* (MDR-TB).
- **Section 4.4 (AMR priority pathogens)** presents percent resistant/intermediate/susceptible (%RIS) statistics, and long-term AMR trends for the UAE (2010-2020) for AMR priority pathogens.

For selected pathogens (*E. coli*, *K. pneumoniae*, *S. aureus*) detailed breakdowns are provided for selected antibiotics, as percent resistant isolates (%R) – by:

- Age category and age group
- Gender
- Nationality status and nationality
- Emirate
- Isolate source
- Location type
- Clinical specialty/department
- Facility (hospitals only)

3.3 Data analysis

Data analysis was conducted with the WHONET 2022 Software for Antimicrobial Resistance Surveillance (WHONET, 2022).

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', 'validation', 'verification', 'proficiency testing', or similar
- Suspected screening isolates, e.g.:
    - *S. aureus* isolates from axilla, nose, groin, umbilicus and perineum
    - *S. agalactiae* (GBS) isolates from vagina (LVS, HVS, rectovaginal, etc.)
- Duplicate isolates (copy strains), i.e., only the first isolate per patient, specimen type and species during the reporting period (one year) was included
- Isolates from primarily contaminated specimen types (e.g., pedibag)
- Other non-diagnostic isolates (e.g., from environmental sampling, infection control)
- Species for which less than 10 isolates are available for analysis
- Antimicrobial agents that are selectively/not routinely tested (i.e., less than 70% of isolates were tested)

De-duplication: As recommended by CLSI guideline M39-ED5:2022, 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). For details see CLSI M39-ED5:2022, Appendix A: Rationale for the "First Isolate per Patient" Analysis Recommendation (CLSI M39, 2022).

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=36/44 labs, 82%), or, if this was technically not feasible, obtained from labs in form of already locally interpreted (S/I/R) results (n=8/44 labs, 18%). Percent RIS interpretations were based on the CLSI interpretation standard CLSI M100 (ED32: 2022) for bacterial isolates and CLSI interpretation standard M60 ED1:2017 for yeast. For amphotericin B (AMB) and tigecycline, EUCAST v12.0:2022 was used (EUCAST, 2022). For *Candida auris*, tentative breakpoints from U.S. CDC were used (CDC C. auris, 2020).

Cumulative antibiograms are presented by adopting the CLSI M39-ED5:2022 standard for the Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data (CLSI M39, 2022).

Definitions used:

- **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. (Magiorakos, et al., 2012).
- **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 susceptibility testing or for patient treatment and should not be interpreted as such.

Statistical considerations:

Statistical analysis is routinely conducted with WHONET 2022. For additional statistical analysis the following software packages are used:

- IBM SPSS Statistics, version 28.0.0.0 (IBM, 2022), or Epi Info™ for Windows v7.2.4.0 (CDC Epi Info, 2022), for statistical significance of proportion trends over time, and an
- online calculation tool, for calculation of Wilson confidence intervals (95% C.I.) (AUSVET, 2018).

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 susceptible/intermediate/resistant (%RIS) 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 SPSS or Epi Info™. 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) (Agresti & Coull, 1998). 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. Error bars in graphs represent the upper limit of the 95% confidence interval.

4. Results

4.1 Patient/isolate characteristics

For the reporting period 2010 to 2020 (11 years), n=1,113,732 isolates were reported by participating surveillance sites/labs. After removal of non-diagnostic isolates (i.e., screening, quality control, and duplicate isolates), a total of n=774,378 (69.5%) isolates (=patients) remained for analysis.

For the reporting period 2020 (one year), n=128,128 diagnostic, non-duplicate isolates from n=318 surveillance sites/labs are available for analysis. For 2020, most frequently reported pathogens were *E. coli* (27.1%), followed by *S. aureus* (13.1%), *K. pneumoniae* (11.2%), and *P. aeruginosa* (7.4%). All AMR priority pathogens together accounted for 71% of all reported isolates (**Figure 4.1.1**).

Figure 4.1.1 Distribution of reported AMR priority pathogens, UAE, 2020, by pathogen (n=128,128)

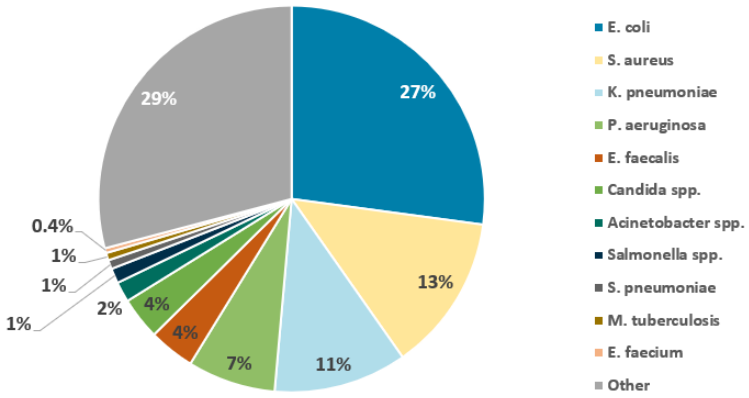


Figure 4.1.2 (next page) presents the distribution of reported patients/isolates by age category, gender, nationality status, Emirate, isolate source, location type, and clinical specialty/department. These figures also give a good indication on the availability of meta data, i.e. the completeness of data reporting.

- **Age:** The data shows a typical age group distribution, with *Salmonella* and pneumococci as expected being more prevalent in the children age group. *M. tuberculosis* affects predominantly adults. All age groups (adults, children, new-borns) are included.
- **Gender:** Distribution by gender is largely balanced. *E. coli*, *K. pneumoniae* and enterococci are more prevalent in females, which is due to the higher prevalence of urinary tract infections in females (*E. coli*, *K. pneumoniae* and enterococci are commonly isolated from the urinary tract). *M. tuberculosis* is predominantly found in males.
- **Nationality status:** UAE nationals represent a significantly higher proportion in the reported data (about 20%) than in the general UAE population (about 12%), which could be partially explained by the higher rate of healthcare utilization by UAE nationals. An exception is *M. tuberculosis*, which is predominantly found in expatriates. Analysis of expatriates by nationality show that most nationalities of the world (n>164) are represented in the data and reflecting the typical distribution of nationalities found in the UAE.
- **Emirate:** Distribution by Emirate shows that patients from all seven Emirates are represented in the sample, except for *M. tuberculosis* (AD and Dubai only). The data is still slightly skewed towards Abu Dhabi Emirate, whereas patients from some of the northern Emirates are slightly underrepresented.
- **Isolate source:** 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.

Candida spp. is isolated mostly from urine, respiratory tract, blood and pus; whereas *M. tuberculosis* is predominantly isolated from the respiratory tract.

- **Location type:** Distribution by location type shows that all relevant location types are included in good numbers (outpatients, emergency, inpatient (non-ICU), and intensive care).
- **Clinical specialty/department:** Distribution by clinical speciality/department specialty shows that all relevant clinical specialties are represented in the data, including internal medicine, surgery, emergency & intensive care, neonatology & paediatrics, obstetrics & gynaecology, etc.

Figure 4.1.2 Distribution of reported pathogens, UAE, 2020, by age category, gender, nationality status, Emirate, isolate source, location type, and clinical specialty/department

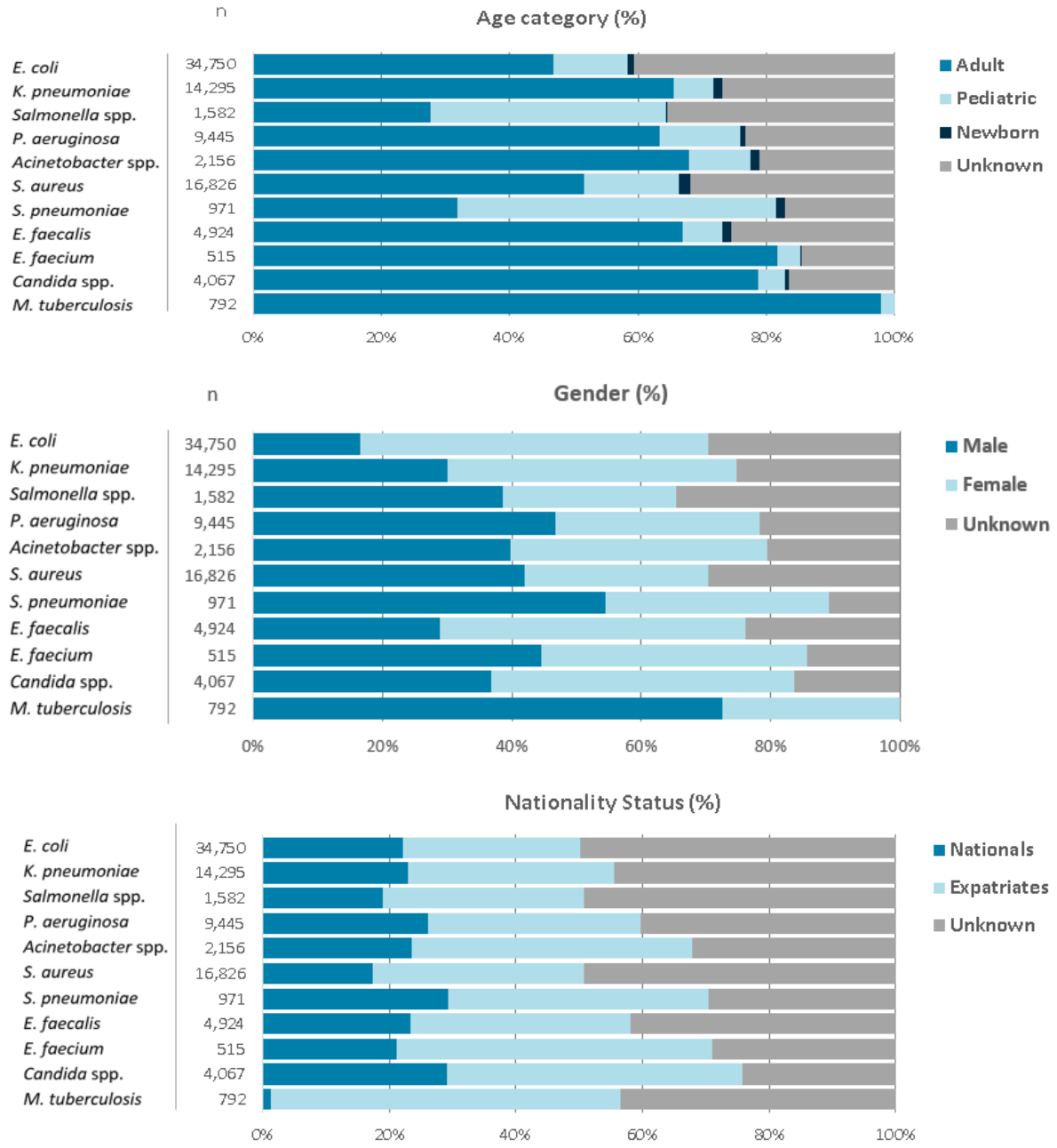
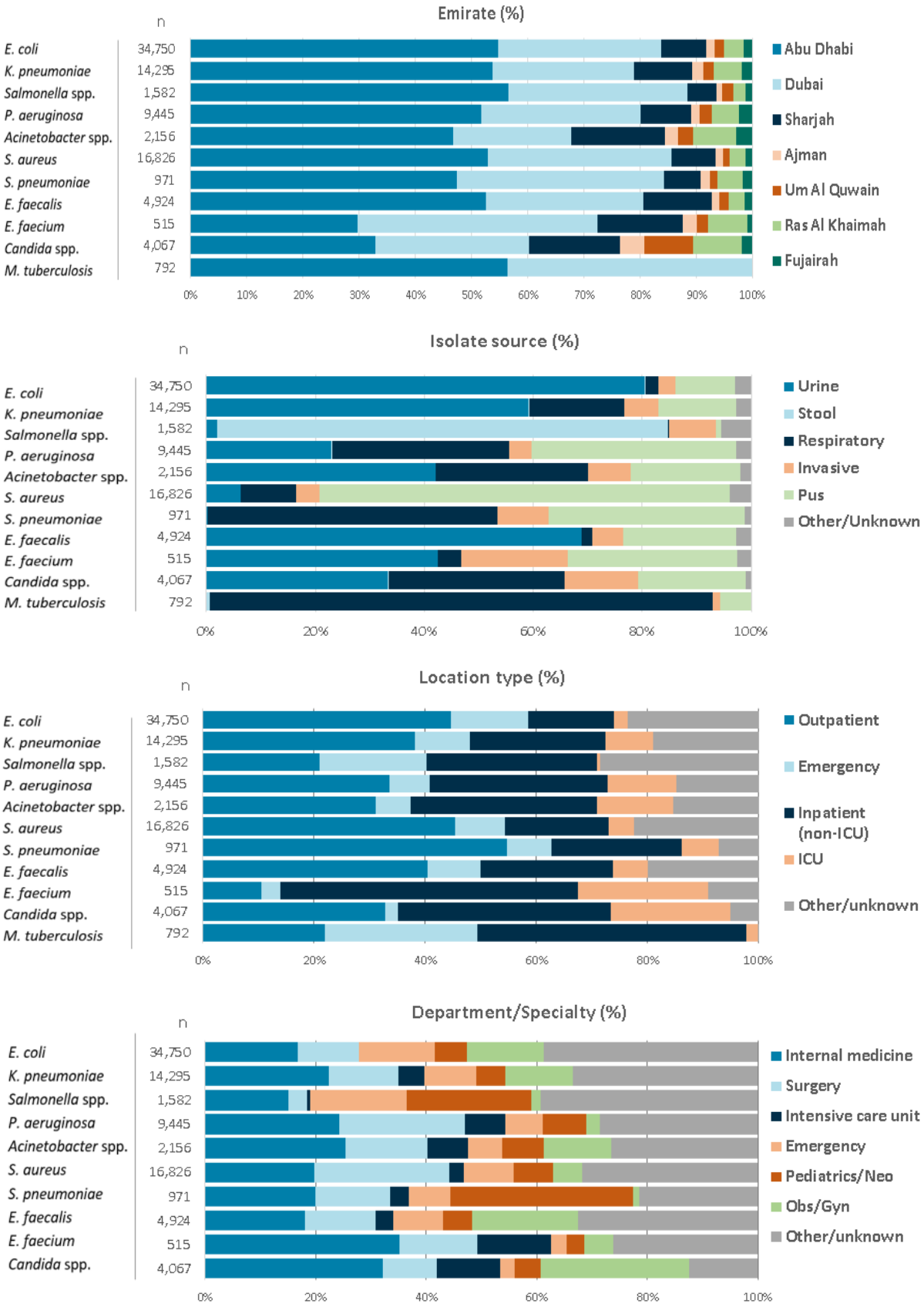


Figure 4.1.2 Distribution of reported pathogens, UAE, 2019, by age category, gender, nationality status, Emirate, isolate source, location type, and clinical specialty/department (continued)



Representativeness of the data for the UAE population:

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

Surveillance sites and labs included in this report were usually identified based on epidemiological needs/gaps, followed by an initial assessment of their location, facility type and size, accessibility, availability of data in the required quality and format, and readiness and willingness to participate. Once identified, strict criteria for enrolment and participation were applied, including management approval, ability of generating and submitting high quality AMR data files, having qualified staff, a quality management system, active participation in external quality control, and lab accreditation.

The data presented in this report is:

- fully representative for public sector healthcare facilities in the UAE (100% sample size for hospitals, centers, and clinics);
- highly representative for private sector healthcare facilities in the UAE, except for the Emirates Ajman, UAQ and Fujairah, from which private healthcare facilities are not yet participating in sufficient numbers (**Table 4.1.1**);
- highly representative for inpatients and ICU patients, with now 87 out of 151 (57.6%) hospitals participating in the system (58%); and
- representative for outpatients: results for outpatients need to be interpreted with some caution, as an increasing, but still relatively small fraction (n=231; 8.5%) of the approximately n=2,730 relevant ambulatory healthcare clinics/centers in the UAE are participating in the national AMR surveillance program.

Table 4.1.1 AMR surveillance sites – by Emirate and ownership (public/private)

Facility Type	Abu Dhabi	Dubai	Sharjah	Ajman	UAQ	RAK	Fujairah	Total
Total number of sites	**140**	**92**	**28**	**10**	**6**	**28**	**14**	**318**
Public ownership	59	27	22	9	6	19	13	155
Private ownership	81	65	6	1	0	9	1	163
Percentage private sites	**57.9**	**70.7**	**21.4**	**10.0**	**0**	**32.1**	**7.1**	**51.3**

The data is still slightly skewed towards Abu Dhabi, because the surveillance system has been established there several years earlier than in the other Emirates, and, over time, a relatively large number of sites has been recruited from that Emirate. However, the balancing of data will further improve over time, as new surveillance sites are now preferably and increasingly selected from Dubai and the northern Emirates, in particular from private sector healthcare providers, and from outpatient centers/clinics.

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.

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 of a sampling bias.

The reported levels and trends of antimicrobial 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 (2020)

4.2.1 United Arab Emirates (National Cumulative Antibiogram)

Table 4.2.1.1 National Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=79,295)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins			Cephalosporins				Carbapenems										
	N	AMP	AMC	TZP	CZO	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	79,295	-	67	90	-	-	72	-	84	91	95	94	97	89	87	70	60	68	72[b]
Haemophilus influenzae[c]	927	66	77	-	-	92	-	-	-	-	-	-	-	-	-	92	-	52	-
Moraxella (Branh.) catarrhalis[d]	160	-	93	-	-	100	-	-	-	-	-	-	-	-	-	95	-	82	-
Enterobacterales	62,643	29	68	92	58	-	74	-	84	93	98	97	98	90	87	69	72	71	-
Citrobacter koseri (diversus)	1,458	R	94	96	90	27/77[i]	94	-	97	98	99	98	100	99	98	97	97	98	67[b]
Enterobacter cloacae	2,010	R	R	86	R	19/41[i]	80	-	91	92	98	93	99	95	92	84	72	87	30[b]
Enterobacter aerogenes (*K. aer.*)	1,682	R	R	84	R	R	81	-	94	73	97	96	99	97	96	92	82	95	20[b]
Escherichia coli [e]	34,717	39	74	94	61	58/63[i]	69	-	80	99	99	98	99	89	86	62	65	63	94[b]
Klebsiella pneumoniae	14,795	R	75	86	65	66/69[i]	76	-	83	95	95	95	96	92	87	74	67	77	26[b]
Klebsiella oxytoca	531	R	84	92	52	75/79[i]	90	-	94	97	97	95	99	96	93	89	81[f]	89	76[b]
Morganella morganii	740	R	R	97	R	R	75	-	95	39	99	98	100	83	81	55	88	65	R
Proteus mirabilis	1,883	63	81	99	67	86/89[i]	90	-	91	16	97	96	96	80	83	65	87	61	R
Proteus vulgaris	58	R	79	100	R	R	95[f]	-	97	6	97	97[f]	100	100	-	87	-	86	R
Providencia spp.	216	R	R	96	R	–	94	-	96	46	99	94	99	84	91	74	-	92	R
Salmonella spp. (non-typhoid)	1,467	76	95	99	-	-	98	-	99	-	-	-	-	-	-	92[g]	-	96	-
Salmonella Typhi/Paratyphi	128	68	85	92	-	25/40[i,f]	85	-	93	-	-	-	-	-	-	39	-	82	-
Serratia marcescens	1,455	R	R	95	R	R	91	-	96	57	98	95	98	97	89	88	92	98	R
Shigella spp.	74	46	80	97	-	-	74	-	95	-	-	-	-	-	-	73	-	47	-
Non-fermenting Gram-neg. rods	14,289	R	R	82	-	-	-	82	83	81	82	R	90	84	87	78	47	72	-
Acinetobacter baumannii	1,816	R	R	71	-	-	-	68	73	76	76	R	97	77	73	70	R	82	-
Pseudomonas aeruginosa	9,402	R	R	88	-	R	R	87	90	85	86	R	96	92	95	84	64	R	R
Stenotrophomonas maltophilia[h]	1,252	R	R	R	-	-	R	53	-	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 the reporting period (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: disc diffusion data (KB): LVX 96 %S, CRO 82 %S, AZM: 96 %S, CLR 61%S. [d] *M. catarrhalis*: CLR: no data, ERY 96 %S, AZM: 98 %S, LVX 91 %S, TCY 82 %S. [e] *E. coli* (urinary tract isolates): FOS 98 %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. (non-typhoid) refer to extra-intestinal (non-stool) isolates only. [h] *S. maltophilia*: MNO 97 %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 ED31:2021. Presentation standard: CLSI M39-A4:2014. Data analysis: WHONET 2021.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 273 surveillance sites from public and private sector (United Arab Emirates), including 84 hospitals and 189 ambulatory healthcare facilities. Version 1.1 (7 Mar 2022).

Table 4.2.1.2 National Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=40,033)

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)	40,033	-	-	-	-	-	-	51	78	-	-	-	69	57	99	98	72	96	99	-	-	-
Enterococcus spp.	5,821	93	-	-	-	R	R	-	R	R	83	94	67	65	98	98	R	93	94	-	-	-
Enterococcus faecalis	4,918	99	-	-	-	R	R	-	R	R	83	94	71	67	99	99	R	97	94	-	-	R
Enterococcus faecium	516	25	-	-	-	R	R	-	R	R	75	91	23	31[j]	90	92	R	31	95	-	-	74
Staphylococcus aureus[k]	16,514	-	-	65[c]	65	-	-	71	89	90	-	-	65	77	100	100	76	100	100	87	100	90
MSSA[k]	10,467	-	-	100	100	-	-	77	97	96	-	-	70	72	100	100	75	100	100	90	100	100
MRSA[k]	4,674	-	-	-	-	-	-	58	83	78	-	-	52	52	100	100	68	98	99	82	99	77
Coagulase-neg. staphylococci (CNS)	6,380	-	-	36[c]	36	-	-	32	68	77	-	-	65	60	99	93	78	99	99	82	94	92
Staphylococcus epidermidis	2,322	-	-	25[c]	25	-	-	28	61	69	-	-	50	50	100	88	67	99	98	82	93	93
Staphylococcus saprophyticus [g]	871	-	-	59[c]	59	-	-	38	83	99	-	-	99	99	100	100	94	100	100	93	99	97
Staphylococcus lugdunensis	354	-	-	77[c]	77	-	-	78	82	97	-	-	99	94	100	99	99	100	100	93	100	97
Streptococcus pneumoniae	969	-	93[d]	-	-	96[e]	95[e]	43	65	-	-	-	94	95	99	98	61	-	100	55	100	98
Streptococcus pyogenes [h]	1,365	100[f]	100	-	-	98	97	74	87	-	-	-	82	-	100	100	-	-	100	75	-	-
Streptococcus agalactiae [i]	5,302	100	98	-	-	100	97	48	57	-	-	-	82	-	99	98	-	96	100	14	-	99
Streptococcus spp. (viridans group)	914	-	59	-	-	89	85	53	76	-	-	-	84	-	99	-	-	-	99	62	-	-

[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 the reporting period (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): 54 %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). Excludes GBS isolates from vagina. [j] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [k] S. aureus: excludes isolates from axilla, nose, groin, perineum, and umbilicus.

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 ED31:2021. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2021.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 273 surveillance sites from public and private sector (United Arab Emirates), including 84 hospitals and 189 ambulatory healthcare facilities. Version 1.1 (7 Mar 2022).

4.2.2 Abu Dhabi Emirate

Table 4.2.2.1 Abu Dhabi Emirate Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=43,244)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins				Cephalosporins				Carbapenems									
	N	AMP	AMC	TZP	CZO	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	43,244	-	67	91	-	-	75	-	85	92	96	96	97	90	87	72	54	73	71[b]
Haemophilus influenzae[c]	429	81	97	-	-	97	91	-	-	-	-	-	-	-	-	94	-	51	-
Moraxella (Bran.) catarrhalis[d]	118	-	94	-	-	100	-	-	-	-	-	-	-	-	-	94	-	81	-
Enterobacterales	34,526	30	68	92	56	-	76	-	85	94	99	98	99	91	88	71	81	72	71[b]
Citrobacter koseri (diversus)	797	R	94	96	89	24/72[i]	94	-	98	99	99	98	100	99	98	97	-	98	66[b]
Enterobacter cloacae	1,045	R	R	85	R	19/39[i]	81	-	91	92	98	94	99	95	92	85	87	87	30[b]
Enterobacter aerogenes (*K. aer.*)	916	R	R	83	R	R	81	-	95	75	97	97	99	97	97	93	96	95	15[b]
Escherichia coli [e]	19,059	39	73	94	61	57/63[i]	71	-	81	99	99	99	100	90	86	64	75	64	94[b]
Klebsiella pneumoniae	8,251	R	77	88	64	67/70[i]	79	-	86	97	97	96	98	93	88	76	84	79	24[b]
Klebsiella oxytoca	281	R	85	91	-	75/80[i]	93	-	95	98	98	98	99	96	93	89	-	90	74[b]
Morganella morganii	404	R	R	96	R	R	77	-	95	45	99	99	100	85	80	55	-	63	R
Proteus mirabilis	992	63	84	99	65	86/90[i]	90	-	94	19	97	96	96	82	85	68	-	63	R
Proteus vulgaris	32	R	81[f]	100[f]	R	R	100[f]	-	100[f]	11[f]	100[f]	94[f]	100[f]	100[f]	-	79[f]	-	83[f]	R
Providencia spp.	108	R	R	96	R	-	94	-	95	53	99	93	97	83	90	75	-	91	R
Salmonella spp. (non-typhoid)	832	75	94	98	-	-	98	-	99	-	-	-	-	-	-	90[g]	-	97	-
Salmonella Typhi/Paratyphi	80	64	79	92	-	-	85	-	95	-	-	-	-	-	-	51	-	80	-
Serratia marcescens	833	R	R	98	R	R	91	-	97	54	99	98	98	96	90	86	100[f]	98	R
Shigella spp.	46	48	79	96	-	-	78	-	92	-	-	-	-	-	-	72	-	48	-
Non-fermenting Gram-neg. rods	7,423	R	R	83	-	-	-	82	83	80	81	R	89	84	86	77	41	80	-
Acinetobacter baumannii	873	R	R	78	-	-	-	74	81	83	83	R	97	82	78	77	R	87	-
Pseudomonas aeruginosa	4,886	R	R	90	-	R	R	86	89	84	84	R	96	92	95	83	63	R	R
Stenotrophomonas maltophilia[h]	632	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 the reporting period (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 97 %S, CRO 98 %S, AZM: 95 %S, CLR: no data. [d] *M. catarrhalis*: CLR: no data, ERY: no data, AZM: 98 %S, LVX 89 %S, TCY 81 %S. [e] *E. coli* (urinary tract isolates): FOS 98 %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: 98 %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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 124 surveillance sites from public and private sector (Abu Dhabi Emirate only), including 38 hospitals and 86 ambulatory healthcare facilities. Version 1.0 (21 May 2022).

