UNITED ARAB EMIRATES
MINISTRY OF HEALTH & PREVENTION

NATIONAL AMR SURVEILLANCE REPORT 2024

In collaboration with:

مؤسسة الإمارات للخدمات الصحية
Emirates Health Services

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DEPARTMENT OF HEALTH

مركز أبوظبي للصحة العامة
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Contributing Bodies (in alphabetical order)

- **Abu Dhabi Public Health Center (ADPHC)**
- **Emirates Health Services Establishment (EHS)**
- **Department of Health, Abu Dhabi (DoH)**
- **Dubai Health Authority (DHA)**
- **H.H. The President Initiatives Hospitals**
- **Khalifa University, Abu Dhabi**
- **Ministry of Health and Prevention (MOHAP)**
- **Mohammed Bin Rashid University, Dubai**
- **Public and private healthcare facilities (see Annex 5.5)**
- **Public and private clinical microbiology laboratories (see Annex 5.6)**
- **RAK Medical and Health Sciences University**
- **Sharjah University, Sharjah**
- **United Arab Emirates University, Al Ain**
- **Zayed University, Dubai**

For media enquiries, please contact:

MOHAP Government Communications Department
E-Mail: gov.comm@MOHAP.gov.ae
Tel.: +971 (4) 230 1000, or
Tel.: +971 (4) 230 1607

For technical enquiries, please contact:

National Sub-Committee for AMR Surveillance
Dr Pramod Chhabrani

Specialist Clinical Microbiology
Al Kuwait Hospital, Dubai
P.O. Box 22241, Dubai, UAE
E-Mail: pramod.chhabrani@ehs.gov.ae
amr.ehs@ehs.gov.ae
Tel.: +971 (0) 4 7078747

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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.

H.E. Dr Hussain A.R. Al Rand	**Dr Najiba Abdulrazzaq**	**Dr Pramod Chhabrani**
Chair, UAE Higher Committee for AMR	Co-Chair, UAE Higher Committee for AMR	Chair, UAE Sub-Committee for AMR Surveillance
Ministry of Health and Prevention, Dubai	Emirates Health Services Establishment, Dubai	Emirates Health Services Establishment, Dubai
February 2026	February 2026	February 2026

Authors

- **Pramod Chhabrani,** Chair, UAE Sub-Committee for AMR Surveillance, Al Kuwait Hospital, Emirates Health Services (EHS)
- **Najiba Abdulrazzaq,** Co-Chair, UAE Higher Committee for AMR

Reviewers

- **Jens Thomsen,** Previous AMR Surveillance Lead & Chair of National AMR Surveillance Sub committee, Medics Labor AG, Bern, Switzerland
- **Adnan Alatoom,** Dubai Health Authority, DHA, UAE

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United Arab Emirates National Sub-Committee for Antimicrobial Resistance Surveillance (in alphabetical order):

Abiola Senok, Adnan Alatoom, Aisha Abdullah Al Marzouqi, Alaa M.M. Enshasy, Anju NabiCarole Ayoub Moubareck, Dean Everett, Duckjin Hong, Farah AlMarzooq, Fathima Rashid, Fatima al Dhaheri, Fouzia Jabeen, Hala Ahmed Fouad Ismail, Hana M S Saleh Salama, Manal Abdel Fattah Ahmed, Maya Habous, Muna Mohamed Al Safi, Mubarak AlFarsi, Nermine Khalifa, Sheikha Ghannam Al Kaabi, Somansu Basu, Stefan Weber, Timothy Collyns

Focal Points from National AMR Surveillance sites:

Abhijith Sidhardhan, Adam Clarke, Ahmed Anaizi, Ajesh K Jayan, Anita Thigale, Anju Nabi, Anup Poddar, Anwar Gampadadda, Arun John, Arun Kumar Jha, Asha Santosh, Ashraf Hussein Abdelhalim Adlan, Ashwani Prasad, Basma Mohamed, Bejoy Peethambaran, Christian Ocampo, Deeba Jafri, Deebu George, Diana Anwar Ghadban, Dirar Abdallah, Duckjin Hong, Eltigani Baloul, Eunjung Kim, Firos CK, Fouzia Jabeen, Gisha Jayakumar, Gitanjali Patil, Hadayatullah, Hafiz Ahmad, Hala Fouad Ismail Fouad, Husain A. Alawadhi, Husam Saleh, Husna Nazar, Ibrahim Alhashmi, Iola Fernandez, Irfan Akhtear, Irfan Hussein Rizvi, Jagadeesha Maharudraiah, Jayalakshmi Sudeep, John Stelling, Joyce N Joseph, Jyoti Talukdar, Kavita Diddi, Khusro Kamal Zia, Khaleelur Rahman Badriya Manzil, Linah Al Zakar, Louis Angelo Garcia, Maja Habous, Mamoun Elzubair, Manal al Fattah, Mangai Gopi, Maria Elizabeth de Leon, Maryam Aly Elsayed, Marivic Astillero, Moawia El Tahir Suliman, Mohamed Khamis Hussien, Mohammad Sartawi, Monet Abraham, Monika Maheshwari, Mubarak Alfaresi, Muhammad Faisal, Muhammed Javid Bhutta, Munish Joneja, Nada Al Boukhari, Nehad Nabeel Al Shirawi, Nesrin Helmy Mahmoud, Niall Jones, Nicholas Carter-Meadows, Nisant Chilukuri, Noora Al Zarouni, Nooramol, Payal Modi, Prashant Nasa, Prejtha Valappil, Rahima Al Balooshi, Rajeshwari T. A. Patil, Ramabhadran Krishnaprasad, Rakesh Kumar Gupta, Rand Ataya, Rand Hussain, Ratna Kurahatti, Ribay Khan, Rita Tanios, Riyaz Amirali Husain, Roa Ahmed Muhammed, Rola Al Fakh, Rubina Lone, Rula Alnafouri, Ryan Rico, Saeid Azizi, Saf Naqvi, Santosh Sharma, Satyam Parmar, Savitha Binoy, Savitha Mudalagiriyappa, Seema Oommen, Shaikha Al Kaabi, Sharukh Aslam, Sherif Mofeed Ekladious, Shoaib Ehsan Hasani, Simantini Jog, Simi Janseer, Somansu Basu, Stefan Weber, Sujith Cyril Joseph, Supriya Jagdale, Sura Khamees Majeed, Suruchi Sharma,Tarek Ghneim Al Hariri, Tigin Thomas, Timothy Collyns, Yasin Ahmed, Youmna Dirani, Zainab Malik, Zulfa Omar Al Deesi.

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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 & patient-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 2024 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 (2024) 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, 2024

Priority[a]	Organism	Antibiotic or antibiotic class	N (Isolates)	% Resistant isolates
Priority 1: Critical group	*Acinetobacter baumannii*	Carbapenems (IPM or MEM)	1,300	**6.8/6.8**
	Enterobacterales (all)	Ceftriaxone/Cefotaxime (ESBL)[b]	93,139	**29.2/29.8**
	Enterobacterales (all)	Carbapenems (IPM or MEM)	93,139	**3.4/1.4**
	Mycobacterium tuberculosis	Rifampicin (Mono-resistant)	1,371	**2.2**
Priority 2: High group	*Salmonella* Typhi	Fluoroquinolones (ciprofloxacin)	163	**48.0**
	Shigella spp.	Fluoroquinolones (ciprofloxacin)	94	**42.9**
	Enterococcus faecium	Vancomycin (VRE)[c]	630	**14.1**
	Pseudomonas aeruginosa	Carbapenems (IPM or MEM)	12,625	**13.5/9.7**
	Salmonella spp. (non-typhoidal)	Fluoroquinolones (ciprofloxacin)	1,773	**9.1**
	Neisseria gonorrhoeae	3rd-generation cephalosporins	344	**0.0**
	Neisseria gonorrhoeae	Fluoroquinolones (ciprofloxacin)	344	**82.5**
	Staphylococcus aureus	Oxacillin (MRSA)[d]	18,659	**40.7**
Priority 3: Medium group	*Streptococcus pyogenes*	Macrolide (Erythromycin)	6,614	**34.0**
	Streptococcus pneumoniae	Macrolide (Erythromycin)	2,958	**59.0**
	Haemophilus influenzae	Ampicillin	1,903	**28.5**
	Streptococcus agalactiae	Penicillin	7,374	**1.0**

[a] Based on: (WHO, 2024), [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 2024, 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.

