UNITED ARAB EMIRATES
MINISTRY OF HEALTH & PREVENTION

NATIONAL AMR SURVEILLANCE REPORT 2023

In collaboration with:

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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

Disclaimer: These data are statistically representative for UAE from all The Seven Emirates.

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**).

Data for the reporting year 2023 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 provides a summary overview of current (2023) levels of antimicrobial resistance (AMR) among relevant and priority pathogens in the United Arab Emirates (percent resistant isolates, %R):

Table 1 Current levels of antimicrobial resistance (AMR) among relevant and priority pathogens in the UAE, Percentage resistant isolates (%R), United Arab Emirates, 2023

Priority[a]	Organism	Antibiotic or antibiotic class	N (Isolates)	% Resistant isolates
Priority 1: Critical	*Acinetobacter* spp.	Carbapenems (IPM or MEM)	1,564	**10.3/10.3**
	Pseudomonas aeruginosa	Carbapenems (IPM or MEM)	8,588	**14.0/10.2**
	Enterobacterales (all)	Carbapenems (IPM or MEM)	87,946	**3.7/2.0**
	Escherichia coli	Carbapenems (IPM or MEM)	32,067	**1.3/1.0**
	Klebsiella pneumoniae	Carbapenems (IPM or MEM)	13,136	**4.5/4.4**
	Enterobacterales (all)	Ceftriaxone/Cefotaxime (ESBL)[b]	87,946	**29.3/28.0**
	Escherichia coli	Ceftriaxone/Cefotaxime (ESBL)[b]	19,120	**35.8/34.4**
	Klebsiella pneumoniae	Ceftriaxone/Cefotaxime (ESBL)[b]	7,449	**25.3/24.9**
Priority 2: High	*Enterococcus faecium*	Vancomycin (VRE)[c]	392	**12.5**
	Staphylococcus aureus	Oxacillin (MRSA)[d]	16,857	**37.9**
	Salmonella spp. (non-typh.)	Fluoroquinolones (ciprofloxacin)	573	**11.2**
	Neisseria gonorrhoeae	3rd-generation cephalosporins	797	**0.2**
	Neisseria gonorrhoeae	Fluoroquinolones (ciprofloxacin)	797	**88.1**
Priority 3: Medium	*Streptococcus pneumoniae*	Penicillin (oral)	1,592	**8.0**
	Streptococcus pneumoniae	Penicillin (meningitis)	1,592	**35.9**
	Streptococcus pneumoniae	Penicillin (non-meningitis)	1,592	**3.6**
	Haemophilus influenzae	Ampicillin	2,671	**39.8**
	Shigella spp.	Fluoroquinolones (ciprofloxacin)	83	**34.9**

[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.

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. (Jim O'Neill, 2014). As per the AMR 2050 burden forecasts estimate, there will be 1·91 million annual deaths attributable to AMR globally and 8·22 million annual deaths associated with AMR & cumulatively from 2025 to 2050, reference scenario forecasts 39·1 million deaths attributable to AMR and 169 million deaths associated with AMR.(The Lancet, 2024). Without effective antibiotics, the success of major surgery and cancer chemotherapy would be compromised (WHO, 2021). AMR and the associated drug-resistant infections are unfortunately not hypothetical problems, but a real threat for all countries, both developing and developed. (World bank, 2017). We are also now seeing pan-resistant infections that are not treatable even with colistin or tigecycline" (Spellberg et al. 2016).

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

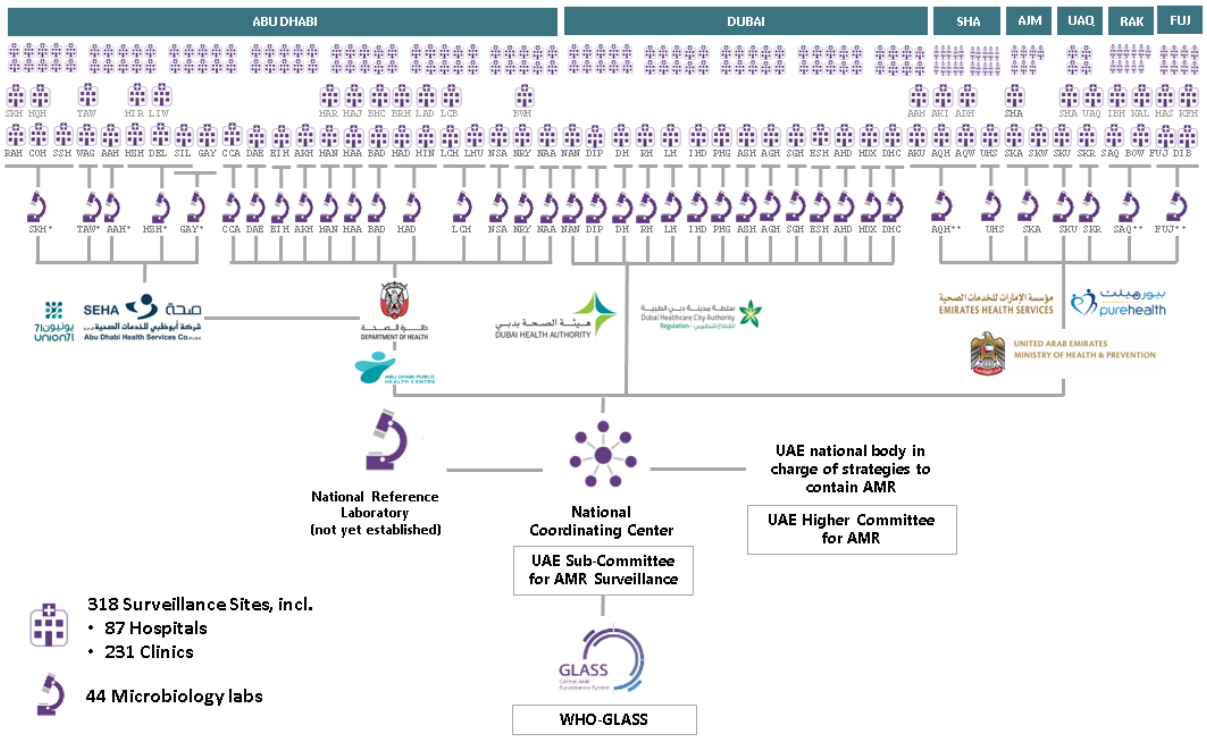
The United Arab Emirates AMR surveillance system was first established in 2010 on a subnational level (Abu Dhabi Emirate, HAAD/DoH). In 2015, the system was expanded and established nationwide by the Ministry of Health and Prevention (MOHAP), in collaboration with the UAE Ministry of Presidential Affairs (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 December 2023, 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



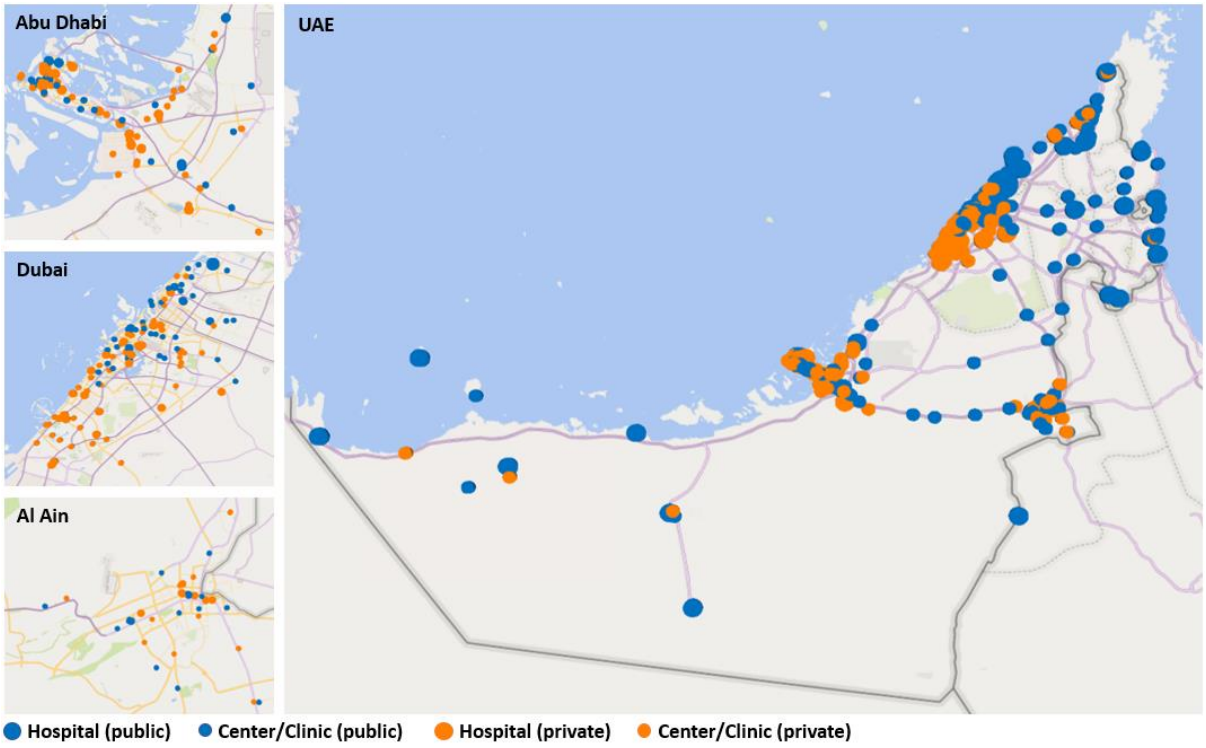
The AMR data submitted includes routine clinical and antibiotic susceptibility testing data from both, governmental as well as private healthcare facilities. There is no central confirmatory testing or central repository of isolates as there is no UAE national reference lab for antimicrobial resistance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

Table 2.3.1 AMR surveillance sites and labs – by Emirate (as of December 2023)

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)



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, 2024). 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, 2024) 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)
- 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. All participating microbiology labs are lab-accredited, by either CAP, or ISO 15189, or both. 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

[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

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.

For reporting period 2023, only the diagnostic (non-duplicate) isolates (total of n=198,771 isolates) are included in the analysis and presented in this report. Screening and quality control isolates as well as copy strains (duplicate isolates) were routinely excluded from the analysis. (see **section 3.3** for details on inclusion, exclusion, and deduplication criteria).

The UAE National AMR surveillance system collects information on all bacteria and yeast grown by cultural methods and tested for antimicrobial susceptibility as part of daily patient routine in participating facilities. For analysis and public health reporting, it focuses then on the following 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, 2024).

Results are presented in this report in section four:

- **Section 4.1 (cumulative antibiograms)** presents the national cumulative antibiogram 2023, 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.
- **Section 4.2 (multidrug resistance)** presents multidrug resistance (%MDR) for Gram-negative and Gram-positive bacteria, and *Mycobacterium tuberculosis* (MDR-TB).
- **Section 4.3 (AMR priority pathogens)** presents percent resistant/intermediate/susceptible (%RIS) statistics.

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

3.3 Data analysis

Data analysis was conducted with the WHONET 2024 Software for Antimicrobial Resistance Surveillance (WHONET, 2024).

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-ED5:2024, 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-ED5:2024, Appendix A: Rationale for the "First Isolate per Patient" Analysis Recommendation (CLSI M39, 2024).