Table 4.2.2.2 Abu Dhabi Emirate Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=23,714)

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)	23,714	-	-	-	-	-	-	52	77	-	-	-	73	61	99	98	71	97	99	-	-	-
Enterococcus spp.	2,972	94	-	-	-	R	R	-	R	R	84	89	72	68	98	98	R	95	96	-	-	-
Enterococcus faecalis	2,598	99	-	-	-	R	R	-	R	R	84	90	73	69	100	100	R	97	97	-	-	R
Enterococcus faecium	153	28	-	-	-	R	R	-	R	R	75	81	24	-	91	92	R	50	96	-	-	79
Staphylococcus aureus	10,185	-	-	64[3]	64	-	-	70	86	91	-	-	68	70	100	100	75	100	100	87	100	90
MSSA	5,332	-	-	100	100	-	-	77	89	96	-	-	75	76	100	100	78	100	100	89	100	94
MRSA	2,529	-	-	-	-	-	-	57	77	81	-	-	53	53	100	100	68	99	99	83	99	76
Coagulase-neg. staphylococci (CNS)	2,752	-	-	38[c]	38	-	-	36	70	79	-	-	72	67	99	91	80	99	99	83	95	94
Staphylococcus epidermidis	1,040	-	-	27[c]	27	-	-	29	62	69	-	-	57	55	100	87	68	99	99	81	95	91
Staphylococcus saprophyticus [g]	399	-	-	55[c]	55	-	-	39	81	99	-	-	100	100	99	99	94	99	99	93	99	97
Staphylococcus lugdunensis	217	-	-	75[c]	75	-	-	79	82	97	-	-	100	95	100	100	99	-	100	93	100	98
Streptococcus pneumoniae	461	-	93[d]	-	-	97[e]	96[e]	47	68	-	-	-	94	98	99	100	60	-	100	55	100	97
Streptococcus pyogenes [h]	1,390	100[f]	100	-	-	100	100	78	87	-	-	-	84	-	100	-	-	-	100	74	-	-
Streptococcus agalactiae [i]	4,699	100	97	-	-	99	95	46	46	-	-	-	90	-	98	-	-	96	99	14	-	100
Streptococcus spp. (viridans group)	488	67	63	-	-	93	87	56	82	-	-	-	86	-	99	-	-	-	99	68	-	-

[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 the reporting period (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): 44 %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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 124 surveillance sites from public and private sector (Abu Dhabi Emirate only), including 38 hospitals and 86 ambulatory healthcare facilities. Version 1.0 (21 May 2022).

4.2.3 Dubai Emirate

Table 4.2.3.1 Dubai Emirate Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=21,228)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins				Cephalosporins				Carbapenems									
	N	AMP	AMC	TZP	CZO	CXM[i]	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	21,228	-	67	92	-	-	66	-	82	92	96	92	98	90	92	73	-	71	79[b]
Haemophilus influenzae[c]	357	58	62	-	-	87	-	-	-	-	-	-	-	-	-	91	-	61	-
Moraxella (Branh.) catarrhalis[d]	35	-	88	-	-	100	-	-	-	-	-	-	-	-	-	-	-	85	-
Enterobacterales	16,905	30	69	93	57	56/64[i]	69	-	80	94	98	95	99	90	90	71	-	71	79[b]
Citrobacter koseri (diversus)	375	R	97	96	91	29/85[i]	98	-	96	98	98	96	100	99	-	97	-	98	60[b]
Enterobacter cloacae	517	R	R	88	R	18/41[i]	80	-	90	89	97	91	99	95	-	85	-	86	34[b]
Enterobacter aerogenes (*K. aer.*)	449	R	R	88	R	R	85	-	92	80	97	93	99	97	-	93	-	96	33[b]
Escherichia coli[e]	9,921	39	74	94	61	59/65[i]	64	-	76	98	99	97	99	88	89	64	-	63	96[b]
Klebsiella pneumoniae	3,476	R	78	85	67	66/68[i]	69	-	78	94	95	92	97	91	91	75	-	76	37[b]
Klebsiella oxytoca	167	R	84	93	65	76/79[i]	77	-	92	93	96	89	100	94	-	89	-	89	79[b]
Morganella morganii	189	R	R	99	R	R	75	-	98	31	98	97	100	88	-	69	-	81	R
Proteus mirabilis	484	63	86	100	72	88/89[i]	83	-	90	30	97	96	96	77	-	70	-	66	R
Proteus vulgaris	19	R	67[f]	100[f]	R	R	-	-	-	-	91[f]	100[f]	100[f]	100[f]	-	100[f]	-	92[f]	R
Providencia spp.	51	R	R	96[f]	R	-	-	-	100[f]	27[f]	100[f]	100[f]	100[f]	82[f]	-	96[f]	-	100[f]	R
Salmonella spp. (non-typhoid)	462	73	95	100	88	84/89[i]	100	-	99	-	-	-	-	-	-	96[g]	-	96	-
Salmonella Typhi/Paratyphi	39	80	100	94	-	-	89	-	87	-	-	-	-	-	-	0[g]	-	88	-
Serratia marcescens	331	R	R	99	R	R	90	-	98	45	96	87	99	99	-	92	-	98	R
Shigella spp.	24	39[f]	82[f]	100[f]	-	-	-	-	100[f]	-	-	-	-	-	-	92[f]	-	42[f]	-
Non-fermenting Gram-neg. rods	3,689	R	R	89	-	-	-	89	89	86	89	R	92	88	94	85	67	72	-
Acinetobacter baumannii	293	R	R	92	-	-	-	88	91	94	92	R	100	90	97	90	R	96	-
Pseudomonas aeruginosa	2,622	R	R	92	-	R	R	93	94	87	91	R	97	93	96	88	-	R	R
Stenotrophomonas maltophilia[h]	362	R	R	R	-	-	R	33	-	R	R	R	R	R	R	-	R	93	-

[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 the reporting period (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 95 %S, CRO 69 %S, AZM: 96 %S, CLR: no data. [d] *M. catarrhalis*: CLR: no data, ERY 92 %S, AZM: no data, 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: 97 %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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 85 surveillance sites from public and private sector (Dubai Emirate only), including 26 hospitals and 59 ambulatory healthcare facilities. Version 1.0 (24 May 2022).

Table 4.2.3.2 Dubai Emirate Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=13,606)

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)	13,606	-	-	-	-	-	-	54	80	-	-	-	68	59	99	98	73	97	99	-	-	-
Enterococcus spp.	1,674	95	-	-	-	R	R	-	R	R	80	99	64	65	98	98	R	94	97	-	-	-
Enterococcus faecalis	1,365	99	-	-	-	R	R	-	R	R	80	99	67	66	99	99	R	97	97	-	-	R
Enterococcus faecium	221	35	-	-	-	R	R	-	R	R	72	100	39	-	88	91	R	40[j]	96	-	-	73[j]
Staphylococcus aureus	5,543	-	-	67[c]	67	-	-	71	91	89	-	-	63	64	100	100	76	99	100	88	100	87
MSSA	3,824	-	-	100[c]	100	-	-	76	94	96	-	-	67	69	100	100	81	100	100	91	100	91
MRSA	1,482	-	-	-	-	-	-	57	88	73	-	-	50	51	100	100	65	93	99	81	99	71
Coagulase-neg. staphylococci (CNS)	1,998	-	-	38[c]	38	-	-	30	68	76	-	-	76	58	99	95	82	100	98	81	94	87
Staphylococcus epidermidis	632	-	-	29[c]	29	-	-	27	63	69	-	-	61	50	100	90	71	100	97	81	94	93
Staphylococcus saprophyticus [g]	356	-	-	64[c]	64	-	-	39	83	99	-	-	99	100	100	100	96	100	100	94	100	93
Staphylococcus lugdunensis	100	-	-	80[c]	80	-	-	71	80	96	-	-	98	91	99	98	100	-	100	93	99	93[j]
Streptococcus pneumoniae	355	-	93[d]	-	-	93[e]	96[e]	36	63	-	-	-	91	91	100	-	64	-	100	57	100[j]	100[j]
Streptococcus pyogenes [h]	444	100[f]	100	-	-	94	96	69	88	-	-	-	79	-	100	-	-	-	100	76	-	-
Streptococcus agalactiae [i]	3,063	99	98	-	-	99	97	46	61	-	-	-	74	-	99	-	-	97	100	15	-	99
Streptococcus spp. (viridans group)	234	79	65	-	-	93	90	39	65	-	-	-	82	-	99	-	-	-	99	47	-	-

[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 the reporting period (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): 79 %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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 85 surveillance sites from public and private sector (Dubai Emirate only), including 26 hospitals and 59 ambulatory healthcare facilities. Version 1.0 (24 May 2022).

4.2.4 Northern Emirates

Table 4.2.4.1 Northern Emirates Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=14,526)

Gram-negative Bacteria	Isolates	β-Lactams											Aminoglycosides			FQ	Other		
		Penicillins				Cephalosporins				Carbapenems									
	N	AMP	AMC	TZP	CZO	CXM	CTX	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gram-negative bacteria (all)	14,526	-	66	84	-	-	64	-	82	88	92	91	96	87	86	65	64	68	68[b]
Haemophilus influenzae[c]	141	47	58	-	-	81	-	-	-	-	-	-	-	-	-	89[f]	-	-	-
Moraxella (Branh.) catarrhalis[d]	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Enterobacterales	11,150	25	67	87	-	53/59[j]	69	-	82	90	96	95	97	88	84	63	68	69	69[b]
Citrobacter koseri (diversus)	283	R	91	90	-	37/73[j]	93	-	97	97	98	96	100	99	97	95	95	96	74[b]
Enterobacter cloacae	4418	R	R	82	R	20/46[j]	74	-	90	93	97	91	98	94	88	80	67	89	27[b]
Enterobacter aerogenes (*K. aer.*)	311	R	R	78	R	R	75	-	92	64	95	94	97	97	86	89	69	94	19[b]
Escherichia coli [e]	5,638	36	75	92	-	55/60[j]	65	-	79	99	98	98	99	87	84	55	61	62	93[b]
Klebsiella pneumoniae	3,019	R	72	76	-	61/64[j]	69	-	80	90	90	90	91	89	77	66	61	72	23[b]
Klebsiella oxytoca	84	R	84	87	-	74/74[j]	81	-	94	98	99	95	99	99	100	88	83[f]	88	76[b]
Morganella morganii	143	R	R	98	R	R	58	-	92	29	97	96	100	76	83	45	86[f]	55	R
Proteus mirabilis	404	57	72	99	-	79/82[j]	90	-	86	6	98	94	97	76	74	54	92	54	R
Proteus vulgaris	8	R	-	-	R	R	-	-	-	-	-	-	-	-	-	-	-	-	R
Providencia spp.	58	R	R	97	R	-	91[f]	-	96	41	100	96[f]	100	88	100[f]	61	-	89	R
Salmonella spp. (non-typhoid)	168	83	97	100	-	-	100	-	99	-	-	-	-	-	-	97[g]	-	96	-
Salmonella Typhi/Paratyphi	9	71[f]	100[f]	89[f]	-	-	-	-	100[f]	-	-	-	-	-	-	-	-	88[f]	-
Serratia marcescens	290	R	R	83	R	R	89	-	94	70	95	92	99	98	84	88	88	96	R
Shigella spp.	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Non-fermenting Gram-neg. rods	3,080	R	R	74	-	-	-	78	80	79	80	R	91	81	87	74	56	59	-
Acinetobacter baumannii	622	R	R	56	-	-	-	52	59	62	61	R	86	64	45	55	R	71	-
Pseudomonas aeruginosa	1,878	R	R	82	-	R	R	87	90	86	86	R	96	90	95	83	65	R	R
Stenotrophomonas maltophilia[i]	248	R	R	R	-	-	R	46	-	R	R	R	R	R	R	-	R	88	-

[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 the reporting period (de-duplicated data). [b] NIT: Nitrofurantoin data from urine isolates only. [c] *H. influenzae*: LVX 98 %S, CRO 68 %S, AZM 98 %S, CLR 58 %S. [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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 75 surveillance sites from public and private sector (Northern Emirates only: Sharjah, Ajman, Um Al Quwain, Ras Al Khaimah, Fujairah), including 23 hospitals and 53 ambulatory healthcare facilities. Version 1.0 (26 May 2022).

Table 4.2.4.2 Northern Emirates Cumulative Antibiogram (2020): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=6,774)

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)	6,774	-	-	-	-	-	-	46	78	-	-	-	65	45	99	98	75	92	97	-	-	-
Enterococcus spp.	1,167	87	-	-	-	R	R	-	R	R	84	98	64	52	97	96	R	87	88	-	-	-
Enterococcus faecalis	959	99	-	-	-	R	R	-	R	R	84	99	71	58	98	98	R	97	87	-	-	R
Enterococcus faecium	142	19	-	-	-	R	R	-	R	R	83[j]	95	16	28[j]	91	94	R	19	93	-	-	74
Staphylococcus aureus	2,439	-	-	63[3]	63	-	-	72	93	90	-	-	62	64	100	100	78	100	100	86	99	97
MSSA	1,615	-	-	100	100	-	-	77	95	96	-	-	67	68	100	100	80	100	100	89	100	98
MRSA	845	-	-	-	-	-	-	62	91	79	-	-	53	54	99	99	75	100	99	81	99	92
Coagulase-neg. staphylococci (CNS)	1,534	-	-	32[c]	32	-	-	27	66	74	-	-	51	50	99	93	71	100	99	80	91	97
Staphylococcus epidermidis	597	-	-	21[c]	21	-	-	26	57	69	-	-	40	40	99	79	62	100	99	83	89	100[j]
Staphylococcus saprophyticus [g]	119	-	-	57[c]	57	-	-	34	89	99	-	-	96	96	100	100	87	99	100	92	100	-
Staphylococcus lugdunensis	37	-	-	78[c]	78	-	-	85	88	97	-	-	97	94	100	100[j]	94	-	100	91	100	-
Streptococcus pneumoniae	153	-	94[d]	-	-	92[e]	91[e]	41	62	-	-	-	96	97	98	90[j]	57	-	99	50	99	-
Streptococcus pyogenes [h]	163	100[f]	100	-	-	98	93	58	90	-	-	-	76	-	99	-	-	-	99	78	-	-
Streptococcus agalactiae [i]	1,043	100	99	-	-	100	99	51	68	-	-	-	86	-	100	100[j]	-	94	100	15	-	93[j]
Streptococcus spp. (viridans group)	153	60	52	-	-	81	82	55	70	-	-	-	86	-	99	-	-	-	100	56	-	-

[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 the reporting period (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): 53 %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 ED32:2022. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2022.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 75 surveillance sites from public and private sector (Northern Emirates only: Sharjah, Ajman, Um Al Quwain, Ras Al Khaimah, Fujairah), including 23 hospitals and 53 ambulatory healthcare facilities. Version 1.0 (26 May 2022).

4.3 Multidrug resistance

4.3.1 MDR, XDR, PDR Summary

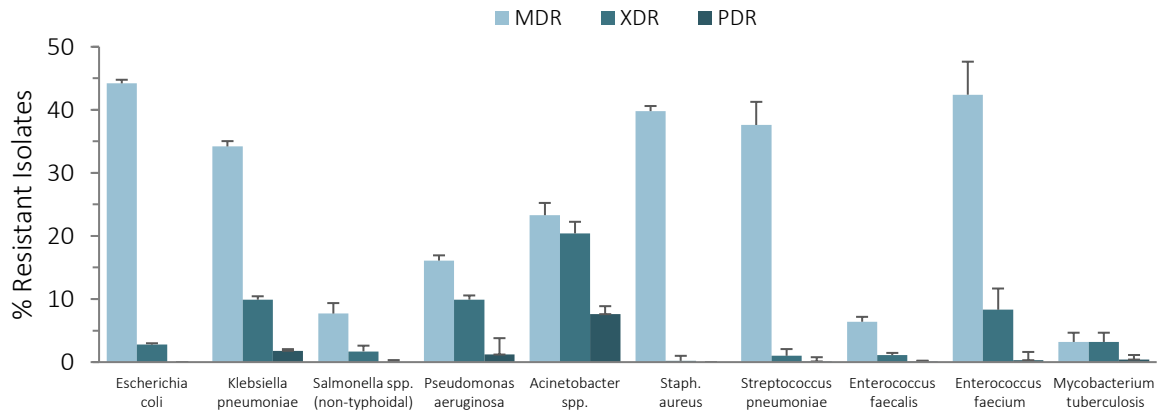
In a 2012 publication, the European Centre for Disease Prevention and Control (ECDC) proposed definitions for common bacterial pathogens resistant to multiple antimicrobials (Magiorakos, et al., 2012). Similar definitions were applied for organisms where these were not available from this publication (*S. pneumoniae*, XDR-TB, PDR-TB). MDR-TB was defined as combined resistance of *M. tuberculosis* to both, isoniazid (INH) and rifampin (RIF). MDR/XDR/PDR results are summarized below.

Table 4.3.1 MDR, XDR, PDR Summary, United Arab Emirates, 2020

Organism	Number of isolates	MDR	Possible XDR	Possible PDR
Escherichia coli	29,139	12,882 (44.2%)	809 (2.8%)	8 (0%)
Klebsiella pneumoniae	12,208	4,171 (34.2%)	1,213 (9.9%)	225 (1.8%)
Salmonella spp. (non-typhoidal)	1,182	91 (7.7%)	20 (1.7%)	0 (0%)
Pseudomonas aeruginosa	7,933	1,276 (16.1%)	785 (9.9%)	93 (1.2%)
Acinetobacter sp.	1,929	450 (23.3%)	394 (20.4%)	147 (7.6%)
Staphylococcus aureus	14,131	5,625 (39.8%)	25 (0.2%)	0 (0%)
Streptococcus pneumoniae	691	260 (37.6%)	7 (1.0%)	1 (0.1%)
Enterococcus faecalis	4,210	271 (6.4%)	47 (1.1%)	1 (0.1%)
Enterococcus faecium	349	148 (42,4%)	29 (8.3%)	1 (0.3%)
Mycobacterium tuberculosis	791	25 (3.2%)	25 (3.2%)	3 (0.4%)
Total	**72,563**	**25,199 (34.7%)**	**3,354 (4.6%)**	**479 (0.7%)**

MDR: Multidrug resistance, XDR: Extensive drug resistance, PDR: Pan-drug resistance.

Figure 4.3.0 MDR, XDR, PDR Summary, United Arab Emirates, 2020



MDR, XDR, PDR Trends

Between 2010 and 2020, multidrug resistance has, overall, increased in the United Arab Emirates, in particular for clinically relevant Enterobacterales (*K. pneumoniae*), all Gram-positive pathogens under enhanced surveillance, and *M. tuberculosis*.

During the same period, prevalence of multidrug resistance decreased for common non-lactose fermenting bacteria such as *P. aeruginosa* and *Acinetobacter* spp.

4.3.2 Multidrug resistance in Gram-negative Bacteria: Enterobacterales

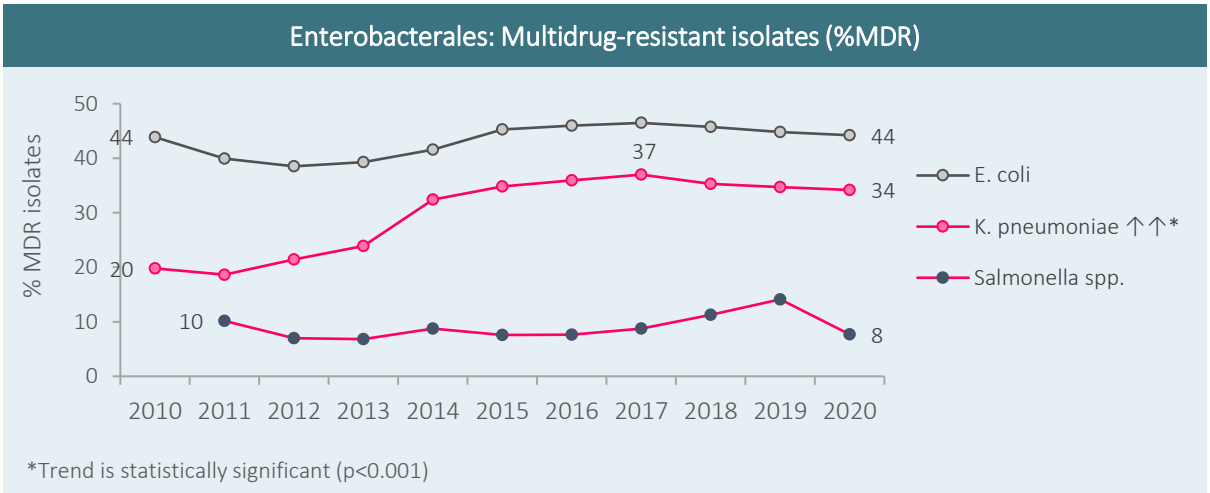
For 2020, prevalence of multidrug resistance (%MDR) in Gram-negative bacteria (Enterobacterales) was 44.2% (*E. coli*), 34.2% (*K. pneumoniae*), and 7.7% (*Salmonella* spp.).

Between 2010 and 2020, multidrug resistance (%MDR), overall, increased for

- *Klebsiella pneumoniae* from 20% to 34% MDR.

However, since 2017, %MDR decreased slightly for *K. pneumoniae*, from 37 (2017) to 34% (2020) (**Fig. 4.3.2).**

Figure 4.3.2 Annual trends for percentage of isolates multidrug resistant (%MDR) for *E. coli*, *K. pneumoniae*, and *Salmonella* spp. (non-typhoid), United Arab Emirates, 2010-2020



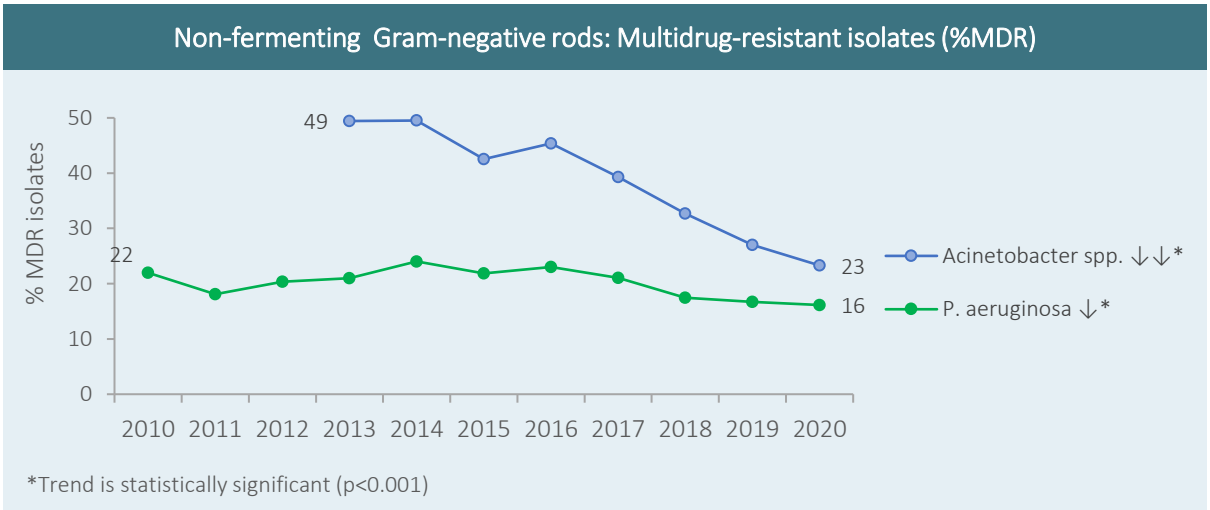
4.3.3 Multidrug resistance in Gram-negative Bacteria: Non-fermenting Gram-neg. rods

For 2020, prevalence of multidrug resistance (%MDR) in non-fermenting Gram-negative rods was 23.3% (*Acinetobacter* spp.), and 16.1% (*P. aeruginosa*).

Between 2010 and 2020, multidrug resistance (%MDR) decreased for lactose non-fermenting Gram-negative bacteria ("Non-fermenters") (**Fig. 4.3.3**):

- *Acinetobacter* spp.: from 49% (2013) to 23%
- *P. aeruginosa:* from 22 % to 16%.