UAE National Network of AMR Surveillance Sites and Labs

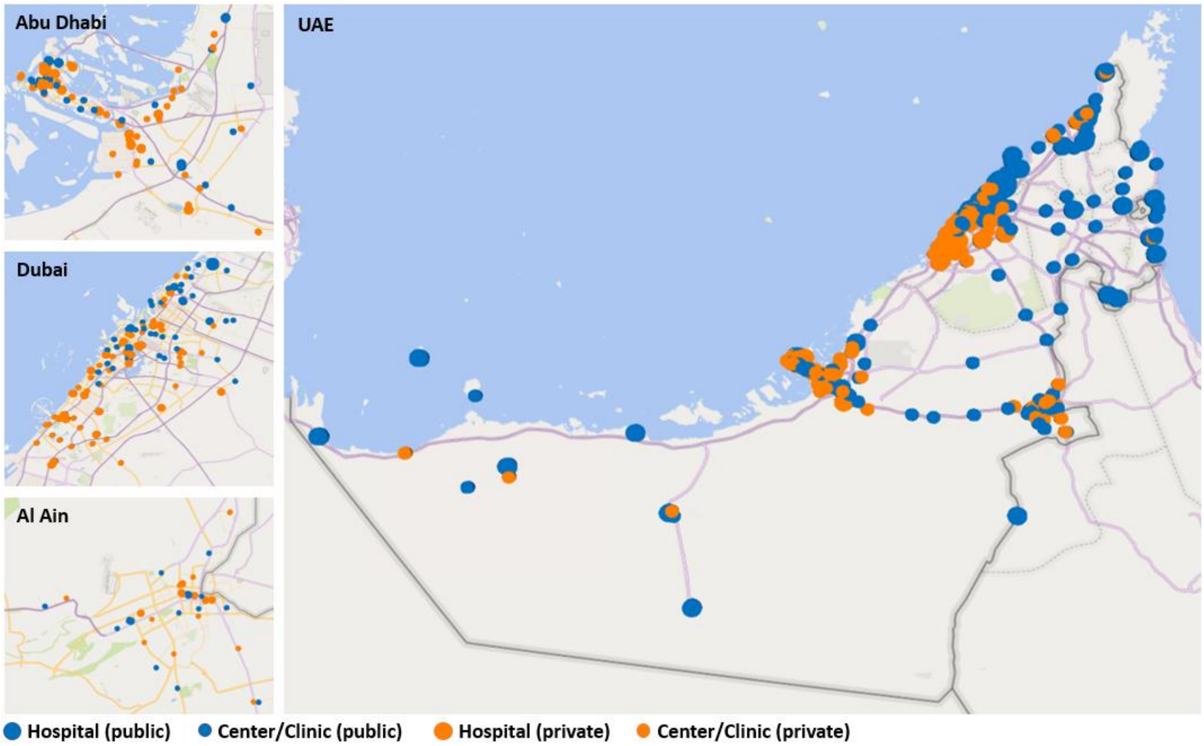
The AMR data submitted includes routine clinical and antibiotic susceptibility testing data from both, governmental as well as private healthcare facilities. There is no central confirmatory testing or central repository of isolates as there is no UAE national reference lab for antimicrobial resistance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

Surveillance sites and microbiology laboratories are sited in all seven Emirates of the UAE (**Figure 2.3.1, 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 2024)

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	**24**	**19**	**5**	**2**	**1**	**2**	**1**	**54**

Figure 2.3.1 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

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[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/

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 system 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 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 2024, 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):

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[5] Minimal inhibitory concentration (MIC, in µg/ml), or the inhibition zone diameter (IZD, in mm)

[6] SIR, susceptible/intermediate/resistant

- *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 4.2 (cumulative antibiograms)** presents the national cumulative antibiogram 2024, 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 4.3 (multidrug resistance)** presents multidrug resistance (%MDR) for Gram-negative and Gram-positive bacteria, and *Mycobacterium tuberculosis* (MDR-TB).
- **Section 4.4 (AMR priority pathogens)** presents percent resistant/intermediate/susceptible (%RIS) statistics.

3.3 Data analysis

Data analysis was conducted with the WHONET Software for Antimicrobial Resistance Surveillance.

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, rectal, 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)

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

- Species for which less than 10 isolates are available for analysis
- Antimicrobial agents that are selectively/not routinely tested (i.e., less than 70% of isolates were tested)

De-duplication: As recommended by CLSI guideline M39-ED5:2022, multiple isolates (copy strains) are routinely excluded from the analysis, considering only the first isolate with antibiotic results of a given species per patient, specimen type, and analysis period (e.g., one year), irrespective of body site, antimicrobial susceptibility profile, or other phenotypical characteristics (e.g., biotype). For details see CLSI M39-ED5:2022, Appendix A: Rationale for the "First Isolate per Patient" Analysis Recommendation (CLSI M39, 2022).