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: 2024) for bacterial isolates and CLSI interpretation standard M60 ED1:2020 for yeast. For amphotericin B (AMB) and tigecycline, EUCAST v12.0:2024 was used (EUCAST, 2024). For *Candida auris*, tentative breakpoints from U.S. CDC were used (CDC C. auris, 2020).

Cumulative antibiograms are presented by adopting the CLSI M39-ED5:2024 standard for the Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data (CLSI M39, 2024).

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 2024. 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

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 (2023)

4.2.1 United Arab Emirates (National Cumulative Antibiogram)

Table 4.2.1.1 National Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=113,400)

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)	113,400	-	69	87	-	-	69	-	81	91	96	95	82	88	84	59	57	70	66[b]
Haemophilus influenzae[c]	3,413	48	85	-	-	79	-	-	-	-	-	-	-	-	-	91	-	46	-
Moraxella (Branh.) catarrhalis[d]	343	-	91	-	-	76	-	-	-	-	-	-	-	-	-	88	-	52	-
Enterobacterales	87,946	28	72	88	57	-	70	-	80	92	98	96	80	88	82	54	71	70	-
Citrobacter koseri (diversus)	2,237	R	94	93	93	55/79[i]	93	-	97	98	99	98	84	98	92	88	94	97	76[b]
Enterobacter cloacae	2,388	R	R	87	R	36/51[i]	81	-	91	92	97	93	76	95	91	71	76	87	41[b]
Enterobacter aerogenes (*K. aer.*)	2,263	R	R	81	R	R	75	-	94	77	97	96	81	96	89	82	47	94	20[b]
Escherichia coli [e]	51,511	36	77	92	56	58/60[i]	64	-	78	98	99	98	81	89	84	45	74	61	96[b]
Klebsiella pneumoniae	19,869	R	80	84	23	67/69[i]	73	-	83	94	95	94	82	91	83	64	69	79	28[b]
Klebsiella oxytoca	1,019	R	82	92	21	81/83[i]	88	-	93	94	97	95	78	95	90	75	-	88	75[b]
Morganella morganii	953	R	R	97	R	R	66	-	95	15	96	97	84	84	76	44	92	64	R
Proteus mirabilis	2,484	61	76	97	22	82/84[i]	82	-	87	23	93	96	76	71	73	55	73	60	R
Proteus vulgaris	69	R	75[f]	100	R	R	83[f]	-	97	6	86	92[f]	74	94	-	65	-	86	R
Providencia spp.	298	R	R	93	R	–	92	-	95	44	91	88	89	74	78	66	-	88	R
Salmonella spp. (non-typhoid)	1,616	81	99	99	-	-	97	-	99	-	-	-	-	-	-	46[g]	-	96	-
Salmonella Typhi/Paratyphi	162	53	85	85	-	25/40[i,f]	56	-	93	-	-	-	-	-	-	9	-	66	-
Serratia marcescens	2,081	R	R	85	R	R	90	-	97	76	97	96	87	96	74	80	77	98	R
Shigella spp.	108	19	90	90	-	-	53	-	95	-	-	-	-	-	-	34	-	40	-
Non-fermenting Gram-neg. rods	14,655	R	R	84	-	-	-	87	90	83	85	R	97	91	91	84	61	70	-
Acinetobacter baumannii	2,270	R	R	78	-	-	-	84	85	90	89	R	92	89	86	84	R	90	-
Pseudomonas aeruginosa	11,981	R	R	84	-	R	R	87	91	83	85	R	97	92	92	85	63	R	R
Stenotrophomonas maltophilia[h]	1,240	R	R	R	-	-	R	33	-	R	R	R	R	R	R	-	R	79	-

[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 95 %S, CRO 81 %S, AZM: 88 %S, CLR 96 %S. [d] *M. catarrhalis*: CLR: no data, ERY 83 %S, AZM: 87 %S, LVX 89 %S, TCY 56 %S. [e] *E. coli* (urinary tract isolates): FOS 99 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. (non-typhoid) refer to extra-intestinal (non-stool) isolates only. [h] *S. maltophilia*: MNO 54 %S, TCC 67 %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 ED34:2024. Presentation standard: CLSI M39-A5:2024. Data analysis: WHONET 2024.

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 1.0 (November 2023)

Table 4.2.1.2 National Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=77,924)

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)	77,924	-	-	-	-	-	-	47	76	-	-	-	75	57	99	99	66	98	99	-	-	-
Enterococcus spp.	7,237	93	-	-	-	R	R	-	R	R	40	73	72	83	98	99	R	90	97	-	-	-
Enterococcus faecalis	6,063	100	-	-	-	R	R	-	R	R	46	78	75	82	99	99	R	99	97	-	-	R
Enterococcus faecium	610	32	-	-	-	R	R	-	R	R	61	68	32	75[j]	88	91	R	22	94	-	-	85
Staphylococcus aureus[k]	24,251	-	-	62[c]	62	-	-	64	87	89	-	-	66	68	100	100	80	100	100	87	100	87
MSSA[k]	11,123	-	-	100	100	-	-	68	90	96	-	-	75	76	100	100	83	100	100	91	100	89
MRSA[k]	6,097	-	-	-	-	-	-	56	81	76	-	-	50	52	99	99	74	99	100	79	99	80
Staphylococcus, coagulase-neg. (SCN)	9,526	-	-	34[c]	34	-	-	32	64	78	-	-	67	63	99	95	82	98	99	81	93	92
Staphylococcus epidermidis	2,553	-	-	21[c]	26	-	-	27	57	68	-	-	53	52	99	90	71	98	100	79	94	95
Staphylococcus saprophyticus [g]	1,496	-	-	44[c]	38	-	-	35	78	99	-	-	98	95	100	100	94	99	99	93	99	94
Staphylococcus lugdunensis	341	-	-	70[c]	70	-	-	77	83	92	-	-	95	92	100	100	100	100	100	94	100	94
Streptococcus pneumoniae	3,764	-	94[d]	-	-	97[e]	96[e]	36	65	-	-	-	91	94	100	100	59	-	100	48	100	99
Streptococcus pyogenes [h]	13,717	95[f]	95	-	-	97	97	50	84	-	-	-	90	-	100	100	-	-	100	79	-	-
Streptococcus agalactiae [i]	7,003	98	98	-	-	98	99	37	49	-	-	-	88	-	99	98	-	96	100	14	-	99
Streptococcus spp. (viridans group)	1,550	-	71	-	-	89	90	34	82	-	-	-	89	-	98	-	-	-	98	45	-	-

[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): 62 %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 ED34:2024. Presentation standard: CLSI M39-A5:2024. Data analysis: WHONET 2024.

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 1.0 (20 Nov 2024).

UAE Resistance Trends comparison between 2022 & 2023, Gram-negative Bacteria:
The 'Good News' and the 'Bad News'

Table: 4.2.1.3

Organism	*Escherichia coli*	*Klebsiella pneumoniae*	*Salmonella* spp. (non-typhoidal)	*Pseudomonas aeruginosa*	*Acinetobacter* sp.
Ampicillin	↑	N/A	→	R	R
Amoxicillin/clavulanic acid	→	↓	↓	R	R
Piperacillin/tazobactam	↑	↑	↓	→	↑
3rd-/4th-Gen. Cephalosporins	↑/↑	↑/↑	↓/↓	↓/↓	↓/↓
Carbapenems (IPM or MEM)	→/→	→/→	N/A	↓/↓	↓/↓
Fluoroquinolones (Ciprofloxacin)	↑	↑	↑	↓	↓
Aminoglycosides (Gentamicin)	↑	↑	N/A	→	↓
Trimethoprim/sulfamethoxazole	↑	↑	↓	R	↑
Multidrug-resistance (≥3 classes NS)	↓	↑	↓	↓	↓

→/↑/↓: horizontal/increasing/decreasing trend of percentage resistant isolates (%R) *R: intrinsic resistance,* *N/A: Not applicable*

UAE Resistance Trends comparison between 2022 & 2023, Gram-positive Bacteria:
The 'Good News' and the 'Bad News'

Table: 4.2.1.4

Organism	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Enterococcus faecalis*	*Enterococcus faecium*
Beta-lactam antibiotics	↑ (OXA)	↓(PEN) / ↓(CTX)	↓ (AMP)	↓ (AMP)
Macrolides (Erythromycin)	↑	↑	N/A	N/A
Lincosamides (Clindamycin)	→	↓	N/A	N/A
Aminoglycosides (Gentamicin)	→	N/A	↑	↑
Fluoroquinolones (Levo/Moxi)	→/→	↑/↑	↑/↑	↑/↑
Glycopeptides	→	→	→	↑ (VRE)
Trimethoprim/sulfamethoxazole	↓	↓	R	R
Multidrug-resistance (≥3 classes NS)	↑	↑	↑	↑

→/↑/↓: horizontal/increasing/decreasing trend of percentage resistant isolates (%R) *R: intrinsic resistance,* *N/A: Not applicable*

4.2.2 Abu Dhabi Emirate

Table 4.2.2.1 Abu Dhabi Emirate Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=34,481)

		Beta Lactams						Macrolides	Aminoglycosides					Fluroqinolones			Glycopeptides		Others									
Organism	Isol	AMP	CTX	FOX	CRO	OXA	PEN	ERY	GEN	GEH	STR	STH	TOB	CIP	LVX	MFX	TEC	VAN	CHL	CLI	FUS	LNZ	NIT	QDA	RIF	TCY	TGC	SXT
Staphylococcus aureus	10,896		68	60		62	10	62	88					66	68	69	99	100		84	0	100	99		100	86	100	77
Streptococcus, beta-haem. Group B	4,999																	100		32								
Enterococcus faecalis	3,535	99				0	98	14	12	53	0	11		71	76		100	100				99	99			23	100	
Streptococcus pyogenes	2,973				98		98	53								25		100		71		100				79		24
Streptococcus, beta-haem. Group A	2,440				100			48												62								
Streptococcus agalactiae	2,129	98	98		99		97	35							90	4		100	95	40		100				13	99	4
Staphylococcus, coagulase negative	1,502	2	42			41		44	84					79	82			100		65		99	93			72		86
Staphylococcus epidermidis	1,266	0	45	33		34	7	27	73					65	69	55	92	100		58	0	99	98		95	78	2	76
Streptococcus pneumoniae	1,187		96		99		97	41							93	98		100		62		100				47		63
Staphylococcus haemolyticus	948	0	26			26	4	30	78					65	69			100		58		100	99			59		82
Staphylococcus saprophyticus	410	2	8			24	2	38	100					100	99	99		100		75		100	99	97	100	91	5	96
Staphylococcus hominis	301			41		39	12	19	97					81	73	75	92	98		64	0	98	94		96	73	2	89
Enterococcus faecium	286	36		22		0	39	10	14	27	0	2		31	38		91	84				94	34	87		36	2	
Streptococcus viridans, alpha-hem.	239	72	90		93		72	54							79			100		73		100				61		60
Staphylococcus capitis	194			36		40	14	49	63				62	63	48	54	92	100		82	0	99	100		93	97	0	100
Corynebacterium sp.	184				71			31	73					51	47			99		37		99				69		32
Staphylococcus lugdunensis	170			71		73	26	75	93					98	99	95	100	99		80	0	100	100	100	100	95	4	100
Streptococcus mitis	131	41	76		84		44	22							83	84		96	97	79		100				63	97	
Enterococcus sp	129	83						0	58	77				64	73			89				91	86			35		
Streptococcus anginosus	90		100		98		93	67							96	86		98		73		99				55		
Streptococcus constellatus	69				96		92	64								96		98		65		100				55		
Enterococcus avium	67	72				0	56	6	0	0	0	0		88	88		100	100				91	58	75		29	0	
Streptococcus dysgalactiae	59				100		100	36								3		100		71		100				48		2
Micrococcus luteus	57	0					96											100		93								
Enterococcus gallinarum	52	83						38				0		74			97	86				92	82			48	0	
Streptococcus parasanguinis	36	9			82		14									70		97		84		100				47		
Staphylococcus warneri	33					70	24	42	91							100	96	100		82		100			100	100	0	97
Streptococcus salivarius	31				72		16	17								100		100		62		100				67		
Bacillus sp.	25																	96										
Streptococcus dysgalactiae ss. equisimilis	23				100		100	43								18		100		62		100				44		19
Enterococcus raffinosus	20	60																				100						