Figure 4.3.3 Annual trends for percentage of isolates multidrug resistant (%MDR) for non-fermenting Gram-negative rods, United Arab Emirates, 2010-2020



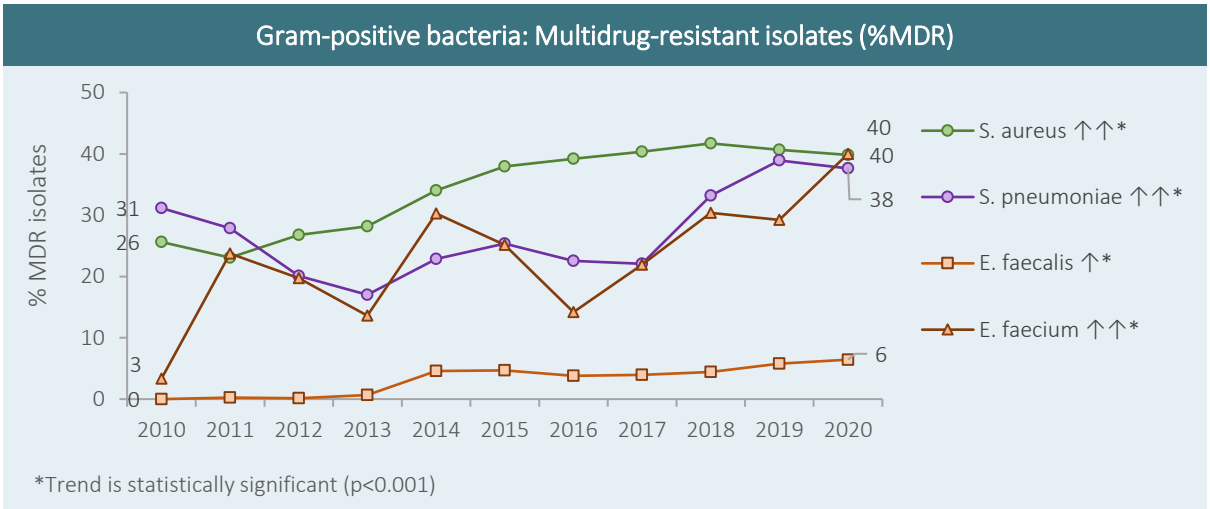
4.3.4 Multidrug-resistance in Gram-positive Bacteria

For 2020, prevalence of multidrug resistance (%MDR) in Gram-positive bacteria was 37.6% (*S. pneumoniae*), 40.0% (*E. faecium*), 39.8% (*S. aureus*) and 6.4% (*E. faecalis*) (**Figure 4.3.4**).

Between 2010 and 2020, multidrug resistance (%MDR) increased for:

- *S. pneumoniae* from 31% to 38%,
- *S. aureus*: from 26% to 40%,
- *E. faecium*: from 3% to 40%, and
- *E. faecalis*: from 0% to 6%.

Figure 4.3.4 Annual trends for percentage of isolates multidrug resistant (%MDR) for Gram-positive bacteria, United Arab Emirates, 2010-2020

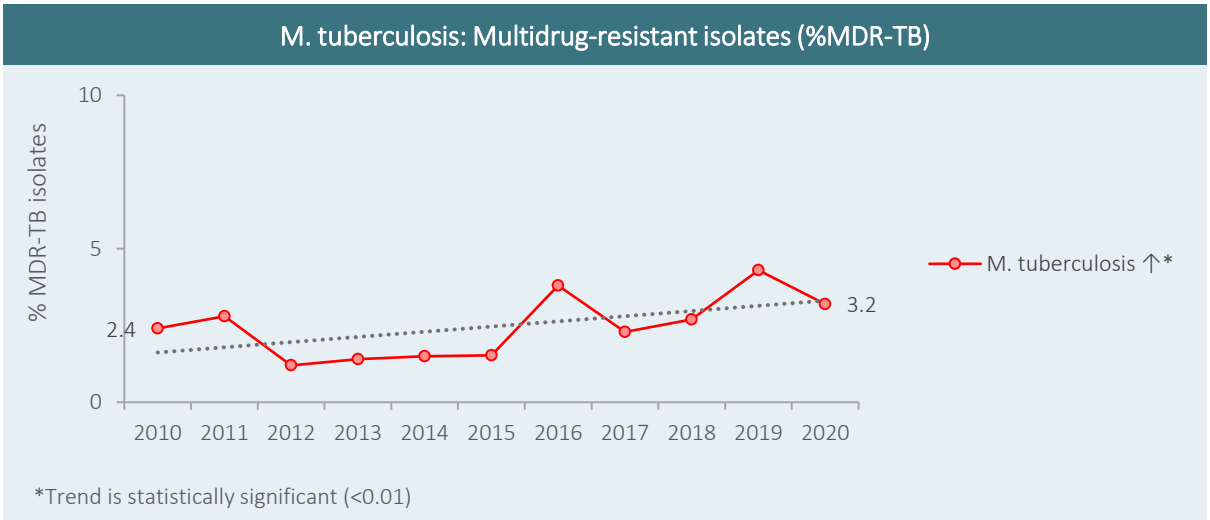


4.3.5 Multidrug-resistance in *Mycobacterium tuberculosis* (MDR-TB)

MDR-TB was defined as combined resistance of *M. tuberculosis* to both, isoniazid (INH) and rifampin (RIF). For 2020, prevalence of multidrug resistance (%MDR-TB) in *Mycobacterium tuberculosis was 3.2%* (**Figure 4.3.5**).

Between 2010 and 2020, multidrug resistance (%MDR) increased for *M. tuberculosis*: from 2.4% to 3.2%.

Figure 4.3.5 Annual trends for percentage of isolates multidrug resistant (%MDR-TB) for *Mycobacterium tuberculosis*, United Arab Emirates, 2010-2020



4.4 AMR priority pathogens

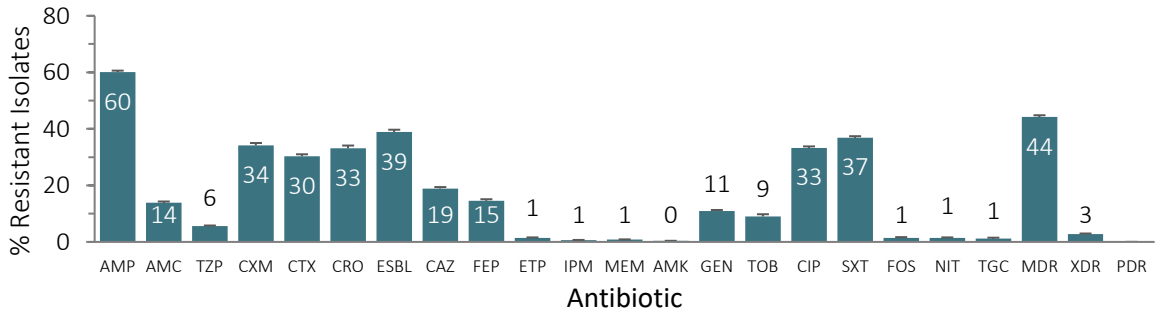
4.4.1 Escherichia coli

Table 4.4.1.1 Percentages of resistant, intermediate, and susceptible isolates for *Escherichia coli*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Escherichia coli* (N=34,717)			
		Isolates (N)	% R	% I	% S
Ampicillin	AMP	28,923	60.1	1.4	38.5
Amoxicillin/clavulanic acid	AMC	27,800	13.8	12.6	73.5
Piperacillin/tazobactam	TZP	28,672	5.6	1.5	93.0
Cefuroxime (oral)	CXM	10,455	34.1	8.6	57.3
Ceftriaxone	CRO	9,373	33.1	0.4	66.5
Cefotaxime	CTX	19,143	30.3	0.6	69.0
Extended-spectrum β-lactamase	ESBL	14,894	38.9	–	61.1
Ceftazidime	CAZ	28,677	18.9	2.1	79.0
Cefepime	FEP	23,348	14.6	5.5	79.9
Ertapenem	ETP	22,364	1.4	0.2	98.4
Imipenem	IPM	26,930	0.6	0.5	98.8
Meropenem	MEM	28,066	0.8	0.2	99.0
Gentamicin	GEN	28,965	10.9	0.4	88.7
Tobramycin	TOB	5,703	9.0	4.9	86.1
Amikacin	AMK	24,920	0.3	0.3	99.4
Ciprofloxacin	CIP	29,004	33.3	4.6	62.1
Trimethoprim/sulfamethoxazole	SXT	28,836	36.8	0	61.1
Fosfomycin[a]	FOS	9,037	1.4[a]	0.3[a]	98.2[a]
Nitrofurantoin[a]	NIT	23,209	1.6[a]	4.3[a]	94.1[a]
Tigecycline[b]	TGC	6,558	1.2	0	98.7
Multidrug-resistance (≥3 classes NS)[c]	MDR	29,139	44.2	–	–
Extensive drug resistance (possible)	XDR	29,139	2.8	–	–
Pan-drug resistance (possible)	PDR	29,139	0	–	–

[a] Fosfomycin and Nitrofurantoin: Isolates from urinary tract only.
[b] Tigecycline: EUCAST breakpoints (S≤0.5, R>0.5)
[c] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

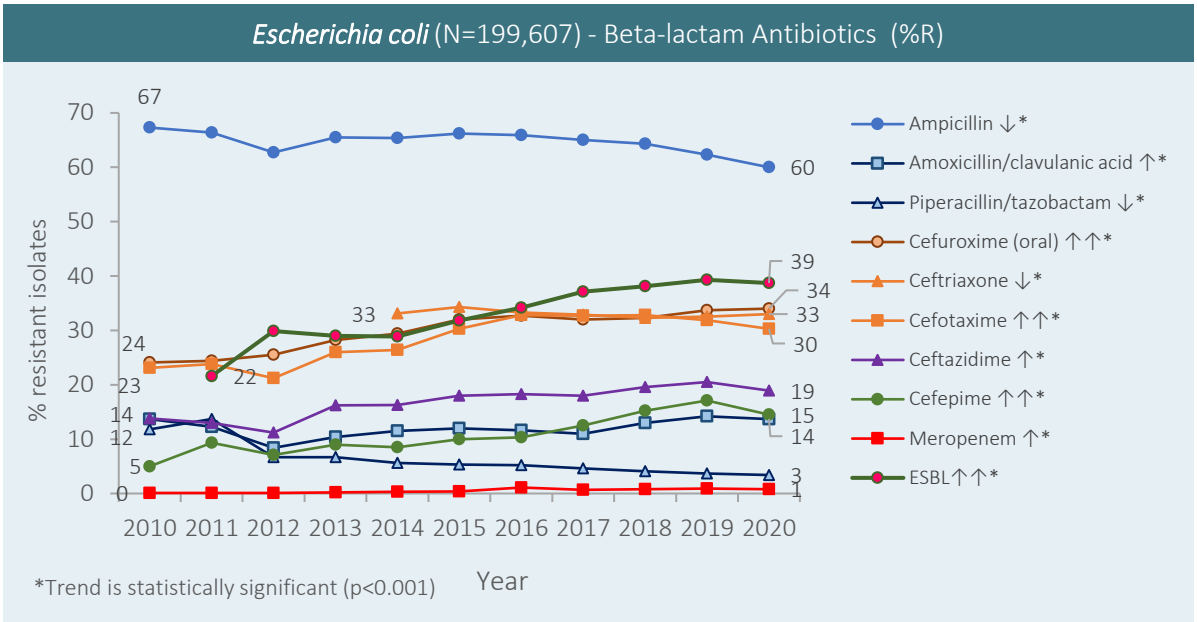
Figure 4.4.1.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Escherichia coli*, isolates from all sources, United Arab Emirates, 2020



For 2020, resistance in *Escherichia coli* ranged from 0.1% for aminoglycosides (amikacin) to 60% for aminopenicillins (ampicillin).

- Susceptibility of urinary tract isolates of *E. coli* to fluoroquinolones (ciprofloxacin) was 64.0%.
- Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *E. coli* was 44.2 %, 2.8%, and 0%, respectively.

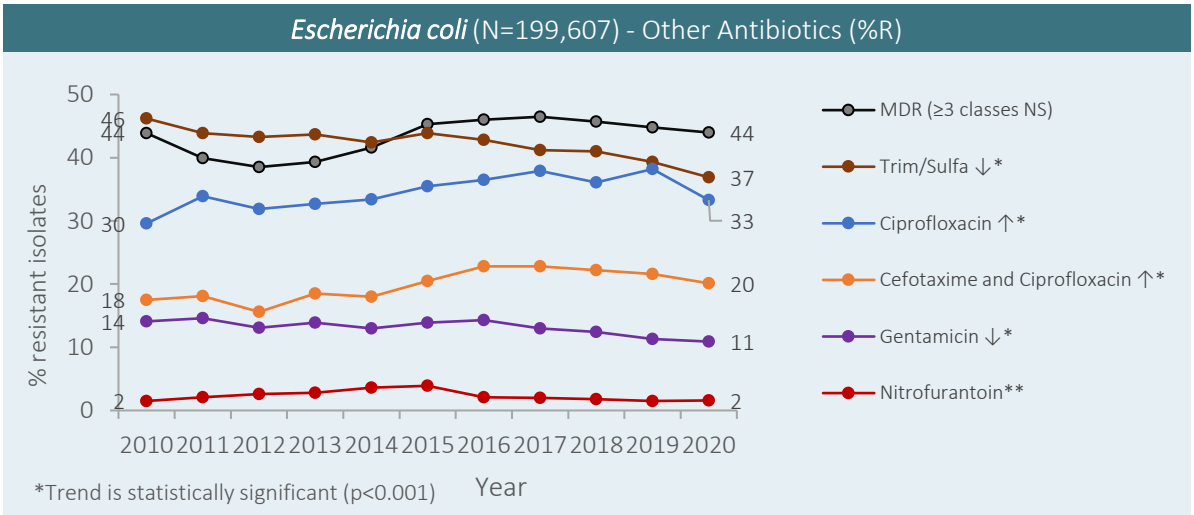
Figure 4.4.1.2 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, United Arab Emirates, 2010-2020 – Beta-lactam Antibiotics



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

- Broad-spectrum penicillins: amoxicillin/clavulanic acid (↑), but not piperacillin/tazobactam (↓),
- Second-generation (cefuroxime ↑↑), third-generation (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, 2010-2020 – Other Antibiotics



E. coli shows increasing trends of resistance for

- Fluoroquinolones (ciprofloxacin ↑) and
- Third generation cephalosporins and fluoroquinolones combined (↑).

E. coli shows decreasing or horizontal trends of resistance for

- Trimethoprim/sulfamethoxazole (↓),
- Aminoglycosides: gentamicin (↓) and amikacin (→),
- Nitrofurantoin (→), and
- Multi-drug resistance (%MDR): horizontal trend (→)

Figure 4.4.1.4 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By age category and age group

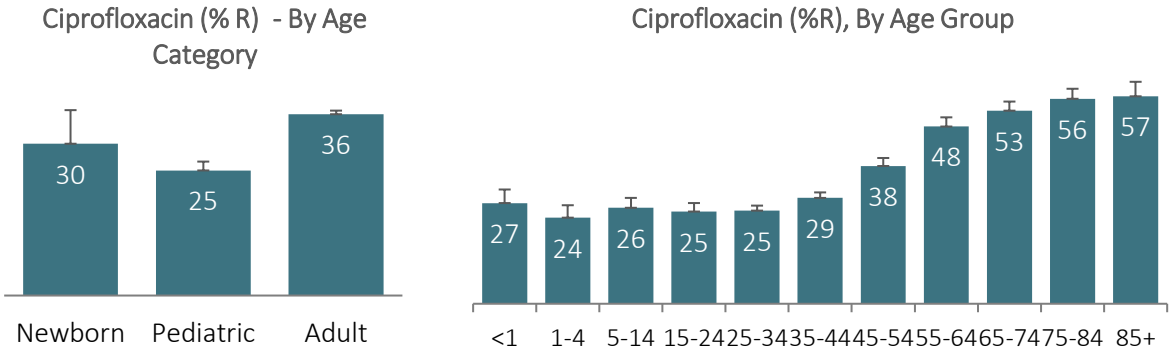


Figure 4.4.1.5 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By gender and nationality status

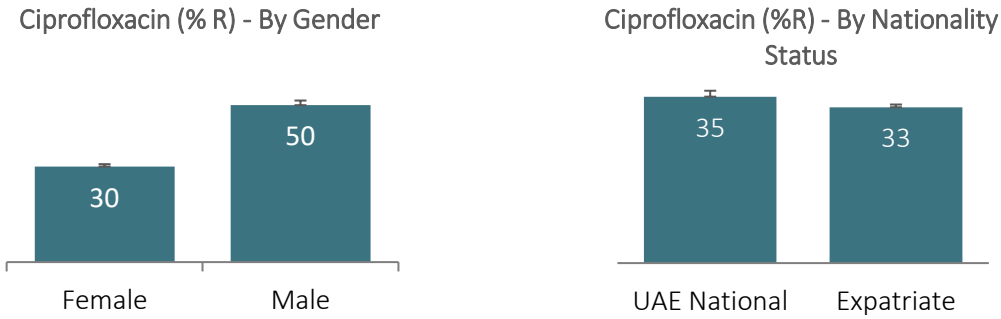


Figure 4.4.1.6 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By patient nationality

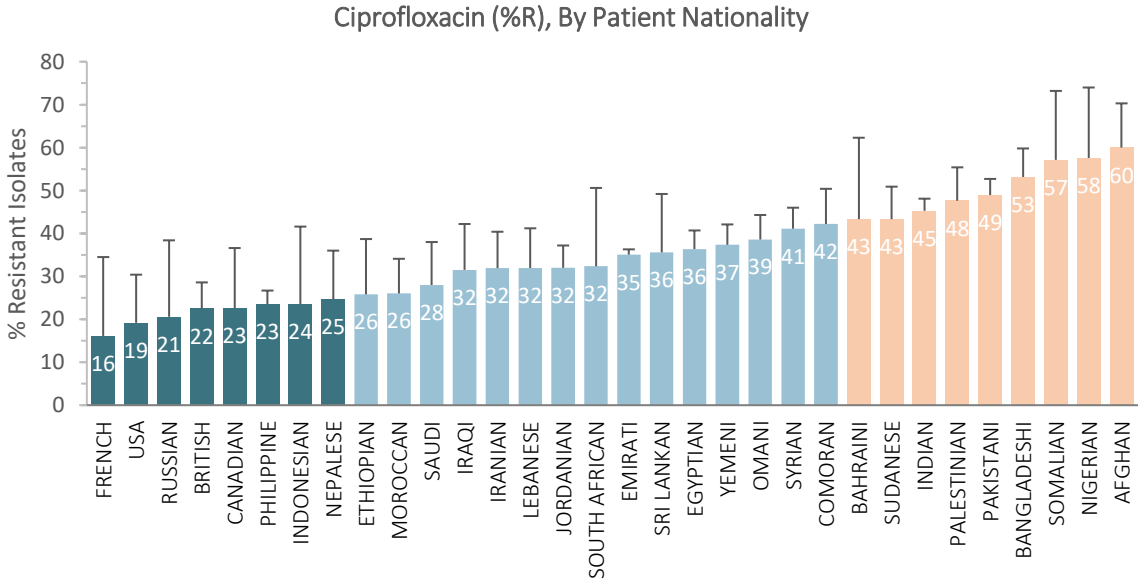


Figure 4.4.1.7 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By Emirate

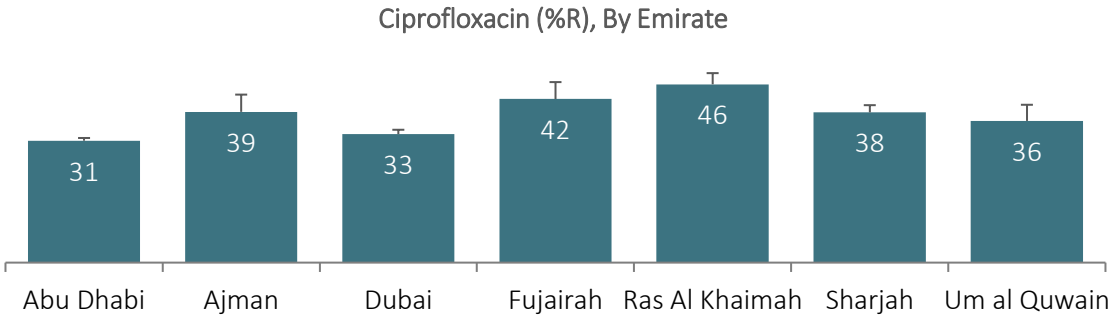


Figure 4.4.1.8 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By isolate source and patient location type

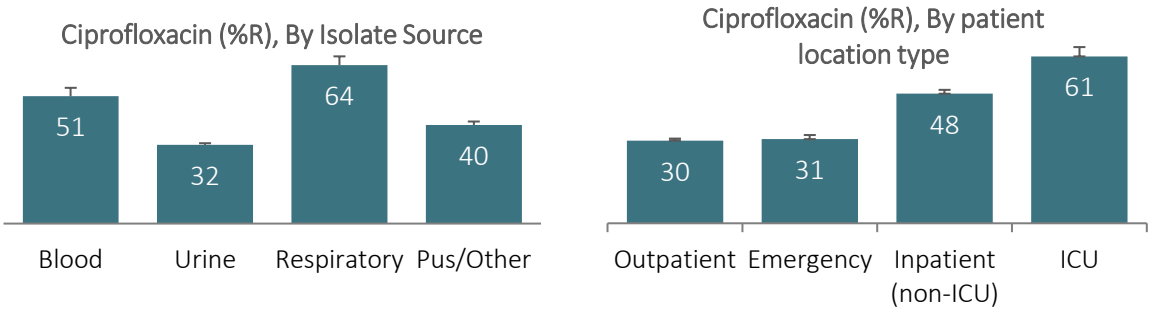


Figure 4.4.1.9 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By clinical specialty/department

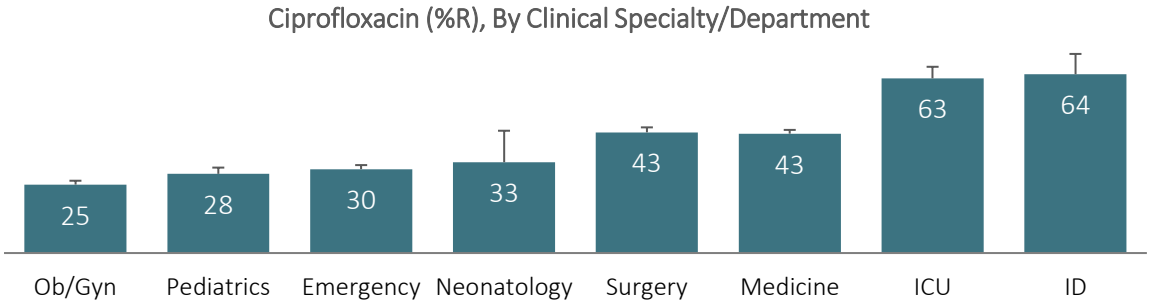
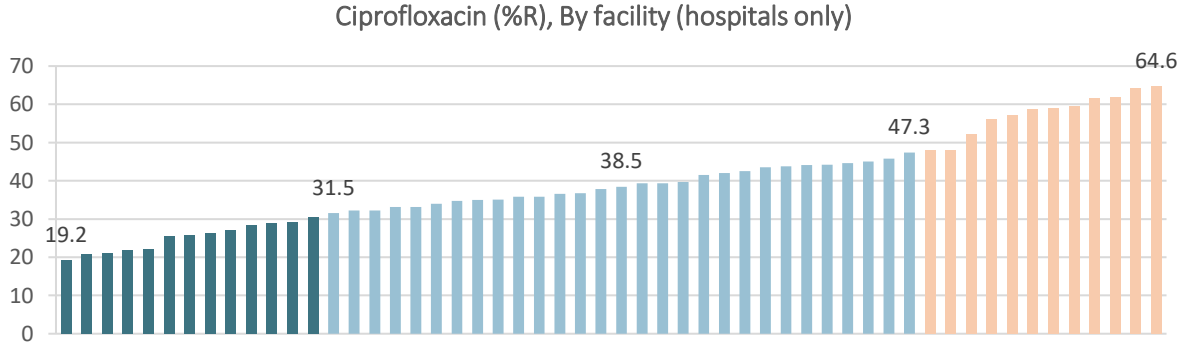


Figure 4.4.1.10 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, United Arab Emirates, 2020 – By facility (hospitals only)



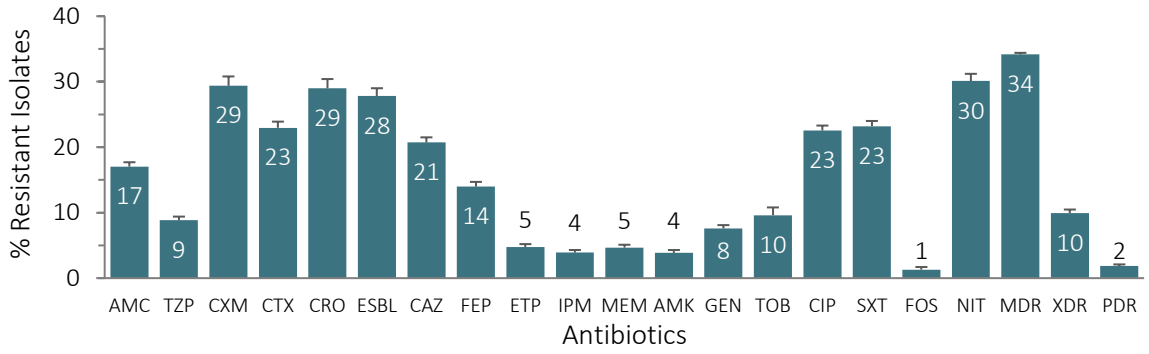
4.4.2 Klebsiella pneumoniae

Table 4.4.2.1 Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Klebsiella pneumoniae* (N=14,287)			
		Isolates (N)	% R	% I	% S
Amoxicillin/clavulanic acid	AMC	11,414	16.9	7.7	75.4
Piperacillin/tazobactam	TZP	12,032	13.1	5.2	80.2
Cefuroxime (oral)	CXM	3,987	28.2	4.4	67.4
Ceftriaxone	CRO	4,340	28.5	0.6	70.9
Cefotaxime	CTX	7,650	23.0	1.2	75.8
Extended-spectrum β-lactamase	ESBL	6,047	27.8	–	72.2
Ceftazidime	CAZ	12,005	20.4	3.1	76.5
Cefepime	FEP	9,842	14.1	2.9	83.1
Ertapenem	ETP	8,601	4.8	0.8	94.4
Imipenem	IPM	11,008	3.9	1.5	94.6
Meropenem	MEM	11,692	4.7	0.3	95.0
Gentamicin	GEN	12,099	7.7	0.7	91.5
Tobramycin	TOB	2,553	9.6	3.4	87.0
Amikacin	AMK	10,432	4.0	0.3	95.6
Ciprofloxacin	CIP	12,126	22.5	3.9	73.6
Trimethoprim/sulfamethoxazole	SXT	12,032	23.1	0	76.8
Nitrofurantoin	NIT	7,165	30.1[a]	44.0[a]	25.8[a]
Multidrug-resistance (≥3 classes NS)[b]	MDR	12,208	34.2	–	–
Extensive drug resistance (possible)	XDR	12,208	9.9	–	–
Pan-drug resistance (possible)	PDR	12,208	1.8	–	–

[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., 2012).