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

The percentage resistant, intermediate, and susceptible (%RIS) isolates were either interpreted at the national AMR Surveillance Center (n=36/44 labs, 82%), or, if this was technically not feasible, obtained from labs in form of already locally interpreted (S/I/R) results (n=8/44 labs, 18%). Percent RIS interpretations were based on the CLSI interpretation standard CLSI M100 (ED32: 2025) for bacterial isolates and CLSI interpretation standard M60 ED1:2020 for yeast. For amphotericin B (AMB) and tigecycline, EUCAST v15.0:2025 was used (EUCAST, 2025). 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) and/or cefoxitin (FOX).
- **VRE** was defined as *Enterococcus faecalis* or *Enterococcus faecium*, resistant to vancomycin (VAN).
- **CRE** was defined as Enterobacterales, 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 2025. For additional statistical analysis the following software packages are used:

- IBM SPSS Statistics, version 28.0.0.0 (IBM, 2022), or Epi Info^{TM} 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 (2024)

4.2.1 United Arab Emirates (National Cumulative Antibiogram)

Table 4.2.1.1 National Cumulative Antibiogram (2024): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=118,442)

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)	118,442	-	68	86	-	-	66	-	79	92	97	97	90	87	69	62	61	64	69[b]
Haemophilus influenzae[c]	1,903	60	85	-	-	80	-	-	-	-	-	-	-	-	-	90	-	58	-
Moraxella (Branh.) catarrhalis[d]	638	-	89	-	-	75	-	-	-	-	-	-	-	-	-	98	-	60	-
Enterobacterales	93,139	24	71	87	16	-	69	-	77	93	98	98	90	87	85	58	62	70	-
Citrobacter koseri (diversus)	2,385	R	94	95	88	61/80[i]	91	-	93	98	99	99	99	99	98	95	85	97	77[b]
Enterobacter cloacae	1,877	R	R	85	R	33/54[i]	78	-	86	92	97	92	98	94	85	80	65	87	37[b]
Enterobacter aerogenes (*K. aer.*)	2,325	R	R	83	R	R	73	-	93	85	98	97	99	97	94	89	-	94	20[b]
Escherichia coli [e]	53,918	34	76	93	51	53/58[i]	63	-	71	98	99	98	97	90	87	50	59	63	95[b]
Klebsiella pneumoniae	21,594	R	78	85	63	67/68[i]	73	-	81	94	97	95	96	94	85	71	70	79	30[b]
Klebsiella oxytoca	994	R	78	90	55	73/74[i]	83	-	86	95	96	94	97	93	83	80	-	83	75[b]
Morganella morganii	1,074	R	R	94	R	R	70	-	95	17	99	98	96	84	85	53	-	69	R
Proteus mirabilis	2,761	60	79	98	68	82/85[i]	82	-	89	33	97	96	88	74	82	65	71	64	R
Proteus vulgaris	82	R	72[f]	100	R	R	80[f]	-	95	16	97	94	95	89	-	81	-	79	R
Providencia spp.	345	R	R	92	R	–	84	-	91	51	96	95	91	63	68[f]	70	-	78	R
Salmonella spp. (non-typhi)	1,773	85	97	99	-	-	96	-	95	-	-	-	-	-	-	73[g]	-	96	-
Salmonella Typhi/Paratyphi	312	76	93	95	-	-	76	-	85	-	-	-	-	-	-	21	-	82	-
Serratia marcescens	2,383	R	R	90	R	R	87	-	96	90	98	97	97	97	81	86	75[f]	98	R
Shigella spp.	94	19[f]	91[f]	97[f]	-	-	-	-	93	-	-	-	-	-	-	48	-	40	-
Non-fermenting Gram-neg. rods	15,273	R	R	80	-	-	-	87	89	84	86	R	96	91	87	84	81	67	-
Acinetobacter baumannii	1,300	R	R	87	-	-	-	88	89	93	93	R	94	93	91	85	R	92	-
Pseudomonas aeruginosa	12,625	R	R	85	-	R	R	87	88	82	86	R	96	91	93	85	67	R	R
Stenotrophomonas maltophilia[h]	1,348	R	R	R	-	-	R	30	-	R	R	R	R	R	R	-	R	82	-

[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 98 %S. [f] A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution. [g] Ciprofloxacin results for *Salmonella* spp. (non-typhi) 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.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 318 surveillance sites from public and private sector (United Arab Emirates), including 87 hospitals and 231 ambulatory healthcare facilities. Version 1.0 (November 2025).