Code	Antibiotic
AMP	Ampicillin
CTX	Cefotaxime
FOX	Cefoxitin
CRO	Ceftriaxone
CHL	Chloramphenicol
CIP	Ciprofloxacin
CLI	Clindamycin
ERY	Erythromycin
FUS	Fusidic acid
GEN	Gentamicin
GEH	Gentamicin-High
LVX	Levofloxacin
LNZ	Linezolid
MFX	Moxifloxacin
NIT	Nitrofurantoin
OXA	Oxacillin
PEN	Penicillin G
QDA	Quinupristin/Dalfopristin
RIF	Rifampin
STR	Streptomycin
STH	Streptomycin-High
TEC	Teicoplanin
TCY	Tetracycline
TGC	Tigecycline
TOB	Tobramycin
SXT	Trimethoprim/Sulfamethoxazole
VAN	Vancomycin

Table 4.2.2.2 Abu Dhabi Emirate Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=54,578)

		Beta Lactams																				Macrolides			Aminoglycosides			Fluroqinolones			Carbepenems			Others								
Organism	Isol	AMC	AMP	SAM	CZO	FEP	CFM	CTX	FOX	CPD	CAZ	CZA	CZT	CRO	CXM	CXA	CEP	PEN	PIP	TZP	TIC	TCC	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	ATM	CHL	COL	FOS	NIT	TCY	TGC	SXT	MNO
Escherichia coli	25,334	72	35		41	75		66	86		74			62	57					93						95	90	87	58		73	98	99	99				98	94			62	
Klebsiella pneumoniae	9,957	77	2		55	84		76	85		78			74	67	67				86						94	93	85	74		90	96	96	97				13	32			81	
Pseudomonas aeruginosa	5,879					90					86	88	89						78	86	5	49				96	90	93	83	78			82	84			0						
Enterobacter sp.	1,247	2	1		1	76					66			54	39					91						95	90		74	54		96	93	97					71			74	
Serratia marcescens	1,179	7			0	96		90	27		96			89	1	0	0			82						97	96	74	82		98	97		98				3	0	64		98	
Proteus mirabilis	1,127	82	60		63	92		88	89	83	93			89	82	82	78			98						89	69	76	63		79	92	27	97				7	1	6		63	
Citrobacter koseri	1,053	92	0		80	96		95	85		94			92	75					94						99	98	96	95		99	99	99	99				20	76			98	
Klebsiella aerogenes	1,036	7	1		5	94		79	11		79			75	59					82						97	96	94	91		96	98	78	97				17	25			94	
Enterobacter cloacae	959	10	6		9	80		81	2	76	77		85	65	47	36	2			88						98	93	93	79	66	95	96	92	98				2	54	85		82	
Salmonella sp.	845	18	85			43		97			30			95						17						0	0		84		19	99	98	100				0	14			97	
Haemophilus influenzae	592	87	45	66		100	96							96	78					93			87	92					93	95			98	96		95			52		45	
Klebsiella oxytoca	564	70	1		45	82		87			79			72	64					90						94	93		84	78	96	97	96	97				19	72			84	
Stenotrophomonas maltophilia	550		0								55																			82												71	
Morganella morganii	474	1	1		2	94		66	42		84			79	2					97						94	84	75	54	50	84	98	23	98				5	2			65	
Acinetobacter baumannii	470					79		53			78								68	76	0	75					84	84	80				83	82			96				86	92
Acinetobacter sp.	347					83					82									84	0	97				92	89	99	90	90			93	93							92	100
Neisseria gonorrhoeae	284						99							100				2					83						18										12			
Moraxella catarrhalis	279	92												97									87		83				88										57		50	
Enterobacter cloacae complex	250	3			2	96		85	4		86			78						83						98	95	90	83		97	95	99	98					35			91	
Enterobacter hormaechei	202	7				90		77			79									79						96	91		77		94	98	94	96				0	32			83	
Klebsiella sp.	153	21	2		9	90		76			80			74	56					87						96	96		87	68	100	96	82	97				9	37			88	
Citrobacter freundii	151	21	5		4	90		85	22		80			62	46					87						98	90	79	67	45	89	97	95	97				4	97			78	
Acinetobacter calcoaceticus-baumannii	122			87	0	88		38			86			33						80						80	90	85	83				94	92								93	
Pantoea agglomerans	119	68	31		43	76					69		83	57	45					97						94	92		73	46		92	100	97					72			75	
Klebsiella pneumoniae ss. ozaenae	115	75	4		58	90		88	87	82	86		75	78	72	73	82			89						92	92	93	84	81	94	92	92	95			0		50	85	91	88	
Citrobacter sp.	106	67	0		30	84					74			74	50					97						96	91		77	51		99	95	99					83			77	

		Beta Lactams																				Macrolides			Aminoglycosides			Fluroqinolones			Carbepenems			Others									
Organism	Isol	AMC	AMP	SAM	CZO	FEP	CFM	CTX	FOX	CPD	CAZ	CZA	CZT	CRO	CXM	CXA	CEP	PEN	PIP	TZP	TIC	TCC	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	ATM	CHL	COL	FOS	NIT	TCY	TGC	SXT	MNO
Achromobacter xylosoxidans	97					17					68								78	81	4	80				10	5	9	8				71	81	0		33					92	64
Pseudomonas sp.	96					91					82									92						98	93		91	92			95	95								73	
Serratia sp.	88	0	0		0	83					76			69	0					99						90	87		88	85		97	82	99					11			90	
Proteus sp.	81	50	13		27	85					85			68	34					98						91	75		73	58		100	32	99					4			72	
Salmonella Typhi	77	0	56			57		58			8			90						0							0		10		0	100	100	100					0			78	
Providencia stuarti	64		17			95		96	100	96	94				81	92	4			100						92	60	63	69		96	90	30	100				0	0	0		87	
Haemophilus parainfluenzae	59		42											98	80								79						76	83			96	100		100				50		40	
Providencia rettgeri	56	5	34		13	100		91			98			91	82					87						96	88		76		100	92	61	91				5	10			89	
Burkholderia cepacia	55					10					80								43	3	0	0				23	3	6	3				0	91	14		0					87	43
Citrobacter braakii	50	50	28		58	94					86			97	78					90						100	100		82			96	93	96					92			80	
Pseudomonas putida	40					95					80									70						97	95	88	88				88	78								19	
Pseudomonas stutzeri	40					100					100								93	94	0	93				97	98	94	95				94	95								87	86
Aeromonas hydrophila	34					97					91									47						100	100		88				36									94	
Acinetobacter lwoffii	33					100					80									44							97	95	93				100	97								89	
Sphingomonas paucimobilis	31					87					75									82						96	90		70				86	89								86	
Enterobacter gergoviae	29	89				93					93									93						100	97		90			89	93	93					79			93	
Moraxella sp.	29	78																					93		96															67		70	
Gram negative rods	28										61									77							87		56				81	83								78	
Proteus vulgaris	28	64	4			96					84				4					100							82		70			90	14	93					5			75	
Citrobacter farmer	27	81	10		52	75					82			61	54					96						100	89		58			92	96	100					96			77	
Cronobacter sakazakii	26	67	17		52	96					91			91	78					96							100		96			96		100								96	
Achromobacter denitrificans	25					22					80									92						17	8		4				81	88								96	
Proteus penneri	24		4								100									96							92		67					100					0			62	
Salmonella Paratyphi A	24					45																							9													100	
Burkholderia cepacia complex	23										96																							91									83	
Burkholderia cenocepacia (genomovar III)	20					10					75															5	5		0					95									65	

Code	Antibiotic	Code	Antibiotic	Code	Antibiotic	Code	Antibiotic	Code	Antibiotic	Code	Antibiotic
AMK	Amikacin	FEP	Cefepime	CZT	Ceftolozane/Tazobactam	CLR	Clarithromycin	LVX	Levofloxacin	TCY	Tetracycline
AMC	Amoxicillin/Clavulanic acid	CFM	Cefixime	CRO	Ceftriaxone	COL	Colistin	MEM	Meropenem	TIC	Ticarcillin
AMP	Ampicillin	CTX	Cefotaxime	CXM	Cefuroxime	ETP	Ertapenem	NIT	Nitrofurantoin	TCC	Ticarcillin/Clavulanic acid
SAM	Ampicillin/Sulbactam	FOX	Cefoxitin	CXA	Cefuroxime axetil	ERY	Erythromycin	NOR	Norfloxacin	TGC	Tigecycline
AZM	Azithromycin	CPD	Cefpodoxime	CEP	Cephalothin	FOS	Fosfomycin	PEN	Penicillin G	TOB	Tobramycin
ATM	Aztreonam	CAZ	Ceftazidime	CHL	Chloramphenicol	GEN	Gentamicin	PIP	Piperacillin	SXT	Trimethoprim/Sulfamethoxazole
CZO	Cefazolin	CZA	Ceftazidime/Avibactam	CIP	Ciprofloxacin	IPM	Imipenem	TZP	Piperacillin/Tazobactam	MNO	Minocycline

4.2.3 Dubai Emirate

Table 4.2.3.1 Dubai Emirate Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=32,254)

		Beta Lactams														Macrolides		Aminoglycosides			Fluroquinolones			Glycopeptides		Others													
Organism	Isol	AMX	AMC	AMP	CZO	FEP	CFM	CTX	FOX	CPT	CRO	CXM	CXA	OXA	PEN	AZM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	DAP	FUS	LNZ	MEM	MTR	MUP	NIT	QDA	RIF	TCY	TGC	SXT
Staphylococcus aureus	9,812							69	66	100				68	12		65	89			66	67	68	100	100		86	100	36	100			22	99	88	100	88	100	81
Streptococcus pyogenes	9,708	100	100			100		98			96				98		48					91		100		98	76			100						78		
Streptococcus, beta-haem. Group B	2,287	100	100	100	100	100	100	99			100	100	100		100	20	38					85		100		91	37	100		100	100			94			11		
Streptococcus pneumoniae	2,209	93				94		94				59			94		37					91	92	100		93	65			100	67						47		56
Streptococcus agalactiae	2,141	100	100	98		99		99							99		28					83	2	99		93	43	100		99							13	96	
Enterococcus faecalis	1,426		98	99					0			0			98		12	34	78	60	63	74	83	99	100			91		96				98	6		25	100	
Staphylococcus saprophyticus	908							67	59					42	3		38	99			99	99	99	100	100		80	100	0	99			28	99	93	100	93	38	94
Staphylococcus epidermidis	573		22						22					25	7		28	69			53	59	55	100	93		58		12	99				100	96	95	78	77	73
Staphylococcus haemolyticus	423							39	13					30	5		24	75			58	61	49	100	98		58	100		100			18	100	88	95	56	50	77
Streptococcus mitis	382	3		65		94		92			88				83		16					89		100		98	92	100		100	99						20		
Streptococcus, beta-haem. Group A	267			99											97												80												
Staphylococcus hominis	251								32					37	11		21	96			72	76	72	99	94		65		12	97				95	93	98	77	79	85
Streptococcus, beta-haem. Group G	229														100		20										47												
Enterococcus faecium	207		17	24					0			0			33		8	20	71	43	24	31		91	90					96				23			31	81	
Staphylococcus capitis	156		26						29			24		34	15		32	56			49	64	48	99	89		36		12	97				100	100	87	97	87	96
Staphylococcus lugdunensis	116		83					87	73					79	42		77	96			96	99	95	99	97		80	100	59	99			71	100	92	99	93	70	100
Streptococcus anginosus	115			97		100		96			97				95		59					87	83	98		66	74			91							51	97	
Gardnerella vaginalis	110																										92					25							
Enterococcus sp.	91			94											38						71			99						99				91			47		
Streptococcus dysgalactiae	74	100		96		100		100			96				99		39					98		100		97	66			100									
Streptococcus constellatus	68			93		100		96			98				98		66					90		98			80			100							64		