Figure 4.4.2.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Klebsiella pneumoniae*, isolates from all sources, United Arab Emirates, 2020

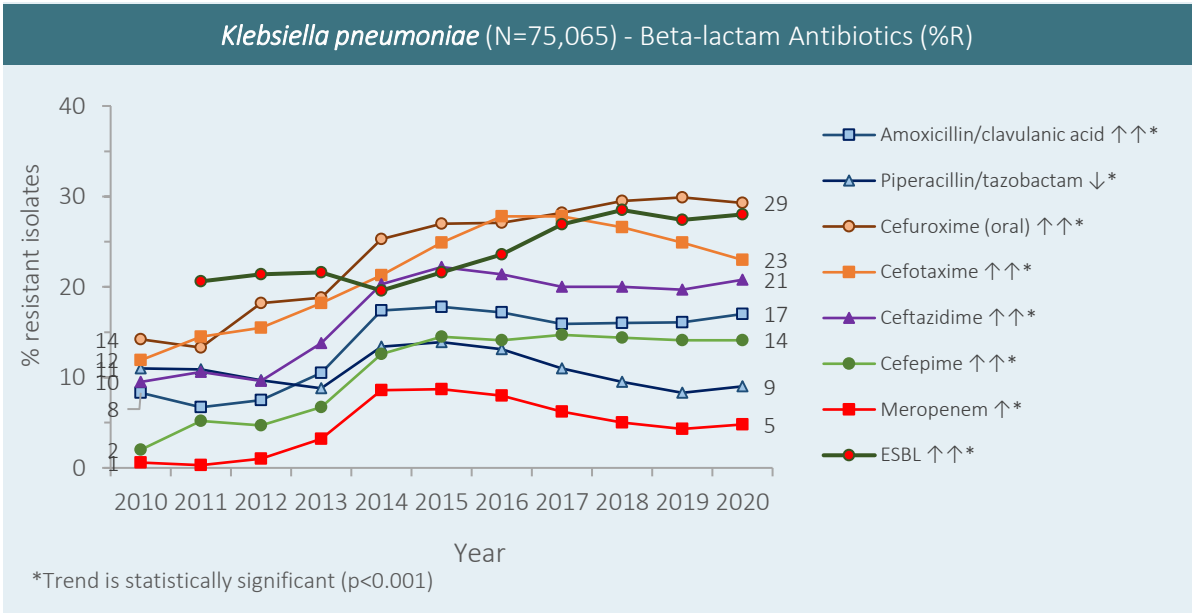


For 2020, resistance in *Klebsiella pneumoniae* ranged from 3.9 %R for amikacin (aminoglycosides) and imipenem, to 29 %R for cefuroxime (CXM) and ceftriaxone (CRO).

- Non-susceptibility (%R+%I) to carbapenems was 5.4%, 5.0%, and 5.5 %NS for imipenem, meropenem and ertapenem, respectively.
- Susceptibility of urinary tract isolates of *K. pneumoniae* to fluoroquinolones (ciprofloxacin) was 60 %S.
- Prevalence of multidrug resistance (%MDR/XDR/PDR[8]) in *K. pneumoniae* was 34.2 %, 9.9%, and 1.8%, respectively.

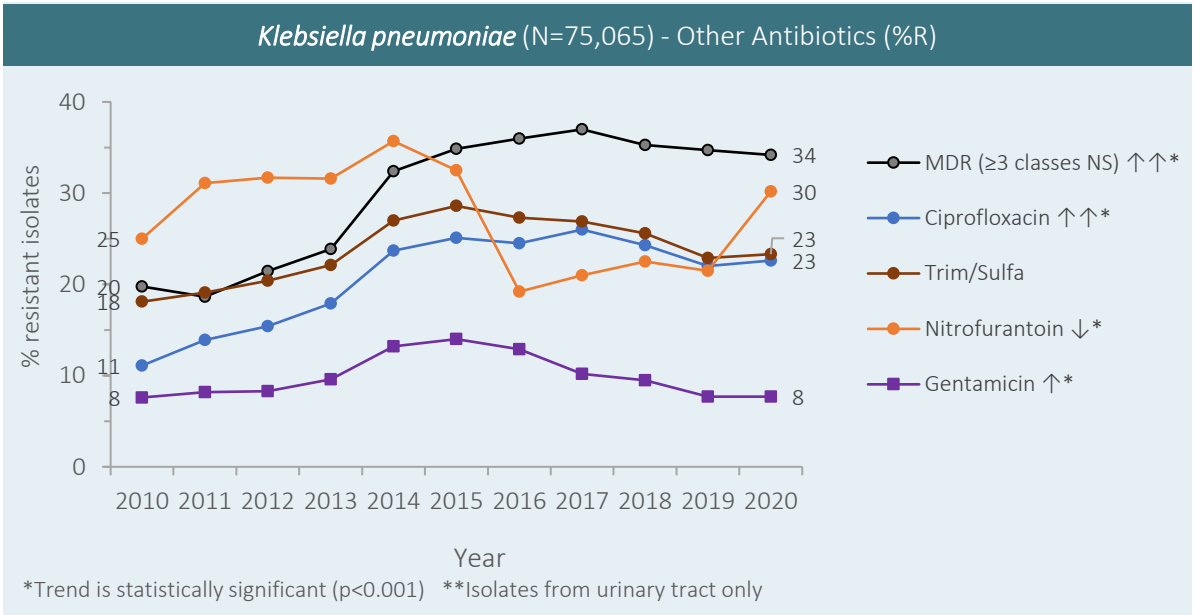
[8] Possible XDR, possible PDR

Figure 4.4.2.2 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, United Arab Emirates, 2010-2020 – 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-generation (cefuroxime ↑↑), third-generation (ceftazidime ↑↑, cefotaxime ↑↑), and fourth-generation (cefepime ↑↑) cephalosporins, and
  - carbapenems (imipenem ↑, meropenem ↑).

Figure 4.4.2.3 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, United Arab Emirates, 2010-2020 – 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 (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By age category and age group

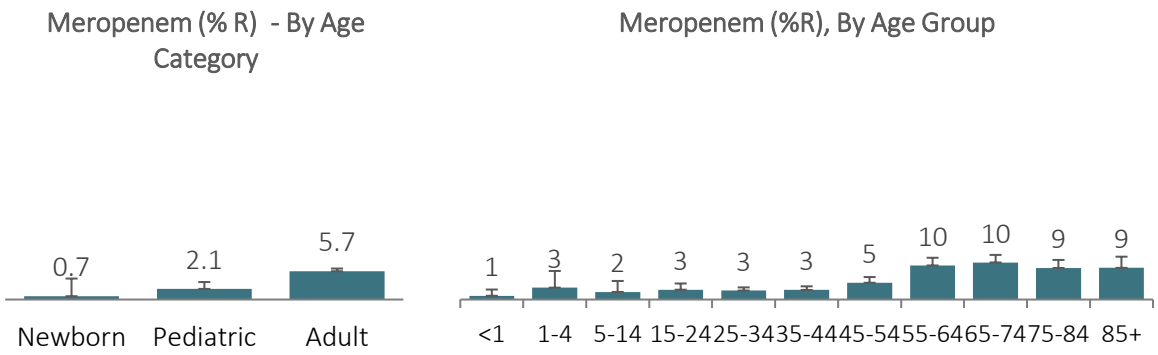


Figure 4.4.2.5 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By gender and nationality status

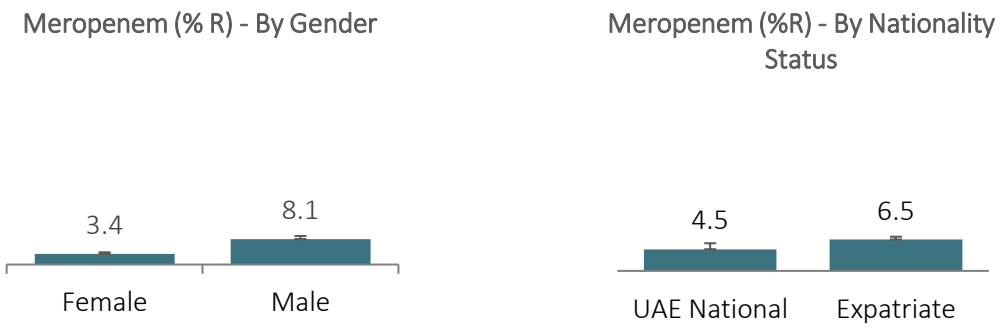


Figure 4.4.2.6 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By patient nationality

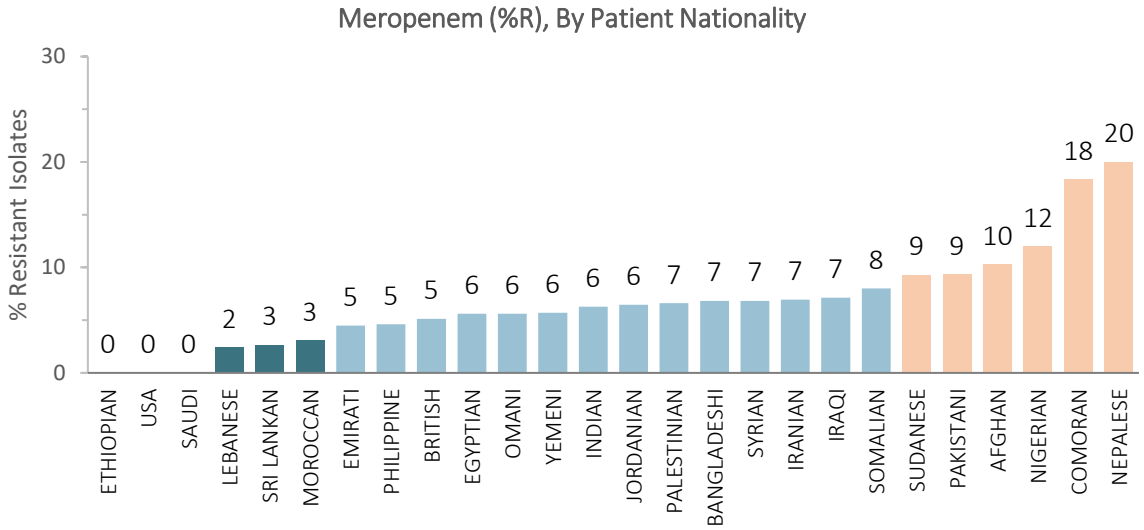


Figure 4.4.2.7 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By Emirate

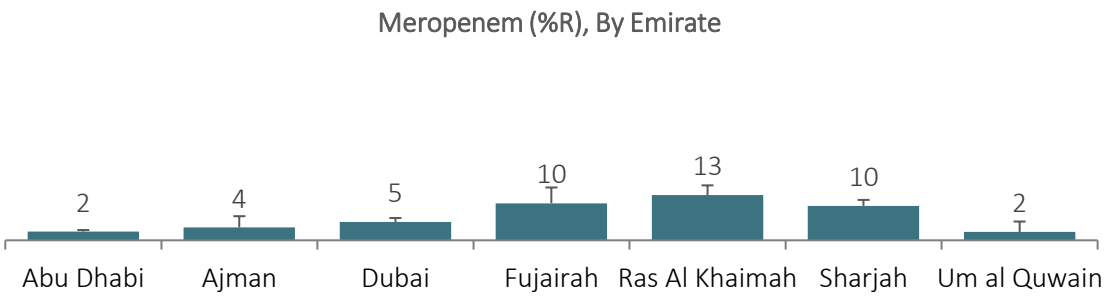


Figure 4.4.2.8 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By isolate source and patient location type

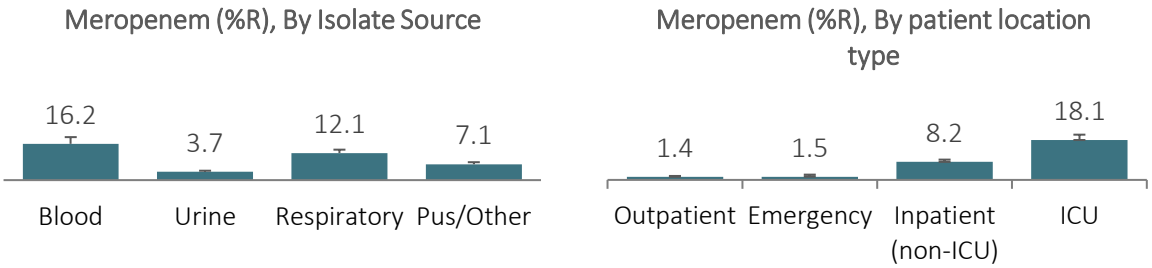


Figure 4.4.2.9 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By clinical specialty/department

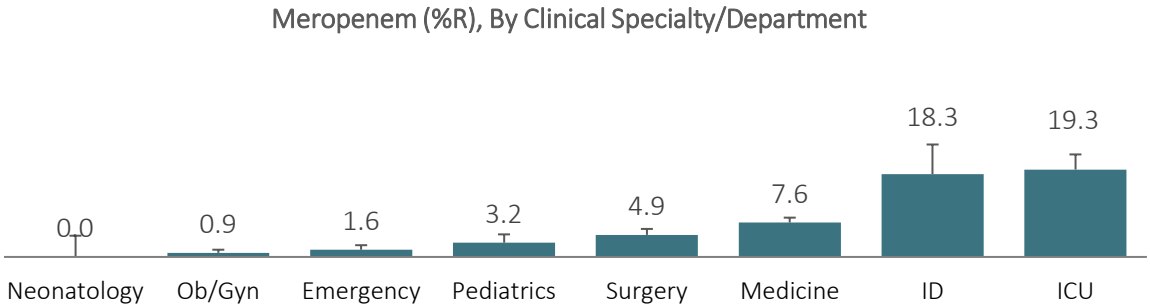
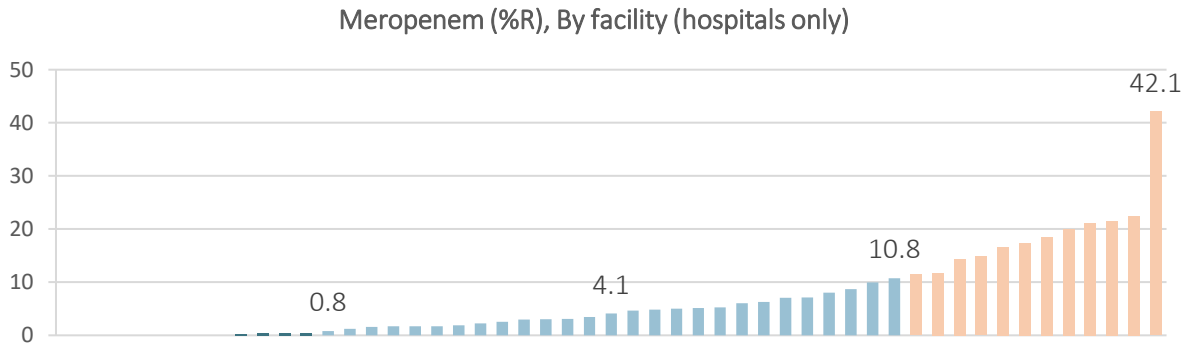


Figure 4.4.2.10 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, United Arab Emirates, 2020 – By facility (hospitals only)



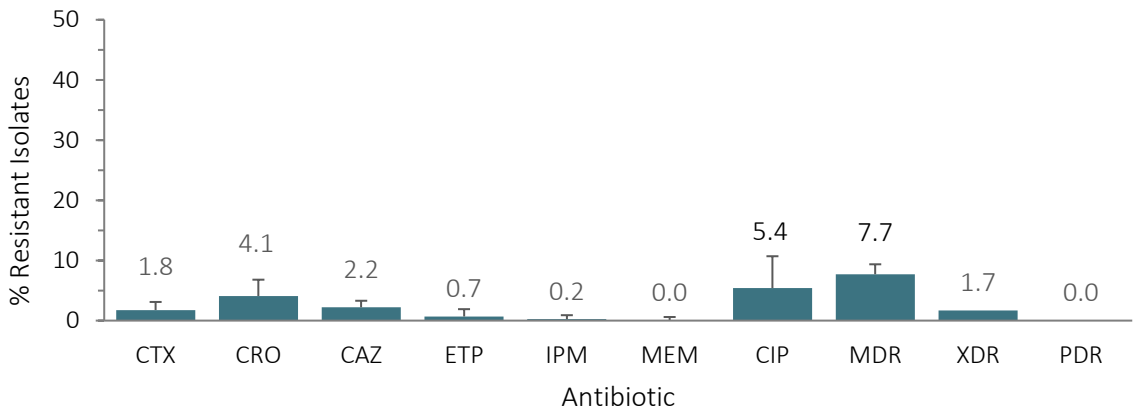
4.4.3 Salmonella spp. (non-typhoidal)

Table 4.4.3.1 Percentages of resistant, intermediate, and susceptible isolates for *Salmonella* spp. (non-typhoidal), isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Salmonella* spp. (non-typhoid) (N=1,467)			
		Isolates (N)	% R	% I	% S
Cefotaxime	CTX	682	1.8	0.3	97.9
Ceftriaxone	CRO	367	4.1	0.5	95.4
Ceftazidime	CAZ	1,042	2.2	0.2	97.6
Ertapenem	ETP	586	0.7	0	99.3
Imipenem	IPM	851	0.2	0.6	99.2
Meropenem	MEM	853	0	0	100
Ciprofloxacin	CIP	149	5.4[a]	2.7[a]	91.9[a]
Multidrug-resistance (≥3 classes NS)[b]	MDR	1,182	7.7	–	–
Extensive drug resistance (possible)	XDR	1,182	1.7	–	–
Pan-drug resistance (possible)	PDR	1,182	0	–	–

[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., 2012).

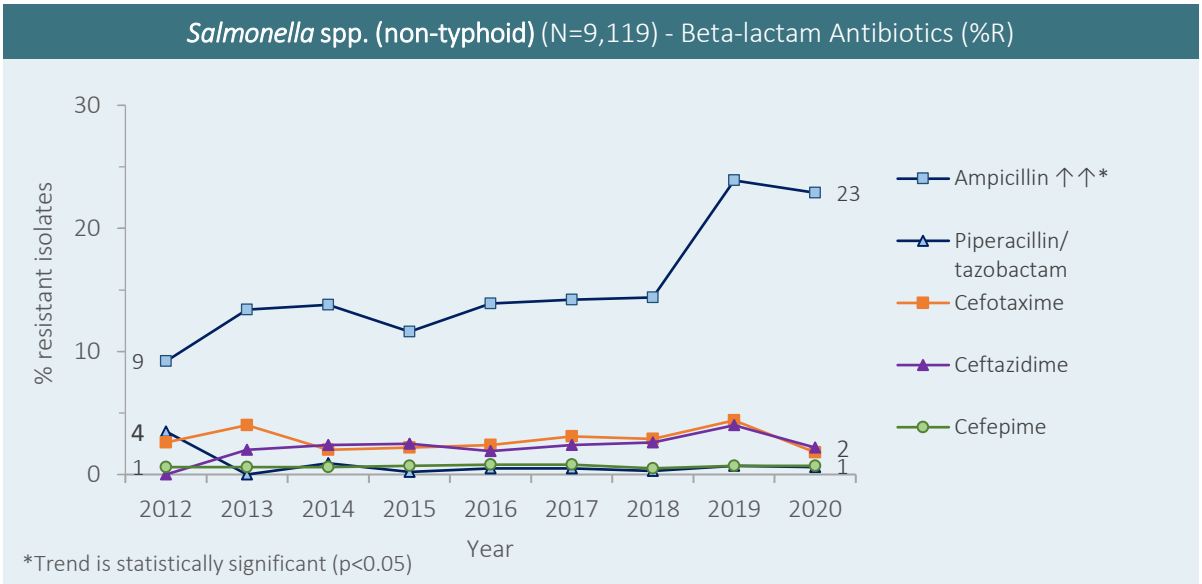
Figure 4.4.3.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Salmonella* spp. (non-typhoidal), isolates from all sources, United Arab Emirates, 2020



For 2020, resistance in *Salmonella* spp. (non-typhoidal) ranged from 0-1 %R for carbapenems (imipenem, meropenem, ertapenem), to 5.4 %R for fluoroquinolones (ciprofloxacin, extraintestinal isolates).

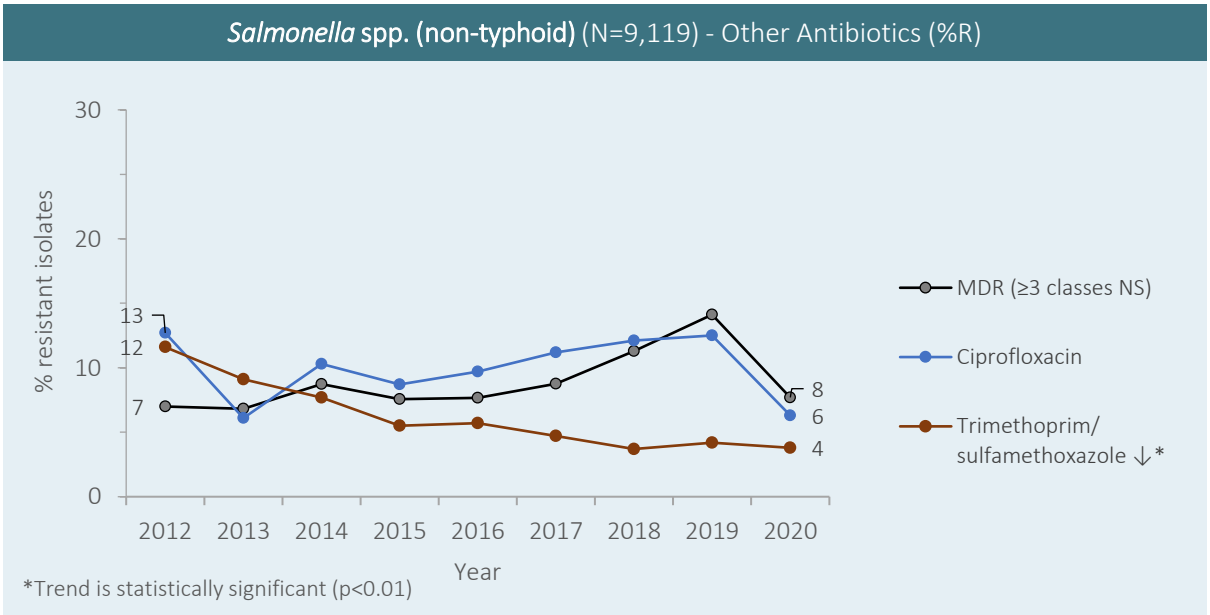
- Susceptibility of non-typhoidal *Salmonella* spp. (extra-intestinal isolates) to ciprofloxacin was 92%.
- Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *Salmonella* spp. (non-typhoidal) was 7.7 %, 1.7% and 0%, respectively.

Figure 4.4.3.2. Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp. (non-typhoidal), United Arab Emirates, 2012-2020 – 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).
- Resistance to carbapenems was very low (<1 %R) during the observation period 2014-2020.

Figure 4.4.3.3 Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp. (non-typhoidal), United Arab Emirates, 2012-2020 – Other Antibiotics



- For trimethoprim/sulfamethoxazole a decreasing trend of resistance (↓) was observed, from 11.6 %R (2012) to 3.8 %R (2020).
- Resistance to fluoroquinolones (ciprofloxacin ↑) increased from 10 %R (2014) to 13 %R (2019).
- Multidrug resistance (≥ 3 classes non-susceptible) was increasing from 7.0 % MDR (2012) to 14.1 %MDR (2019), however, in 2020 it decreased again to 7.7 %MDR.

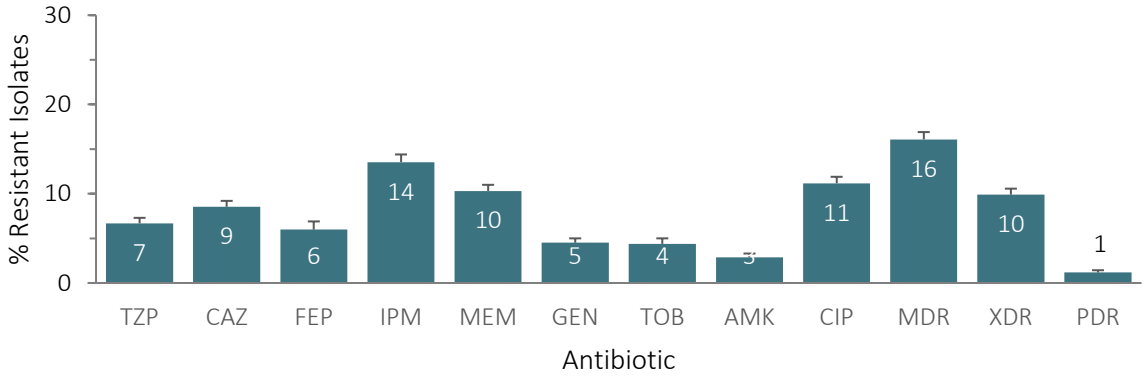
4.4.4 Pseudomonas aeruginosa

Table 4.4.4.1 Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Pseudomonas aeruginosa* (N=9,402)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	7,355	6.7	5.1	88.2
Ceftazidime	CAZ	7,813	8.5	4.1	87.4
Cefepime	FEP	7,437	6.0	3.5	90.1
Imipenem	IPM	7,347	13.5	1.3	85.2
Meropenem	MEM	7,574	10.3	3.9	85.6
Gentamicin	GEN	7,831	4.5	4.0	91.5
Tobramycin	TOB	5,432	4.4	0.5	95.1
Amikacin	AMK	7,436	2.9	1.1	96.0
Ciprofloxacin	CIP	7,797	11.2	4.6	84.2
Multidrug-resistance (≥3 classes NS)[a]	MDR	7,933	16.1	–	–
Extensive drug resistance (possible)	XDR	7,933	9.9	–	–
Pan-drug resistance (possible)	PDR	7,933	1.2	–	–

[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., 2012).