Table 4.2.1.2 National Cumulative Antibiogram (2024): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=76,666)

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)	76,666	-	-	-	-	-	-	47	67	-	-	-	75	62	99	97	67	95	99	-	-	-
Enterococcus spp.	7,700	93	-	-	-	R	R	-	R	R	74	74	71	80	98	98	R	95	97	-	-	-
Enterococcus faecalis	6,760	100	-	-	-	R	R	-	R	R	75	66	74	80	99	99	R	99	98	-	-	R
Enterococcus faecium	630	30	-	-	-	R	R	-	R	R	66	47	31	-	85	87	R	40	90	-	-	84
Staphylococcus aureus[k]	24,771	-	-	59[c]	59	-	-	60	79	88	-	-	66	66	100	100	81	99	100	87	99	82
MSSA[k]	11,792	-	-	100	100	-	-	65	86	96	-	-	76	77	100	100	84	99	100	91	99	84
MRSA[k]	6,923	-	-	-	-	-	-	51	73	72	-	-	48	51	100	100	71	99	100	79	99	76
Staphylococcus, coagulase-neg. (SCN)	10,478	-	-	36[c]	36	-	-	36	65	82	-	-	77	67	99	91	79	98	99	81	95	88
Staphylococcus epidermidis	2,733	-	-	33[c]	33	-	-	27	57	73	-	-	58	54	99	85	71	99	100	79	95	90
Staphylococcus saprophyticus [g]	1,758	-	-	43[c]	43	-	-	40	78	99	-	-	98	91	99	98	85	100	98	92	99	91
Staphylococcus lugdunensis	411	-	-	72[c]	72	-	-	75	77	94	-	-	95	86	100	99	97	99	100	92	100	86
Streptococcus pneumoniae	2,958	-	88[d]	-	-	98[e]	94[e]	41	66	-	-	-	93	98	99	-	61	-	100	46	100	99
Streptococcus pyogenes [h]	6,614	99[f]	99	-	-	98	98	66	82	-	-	-	89	-	100	100	-	-	100	83	-	-
Streptococcus agalactiae [i]	7,374	99	99	-	-	100	99	39	41	-	-	-	87	-	100	-	-	96	99	17	-	99
Streptococcus spp. (viridans group)	1,604	-	69	-	-	91	88	46	75	-	-	-	86	-	98	-	-	-	98	58	-	-

[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): 52 %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.

Data source: United Arab Emirates Antimicrobial Resistance Surveillance System. Data shown is from 318 surveillance sites from public and private sector (United Arab Emirates), including 87 hospitals and 231 ambulatory healthcare facilities. Version 1.0 (November 2025).

UAE Resistance Trends comparison between 2023 & 2024, 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 2023 & 2024, 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	→	→	→	↑
Trimethoprim/sulfamethoxazole	↑	↑	**R**	**R**
Multidrug-resistance (≥3 classes NS)	↑	↓	↓	↑

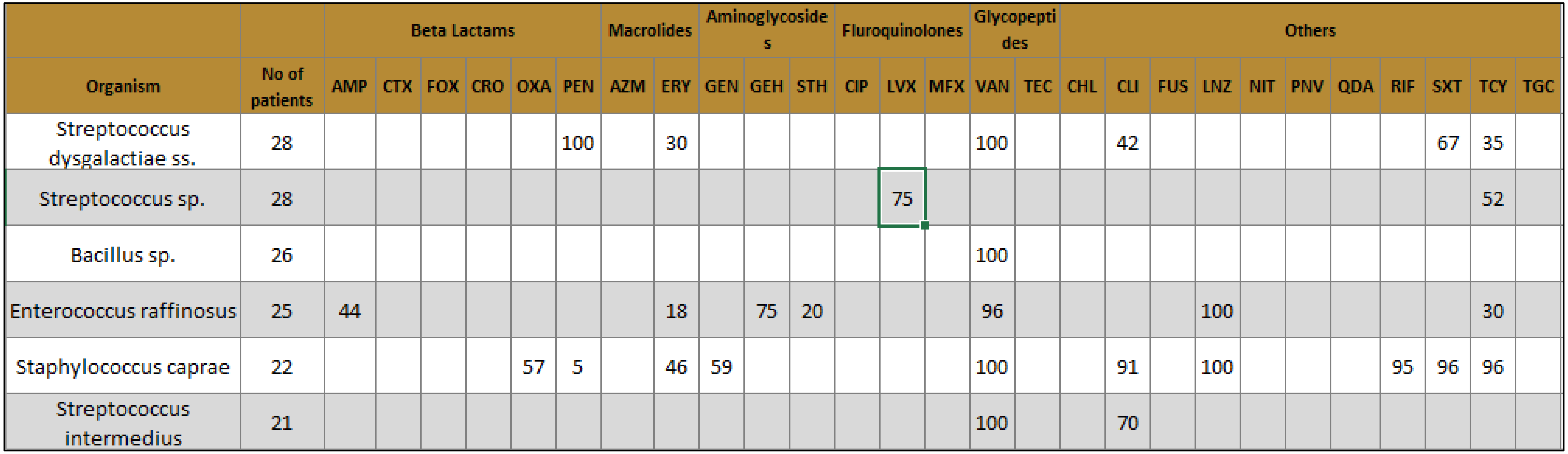
→/↑/↓: horizontal/increasing/decreasing trend of percentage resistant isolates (%R) *R: intrinsic resistance,* *N/A: Not applicable*