		Beta Lactams														Macrolides		Aminoglycosides			Fluroquinolones			Glycopeptides		Others																
Organism	Isol	AMX	AMC	AMP	CZO	FEP	CFM	CTX	FOX	CPT	CRO	CXM	CXA	OXA	PEN	AZM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	DAP	FUS	LNZ	MEM	MTR	MUP	NIT	QDA	RIF	TCY	TGC	SXT
Streptococcus dysgalactiae ss. equisimilis	68			100		100		100			100				98		35					95	6	98		93	61			98							52	100	6
Staphylococcus, coagulase negative	64								68					35	24		54	93			75	70		100			73			100				87			73		91
Streptococcus, beta-haem. Group F	56														100		57										66												
Staphylococcus warneri	49								54					55	14		45	84			82	92	86	100			71			100				92	88	96	96	70	96
Streptococcus, beta-haem. Group C	33														91		54										73												
Streptococcus sp.	32					91		83							73		32					84		92			77										46		
Streptococcus, beta-haemolytic	31	93	97			100	100	100			100	100			97	26	23					97		100		93	39	100		100	100						29		
Enterococcus avium	31			64											60		21		100	58	82			100	100					97							48	86	
Enterococcus gallinarum	27			96											71		33		96	52	56			11	100					93							48	85	
Staphylococcus intermedius	25													48			50	88			92	92	100	100			64	100		100						100	80		92
Streptococcus salivarius	24					100					100													100															
Streptococcus gordonii	23										96				75												65												

Code	Antibiotic	Code	Antibiotic	Code	Antibiotic
AMX	Amoxicillin	CHL	Chloramphenicol	MUP	Mupirocin
AMC	Amoxicillin/Clavulanic acid	CIP	Ciprofloxacin	NIT	Nitrofurantoin
AMP	Ampicillin	CLI	Clindamycin	OXA	Oxacillin
AZM	Azithromycin	DAP	Daptomycin	PEN	Penicillin G
CZO	Cefazolin	ERY	Erythromycin	QDA	Quinupristin/Dalfopristin
FEP	Cefepime	FUS	Fusidic acid	RIF	Rifampin
CFM	Cefixime	GEN	Gentamicin	STH	Streptomycin-High
CTX	Cefotaxime	GEH	Gentamicin-High	TEC	Teicoplanin
FOX	Cefoxitin	LVX	Levofloxacin	TCY	Tetracycline
CPT	Ceftaroline	LNZ	Linezolid	TGC	Tigecycline
CRO	Ceftriaxone	MEM	Meropenem	SXT	Trimethoprim/Sulfamethoxazole
CXM	Cefuroxime	MTR	Metronidazole	VAN	Vancomycin
CXA	Cefuroxime axetil	MFX	Moxifloxacin		

Table 4.2.3.2 Dubai Emirate Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=39,041)

		Beta Lactams															Macrolides		Aminoglycosides			Fluroqinolones				Carbepenems			Others						
Organism	Isol	AMC	AMP	CZO	FEP	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	TZP	PEN	AZM	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	CHL	COL	FOS	NIT	TCY	TGC	SXT
Escherichia coli	18,191	77	36	57	70		60	68		96	64	60	57	94				99	90		51	57		66	98	96	99			98	96			61
Klebsiella pneumoniae	6,114	80	0	69	79	76	70	73		92	76	69	68	88				98	93		69	83		86	94	94	96			53	32		92	79
Pseudomonas aeruginosa	3,719				92		0	91	89	95	1			91				98	95	96	89	88		87		84	90		56					
Haemophilus influenzae	2,722	84	49			88					79					88					91	94						93						
Proteus mirabilis	856	82	68	75	88	90	82	89		90	88	86	86	99				90	73		62	63		83	96	30	96			62	1			65
Enterobacter cloacae	847	5	6	7	90		57	73		90	75	42	37	76				99	95		80	84		93	93	90	98			39	35		93	86
Klebsiella aerogenes	811	3		6	93		63	80		96	81	52	33	82				99	98		88	97			96	77	98			54	20		95	95
Citrobacter koseri	746	95		93	97		92	94		97	94	85	68	96				100	100		93	95		99	97	98	99			63	69			98
Serratia marcescens	547	2		0	96		78	90		90	89	1	3	92				97	97	89	90	97		99	95	65	95			63	0		43	98
Acinetobacter baumannii	437			0	85		42	83			64	1		82				88	88	78	83	86				88	86				0			90
Salmonella sp.	396	25	80	2	25			26		30	93	1	68	27				2	2		64	59			99	99	99			7	13		94	97
Haemophilus sp.	343	69	61					81			82	60				93					93	96	98				100							47
Stenotrophomonas maltophilia	318							51														87												91
Klebsiella oxytoca	300	84	1	67	92		84	91		95	90	85	83	96				100	97		82	84			95	93	98			52	76		93	88
Morganella morganii	261	2	3	2	94		44	70		94	74	3	7	85				98	88	94	54	48		86	96	15	98			7	0			74
Moraxella sp.	253	92					99	98			98	89					83				98	98					100							56
Neisseria gonorrhoeae	195					93					97				16	94					3											16		
Citrobacter freundii	147	22	0	12	90		74	85		94	86	33	55	90				99	90		74	71		94	96	91	98			52	98		95	84
Enterobacter cloacae complex	134	0		0	92			79			78	0	0	87				99	95		80				94	98	99			48	54			90
Acinetobacter calcoaceticus-baumannii complex	102			0	86			86			73	6		86				89	85		87	87				90	91				0			92
Salmonella Typhi	65	47	59	0	40			39		46	77	0		49				0	0		8	46			100	100	100			33	43		100	67
Pseudomonas putida	63				97			92			58			89				96	98		90	88				95	94							31
Moraxella catarrhalis	60	91	56				100	100			100					86	81				92	92												66

		Beta Lactams														Macrolides		Aminoglycosides			Fluroqinolones				Carbepenems			Others					
Organism	Isol	AMC	AMP	CZO	FEP	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	TZP	PEN	AZM	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	CHL	COL	FOS	NIT	TCY	TGC	SXT
Klebsiella pneumoniae ss. ozaenae	57	75	6	67	84			82		93	80	78	70	95				95	95		72				93	91	98			44	55		80	90
Burkholderia cepacia	53				16		8	90			5			18				16	13		26	65		48		16	86							82
Acinetobacter sp.	51	0	4	4	90	71		88			70	0		87		56		96	90		88	91			22	91	94							94
Salmonella Group D (D1, D2, D3)	47		93								98					97		5			83	78			100		100							100
Vibrio cholerae	47		34													94															92		79
Achromobacter sp	42				24			67			4			95				24	14		17	55				84								98
Citrobacter farmer	39	69	23	45	67			71			64	57		100				100	90		41	42			97	92	100				86			72
Klebsiella sp.	39	47	0	25	73	54		70		88	66	46		89		50		100	97		81	81			84	82	95						85	70
Citrobacter sp.	37	56	0	41	86			67		92	63	30		78				100	97		81	78			86	94	97				77			89
Enterobacter sp.	36	23	10	17	86			83		96	71	52		94				100	100		85	83			91	85	94						96	74
Providencia stuarti	36				91			94			94	89		94				97	40		84				91	34	91			21	0			94
Salmonella Group B (O:4)	34		81								97					96					85	84												90
Achromobacter xylosoxidans	32				25			78						90				4	3		19					77	86							97
Serratia sp.	31	7			100		91	33			43	0		36				100	100	100	97	100		100	100		100			83	0			100
Salmonella enterica ss. enterica (Subgroup I)	31	0		0	0			0			84	0	64	0				0	0		64				100	100	100			0	0			100
Acinetobacter lwoffii	28				86			82			65							90	89		79					88	92							71
Pseudomonas stutzeri	28				96			93						96				96			96					96	96							89

		Beta Lactams														Macrolides		Aminoglycosides			Fluroqinolones				Carbepenems			Others							
Organism	Isol	AMC	AMP	CZO	FEP	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	TZP	PEN	AZM	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	CHL	COL	FOS	NIT	TCY	TGC	SXT
Proteus vulgaris	27	74	10		89			85			60			100				100	100		82				96	4	96							80
Haemophilus parainfluenzae	26		80																															
Pseudomonas sp.	26				92			88						96				90			88	87				91	90							
Sphingomonas paucimobilis	26				88			77			86			86					72		73					84	83							88
Shigella sonnei	25	42			29			33			35			39				0	0		48				100	100	100				38			18
Enterobacter gergoviae	23	61		60	87			87			86			96				100	100						96	83	100							95
Providencia rettgeri	22							85						86				81	86						76	29	86							85
Citrobacter braakii		45			90			80			75			95					90							90	100							
Pantoea agglomerans	21	90			81			86						95				100	100						81		95							95
Salmonella Group A (O:2)	20		90								100										90														95

Code	Antibiotic	Code	Antibiotic	Code	Antibiotic
AMK	Amikacin	CRO	Ceftriaxone	LVX	Levofloxacin
AMC	Amoxicillin/Clavulanic acid	CXM	Cefuroxime	MEM	Meropenem
AMP	Ampicillin	CXA	Cefuroxime axetil	MFX	Moxifloxacin
AZM	Azithromycin	CHL	Chloramphenicol	NIT	Nitrofurantoin
CZO	Cefazolin	CIP	Ciprofloxacin	NOR	Norfloxacin
FEP	Cefepime	COL	Colistin	PEN	Penicillin G
CFM	Cefixime	ETP	Ertapenem	TZP	Piperacillin/Tazobactam
CTX	Cefotaxime	ERY	Erythromycin	TCY	Tetracycline
CAZ	Ceftazidime	FOS	Fosfomycin	TGC	Tigecycline
CZA	Ceftazidime/Avibactam	GEN	Gentamicin	TOB	Tobramycin
CZT	Ceftolozane/Tazobactam	IPM	Imipenem	SXT	Trimethoprim/Sulfamethoxazole

4.2.4 Northern Emirates

Table 4.2.4.1 Northern Emirates Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=11,754)