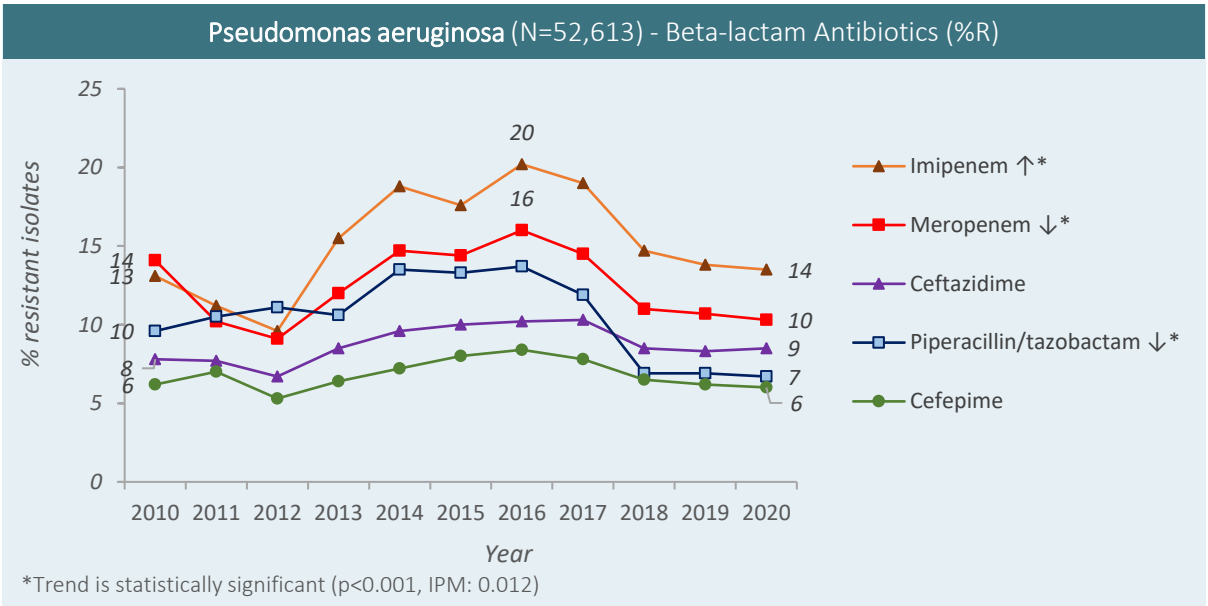
Figure 4.4.4.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Pseudomonas aeruginosa,* isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Pseudomonas aeruginosa* ranged from 3-5 %R for aminoglycosides, to 11 %R for fluoroquinolones (ciprofloxacin), and 10-14 %R for carbapenems (meropenem: 10 %R, imipenem: 14 %R).
- Prevalence of multidrug resistance (%MDR/XDR/PDR[9]) in *Pseudomonas aeruginosa* was 16.1 %, 9.9%, and 1.2%, respectively.

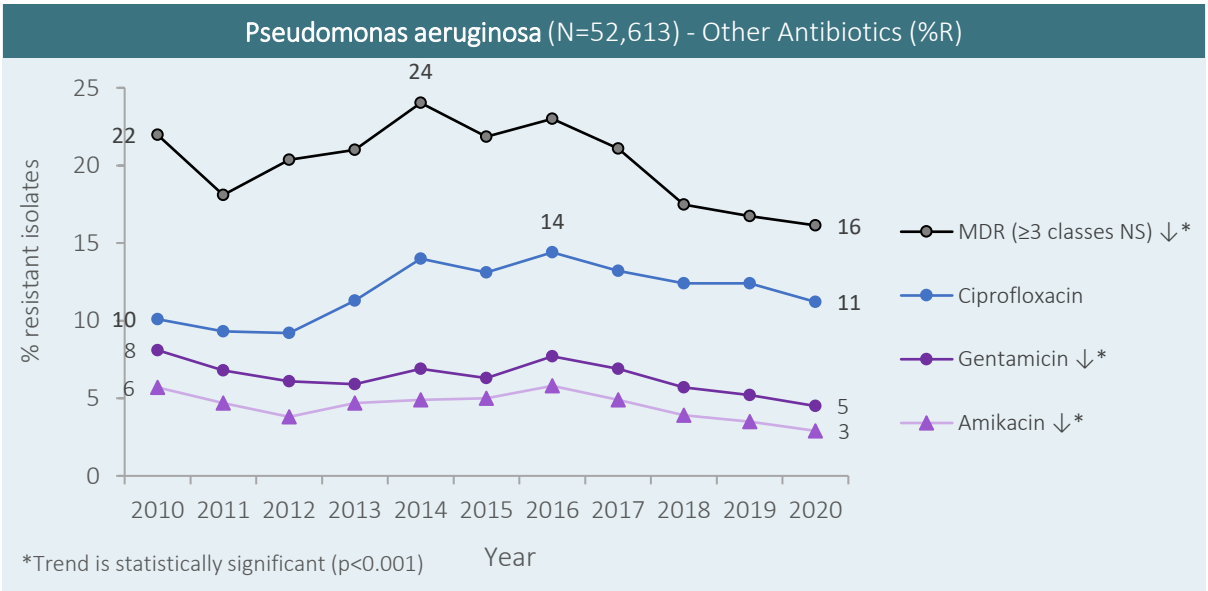
[9] Possible XDR, possible PDR

Figure 4.4.4.2 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, United Arab Emirates, 2010-2020 – Beta-lactam Antibiotics



- *Pseudomonas aeruginosa* shows decreasing (↓) resistance to broad-spectrum penicillins (piperacilllin-tazobactam: from 10 %R (2010) to 7 %R (2020).
- Horizontal (→) trends for resistance to 3rd- and 4th-gen. cephalosporins (ceftazidime, cefepime).
- Resistance trends for carbapenems are diverse: imipenem (IMP) shows a slightly increasing long-term trend of resistance (from 13 to 14 %R, p=0.012), whereas meropenem (MEM) shows a decreasing long-term trend of resistance (from 10 to 10 %R, p<0.001). For the past five years (short term, 2016-2020), both carbapenems (IMP, MEM) are showing a decreasing trend of resistance.

Figure 4.4.4.3 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, United Arab Emirates, 2010-2020 – Other Antibiotics



- Multidrug resistance in *P. aeruginosa* (%MDR) decreased from 22% (2010) to 16% (2020).
- *Pseudomonas aeruginosa* shows a horizontal (→) trend of resistance for fluoroquinolones (ciprofloxacin).
- Decreasing (↓) trends of resistance for aminoglycosides (gentamicin, amikacin).

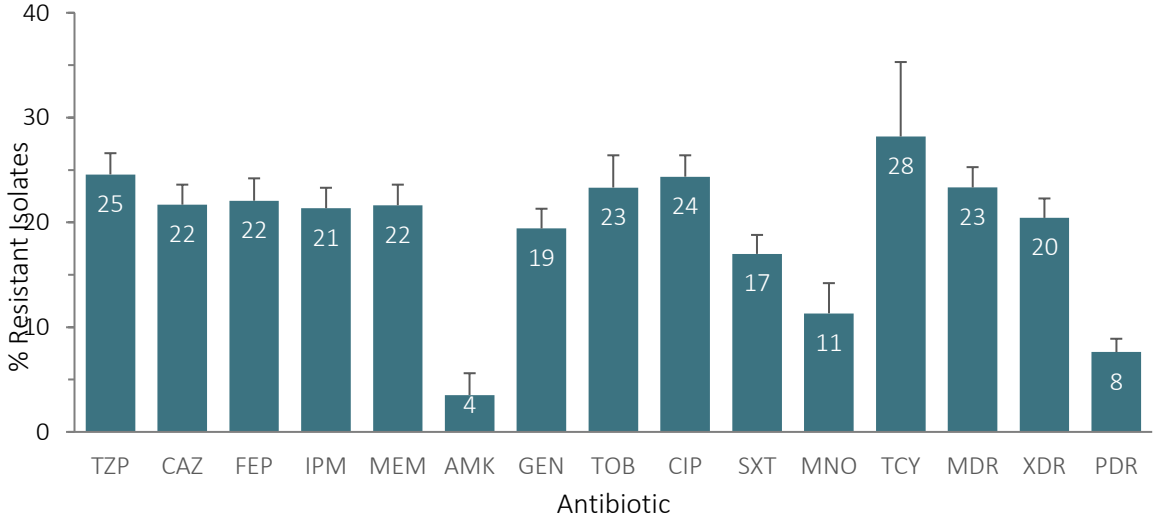
4.4.5 Acinetobacter spp.

Table 4.4.5.1 Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp., isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Acinetobacter* spp. (N=2,165)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	1,807	24.6	3.0	72.4
Ceftazidime	CAZ	1,900	21.7	8.9	69.4
Cefepime	FEP	1,677	22.1	2.1	75.8
Imipenem	IPM	1,785	21.3	0.2	78.4
Meropenem	MEM	1,863	21.6	0.4	77.9
Gentamicin	GEN	1,911	19.4	1.8	78.8
Tobramycin	TOB	819	23.3	1.0	75.7
Amikacin	AMK	511	3.5	0.6	95.9
Ciprofloxacin	CIP	1,868	24.4	3.3	72.4
Trimethoprim/Sulfamethoxazole	SXT	1,860	17.0	0	83.0
Minocycline	MNO	601	11.3	8.8	79.9
Tetracycline	TCY	188	28.2	1.1	70.7
Multidrug-resistance (≥3 classes NS)[a]	MDR	1,929	23.3	–	–
Extensive drug resistance (possible)	XDR	1,929	20.4	–	–
Pan-drug resistance (possible)	PDR	1,929	7.6	–	–

[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., 2012).
[d] Includes duplicate isolates.

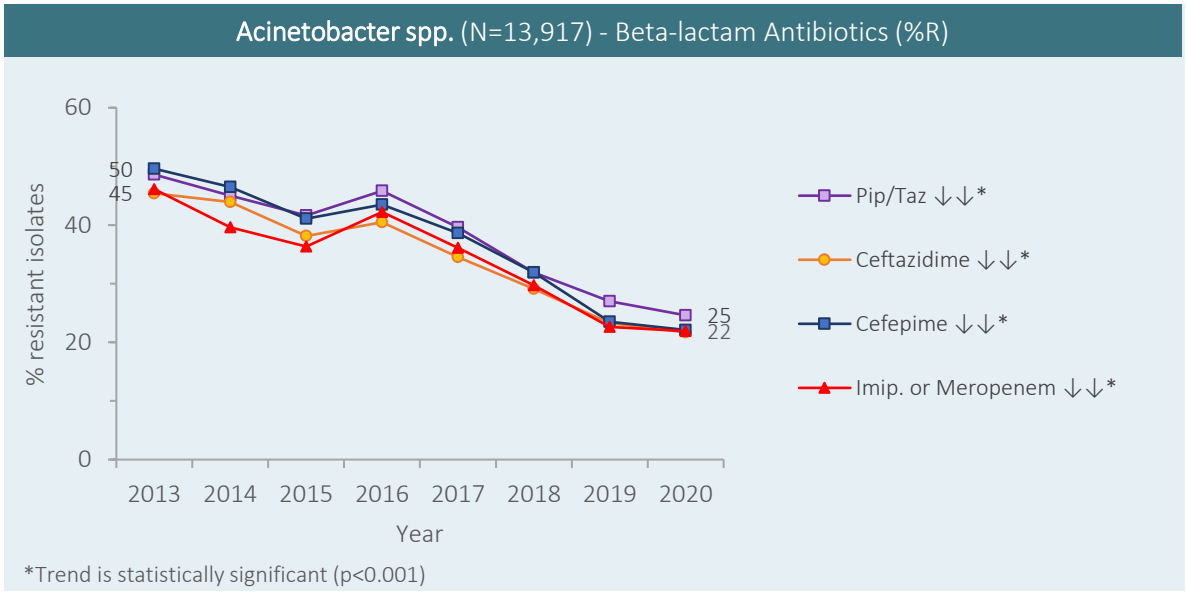
Figure 4.4.5.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Acinetobacter* spp., isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Acinetobacter* spp. ranged from 4 %R for amikacin (aminoglycosides) to 28 %R for tetracycline.
- Prevalence of multidrug resistance (%MDR/XDR/PDR[10]) in *Acinetobacter* spp. was 23.3 %, 20.4%, and 7.6%, respectively.

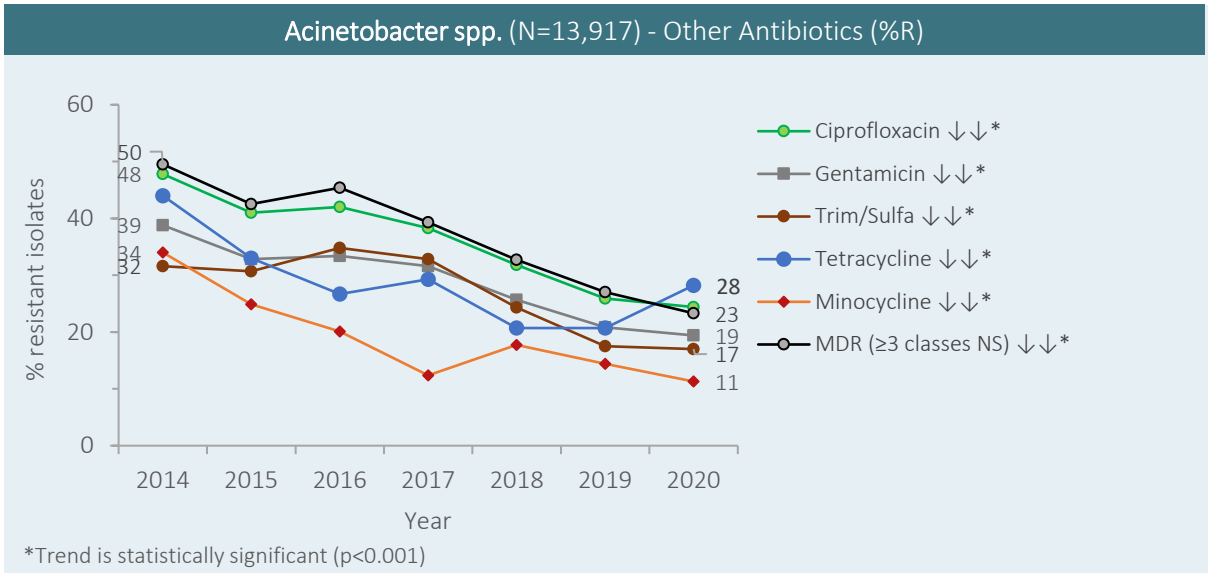
[10] Possible XDR, possible PDR

Figure 4.4.5.2 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., United Arab Emirates, 2013-2020 – Beta-lactam antibiotics



- *Acinetobacter* spp. shows decreasing trends of resistance for all beta-lactam antibiotics, including
  - Broad-spectrum penicillins (piperacillin-tazobactam ↓↓),
  - Third-generation (ceftazidime ↓↓), and fourth-gen. (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, 2014-2020 – Other Antibiotics



- *Acinetobacter* spp. shows decreasing trends of resistance for
  - Aminoglycosides (gentamicin ↓↓),
  - Fluoroquinolones (ciprofloxacin ↓↓),
  - Trimethoprim/sulfamethoxazole ↓↓,
  - Minocycline ↓↓, and
  - Tetracycline ↓↓.
- Multidrug resistance (%MDR) decreased from 50% (2014) to 23% (2020).

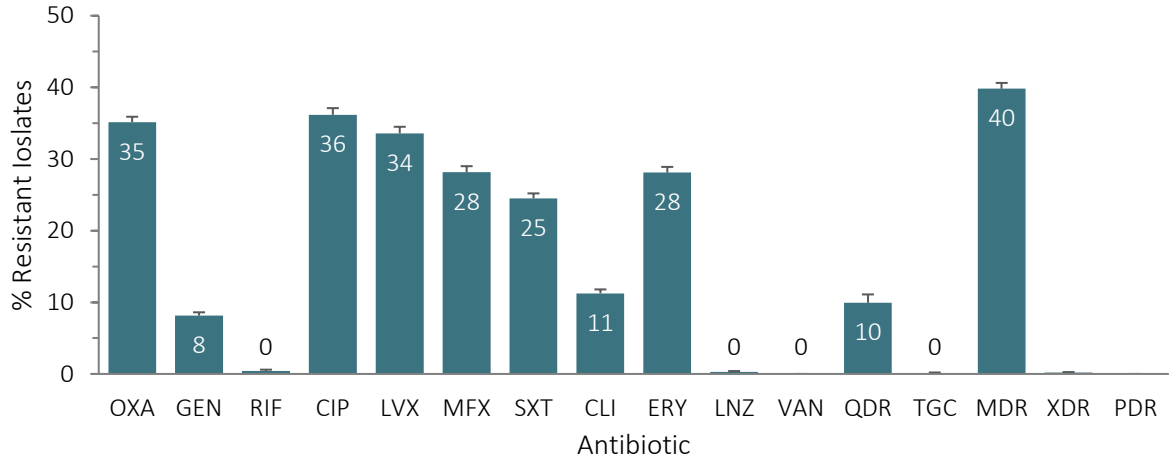
4.4.6 Staphylococcus aureus

Table 4.4.6.1 Percentages of resistant, intermediate, and susceptible isolates for *Staphylococcus aureus*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Staphylococcus aureus* (n=16,514)			
		Isolates (N)	% R	% I	% S
Oxacillin	OXA	14,076	35.1[a]	–	64.9[a]
Gentamicin	GEN	14,027	8.1	1.5	90.3
Rifampicin	RIF	12,071	0.4	0	99.5
Ciprofloxacin	CIP	9,529	36.2	1.0	62.8
Levofloxacin	LVX	9,996	33.6	1.8	64.6
Moxifloxacin	MFX	12,219	28.2	4.9	67.0
Trimethoprim/sulfamethoxazole	SXT	13,617	24.4	0	75.6
Clindamycin	CLI	13,872	11.2	0.2	88.6
Erythromycin	ERY	13,873	27.7	1.4	70.9
Linezolid	LNZ	13,349	0.3	0	99.7
Vancomycin	VAN	13,680	0	0	100.0
Quinupristin/Dalfopristin	QDA	2,924	9.9	0.1	90.0
Tigecycline	TGC	11,290	0.1	0	99.9
Multidrug-resistance (≥3 classes NS)[c]	MDR	14,131	39.8	–	–
Extensive drug resistance (possible)	XDR	14,131	0.2	–	–
Pan-drug resistance (possible)	PDR	14,131	0	–	–

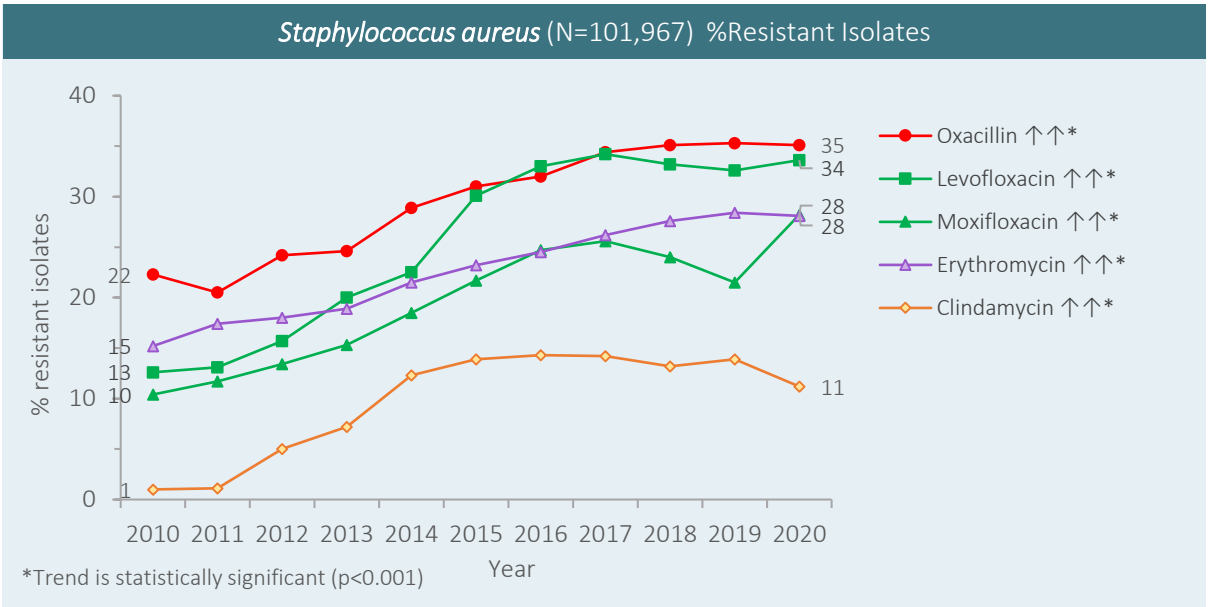
[a] MRSA/MSSA is calculated as resistance/susceptibility to oxacillin: %MRSA = 35.1% and %MSSA = 64.9.
[b] Tigecycline: EUCAST breakpoints (S≤0.5, R>0.5)
[c] Multidrug resistance (MDR) was defined as isolate being either a MRSA or having acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

Figure 4.4.6.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Staphylococcus aureus,* isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Staphylococcus aureus* ranged from 0% for rifampin, linezolid, vancomycin, and tigecycline, to 36% for ciprofloxacin.
- Percentage MRSA was 35% for all isolates (41% for blood culture isolates).
- Percentage MRSA was 31% for outpatients, 40% for inpatients (non-ICU), and 41% for ICU patients.
- Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *S. aureus* was 39.8%, 0.2%, and 0%, respectively.

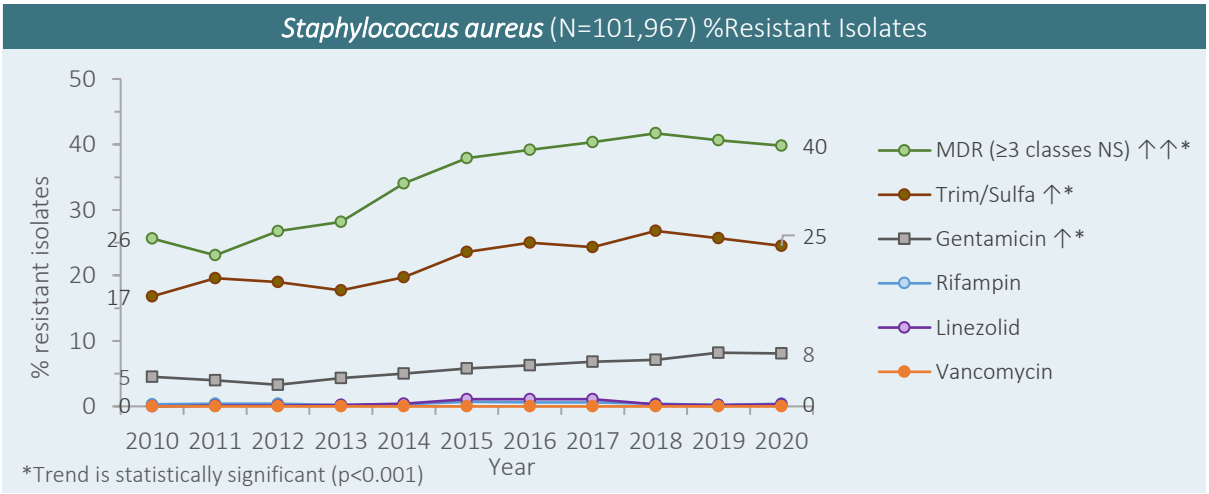
Figure 4.4.6.2 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, United Arab Emirates, 2010-2020 – Beta-lactams, fluoroquinolones, macrolides and lincosamides



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

- Beta-lactam antibiotics: %MRSA (↑↑) increased from 22% (2010) to 35% (2020).
- Fluoroquinolones: resistance to levofloxacin (↑↑) and moxifloxacin (↑↑) increased from 13%/10% (2010) to 34%/28% (2019), respectively.
- Macrolides: resistance to erythromycin (↑↑) increased from 15% (2010) to 28% (2020).
- Lincosamides: resistance to clindamycin (↑↑) increased from 1% (2010) to 11 % (2020).

Figure 4.4.6.3 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, United Arab Emirates, 2010-2020 – Other Antibiotics



Staphylococcus aureus shows increasing trends of resistance for:

- Trimethoprim/sulfamethoxazole (↑↑): resistance increased from 17% (2010) to 25% (2020).
- Aminoglycosides (gentamicin ↑): resistance increased from 5 % (2010) to 8% (2020).
- Resistance to rifampin and linezolid remains very low (< 1%).
- Confirmed resistance to glycopeptides (vancomycin, teicoplanin) was not observed.
- Multidrug resistance (MDR) increased from 26 %MDR (2010) to 40 %MDR (2020).

Figure 4.4.6.4 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 – By age category and age group (years)

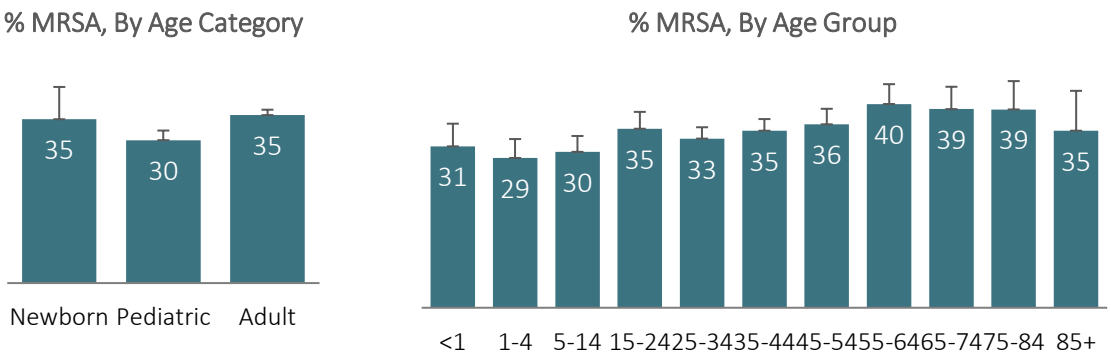


Figure 4.4.6.5 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 – By gender and nationality status

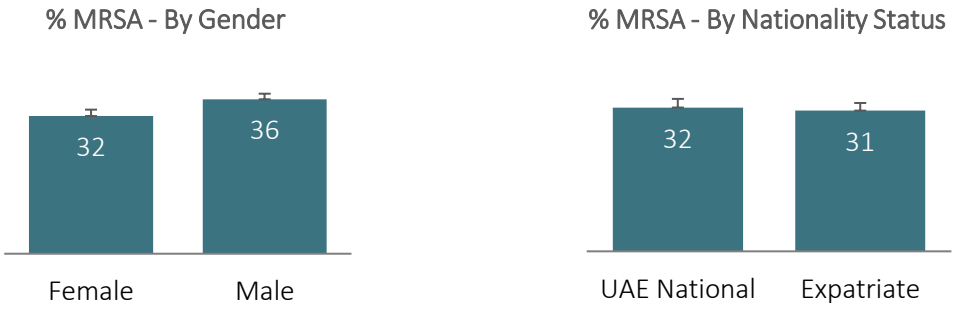


Figure 4.4.6.6 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 – By patient nationality

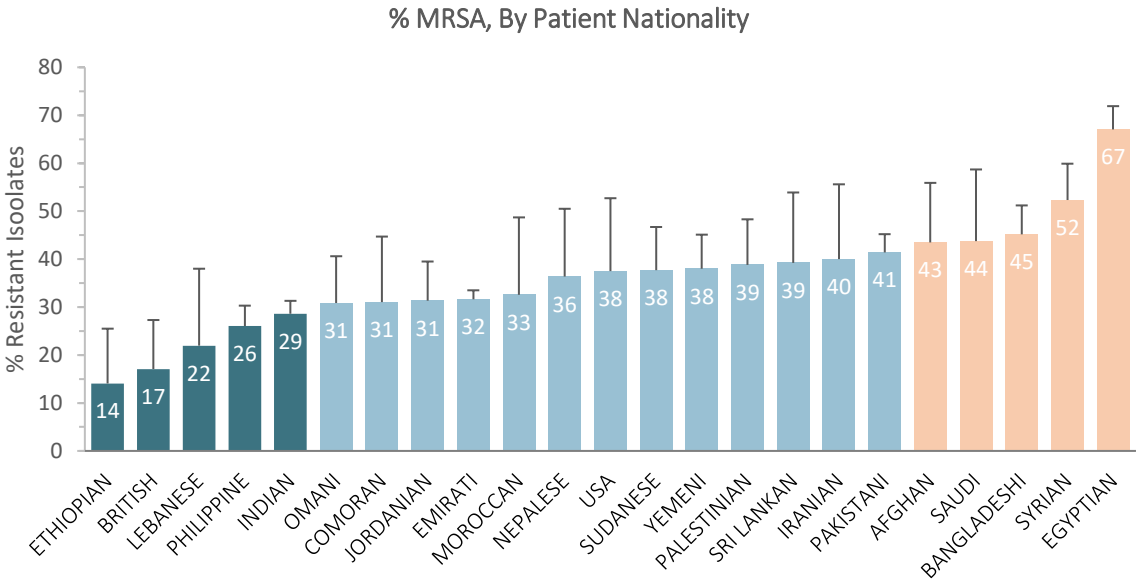


Figure 4.4.6.7 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 –By Emirate

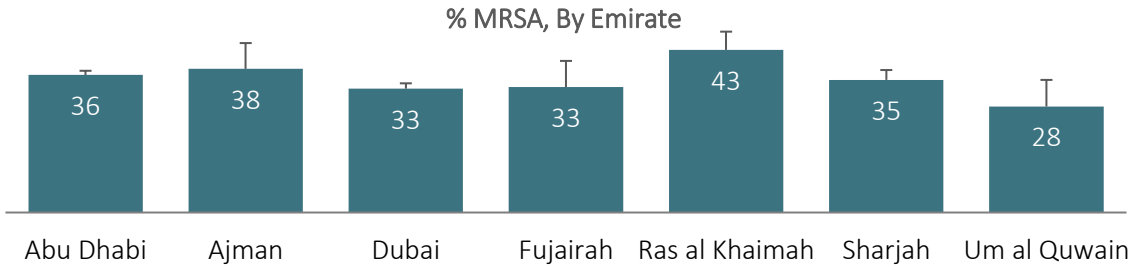


Figure 4.4.6.8 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 –By isolate source and patient location type

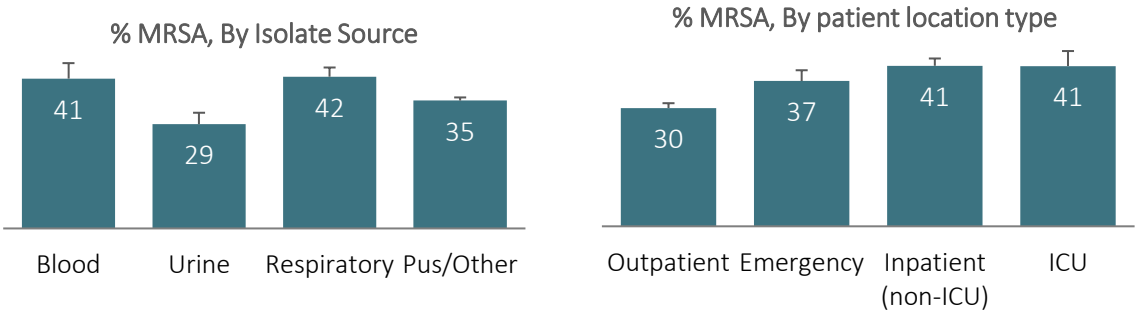


Figure 4.4.6.9 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, United Arab Emirates, 2020 –By clinical specialty/department

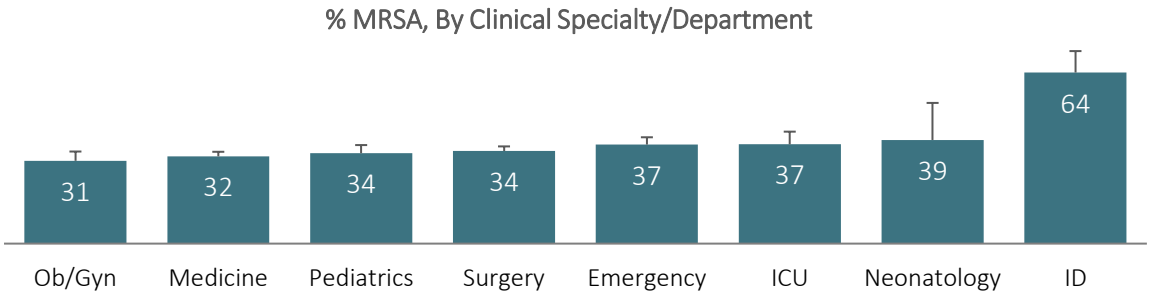
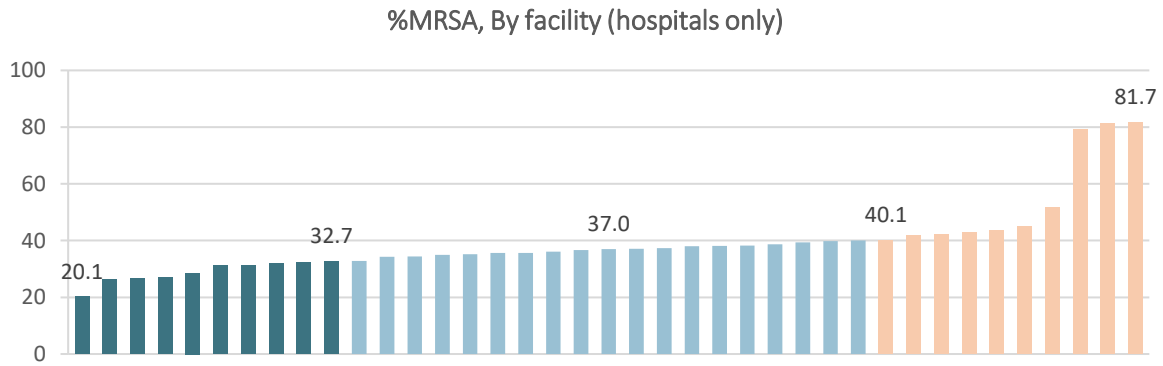


Figure 4.4.6.10 Percentage of isolates resistant to oxacillin (%MRSA) for Staphylococcus aureus, United Arab Emirates, 2020 – By facility (hospitals only)



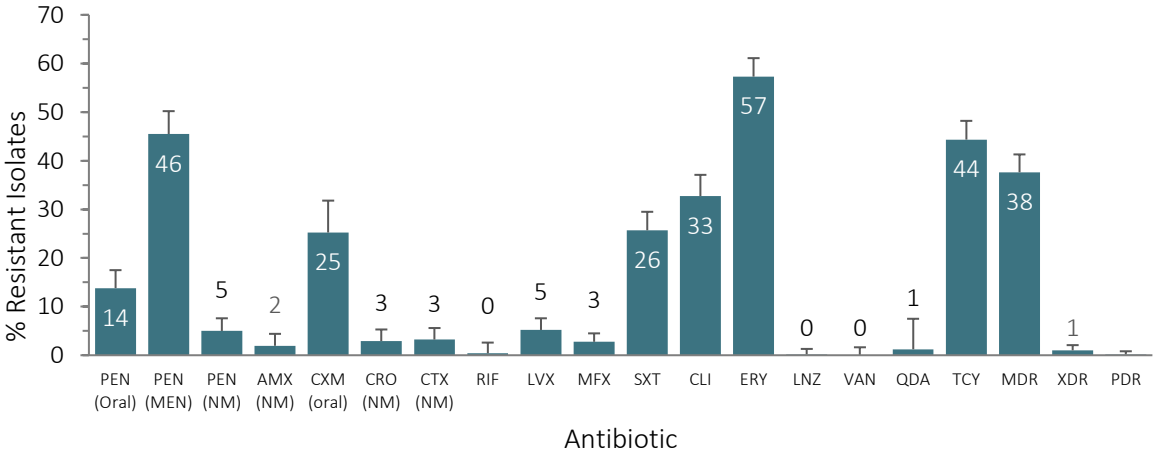
4.4.7 Streptococcus pneumoniae

Table 4.4.7.1 Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Streptococcus pneumoniae* (N=969)			
		Isolates (N)	% R	% I	% S
Penicillin G (oral breakpoints)	PEN (oral)	442	13.8	31.9	54.3
Penicillin G (non-meningitis breakpoints)	PEN (NM)	442	5.0	2.0	93.0
Penicillin G (meningitis breakpoints)	PEN (MEN)	442	45.5	0.2	54.3
Amoxicillin (non-meningitis breakpoints)	AMX (NM)	308	1.9	3.9	94.2
Cefuroxime (oral breakpoints)	CXM (oral)	210	25.2	1.9	72.9
Cefotaxime (non-meningitis breakpoints)	CTX (NM)	403	3.2	1.7	95.0
Ceftriaxone (non-meningitis breakpoints)	CRO (NM)	378	2.9	1.3	95.8
Rifampin	RIF	250	0.4	0	99.6
Levofloxacin	LVX	519	5.2	1.2	93.6
Moxifloxacin	MFX	615	2.8	1.8	95.4
Trimethoprim/Sulfamethoxazole	SXT	576	25.7	13.5	60.7
Clindamycin	CLI	489	32.7	2.0	65.2
Erythromycin	ERY	665	57.3	0.2	42.6
Linezolid	LNZ	611	0.2	0	99.7
Vancomycin	VAN	607	0.2	0	99.3
Quinupristin/Dalfopristin	QDA	82	1.2	1.2	97.6
Tetracycline	TCY	654	44.3	1.1	54.6
Multidrug-resistance (≥3 classes NS)[a]	MDR	691	37.6	–	–
Extensive drug resistance (possible)	XDR	691	1.0	–	–
Pan-drug resistance (possible)	PDR	691	0.1	–	–

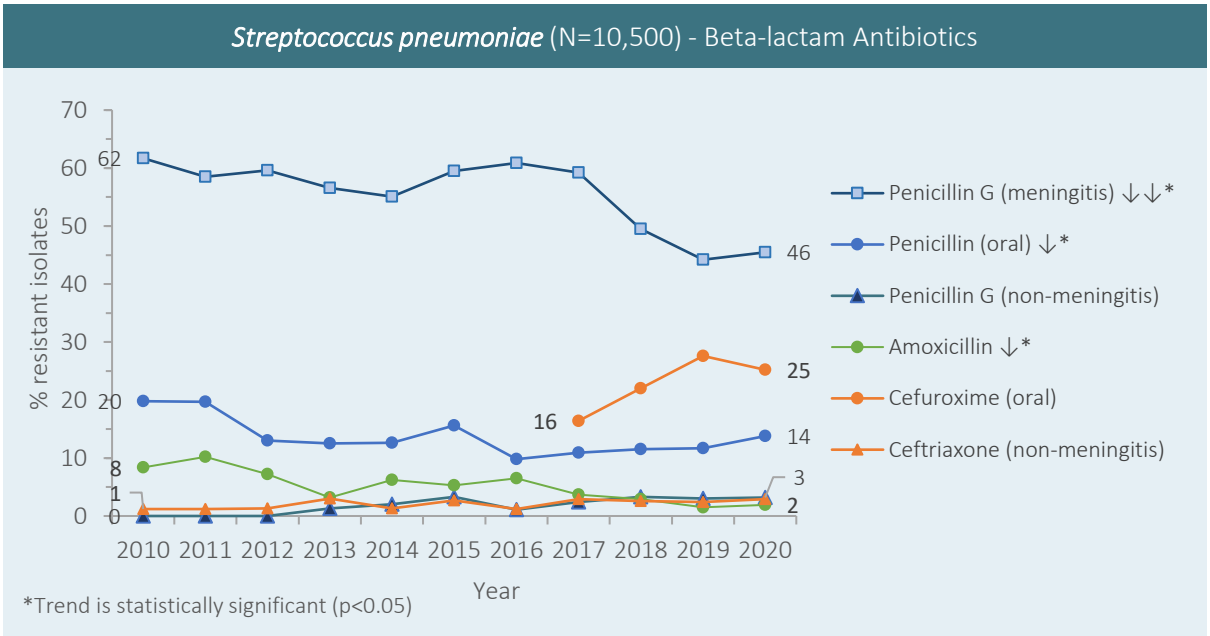
[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes.

Figure 4.4.7.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Streptococcus pneumoniae,* isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Streptococcus pneumoniae* ranged from 0% for rifampin, linezolid, and vancomycin, to 57% for erythromycin.
- Prevalence of multidrug resistance (%MDR/XDR/PDR) in *S. pneumoniae* was 37.6%, 1.0%, and 0%, respectively.
- Prevalence of the different pneumococcal serotypes in the UAE is currently unknown (no routine testing of serotypes in participating facilities, no reference lab).

Figure 4.4.7.2 Annual trends for percentage of isolates resistant (%R) for *Streptococcus pneumoniae*, United Arab Emirates, 2010-2020 – Beta-lactam Antibiotics

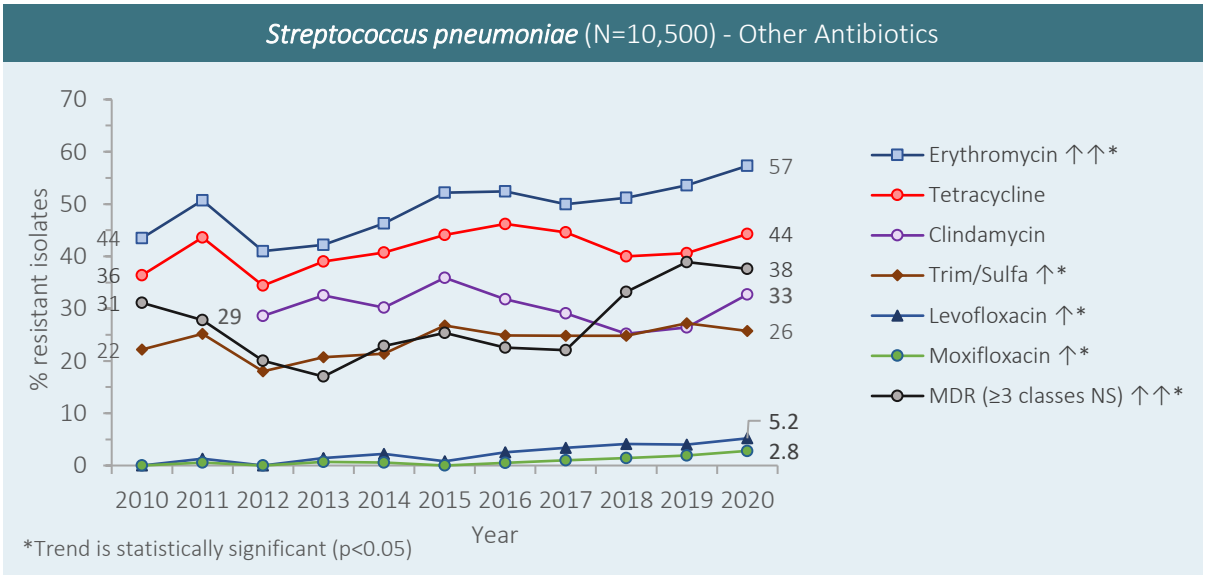


For beta-lactam antibiotics, *Streptococcus pneumoniae* shows no statistically significant increasing trends of resistance.

Antibiotic resistance decreased for:

- Penicillin G (↓, oral breakpoints): from 20 %R (2010) to 14 %R (2020) (p<0.05)
- Penicillin G (↓↓, meningitis breakpoints): from 62 %R (2010) to 46 %R (2020) (p<0.001).
- Amoxicillin (↓, non-meningitis breakpoints): from 8 %R (2010) to 2 %R (2020) (p<0.001).

Figure 4.4.7.3 Annual trends for percentage of isolates resistant (%R) for *Streptococcus pneumoniae*, United Arab Emirates, 2010-2020 – Other Antibiotics



For non-beta-lactam antibiotics, *Streptococcus pneumoniae* shows increasing trends of resistance for

- Macrolides: resistance to erythromycin (↑↑) increased from 44 % (2010) to 57 % (2020).
- Trimethoprim/sulfamethoxazole (↑): resistance increased from 22 % (2010) to 26 % (2020).
- Fluoroquinolones (↑): resistance increased from 0 %R (2010) to 5.2 %R, and 2.8 %R (2020) for levofloxacin and moxifloxacin, respectively.

Multidrug resistance (MDR) increased from 31 %MDR (2010) to 37 %MDR (2020).

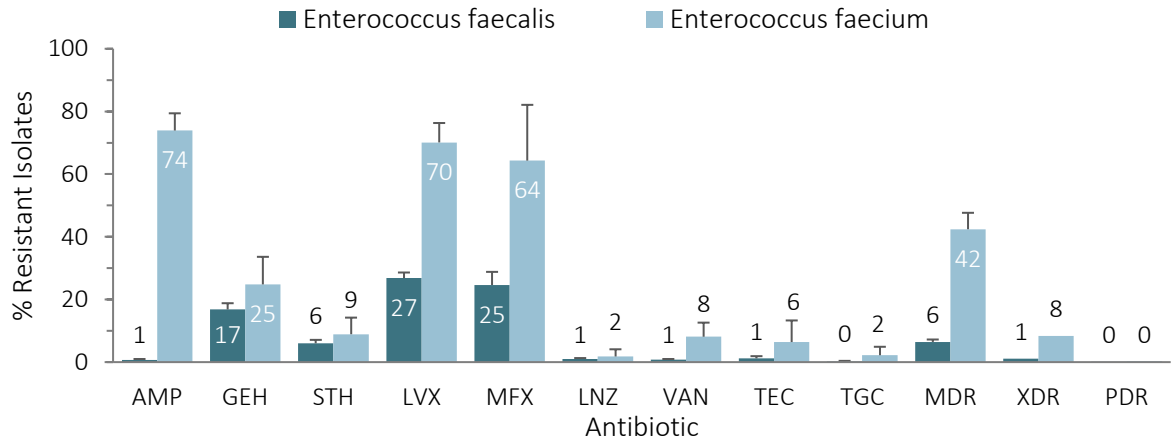
4.4.8 Enterococcus faecalis and Enterococcus faecium

Table 4.4.8.1 Percentages of resistant, intermediate, and susceptible isolates for *Enterococcus faecalis* and *Enterococcus faecium*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*Enterococcus faecalis* (N=4,893)				*Enterococcus faecium* (N=512)			
		N	% R	% I	% S	N	% R	% I	% S
Ampicillin	AMP	4,213	0.7	0	99.3	349	73.9	0	26.1
Gentamicin (high level)	GEH	1,635	16.8	0	83.2	121	24.8	0	75.2
Streptomycin (high level)	STH	2,321	6.0	0	94.0	214	8.9	0	91.1
Levofloxacin	LVX	2,813	26.8	2.4	70.8	234	70.1	6.0	23.9
Moxifloxacin	MFX	532	24.6	7.9	67.5	28	64.3[a]	3.6[a]	32.1[a]
Linezolid	LNZ	3,832	1.0	4.8	94.2	341	1.8	3.5	94.7
Vancomycin	VAN	4,008	**0.8**[b]	0.1	99.1	346	**8.1**[b]	1.2	90.8
Teicoplanin	TEC	1,850	1.2	0.1	98.7	171	6.4	0	93.6
Tigecycline[c]	TGC	3,294	0.2	0	99.8	275	2.2	0	97.8
Multidrug-resistance (≥3)[d]	MDR	4,210	6.4	–	–	349	42.4	–	–
Extensive drug resistance	XDR	4,210	1.1	–	–	349	8.3	–	–
Pan-drug resistance	PDR	4,210	0	–	–	349	0.3	–	–

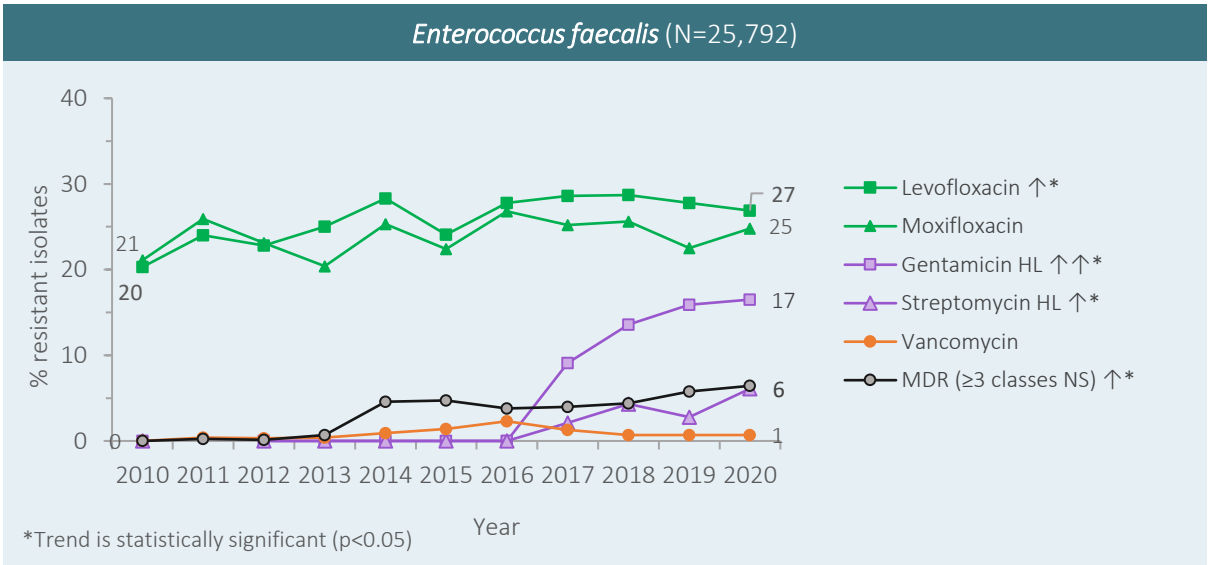
[a] A small number of isolates were tested (N<30): percentage resistance should be interpreted with caution.
[b] %VRE for *Enterococcus* spp. = 1.5%.
[c] Tigecycline: EUCAST breakpoints (S≤0.25, R>0.25).
[d] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

Figure 4.4.8.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Enterococcus faecalis* and *Enterococcus faecium*, isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Enterococcus faecalis* ranged from 0%-1% for tigecycline, aminopenicillins (ampicillin), oxazolidinones (linezolid), and glycopeptides (vancomycin, teicoplanin), to 25-27% for fluoroquinolones (levofloxacin, moxifloxacin).
- For *Enterococcus faecium*, resistance ranged from 2% for oxazolidinones (linezolid) and tigecycline, to 65-71% for fluoroquinolones (moxifloxacin, levofloxacin) and 75 %R for aminopenicillins (ampicillin).
- Vancomycin-resistant Enterococci (VRE) were observed in 0.7 % of *E. faecalis*, and 8.9 % of *E. faecium* isolates, respectively, and in 1.3 % of all *Enterococcus* spp. isolates (combined).
- Prevalence of multidrug-resistance (%MDR/possible XDR/possible PDR) was 6.4%, 1.1%, and 0% for *E. faecalis*, and 42.4%, 8.3%, and 0.3% for *E. faecium*, respectively.