		Beta Lactams								Macrolides	Aminoglycosides			Fluroqinolones			Glycopeptides		Others									
Organism	Isol	AM	AM	CTX	FOX	CRO	OXA	PEN	PNV	ERY	GEN	GEH	STH	CIP	LVX	MFX	TEC	VAN	CHL	CLI	DAP	DOX	LNZ	NIT	TCY	TGC	SXT	QD	RIF
Staphylococcus aureus	4,124				38		45			62	89			61	62	63		99		85	100	98	100	100	85	100	79		100
Streptococcus agalactiae	2,370		100	100		100		99		43					89	22		100	96	57			100		16	100	10		
Enterococcus faecalis	1,102		99					93		10			0	69	72			99			58	31	96	98	26	97			
Streptococcus pyogenes	1,035	1	99	100		100		99	0	44					81	13		100	100	92			100		82	100	13		
Staphylococcus epidermidis	714				19		22			22	64			46	47	46		99		52	100	88	100	98	79	19	65		90
Streptococcus pneumoniae	368			94		96		92		36					94	98		100	93	68			100		47	100	66		100
Staphylococcus hominis	356				27		36			26	97			66	68	68		100		72	100	94	100	94	72	17	76		97
Staphylococcus capitis	295				18		20			26	34			28	27	28		100		42	100	100	100	100	99	9	79		69
Staphylococcus haemolyticus	290				13		15			13	60			35	37	35		99		46	100	70	99	98	60	18	78		79
Staphylococcus saprophyticus	178				26		34	15		32	99			97	95	81	100	99		66	99	99	99	98	90	16	90		98
Enterococcus faecium	117		27					17		7	3		0	19	22			90				35	95	14	30	4		74	
Streptococcus, beta-haem. Group A	72		100							71					76					81									
Streptococcus dysgalactiae ss. equisimilis	72	3	91	98		97		97	0	26					94	9		97	100	73			100		59				
Streptococcus anginosus	62		80	94		91		85		55					96	92		98	62	69			98		57	100			
Streptococcus mitis	56		48	86		86		30		33					74	78		100	100	94			100		57	100			
Staphylococcus lugdunensis	55				64		63			82	88			89	89	86		100		80	100	100	100	100	98	33	100		100
Streptococcus dysgalactiae	50	0							0	37										81									
Enterococcus sp.	49		89									88		73	71			93					96	91	34				
Staphylococcus warneri	46						56			44	77			71	73	76		100		80	100	98	100	100	87	27	98		98
Gram positive cocci	32																	100											
Staphylococcus, coagulase negative	30				70					38	85			73	72					65			100		75				
Streptococcus sp.	29		96							29					15	78		100		81			100		52				
Streptococcus sanguinis	25		68	90		90		85		56					96	96		100		90			100		72				
Streptococcus viridans, alpha-hem.	25		75	78		83		68										96		91									
Enterococcus avium	20																	100											

Code	Antibiotic
AMX	Amoxicillin
AMP	Ampicillin
CTX	Cefotaxime
FOX	Cefoxitin
CRO	Ceftriaxone
CHL	Chloramphenicol
CIP	Ciprofloxacin
CLI	Clindamycin
DAP	Daptomycin
DOX	Doxycycline
ERY	Erythromycin
GEN	Gentamicin
GEH	Gentamicin-High
LVX	Levofloxacin
LNZ	Linezolid
NIT	Nitrofurantoin
OXA	Oxacillin
PEN	Penicillin G
PNV	Penicillin V
TEC	Teicoplanin
TCY	Tetracycline
TGC	Tigecycline
SXT	Trimethoprim/Sulfamethoxazole
VAN	Vancomycin
MFX	Moxifloxacin
QDA	Quinupristin/Dalfopristin
RIF	Rifampin
STH	Streptomycin-High

Table 4.2.4.2 Northern Emirates Cumulative Antibiogram (2023): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=19,171)

		Beta Lactams																	Aminoglycosides			Fluroqinolones			Carbepenems			Others							
Organism	Isol	AMC	AMP	CEC	CZO	FEP	CFM	CTX	FOX	CAZ	CRO	CXM	CXA	CEP	PIP	TZP	TIC	TCC	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	ATM	COL	FOS	MNO	NIT	TCY	TGC	SXT
Escherichia coli	7,985	75	33		36	76		61		69	58	52				93			96	88		43		66	98	98	98			98		94			60
Klebsiella pneumoniae	3,799	76	1		52	78		67		69	68	63				82			92	89		62		82	91	90	92			11		24		78	74
Pseudomonas aeruginosa	2,382				1	89				86					72	78	10	43	97	91	94	84				84	85		16						
Enterobacter cloacae	582	10			7	94		82	2	82	76	46				87			98	96		81			94	95	98			5		40		90	89
Acinetobacter baumannii	526				0	85		42		86	58					80			93	89		84				91	90								92
Proteus mirabilis	500	65	54		51	83		76		84	82	82				97			87	75		58		78	96	20	97			17		1		21	58
Citrobacter koseri	438	95			85	96		92		94	89	76				96			99	99		86		99	99	98	98			12		80		85	97
Klebsiella aerogenes	416	10			11	94		74		79	80	71				81			98	96		84		94	94	80	96			8		22		85	93
Stenotrophomonas maltophilia	372																																		87
Serratia marcescens	355	5			0	96		89	11	95	92	0							98	97		84		97	97	92	96			11		0		91	98
Morganella morganii	218	1	1		0	95		65	34	78	72	3		0		97			96	82		43			98	13	98			0		1		67	64
Salmonella sp.	156	30	79		0	32			0	32	95	0				33			0	0		78			95	97	98			14		36		96	98
Klebsiella oxytoca	155	85	5		65	89	78	85		86	82	72				92			99	95		79	69		96	96	97			11		68		90	86
Haemophilus influenzae	99	86	35								50	80	82									34					14								
Burkholderia cepacia	96				0	17		0		94	0					7			54	11		2				10	92								84
Citrobacter freundii	87	32	12		10	88		68	24	74	61	37				86			92	89		63	59	85	92	90	95			13		91		83	73
Achromobacter xylosoxidans	86				0	17		4		91	3				96	92			28	15	10	5				73	89	5	29		56				96
Neisseria gonorrhoeae	65						50				56											7											2		
Providencia stuarti	63		0			100		100		93	92	74				97			98	58		52			96	37	94			9		0		15	84
Acinetobacter lwoffii	50					79				79	54					57			89	85		64				96	96								87
Klebsiella pneumoniae ss. ozaenae	50	76	14			80				70	76	76				86			94	94		65			94	91	94			11		46			88
Providencia rettgeri	38		30			95				90	90					87			97	92		82			91	68	87			8		45			97
Sphingomonas paucimobilis	32					70				53						73			89	90		73				80	80								77
Enterobacter cloacae complex	30	0		4		93	40	71		76	73	10		0		83			100	93	93	90			97	97	97					50	90		93
Gram negative rods	30					59				63						67			93	86		32				70	85								76
Pseudomonas putida	28					85				85						65			96			78				82	89								14
Elizabethkingia meningoseptica	26					8				0						0			8	4		42				0	0								48
Acinetobacter calcoaceticus-baumannii complex	24									83										96		96				100	100								100
Pseudomonas fluorescens	23					91										68			90			82				68	70								
Proteus sp.	22					100				100						100			100	100		71				14	96								82
Aeromonas hydrophila	21					95				95									100	100		95				29									95

Code	Antibiotic
AMK	Amikacin
AMC	Amoxicillin/Clavulanic acid
AMP	Ampicillin
ATM	Aztreonam
CEC	Cefaclor
CZO	Cefazolin
FEP	Cefepime
CFM	Cefixime
CTX	Cefotaxime
FOX	Cefoxitin
CAZ	Ceftazidime
CRO	Ceftriaxone
CXM	Cefuroxime
CXA	Cefuroxime axetil
CEP	Cephalothin
CIP	Ciprofloxacin
COL	Colistin
ETP	Ertapenem
FOS	Fosfomycin
GEN	Gentamicin
IPM	Imipenem
LVX	Levofloxacin
MEM	Meropenem
MNO	Minocycline
NIT	Nitrofurantoin
PIP	Piperacillin
TZP	Piperacillin/Tazobactam
TCY	Tetracycline
TGC	Tigecycline
TOB	Tobramycin
SXT	Trimethoprim/Sulfamethoxazole
NOR	Norfloxacin
TIC	Ticarcillin
TCC	Ticarcillin/Clavulanic acid

4.3 Multidrug resistance

4.3.1 MDR, XDR, PDR Summary

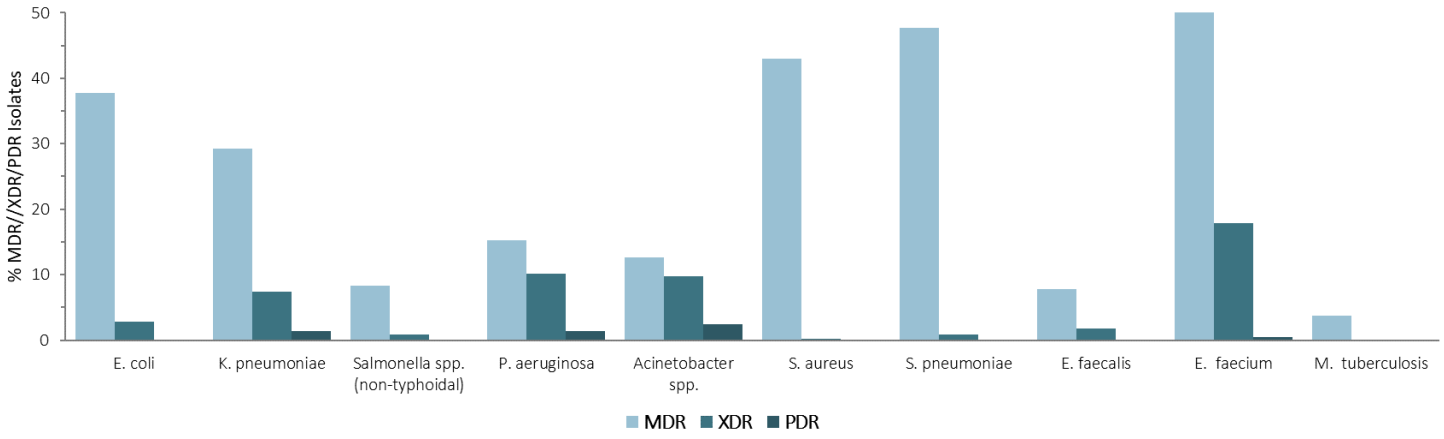
In a 2012 publication, the European Centre for Disease Prevention and Control (ECDC) proposed definitions for common bacterial pathogens resistant to multiple antimicrobials (Magiorakos, et al., 2012). Similar definitions were applied for organisms where these were not available from this publication (*S. pneumoniae*). 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, 2023

Organism	Number of isolates	MDR	Possible XDR	Possible PDR
Escherichia coli	51,511	19,441 (37.7%)	1,447 (2.8%)	14 (0%)
Klebsiella pneumoniae	19,869	5,816 (29.3%)	1,478 (7.4%)	273 (1.4%)
Salmonella spp. (non-typhoidal)	957	78 (8.3%)	9 (0.9%)	0 (0%)
Pseudomonas aeruginosa	11,981	1,829 (15.3%)	1,217 (10.2%)	170 (1.4%)
Acinetobacter sp.	2,270	287 (12.6%)	221 (9.7%)	54 (2.4%)
Staphylococcus aureus	24,833	10,682 (43.0%)	46 (0.2%)	3 (0%)
Streptococcus pneumoniae	2,707	1,290 (47.7%)	22 (0.8%)	3 (0.1%)
Enterococcus faecalis	3,994	312 (7.8%)	70 (1.8%)	0 (0%)
Enterococcus faecium	395	214 (54.2%)	71 (17.9%)	2 (0.5%)
Mycobacterium tuberculosis	1,200	44 (3.7 %)	No data	No data
Total	118,517	39,949 (33.7%)	4,581 (3.9%)	519 (0.4%)