Figure 4.4.8.2 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecalis*, United Arab Emirates, 2010-2020

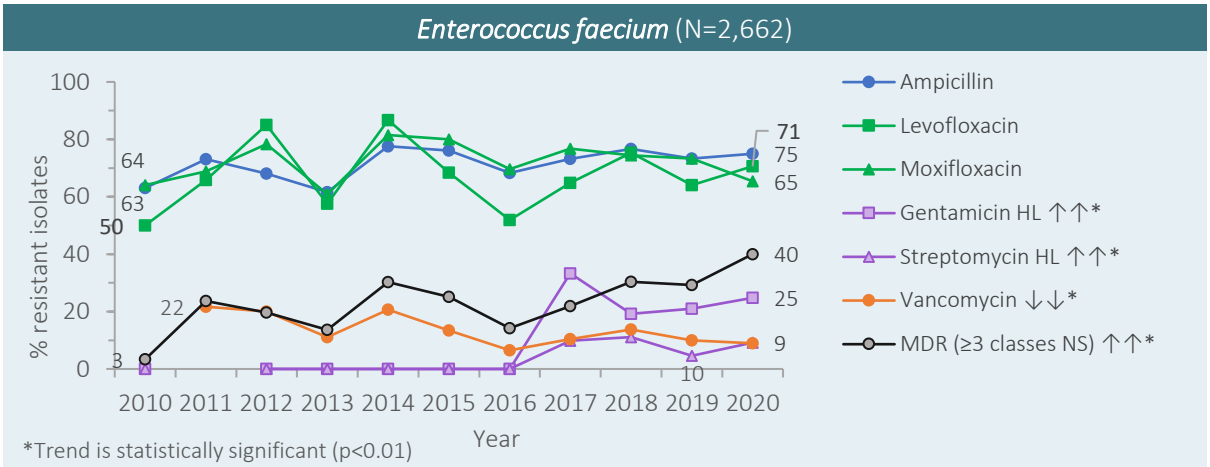


Enterococcus faecalis shows an increasing trend of resistance for

- Fluoroquinolones: resistance to levofloxacin (↑) increased from 20% (2010) to 27% (2020).
- Aminoglycosides: resistance to gentamicin-HL (↑ ↑, high level) increased since 2016 from 0% to 17 %R in 2020. Resistance to streptomycin-HL also increased since 2016 from 0 % to 6 % (2020).

Multidrug resistance (MDR) increased from 0 %MDR (2010) to 6.4 %MDR (2020).
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, 2010-2020



Enterococcus faecium shows a decreasing trend of resistance for glycopeptides (vancomycin):

- Resistance to vancomycin (%VRE) decreased (↓↓) from 22 %VRE (2011) to 8.9 %VRE (2020).

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.

Resistance of *E. faecium* to gentamicin-HL and streptomycin-HL was not observed in the period 2010-2016, however, starting in 2017, both antibiotics show an increasing trend of resistance, currently at 24.8 %R for gentamicin (high level), and 9.2 %R for streptomycin (high level).

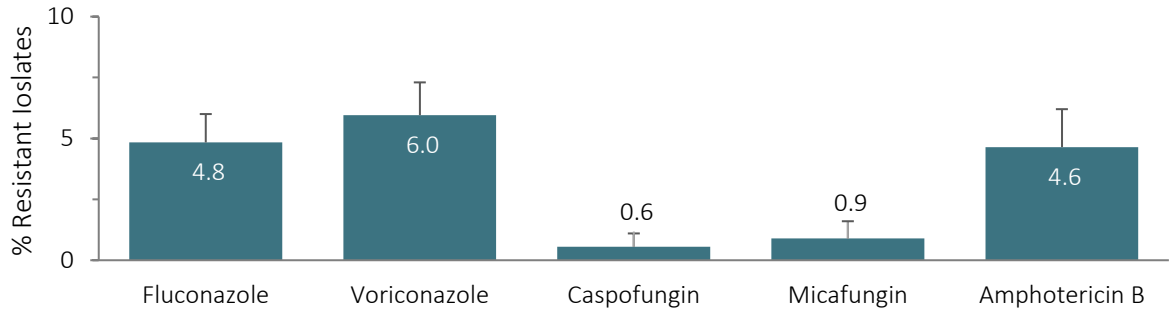
Multidrug resistance (%MDR) increased (↑↑) from 3.3 %MDR (2010) to 40.0 %MDR (2020).

4.4.9 Candida spp.

Table 4.4.9.1 Percentages of resistant, intermediate, and susceptible isolates for *Candida albicans*, isolates from all sources, United Arab Emirates, 2020

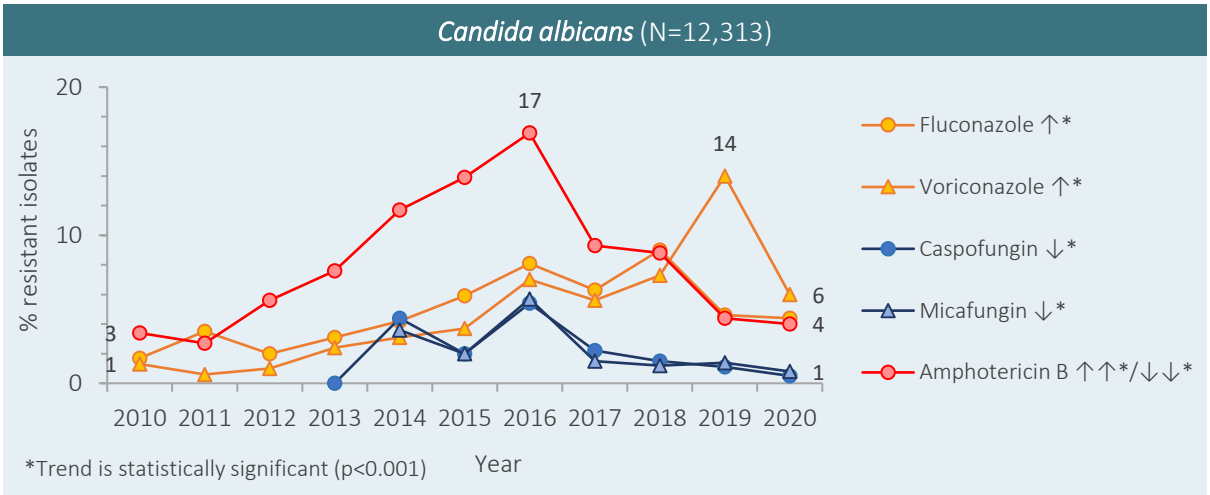
Antibiotic	Code	*Candida albicans* (N=1,615)			
		Isolates (N)	% R	% I	% S
Fluconazole	FLU	1,593	4.8	1.6	93.6
Voriconazole	VOR	1,579	6.0	3.6	90.4
Caspofungin	CAS	1,454	0.6	0.1	99.4
Micafungin	MIC	1,455	0.9	0.1	99.0
Amphotericin B	AMB	1,034	4.6	-	95.4

Figure 4.4.9.1 Percentages of resistant (%R) isolates for *Candida albicans*, isolates from all sources, United Arab Emirates, 2020



- For 2020, resistance in *Candida albicans* ranged from 0.6-0.9% for echinocandins (caspofungin, micafungin) to 5-6% for azoles (fluconazole, voriconazole) and amphotericin B.

Figure 4.4.9.2 Annual trends for percentage of isolates resistant (%R) for *Candida albicans*, United Arab Emirates, 2010-2020



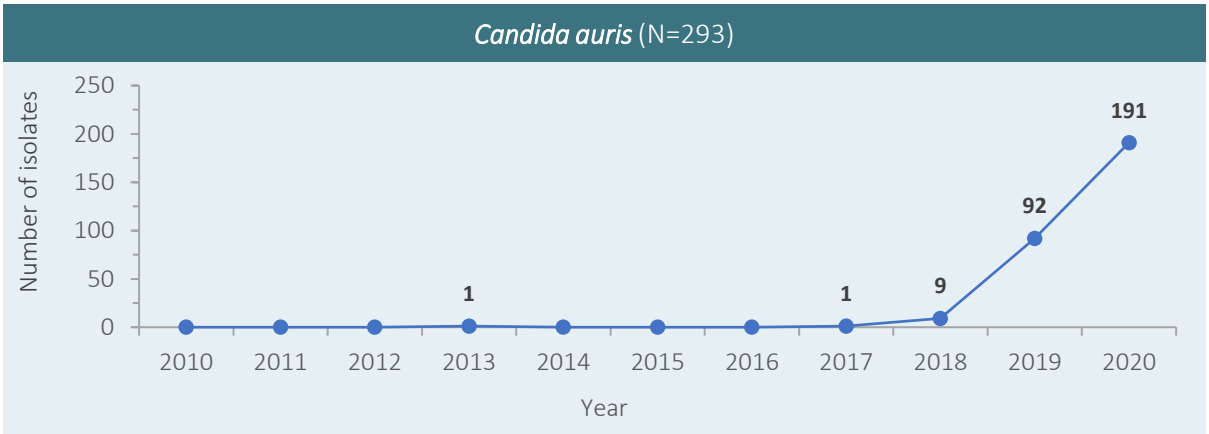
- Resistance of *C. albicans* to polyenes (amphotericin B) increased from 3 %R (2010) to 17 %R in 2016, and then decreased to 4.0 %R in 2020.
- Resistance of *C. albicans* to azoles is increasing: resistance to fluconazole increased from 1.7 % (2010) to 4.4 % (2020); resistance to voriconazole increased from 1.3 % (2010) to 6.0 % (2020).
- Resistance of *C. albicans* to echinocandins is decreasing. Resistance to caspofungin decreased from 4.4 %r (2014) to 0.5 %r (2020); resistance to micafungin decreased from 3.6 % (2014) to 0.8% (2020).

Table 4.4.9.2 Percentage of susceptible isolates for *Candida* spp. and other Yeasts, isolates from all sources, United Arab Emirates, 2020 (Cumulative antibiogram)

	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU[a]	VOR[b]	AMB [c]	CAS[d, e]	MIF[e]
***Candida* spp.**	4,531	100.0	81	74	–	86	92
Candida albicans	1,901	42.0	94	91	96	99	99
Candida spp. (non-albicans)	2,630	58.0	67	58	83	73	85
C. tropicalis	704	15.5	93	96	99	99	99
C. parapsilosis	465	10.3	78	81	96	99	98
C. glabrata[f]	315	7.0	3	–[g]	100	42	99
C. auris[h]	191	4.2	46	–	11	100	100
C. dubliniensis	55	1.2	100	98	100	–	–
C. haemulonii	32	0.7	–	–	–	–	–
C. duobushaemulonii	7	0.2	–	–	–	–	–
Other (C.non-albicans)	861	19.0	–	–	–	–	–
Other Yeasts							
Pichia kudriavzevii[i]	110		R	100	98	49	100
Clavispora lusitaniae[i]	96		–	–	–	–	–
Debaryomyces hansenii[i]	48		–	–	–	–	–
Meyerozyma guilliermondiii[i]	36		–	–	–	–	–
Trichomonascus ciferrii[i]	23		–	–	–	–	–

[a]FLU=Fluconazole [b]VOR=Voriconazole [c]AMB=Amphotericin B. EUCAST breakpoints (S≤1, R>1) are used for amphotericin B for *C. albicans, C. glabrata, C. krusei, C. parapsilosis*, and *C. tropicalis* (EUCAST, 2022). Note: some automated systems overcall amphotericin resistance for *Candida* species [d]CAS=Caspofungin. Note: caspofungin susceptibility testing *in vitro* has been associated with significant inter-laboratory variability. [e]MIF=Micafungin. Note: micafungin is a better surrogate than caspofungin for echinocandin susceptibility [f]New name: *Nakaseomyces glabrataa* (Borman & Johnson, 2021) [g]For *C. glabrata* and voriconazole, current data are insufficient to demonstrate a correlation between in vitro susceptibility testing and clinical outcome [h]CDC tentative breakpoints for *Candida auris* (CDC C. auris, 2020) [i]*Pichia kudriavzevii*: formerly known as *Candida krusei*; *Clavispora lusitaniae*: formerly known as *Candida lusitaniae*; *Debaryomyces hansenii*: formerly known as *Candida famata; Meyerozyma guilliermondii*: formerly known as *Candida guilliermondii; Trichomonascus ciferrii*: formerly known as *Candida ciferrii* (Borman & Johnson, 2021).

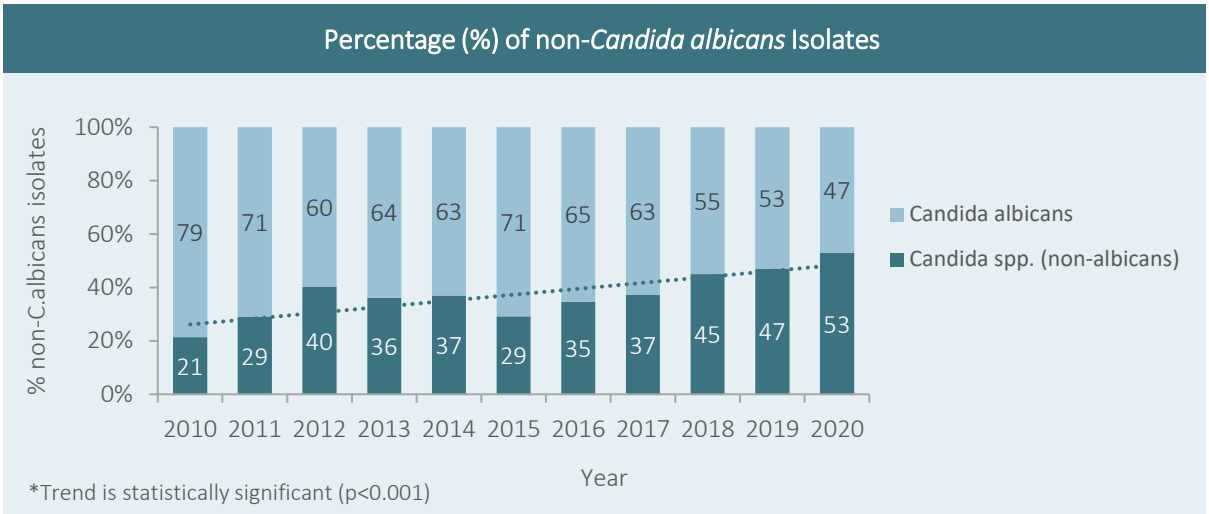
Figure 4.4.9.3 *Candida auris*: Number of isolates reported, by year



Candida auris is a new, emerging, often multidrug-resistant yeast:

- The number of reported isolates of *Candida auris* increased between 2016 and 2020 from n=0 to n=191
- During the same time period, the percentage of *Candida auris* among all non-*C. albicans* species increased from 0% to now 4.2 % (2020).

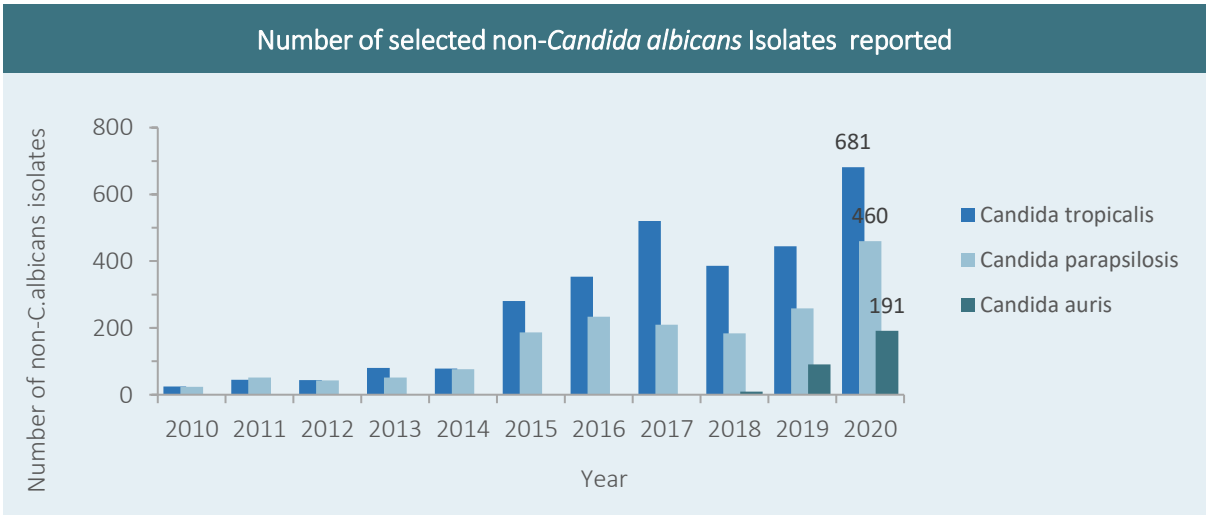
Figure 4.4.9.4 Annual trend for percentage of *Candida* (non-albicans) isolates, among all *Candida* isolates (C*andida* spp.), United Arab Emirates, 2010-2020



During the observation period (2010-2020), a statistically highly significant shift, from *Candida albicans* to non-*C. albicans* species is observed:

- In 2010, *C. albicans* accounted for 79% of all *Candida* spp. isolates, whereas in 2020 it was only 47%.
- The proportion of non-*Candida albicans* species among all *Candida* spp. accordingly increased from 21.4% (2010) to now 53.8% (2020).

Figure 4.4.9.5 Annual trend for number of selected non-albicans *Candida* spp., United Arab Emirates, 2010-2020



The observed increase over time of non-albicans *Candida* species is mostly due to an increase in the number of reported isolates of the following three non-albicans *Candida* species (see Figure 4.4.9.):

- *Candida tropicalis*
- *Candida parapsilosis*
- *Candida auris* (newly emerging multidrug-resistant yeast, since 2017)

4.4.10 Mycobacterium tuberculosis

Table 4.4.10.1 Percentages of resistant, intermediate, and susceptible isolates for *Mycobacterium tuberculosis*, isolates from all sources, United Arab Emirates, 2020

Antibiotic	Code	*M. tuberculosis* (N=792)			
		Isolates (N)	% R	% I	% S
Rifampin	RIF	791	3.3	0	96.7
Ethambutol	EMB	791	1.3	0.3	98.5
Isoniazid	INH	791	11.1	1.4	87.5
Pyrazinamide	PZH	789	3.0	0	97.0
Streptomycin	STM	481	6.4	0	93.6
Multidrug-resistance (INH+RIF)	MDR	791	3.2	–	–
Extensive drug resistance	XDR	791	3.2	–	–
Pan-drug resistance	PDR	791	0.4	–	–

Figure 4.4.10.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Mycobacterium tuberculosis*, isolates from all sources, United Arab Emirates, 2020

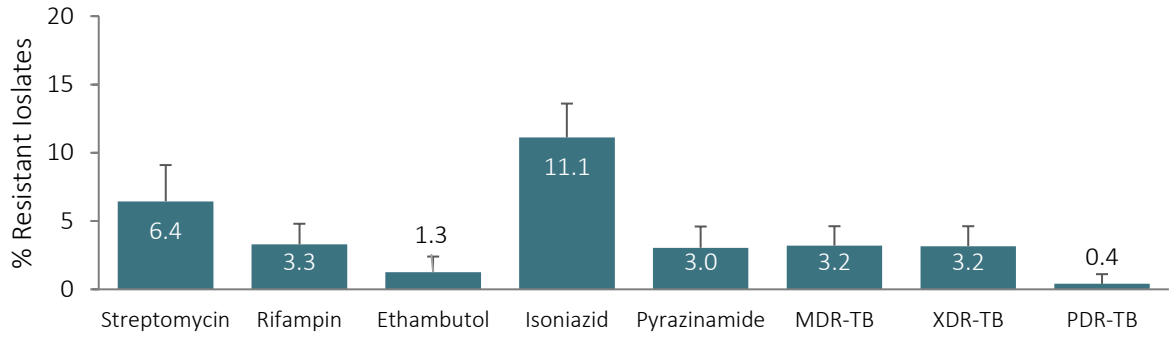
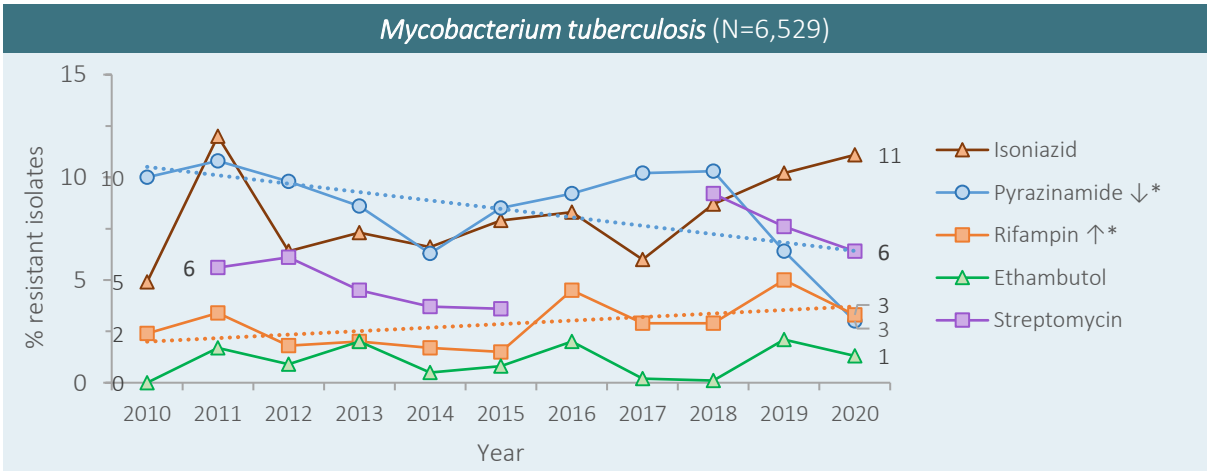
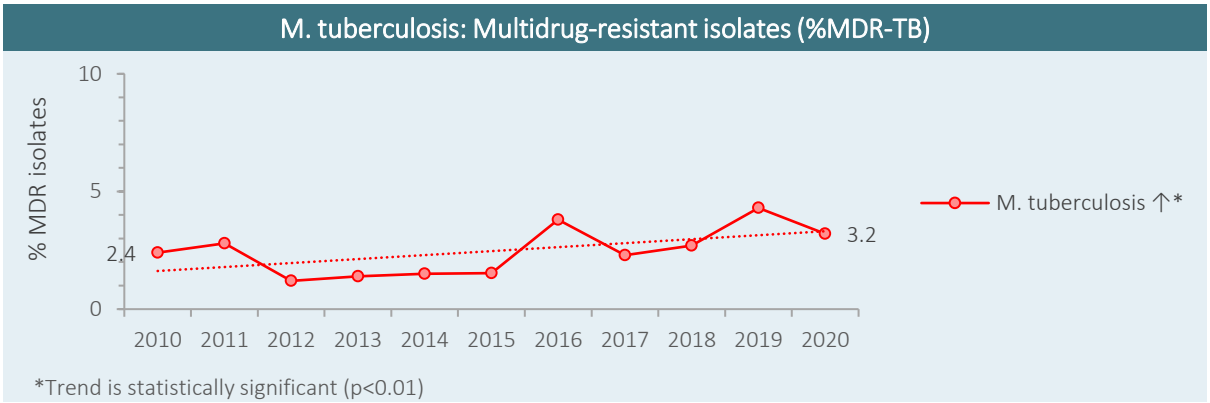


Figure 4.4.10.2 Annual Trends for percentage of isolates resistant (%R) for *Mycobacterium tuberculosis*, United Arab Emirates, 2010-2020



- In 2020, resistance of *M. tuberculosis* to first-line antibiotics ranged from 1% for ethambutol to 11% for isoniazid.
- Rifampin showed a slightly increasing trend of resistance, from 2.4 %R (2010) to 3.4 %R (2020).
- Pyrazinamide showed a decreasing resistance trend, from 10.0% (2010) to 3.0 % (2020)
- Susceptibility data for second-line antibiotics is not available as it is not tested (Abu Dhabi), or not routinely tested (Dubai).

Figure 4.4.10.3 Annual trend for percentage of isolates multidrug-resistant[a] (%MDR-TB) for *Mycobacterium tuberculosis*, United Arab Emirates, 2010-2020



[a]Multidrug-resistant TB (MDR-TB) was defined as full resistance to both, isoniazid and rifampin.

- For 2020, prevalence of multidrug resistance (%MDR-TB/XDR-TB/PDR-TB) in *Mycobacterium tuberculosis* was 3.2%, 3.2%, and 0.4%, respectively.
- Between 2010 and 2020, multidrug-resistance in *Mycobacterium tuberculosis* increased from 2.4 % MDR-TB (2010) to 3.2. %MDR-TB (2020).

Table 4.4.10.2 Percentage of susceptible isolates for *Mycobacterium tuberculosis*, isolates from all sources, United Arab Emirates, 2020, By Emirate

	Isolates (N)	Rifampin (%S)	Ethambutol (%S)	Isoniazid (%S)	Pyrazinamide (%S)	Streptomycin (%S)
UAE	792	97	99	88	97	94
Abu Dhabi	447	97	98	88	96	94 [a]
Dubai	345	97	99	87	98	93

[a] n=137 isolates only were tested for streptomycin.

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 (WHO, 2014) and the annual report of the EARS-Net published by the ECDC in 2015 (ECDC, 2015).

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 (Majowicz, et al., 2010).

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) (Albrecht, Jatzwauck, Slickers, Ehricht, & Monecke, 2011). 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 (Sonnevend, et al., 2012).

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 (O'Brien, et al., 2009).

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
IZD	Inhibition zone diameter (mm)
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
RAK	Ras Al Khaimah
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
UAQ	Umm al Quwain
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
ATM	Aztreonam
AZM	Azithromycin
CAS	Caspofungin
CAZ	Ceftazidime
CIP	Ciprofloxacin
CLI	Clindamycin
CLR	Clarithromycin
CRO	Ceftriaxone
CTX	Cefotaxime
CXM	Cefuroxime
CZO	Cefazolin
DAP	Daptomycin
ERY	Erythromycin
ETH	Ethambutol
ETP	Ertapenem
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
MEM	Meropenem
MFX	Moxifloxacin
MIF	Micafungin
MNO	Minocycline
MUP	Mupirocin
NIT	Nitrofurantoin
NOR	Norfloxacin
OXA	Oxacillin
PEN	Penicillin G
PTH	Protionamide
PZA	Pyrazinamide
QDA	Quinupristin/dalfopristin
RIF	Rifampin, rifampicin
SAM	Ampicillin/sulbactam
STH	Streptomycin (high level)
SXT	Trimethoprim/sulfamethoxazole
TCC	Ticarcillin/clavulanic acid
TCY	Tetracycline
TGC	Tigecycline
TEC	Teicoplanin
TOB	Tobramycin
TZP	Piperacillin/tazobactam
VAN	Vancomycin
VOR	Voriconazole

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Annex 5.5 AMR surveillance sites

Annex 5.5.1 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	Public
16	DAE	Danat Al Emarat Hospital	Abu Dhabi	Private
17	EIH	Emirates International Hospital Al Ain	Abu Dhabi	Private
18	AKH	Ain Al Khaleej Hospital Al Ain	Abu Dhabi	Private
19	MAN	Mediclinic Al Noor Hospital Abu Dhabi	Abu Dhabi	Private
20	MAR	Mediclinic Al Noor Hospital Airport Road	Abu Dhabi	Private
21	MAA	Mediclinic Al Ain Hospital	Abu Dhabi	Private
22	MAJ	Mediclinic Al Jowhara Hospital	Abu Dhabi	Private
23	BAD	VPS Burjeel Hospital Abu Dhabi	Abu Dhabi	Private
24	BRH	VPS Burjeel Royal Hospital Al Ain	Abu Dhabi	Private
25	LCB	VPS Lifecare Hospital Baniyas	Abu Dhabi	Private
26	LCM	VPS Lifecare Hospital Mussafah	Abu Dhabi	Private
27	LAD	VPS LLH Hospital Abu Dhabi	Abu Dhabi	Private
28	LMU	VPS LLH Hospital Musaffah	Abu Dhabi	Private
29	MAD	VPS Medeor 24x7 Hospital Abu Dhabi	Abu Dhabi	Private
30	MIN	VPS Burjeel Farha Hospital Al Ain	Abu Dhabi	Private
31	NSA	NMC Specialty Hospital Abu Dhabi	Abu Dhabi	Private
32	NRY	NMC Royal Hospital Khalifa City A	Abu Dhabi	Private
33	BWH	NMC Royal Women's Hospital Abu Dhabi	Abu Dhabi	Private
34	NAA	NMC Specialty Hospital Al Ain	Abu Dhabi	Private
35	REM	Reem Hospital	Abu Dhabi	Private
36	BMC	VPS Burjeel Medical City	Abu Dhabi	Private
37	NAN	NMC Specialty Hospital Al Nahda	Dubai	Private
38	DIP	NMC Royal Hospital, DIP	Dubai	Private
39	BLUE	NMC Blue Hospital	Dubai	Private
40	DH	Dubai Hospital	Dubai	Public
41	RH	Rashid Hospital	Dubai	Public
42	LH	Latifa Hospital	Dubai	Public
43	HAT	Hatta Hospital	Dubai	Public
44	NHD	Neurospinal Hospital Dubai	Dubai	Private
45	IHD	Iranian Hospital	Dubai	Private
46	PHG	Prime Health Hospital	Dubai	Private
47	AZH	Al Zahra Hospital Dubai	Dubai	Private
48	AGH	Al Garhoud Hospital	Dubai	Private
49	SGH	Saudi German Hospital	Dubai	Private
50	ESH	Emirates Specialty Hospital	Dubai	Private
51	AHD	American Hospital Dubai	Dubai	Private
52	AKU	Al Kuwait Hospital (previously: Al Baraha Hospital)	Dubai	Public
53	AAM	Al Amal Psychiatric Hospital	Dubai	Public
54	BAS	Burjeel Hospital for Advanced Surgery	Dubai	Private

Annex 5.5.1 AMR Surveillance Sites – Hospitals (continued):

Nr.	Code	Hospital name	Emirate	Ownership
55	MDX	Medeor 24x7 Hospital Dubai	Dubai	Private
56	MCIT	Mediclinic City Hospital Dubai	Dubai	Private
57	MWEL	Mediclinic Welcare Hospital	Dubai	Private
58	MPAR	Mediclinic Parkview Hospital	Dubai	Private
59	MCOS	Cosmesurge Hospital Umm Suqeim	Dubai	Private
60	MIRD	Mirdif Private Hospital	Dubai	Private
61	CLEM	Clemenceau Medical Center Dubai	Dubai	Private
62	FAK	Fakeeh University Hospital	Dubai	Private
63	KING	King´s College London Hospital Dubai	Dubai	Private
64	ZULD	Zulekha Hospital Dubai	Dubai	Private
65	AQH	Al Qassimi Hospital	Sharjah	Public
66	AQW	Al Qassimi Women's and Children's Hospital	Sharjah	Public
67	AKI	Al Kuwaiti Hospital	Sharjah	Public
68	KFH	Khor Fakkan Hospital	Sharjah	Public
69	ADH	Al Dhaid Hospital	Sharjah	Public
70	UHS	University Hospital Sharjah	Sharjah	Public
71	BSS	Burjeel Specialty Hospital Sharjah	Sharjah	Public
72	SKA	Sheikh Khalifa Medical City Ajman (SKMCA)	Ajman	Public
73	SKW	Sheikh Khalifa Women's and Children's Hospital	Ajman	Public
74	SMA	Sheikh Khalifa Hospital - Masfout	Ajman	Public
75	SKU	Sheikh Khalifa General Hospital (SKGH) UAQ	Um Al Quwain	Public
76	UAQ	Um Al Quwain Hospital	Um Al Quwain	Public
77	SKRAK	Sheikh Khalifa Specialty Hospital (SKSH) RAK	Ras Al Khaimah	Public
78	IBHO	Ibrahim Bin Hamad Obaidullah Hospital/RAK Psych.	Ras Al Khaimah	Public
79	SAQR	Saqr Hospital	Ras Al Khaimah	Public
80	BOW	Abdullah Bin Omran Hospital for Obstetrics and Gyn.	Ras Al Khaimah	Public
81	SHA	Shaam Hospital	Ras Al Khaimah	Public
82	PRAK	Psychiatric Hospital RAK	Ras Al Khaimah	Public
83	RAKH	RAK Hospital	Ras Al Khaimah	Private
84	FUJ	Fujairah Hospital	Fujairah	Public
85	DIB	Dibba Hospital	Fujairah	Public
86	KAL	Al Kalba Hospital	Fujairah	Public
87	MAS	Masafi Hospital	Fujairah	Public

Annex 5.5 AMR surveillance sites (continued)

Annex 5.5.2. AMR Surveillance Sites – Center/Clinics

Nr.	Center/Clinic name	Emirate	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	Al Ettihad Health Center	Abu Dhabi	Public
38	Al Faqah Health Center	Abu Dhabi	Public
39	Al Khaleej Primary Health Center	Abu Dhabi	Public
40	Al Manhal Primary Health Center	Abu Dhabi	Public
41	SEHA Kidney Care Center - Abu Dhabi	Abu Dhabi	Public
42	SEHA Kidney Care Center - Al Ain	Abu Dhabi	Public
43	SEHA Kidney Care Center - Central	Abu Dhabi	Public
44	Sir Baniyas Clinic	Abu Dhabi	Public
45	Danat Al Emarat Clinic for Women and Children	Abu Dhabi	Private
46	Health Plus Diabetes and Endocrinology Center	Abu Dhabi	Private
47	Health Plus Family Health Center - Al Bandar	Abu Dhabi	Private
48	Health Plus Family Health Center - Al Forsan	Abu Dhabi	Private
49	Health Plus Fertility and Women's Health Center – Al Karama area	Abu Dhabi	Private
50	Moorfields Eye Hospital Center – Al Marina	Abu Dhabi	Private
51	Imperial College London Diabetes Center Abu Dhabi	Abu Dhabi	Private
52	Imperial College London Diabetes Center Al Ain	Abu Dhabi	Private
53	Imperial College London Diabetes Center ZSC Branch	Abu Dhabi	Private
54	Mediclinic Al Bateen	Abu Dhabi	Private
55	Mediclinic Al Bawadi	Abu Dhabi	Private
56	Mediclinic Al Madar	Abu Dhabi	Private
57	Mediclinic Al Marmoura	Abu Dhabi	Private
58	Mediclinic Al Mussafah	Abu Dhabi	Private
59	Mediclinic Al Yahar	Abu Dhabi	Private
60	Mediclinic Baniyas	Abu Dhabi	Private
61	Mediclinic ENEC	Abu Dhabi	Private
62	Mediclinic Gayathi	Abu Dhabi	Private
63	Mediclinic Khalifa City A	Abu Dhabi	Private
64	Mediclinic Madinat Zayed	Abu Dhabi	Private
65	Mediclinic Zakher	Abu Dhabi	Private

Annex 5.5.2 AMR Surveillance Sites – Centers/Clinics (continued)

Nr.	Center/Clinic name	Emirate	Ownership
66	NMC ADNOC OHC	Abu Dhabi	Private
67	NMC Family Medical Center, Al Bateen	Abu Dhabi	Private
68	NMC Medical Center Al Wadi	Abu Dhabi	Private
69	NMC Medical Centre Mohammed Bin Zayed	Abu Dhabi	Private
70	NMC Provita International Medical Center, Abu Dhabi	Abu Dhabi	Private
71	NMC Provita International Medical Center, Al Ain	Abu Dhabi	Private
72	NMC Royal Family Medical Center, Al Musaffah	Abu Dhabi	Private
73	NMC Royal Medical Center Sama Tower Abu Dhabi	Abu Dhabi	Private
74	NMC Oxford Medical Center	Abu Dhabi	Private
75	NMC Alpha Medical Center, Abu Dhabi	Abu Dhabi	Private
76	NMC Mesk AlMadina Medical Centre LLC	Abu Dhabi	Private
77	NMC Golden Sands Medical Center	Abu Dhabi	Private
78	NMC Medical Specialty Medical Center, Khalidiya	Abu Dhabi	Private
79	NMC Karama Medical Center	Abu Dhabi	Private
80	NMC Shahama Medical Center	Abu Dhabi	Private
81	American Surge Center	Abu Dhabi	Private
82	Cosmesurge and NMC Clinic Delma Street	Abu Dhabi	Private
83	Cosmesurge BAS Clinic	Abu Dhabi	Private
84	Cosmesurge Conrad Clinic	Abu Dhabi	Private
85	Cosmesurge Al Ain Clinic	Abu Dhabi	Private
86	Cosmesurge Khalifa Clinic	Abu Dhabi	Private
87	Cosmesurge Zakher Al Ain Clinic	Abu Dhabi	Private
88	IMA - Sehaty Medical Center	Abu Dhabi	Private
89	IMA - Golden Health Mobile Medical Unit	Abu Dhabi	Private
90	Sheikh Zayed Mosque Clinic	Abu Dhabi	Private
91	NMC UAE University Clinics	Abu Dhabi	Private
92	VPS Burjeel Day Surgery Center, Al Reem island	Abu Dhabi	Private
93	VPS Burjeel Medical Center, Al Zeina	Abu Dhabi	Private
94	VPS Burjeel Medical Center, Shahama	Abu Dhabi	Private
95	VPS Burjeel Medical Center, Shamkha	Abu Dhabi	Private
96	VPS Burjeel Medical Center, Yas Mall	Abu Dhabi	Private
97	VPS Burjeel MHPC Marina Medical Center	Abu Dhabi	Private
98	VPS Burjeel Tajmeel Kid's Park Medical Center	Abu Dhabi	Private
99	VPS Lifeline Medical Center	Abu Dhabi	Private
100	VPS Burjeel Oasis Medical Center	Abu Dhabi	Private
101	VPS Burjeel Medical Center, Barari Mall Al Ain	Abu Dhabi	Private
102	VPS LLH Medical Centre (Shabiya 11)	Abu Dhabi	Private
103	VPS Occupational Medicine Center Mussafah	Abu Dhabi	Private
104	VPS Lifecare Razeen Medical Center	Abu Dhabi	Private
105	Abu Hail Clinic	Dubai	Public
106	Al Badaa Health Center	Dubai	Public
107	Al Khawaneej Clinic	Dubai	Public
108	Al Lussily Health Center	Dubai	Public
109	Al Mamzar Health Center	Dubai	Public
110	Al Mankhool Health Center	Dubai	Public
111	Al Muhaisnah Medical Fitness Center	Dubai	Public
112	Al Qusais 2 Clinic	Dubai	Public
113	Al Rashidya Medical Fitness Center	Dubai	Public
114	Al Towar Clinic	Dubai	Public
115	Dubai Diabetic Centre	Dubai	Public
116	Police Clinics	Dubai	Public
117	Zabeel Health Center	Dubai	Public
118	Al Aweer Health Center	Dubai	Public
119	Al Ittihad Health Center	Dubai	Public
120	Al Muhaisnah Health Center	Dubai	Public
121	Al Quoz Health Center	Dubai	Public
122	Al Qusais Health Center	Dubai	Public
123	Al Rashidiya Health Center	Dubai	Public
124	Al Refaa Health Center	Dubai	Public
125	Hor Al Anz Health Center	Dubai	Public
126	Cosmesurge Jumeirah Clinic	Dubai	Private
127	Cosmesurge Marina Clinic	Dubai	Private
128	Dr Reena Begaum Clinic	Dubai	Private
129	Al Garhoud Private hospital Clinic, Shorouq	Dubai	Private
130	Al Garhoud Private hospital, FIFA Centre of Excellence	Dubai	Private
131	American hospital clinic, Al Barsha	Dubai	Private
132	American hospital clinic, Media city	Dubai	Private

Annex 5.5.2 AMR Surveillance Sites – Centers/Clinics (continued)

Nr.	Center/Clinic name	Emirate	Ownership
133	American hospital clinic, Al Khawaneej	Dubai	Private
134	American Hospital Clinics - Jumeirah Clinic	Dubai	Private
135	American Hospital Clinics - Mira	Dubai	Private
136	Private Clinics (DHA)	Dubai	Private
137	Day Surgery Center (Karama)	Dubai	Private
138	Safa Polyclinic	Dubai	Private
139	King´s Jumeirah Medical Center	Dubai	Private
140	King´s Marina Medical Center	Dubai	Private
141	Mediclinic Al Sufouh Clinic	Dubai	Private
142	Mediclinic Arabian Ranches Clinic	Dubai	Private
143	Mediclinic Deira City Center Clinic	Dubai	Private
144	Mediclinic Dubai Mall Clinic	Dubai	Private
145	Mediclinic Ibn Battuta Clinic	Dubai	Private
146	Mediclinic Meadows Clinic	Dubai	Private
147	Mediclinic Me'aisem Clinic	Dubai	Private
148	Mediclinic Mirdif Clinic	Dubai	Private
149	Mediclinic Qusais Clinic	Dubai	Private
150	Mediclinic Springs Clinic	Dubai	Private
151	Mediclinic Al Barsha Dialysis Centre	Dubai	Private
152	NMC BR Medical Suites	Dubai	Private
153	NMC DIC Clinic and Pharmacy	Dubai	Private
154	NMC Medical Center, Deira	Dubai	Private
155	NMC Family Clinic Satwa	Dubai	Private
156	Premier Diagnostics and Medical Center, Deira	Dubai	Private
157	Prime Medical Center, Al Qusais	Dubai	Private
158	Prime Medical Center, Al Warqa	Dubai	Private
159	Prime Medical Center, Barsha Heights	Dubai	Private
160	Prime Medical Center, Bur Dubai	Dubai	Private
161	Prime Medical Center, Deira	Dubai	Private
162	Prime Medical Center, Homecare	Dubai	Private
163	Prime Medical Center, Jumeirah	Dubai	Private
164	Prime Medical Center, Mizhar	Dubai	Private
165	Prime Medical Center, Motor city	Dubai	Private
166	Prime Medical Center - Prime Corp (Camps, various locations)	Dubai	Private
167	Prime Medical Center, Reef Mall	Dubai	Private
168	Prime Medical Center, Sheikh Zayed Road	Dubai	Private
169	Al Batayeh Health Center	Sharjah	Public
170	Al Hamriya Health Center	Sharjah	Public
171	Al Maliha Medical Center	Sharjah	Public
172	Al Rafa Medical Center	Sharjah	Public
173	Al Riqqa Health Center	Sharjah	Public
174	Dhaid Medical Center	Sharjah	Public
175	Dibba Al Hisn Clinic	Sharjah	Public
176	Family Health Promotion Center	Sharjah	Public
177	Khalidiya Health Center	Sharjah	Public
178	Lualuea Health Center	Sharjah	Public
179	Madam Health Center	Sharjah	Public
180	Qarain Health Center	Sharjah	Public
181	Sabkha Health Center	Sharjah	Public
182	Sharjah Health Center	Sharjah	Public
183	Thameed Health Center	Sharjah	Public
184	Wasit Health Center	Sharjah	Public
185	Cosmesurge Sharjah Clinic	Sharjah	Private
186	Prime Medical Center, Al Nahda	Sharjah	Private
187	Prime Medical Center, Al Qasimia	Sharjah	Private
188	Prime Medical Center, Zero-6 mall	Sharjah	Private
189	Prime Medical Specialist Center, King Faisal Road/Safeer Mall	Sharjah	Private
190	LAIQ Medical Screening Center	Ajman	Public
191	Rashid Centre for Diabetes and Research	Ajman	Public
192	Al Hamidiyah Health Center	Ajman	Public
193	Al Madina Clinic	Ajman	Public
194	Manama Medical Center	Ajman	Public
195	Mushairef Health Center	Ajman	Public
196	Premier Diagnostics and Medical Center, Ajman	Ajman	Private
197	Al Khazan Health Center	Um Al Quwain	Public
198	Al Raffa Health Center	Um Al Quwain	Public

Annex 5.5.2 AMR Surveillance Sites – Centers/Clinics (continued)

Nr.	Center/Clinic name	Emirate	Ownership
199	Al Salamah Health Center	Um Al Quwain	Public
200	Falaj Clinic	Um Al Quwain	Public
201	Al Dhait Health Center	RAK	Public
202	Al Digdagga Health Center	RAK	Public
203	Al Hemrania Health Center	RAK	Public
204	Al Jazeera Medical Clinic	RAK	Public
205	Al Jeer Health Center	RAK	Public
206	Al Mamourah Health Center	RAK	Public
207	Al Nakheel Health Center	RAK	Public
208	Al Rams Clinic	RAK	Public
209	Julphar Clinic	RAK	Public
210	Kadra Health Center	RAK	Public
211	Ras Al Khaimah Health Center	RAK	Public
212	Saif Bin Ali Health Center	RAK	Public
213	Shamal Health Center	RAK	Public
214	Cosmesurge RAK Julphar Clinic	RAK	Private
215	Cosmesurge RAK Villa Clinic	RAK	Private
216	Al Hamra Medical Center	RAK	Private
217	Al Ghalila Medical Center	RAK	Private
218	Al Jazeera Medical Center	RAK	Private
219	Retaj Medical Center	RAK	Private
220	Aster clinic	RAK	Private
221	European Medical Center	RAK	Private
222	Cosmesurge Fujairah Clinic	Fujairah	Private
223	Al Faseel Family Health	Fujairah	Public
224	Al Halah Health Center	Fujairah	Public
225	Al Khalibia Health Center	Fujairah	Public
226	Al Qidfaa Health Center	Fujairah	Public
227	Al Qurrayah Health Center	Fujairah	Public
228	Dhadna Health Center	Fujairah	Public
229	Madina Medical Center	Fujairah	Public
230	Murbah Health Center	Fujairah	Public
231	Murishid Primary Health Clinic	Fujairah	Public

Annex 5.6 AMR surveillance laboratories

Nr.	Code	Hospital name	Emirate	Ownership
1	SKM	Union71 - Sheikh Khalifa Medical City	Abu Dhabi	Public
2	AAH	Union 71 - Al Ain hospital	Abu Dhabi	Public
3	TAW	Union 71 - Tawam hospital	Abu Dhabi	Public
4	MZH	Union 71 - Al Dhafra hospitals – MZH	Abu Dhabi	Public
5	GYH	Union71 - Al Dhafra hospitals – Gayathi hospital	Abu Dhabi	Public
6	CCA	Cleveland Clinic Abu Dhabi hospital	Abu Dhabi	Public
7	DAE	Danat Al Emarat hospital	Abu Dhabi	Private
8	EIH	Emirates International Hospital Al Ain	Abu Dhabi	Private
9	AKH	Ain Al Khaleej Hospital Al Ain	Abu Dhabi	Private
10	MAR	Mediclinic Al Noor hospital Airport Road	Abu Dhabi	Private
11	MAA	Mediclinic Al Ain hospital	Abu Dhabi	Private
12	BMC	VPS Burjeel Medical City	Abu Dhabi	Private
13	NSA	NMC Specialty hospital Abu Dhabi	Abu Dhabi	Private
14	NRY	NMC Royal hospital Khalifa City A	Abu Dhabi	Private
15	NAA	NMC Specialty hospital Al Ain	Abu Dhabi	Private
16	NRL	National Reference Laboratory Abu Dhabi	Abu Dhabi	Private
17	PHD	Proficiency Healthcare Diagnostics for Laboratories	Abu Dhabi	Private
18	NAN	NMC Specialty hospital Al Nahda	Dubai	Private
19	DIP	NMC Royal hospital, DIP	Dubai	Private
20	DH	DHA - Dubai hospital	Dubai	Public
21	HAT	DHA - Hatta hospital	Dubai	Public
22	RH	DHA - Rashid hospital	Dubai	Public
23	LH	DHA - Latifa hospital	Dubai	Public
24	IHD	Iranian hospital	Dubai	Private
25	PHG	Premier Diagnostics (Prime Health Group)	Dubai	Private
26	AZH	Al Zahra hospital Dubai	Dubai	Private
27	MIR	Mirdif hospital	Dubai	Private
28	SGH	Saudi German hospital	Dubai	Private
29	ESH	Emirates Specialty hospital	Dubai	Private
30	AHD	American hospital Dubai	Dubai	Private
31	MDX	Medeor 24x7 hospital Dubai	Dubai	Private
32	MCIT	Mediclinic City hospital Dubai	Dubai	Private
33	ZULD	Zulekha hospital Dubai	Dubai	Private
34	CLEM	Clemenceau Medical Center Dubai	Dubai	Private
35	KING	King´s College London hospital Dubai	Dubai	Private
36	FAK	Fakeeh University hospital	Dubai	Private
37	AQH	Purehealth Lab (Al Qassimi hospital)	Sharjah	Public
38	UHS	University hospital Sharjah	Sharjah	Public
39	SKA	MOPA - Sheikh Khalifa Medical City Ajman (SKMCA)	Ajman	Public
40	SKU	MOPA - Sheikh Khalifa General hospital (SKGH) UAQ	Um Al Quwain	Public
41	SKRAK	MOPA - Sheikh Khalifa Specialty hospital (SKSH) RAK	Ras Al Khaimah	Public
42	SAQR	Purehealth Lab (Saqr hospital)	Ras Al Khaimah	Public
43	RAK	RAK Hospital	Ras Al Khaimah	Public
44	FUJ	Purehealth Lab (Fujairah hospital)	Fujairah	Public

Annex 5.7 Data fields collected for AMR Surveillance

Nr.	Data Field	Description	Format	Classification
1	PATIENT_ID	Patient ID (medical record number)	Required	TEXT
2	PATIENT_EID	Patient Emirates ID nr.	Desirable	TEXT
3	PATIENT_NAME	Patient name	Desirable	TEXT
4	PATIENT_DOB	Patient date of birth (DOB)	Required	DATE (dd/mm/yyyy)
5	PATIENT_AGE	Patient age	Required	NUMERICAL
6	PATIENT_GENDER	Patient gender	Optional	TEXT
7	PATIENT_NATIONALITY	Patient nationality	Desirable	TEXT
8	PATIENT_NAT_STATUS	Patient nationality status	Desirable	TEXT
9	PATIENT_ADM_DATE	Date of patient admission	Required	DATE (dd/mm/yyyy)
10	PATIENT_DISC_DATE	Date of discharge (for inpatients)	Desirable	DATE (dd/mm/yyyy)
11	FACILITY_NAME	Healthcare facility name	Required	TEXT
12	FACILITY_ID	Healthcare facility ID	Optional	TEXT
13	FACILITY_LICENCE_NR	Healthcare facility licensing number	Required	TEXT
14	FACILITY_EMIRATE	Healthcare facility Emirate	Conditional	TEXT
15	FACILITY_DEPT_NAME	Department/specialty name	Required	TEXT
16	PATIENT_LOCATION_NAME	Patient location name	Required	TEXT
17	PATIENT_LOCATION_TYPE	Patient location type	Desirable	TEXT
18	LAB_NAME	Laboratory name	Required	TEXT
19	SPECIMEN_PROC_ORDER_NAME	Microbiological procedure ordered	Required	TEXT
20	SPECIMEN_LAB_NR	Specimen lab number	Required	TEXT
21	SPECIMEN_TYPE	Specimen type	Required	TEXT
22	SPECIMEN_DATE_COLLECTED	Specimen collection date	Required	DATE (dd/mm/yyyy)
23	ORGANISM_NAME	Name of identified organism	Required	TEXT
24	AST_METHOD	AST susceptibility Method	Conditional	TEXT
25	AST_RESULT_CAT	AST result (categorical/interpreted)	Required	TEXT
26	AST_RESULT_NUM	AST result (numerical)	Required	TEXT
27	ANTIBIOTIC_NAME	Antimicrobial agent tested	Required	TEXT
28	PATIENT_DISC_STATUS	Patient discharge status	Desirable	TEXT
29	DIAGNOSIS	Diagnosis	Desirable	TEXT

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