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

Figure 4.3.1 MDR, XDR, PDR Summary, United Arab Emirates, 2023



4.4 AMR priority pathogens

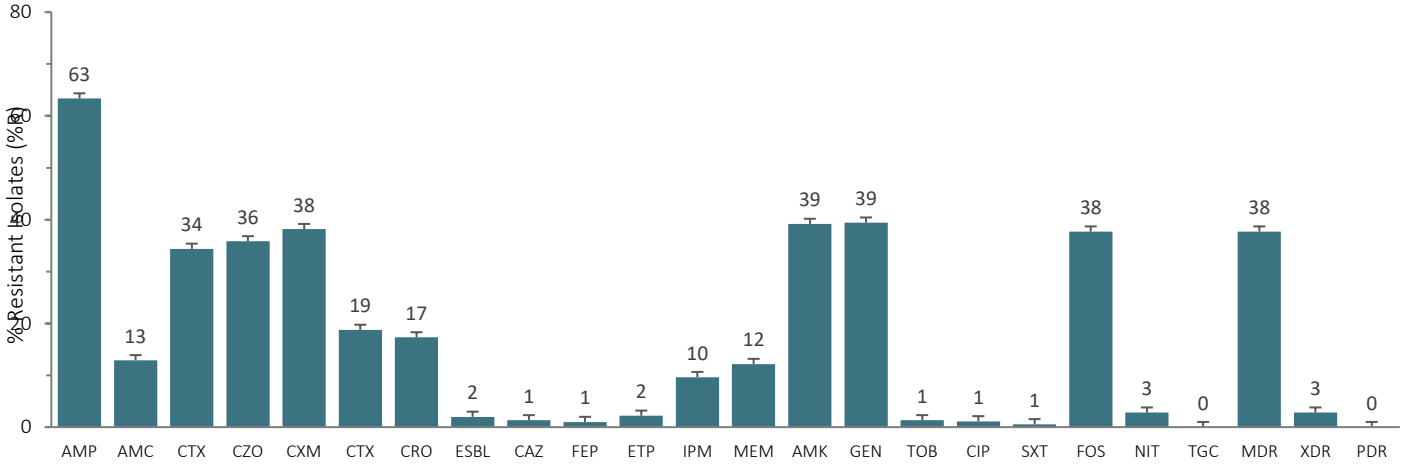
4.4.1 *Escherichia coli*

Table 4.4.1.1 Percentages of resistant, intermediate, and susceptible isolates for *Escherichia coli*, isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Escherichia coli* (N=51,511)			
		Isolates (N)	% R	% I	% S
Ampicillin	AMP	23,530	63.3	1.0	35.6
Amoxicillin/clavulanic acid	AMC	30,877	12.9	10.2	76.9
Piperacillin/tazobactam	TZP	32,025	5.8	1.4	92.1
Cefuroxime (oral)	CXM	20,483	38.0	6.0	55.3
Ceftriaxone	CRO	19,120	35.8	0.2	64.0
Cefotaxime	CTX	13,385	34.4	1.2	64.3
Extended-spectrum β-lactamase	ESBL	9,094	38.5	–	61.5
Ceftazidime	CAZ	31,880	18.7	5.8	75.5
Cefepime	FEP	28,493	17.3	4.3	77.9
Ertapenem	ETP	27,005	2.0	0.3	97.7
Imipenem	IPM	30,851	1.3	1.1	97.6
Meropenem	MEM	32,067	1.0	0.2	98.8
Gentamicin	GEN	32,364	9.6	0.4	89.3
Tobramycin	TOB	5,246	12.2	0.5	83.5
Amikacin	AMK	28,559	2.2	1.5	80.9
Ciprofloxacin	CIP	30,008	39.2	11.7	44.8
Trimethoprim/sulfamethoxazole	SXT	31,856	39.4	0.0	60.6
Fosfomycin[a]	FOS	19,231	1.2	0.2	98.4
Nitrofurantoin[a]	NIT	30,703	1.1	3.4	95.5
Tigecycline[b]	TGC	4,382	0.5	0.6	90.7
Multidrug-resistance (≥3 classes NS)[c]	MDR	51,511	37.7	–	–
Extensive drug resistance (possible)	XDR	51,511	2.8	–	–
Pan-drug resistance (possible)	PDR	51,511	0.0	–	–

[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, 2023



For 2023, resistance in *Escherichia coli* ranged from 1.0% for carbapenems (Meropenem) to 63% for aminopenicillins (ampicillin). Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *E. coli* was 37.7%, 2.8%, and 0%, respectively.

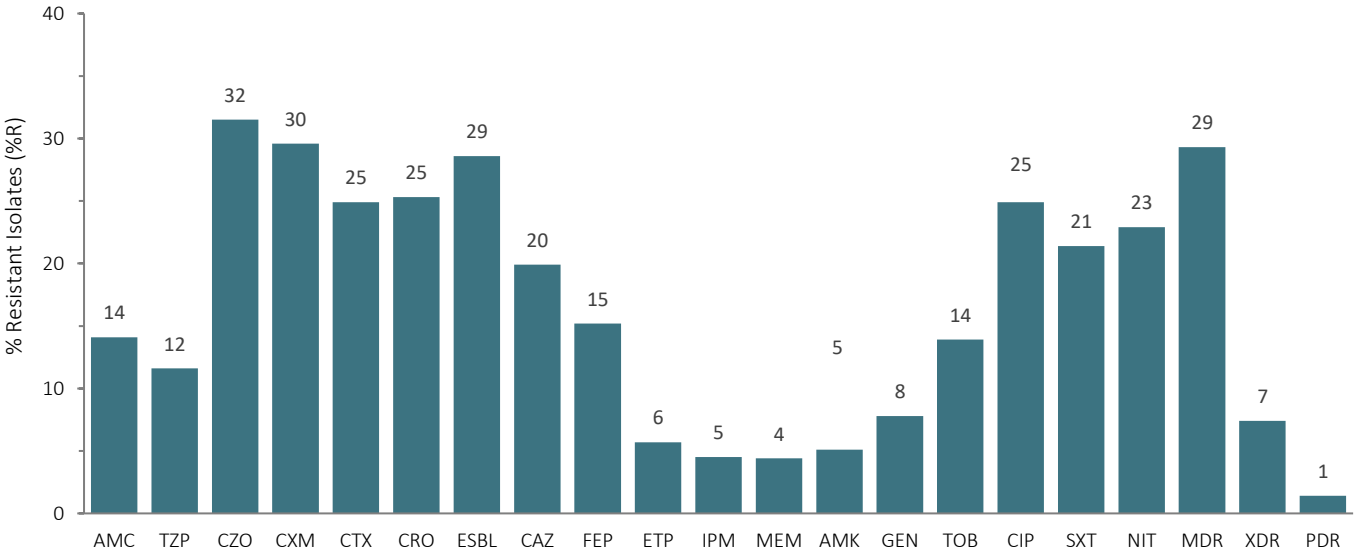
4.4.2 *Klebsiella pneumoniae*

Table 4.4.2.1 Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae*, isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Klebsiella pneumoniae* (N=19,869)			
		Isolates (N)	% R	% I	% S
Amoxicillin/clavulanic acid	AMC	12386	14.1	6.4	79.5
Piperacillin/tazobactam	TZP	13061	11.6	4.0	83.7
Cefuroxime (oral)	CXM	7795	29.6	2.8	67.0
Ceftriaxone	CRO	7449	25.3	0.4	74.3
Cefotaxime	CTX	5810	24.9	2.1	72.9
Extended-spectrum β-lactamase	ESBL	5,958	28.6	–	71.4
Ceftazidime	CAZ	13,026	19.9	4.4	75.7
Cefepime	FEP	11,526	15.2	2.1	82.6
Ertapenem	ETP	10,331	5.7	0.7	93.6
Imipenem	IPM	12,458	4.5	1.8	93.7
Meropenem	MEM	13,139	4.4	0.3	95.2
Gentamicin	GEN	13,248	7.8	0.3	91.3
Tobramycin	TOB	2,567	13.9	0.4	82.8
Amikacin	AMK	11,519	5.1	0.3	81.6
Ciprofloxacin	CIP	12,416	24.9	6.2	63.6
Trimethoprim/sulfamethoxazole	SXT	13,081	21.4	0.0	78.6
Nitrofurantoin[a]	NIT	12,021	22.9	49.2	27.9
Multidrug-resistance (≥3 classes NS)[b]	MDR	19,869	29.0	–	–
Extensive drug resistance (possible)	XDR	19,869	7.0	–	–
Pan-drug resistance (possible)	PDR	19,869	1.4	–	–

[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, 2023



For 2023, resistance in *Klebsiella pneumoniae* ranged from 4.4 %R for meropenem (Carbapenems), to 30 %R for cefuroxime (CXM).

Non-susceptibility (%R+%I) to carbapenems was 4.5%, 4.4%, and 5.7 %NS for imipenem, meropenem and ertapenem, respectively.

Prevalence of multidrug resistance (%MDR/XDR/PDR[8]) in *K. pneumoniae* was 29.0 %, 7.0%, and 1.4%, respectively.

4.4.3 *Salmonella spp. (non-typhoidal)*

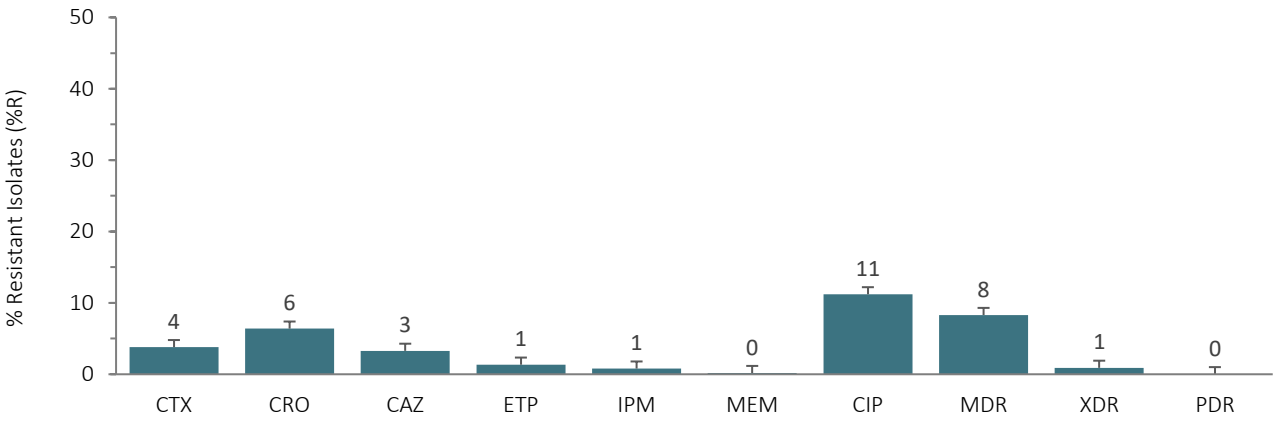
Table 4.4.3.1 Percentages of resistant, intermediate, and susceptible isolates for *Salmonella* spp. (non-typhoidal), isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Salmonella* spp. (non-typhoid) (N=1,616)			
		Isolates (N)	% R	% I	% S
Cefotaxime	CTX	365	3.3	0.0	96.7
Ceftriaxone	CRO	551	7.8	0.0	92.0
Ceftazidime	CAZ	901	0.3	0.0	99.7
Ertapenem	ETP	801	1.2	0.1	98.6
Imipenem	IPM	882	1.1	0.7	98.2
Meropenem	MEM	892	0.2	0.1	99.7
Ciprofloxacin[a]	CIP	573	11.2	5.8	45.7
Multidrug-resistance (≥3 classes NS)[b]	MDR	957	8.3	–	–
Extensive drug resistance (possible)	XDR	957	0.9	–	–
Pan-drug resistance (possible)	PDR	957	0.0	–	–

[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).

[8] Possible XDR, possible PDR

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, 2023



For 2023, resistance in *Salmonella* spp. (non-typhoidal) ranged from 0.2 %R for carbapenems (meropenem), to 11.2 %R for fluoroquinolones (ciprofloxacin, extraintestinal isolates).

Susceptibility of non-typhoidal *Salmonella* spp. (extra-intestinal isolates) to ciprofloxacin was 46%.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *Salmonella* spp. (non-typhoidal) was 8.3 %, 0.9% and 0%, respectively.

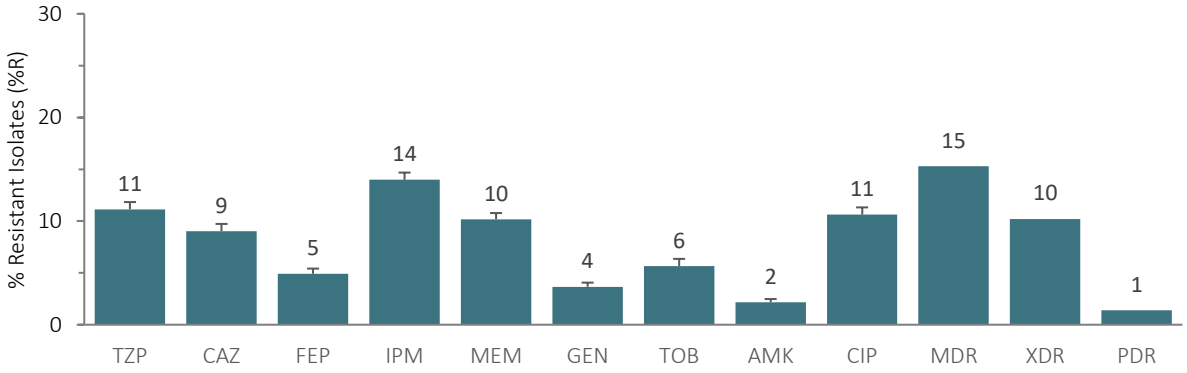
4.4.4 *Pseudomonas aeruginosa*

Table 4.4.4.1 Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa*, isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Pseudomonas aeruginosa* (N=11,981)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	8,289	11.1	4.4	84.4
Ceftazidime	CAZ	8,586	9.0	3.6	87.4
Cefepime	FEP	8,605	4.9	4.4	90.5
Imipenem	IPM	8,554	14.0	3.2	82.9
Meropenem	MEM	8,588	10.2	4.4	85.4
Gentamicin	GEN	6,880	3.7	4.4	92.0
Tobramycin	TOB	4,158	5.7	1.7	91.6
Amikacin	AMK	8,353	2.2	0.8	97.0
Ciprofloxacin	CIP	8,625	10.6	4.2	84.7
Multidrug-resistance (≥3 classes NS)[a]	MDR	11,981	15.3	–	–
Extensive drug resistance (possible)	XDR	11,981	10.2	–	–
Pan-drug resistance (possible)	PDR	11,981	1.3	–	–

[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, 2023



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.

4.4.5 *Acinetobacter spp.*

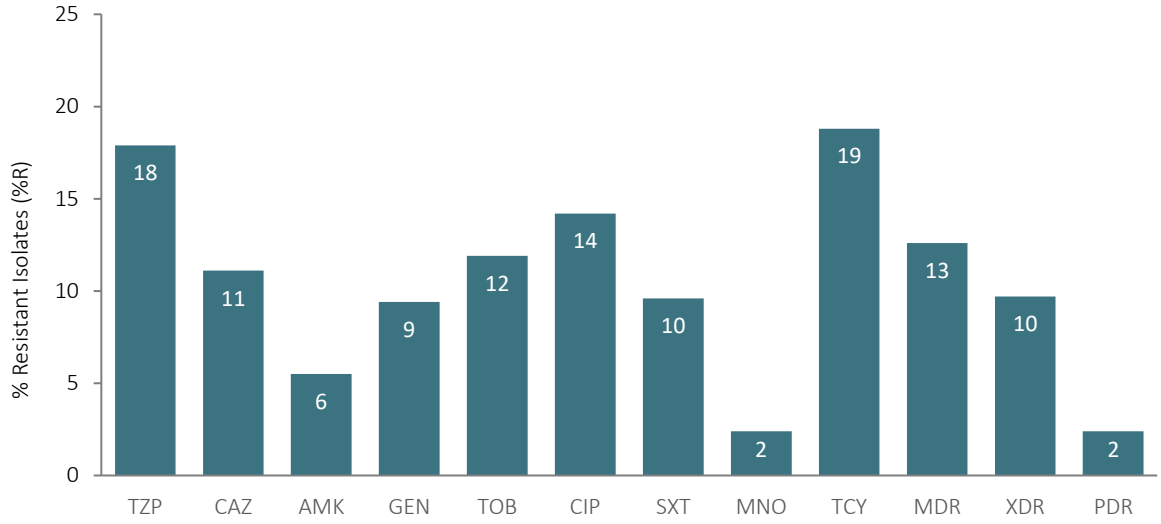
Table 4.4.5.1 Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp., isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Acinetobacter* spp. (N=2,270)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	1,491	17.9	4.2	77.9
Ceftazidime	CAZ	1,561	11.1	5.1	83.7
Cefepime	FEP	1,452	11.2	3.1	85.4
Imipenem	IPM	1,488	10.3	0.2	89.5
Meropenem	MEM	1,564	10.3	0.7	89.0
Gentamicin	GEN	1,577	9.4	2.0	88.6
Tobramycin	TOB	540	11.9	2.4	85.7
Amikacin	AMK	841	5.5	1.4	91.9
Ciprofloxacin	CIP	1,575	14.2	1.5	84.3
Trimethoprim/Sulfamethoxazole	SXT	1,555	9.6	0.0	90.4
Minocycline	MNO	381	2.4	5.5	92.1
Tetracycline	TCY	112	18.8	2.7	78.6
Multidrug-resistance (≥3 classes NS)[a]	MDR	2,270	12.6	–	–
Extensive drug resistance (possible)	XDR	2,270	9.7	–	–
Pan-drug resistance (possible)	PDR	2,270	2.4	–	–

[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).
[d] Includes duplicate isolates.

[9] Possible XDR, possible PDR

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, 2023



For 2023, resistance in *Acinetobacter* spp. ranged from 2.4 %R for minocycline to 18.8 %R for tetracycline.

Prevalence of multidrug resistance (%MDR/XDR/PDR[10]) in *Acinetobacter* spp. was 12.6 %, 9.7%, and 2.4%, respectively.

4.4.6 *Staphylococcus aureus*

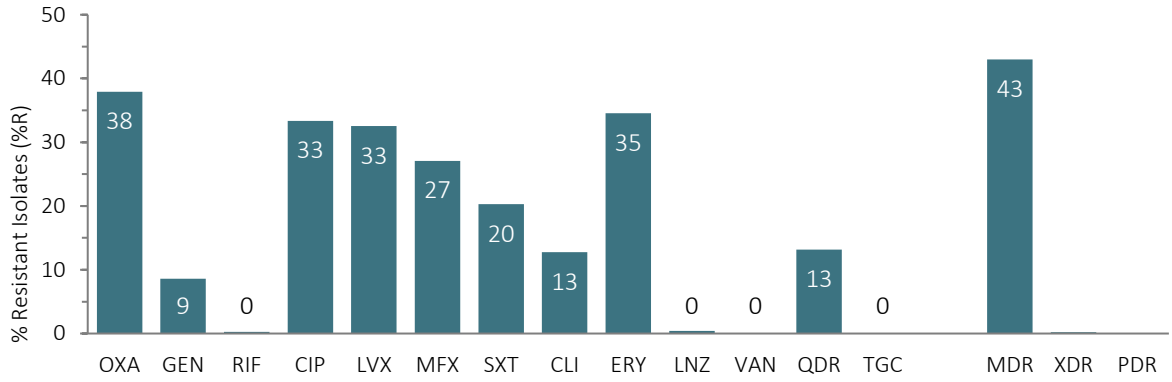
Table 4.4.6.1 Percentages of resistant, intermediate, and susceptible isolates for *Staphylococcus aureus*, isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Staphylococcus aureus* (n=24,833)			
		Isolates (N)	% R	% I	% S
Oxacillin	OXA	16,857	37.9[a]	–	62.1[a]
Gentamicin	GEN	16,799	8.6	2.1	89.3
Rifampicin	RIF	16,617	0.3	0.1	99.7
Ciprofloxacin	CIP	11,907	33.3	1.5	65.1
Levofloxacin	LVX	13,176	32.5	1.6	65.9
Moxifloxacin	MFX	16,316	27.1	5.2	67.6
Trimethoprim/sulfamethoxazole	SXT	16,680	20.3	0.0	79.7
Clindamycin	CLI	16,743	12.7	0.2	87.0
Erythromycin	ERY	16,689	34.5	1.5	63.9
Linezolid	LNZ	16,644	0.4	0.0	99.6
Vancomycin	VAN	16,638	0.4	0.1	99.5
Quinupristin/Dalfopristin	QDA	2,989	13.2	0.1	86.8
Tigecycline	TGC	16,068	0.0	0.0	99.8
Multidrug-resistance (≥3 classes NS)[c]	MDR	24,833	43.0	–	–
Extensive drug resistance (possible)	XDR	24,833	0.2	–	–
Pan-drug resistance (possible)	PDR	24,833	0	–	–

[a] MRSA/MSSA is calculated as resistance/susceptibility to oxacillin: %MRSA = 37.9% and %MSSA = 62.1.
[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).

[10] Possible XDR, possible PDR

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, 2023



For 2023, resistance in *Staphylococcus aureus* ranged from 0% for rifampin, linezolid, vancomycin, and tigecycline, to 33% for ciprofloxacin.

Percentage MRSA was 38% for all isolates.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *S. aureus* was 43.0%, 0.2%, and 0%, respectively.

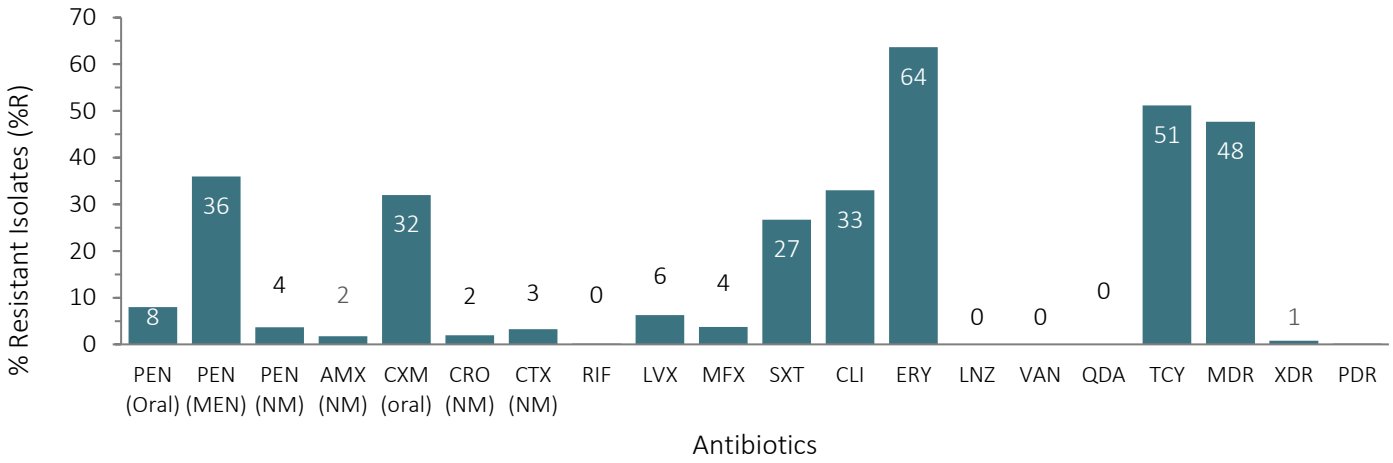
4.4.7 *Streptococcus pneumoniae*

Table 4.4.7.1 Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae*, isolates from all sources, United Arab Emirates, 2023

Antibiotic	Code	*Streptococcus pneumoniae* (N=3,764)			
		Isolates (N)	% R	% I	% S
Penicillin G (oral breakpoints)	PEN (oral)	1592	8.0	29.2	62.1
Penicillin G (non-meningitis breakpoints)	PEN (NM)	1592	3.6	2.1	93.7
Penicillin G (meningitis breakpoints)	PEN (MEN)	1592	35.9	1.3	62.1
Amoxicillin (non-meningitis breakpoints)	AMX (NM)	1677	1.7	3.7	94.6
Cefuroxime (oral breakpoints)	CXM (oral)	1513	32.0	3.2	64.8
Cefotaxime (non-meningitis breakpoints)	CTX (NM)	1896	3.3	1.2	95.5
Ceftriaxone (non-meningitis breakpoints)	CRO (NM)	1085	1.9	0.9	97.1
Rifampin	RIF	636	0.2	0.0	99.8
Levofloxacin	LVX	2209	6.2	2.6	91.2
Moxifloxacin	MFX	2622	3.7	1.8	94.4
Trimethoprim/Sulfamethoxazole	SXT	2581	26.7	14.2	59.1
Clindamycin	CLI	2488	33.0	1.7	65.2
Erythromycin	ERY	2688	63.7	0.5	35.9
Linezolid	LNZ	2635	0.0	0.0	100.0
Vancomycin	VAN	2666	0.0	0.0	99.9
Quinupristin/Dalfopristin	QDA	102	0.0	1.0	99.0
Tetracycline	TCY	2689	51.2	1.2	47.6
Multidrug-resistance (≥3 classes NS)[a]	MDR	2,707	47.7	–	–
Extensive drug resistance (possible)	XDR	2,707	0.8	–	–
Pan-drug resistance (possible)	PDR	2,707	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, 2023

For 2023, resistance in *Streptococcus pneumoniae* ranged from 0% for rifampin, linezolid, and vancomycin, to 64% for erythromycin.

Prevalence of multidrug resistance (%MDR/XDR/PDR) in *S. pneumoniae* was 47.7%, 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).

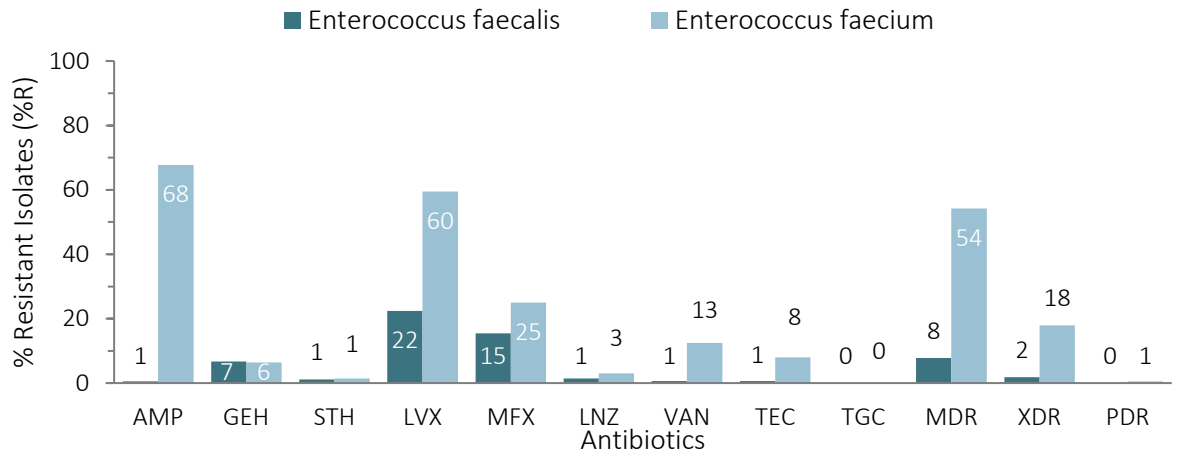
4.4.8 *Enterococcus faecalis and Enterococcus faecium*

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, 2023

Antibiotic	Code	*Enterococcus faecalis* (N=6,063				*Enterococcus faecium* (N=610)			
		N	% R	% I	% S	N	% R	% I	% S
Ampicillin	AMP	4001	0.5	0.0	99.5	397	67.8	0.0	32.2
Gentamicin (high level)	GEH	853	6.7	0.0	35.9	109	6.4	0.0	20.2
Streptomycin (high level)	STH	2133	1.1	0.0	5.7	279	1.4	0.0	3.2
Levofloxacin	LVX	2379	22.4	2.3	75.3	242	59.5	8.7	31.8
Moxifloxacin	MFX	323	15.5	1.9	82.4	8	25.0	0.0	75.0
Linezolid	LNZ	3982	1.4	1.2	97.4	395	3.0	2.5	94.4
Vancomycin	VAN	3991	0.6[b]	0.1	99.3	392	12.5[b]	0.0	87.5
Teicoplanin	TEC	2009	0.6	0.0	99.4	176	8.0	1.1	90.9
Tigecycline[c]	TGC	3673	0.0	0.0	99.1	360	0.3	0.0	3.9
Multidrug-resistance (≥3)[d]	MDR	3,994	7.8	–	–	395	54.2	–	–
Extensive drug resistance	XDR	3,994	1.8	–	–	395	17.9	–	–
Pan-drug resistance	PDR	3,994	0	–	–	395	0.5	–	–

[a] A small number of isolates were tested (N<30): percentage resistance should be interpreted with caution.
[b] %VRE.
[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, 2023



For 2023, 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.

4.4.9 *Candida spp.*

Table 4.4.9.1 Percentage of susceptible isolates for *Candida* spp. (Candida albicans & Candida non-albicans), isolates from all sources, United Arab Emirates, 2023 (Cumulative antibiogram)

	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU[a]	VOR[b]	AMB [c]	CAS[d, e]	MIF[e]
***Candida* spp.**	15,798	100.0	4.0	8.0	1.0	2.0	0
Candida albicans	5,372	34.0	92	89	16	98	99
Candida spp. (non-albicans)	10,426	66.0					
C. tropicalis	1063	6.7	93	96	8.0	98	98
C. parapsilosis	562	3.5	81	90	16	99	99
C. glabrata[f]	782	4.9	0	9[g]	8.0	37	98
C. auris[h]	655	4.1	0	2	1.0	2.0	0
C. dubliniensis	86	0.54	0	8	5.0	8.0	0

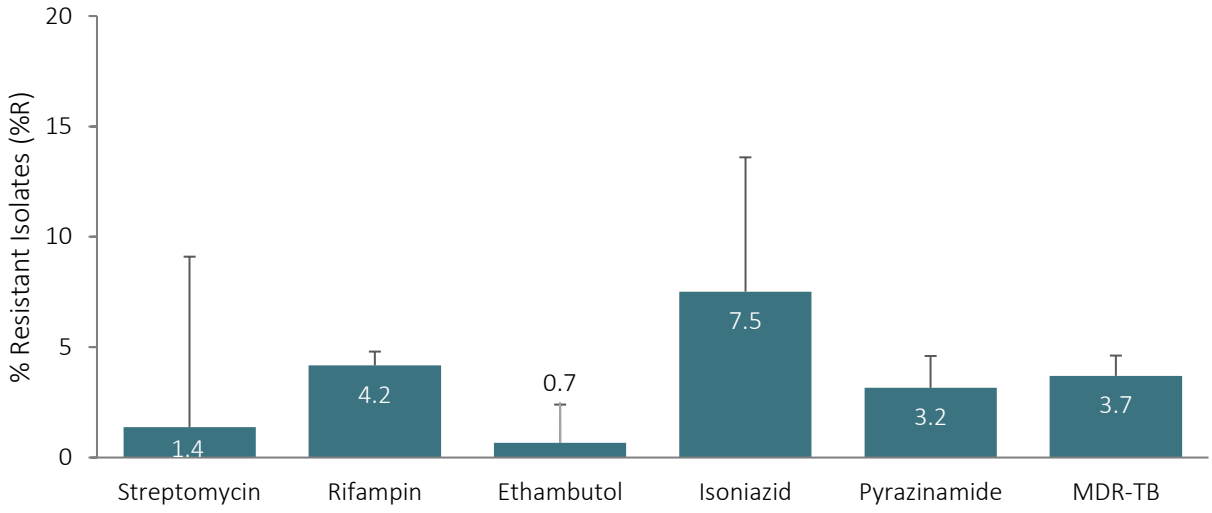
[a]FLU=Fluconazole [b]VOR=Voriconazole [c]AMB=Amphotericin B. EUCAST breakpoints (S≤1, R>1) are used for amphotericin B for *C. albicans, C. glabrata, C. parapsilosis*, and *C. tropicalis* (EUCAST, 2024) Note: Some automated systems overcall amphotericin resistance for *Candida* species [d]CAS=Caspofungin. 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).

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, 2023

Antibiotic	Code	*M. tuberculosis* (N=1,405)			
		Isolates (N)	% R	% I	% S
Rifampin	RIF	1,343	**4.2** ↑	**0**	**95.8**
Ethambutol	EMB	1,343	**0.7**	**0.2**	**99.1**
Isoniazid	INH	1,344	**7.5** ↓	**1.1**	**91.4**
Pyrazinamide	PZH	1,331	**3.2**	**0**	**96.8**
Streptomycin	STM	289	**1.4** ↓↓	**0**	**98.6**
Multidrug-resistance (INH+RIF)	MDR	1200	**3.7**↑	**–**	**–**

Figure 4.4.9.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Mycobacterium tuberculosis*, isolates from all sources, United Arab Emirates, 2023



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

Annex 5.3 List of Figures

Annex 5.4 List of Tables

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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