4.2.2 Abu Dhabi Emirate

Table 4.2.2.1 Abu Dhabi Emirate Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-positive bacteria (isolates from all sources, N=39,994)

		Beta Lactams						Macrolides		Aminoglycosides			Fluroquinolones			Glycopeptides		Others										
Organism	No of patients	AMP	CTX	FOX	CRO	OXA	PEN	AZM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	FUS	LNZ	NIT	PNV	QDA	RIF	SXT	TCY	TGC
Staphylococcus aureus	13,082			45		58	8		59	88			66	71	67	100	100		79		100	99			99	79	87	100
Streptococcus, beta-haem. Group B	5,356						100									100			28									
Enterococcus faecalis	3,977	100					99		17		74	68	65	75		100	100				99	99					25	100
Streptococcus agalactiae	2,950	98	98		99		98	41	32					90	47	99		96	36		100					47	14	98
Streptococcus, beta-haem. Group A	2,187				100		100		57										69				100					
Streptococcus pyogenes	1,792	99			99		99	84	60					89	86	99			77		100					82	81	
Streptococcus pneumoniae	1,574		92		99		59		41					93	99	99		93	64		100				99	61	45	
Staphylococcus, coagulase negative	1,546	1				47	1		48	84			77	80		100			70		100	94				87	75	
Staphylococcus epidermidis	1,354			29		37	5		27	76			60	72	54	99	86		60	8	100				97	73	77	65
Staphylococcus haemolyticus	958	0				29	3		28	72			63	68		99			56		100	100				79	60	
Streptococcus, beta-haemolytic	748						100		40										59									
Staphylococcus saprophyticus	707	0				22	2		46	99			99	98	74	98			76		99	100		1	99	91	93	24
Corynebacterium sp. (diphtheroids)	455				78		66		35	81			39	44		99			36		99		48			28	80	
Staphylococcus, coagulase positive	411	0				0	0		55	67						100			73		100					74	78	
Staphylococcus hominis	331			36		41	12		22	97			83	87	74	99	94		66	5	100	96			98	87	72	73
Streptococcus viridans, alpha-hem.	309	62	88		95		79		51					80		100			74		100		45			56	58	

		Beta Lactams						Macrolides		Aminoglycosides			Fluroquinolones			Glycopeptides		Others										
Organism	No of patients	AMP	CTX	FOX	CRO	OXA	PEN	AZM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	FUS	LNZ	NIT	PNV	QDA	RIF	SXT	TCY	TGC
Enterococcus faecium	305	37					47		10		59	41	36	44		80	89				92	59		82			34	72
Staphylococcus capitis	201			49		42	16		52	63			50	55	52	100	86		58	8	100	100			94	98	95	74
Streptococcus mitis	185	64	72		82		54		44					82	54	98		100	80		99						64	100
Staphylococcus lugdunensis	176			71		69	34		72	91			94	96	80	99	99		74	28	100	100		0	100	94	90	42
Streptococcus anginosus	173	89			98		90	63	51					81	68	99			70		99						57	
Enterococcus sp.	130	91					85		22		81		66	78		86					84	92	74				32	
Streptococcus constellatus	92	100			99		96		64						94	100			73		100						72	
Micrococcus luteus	81						96									100			93									
Streptococcus, beta-haem. Group G	72	100			100			50								100			61								32	
Streptococcus dysgalactiae	59				100		100		28						98	100			28		100					98	38	
Staphylococcus warneri	59			59		58	20		47	89			93		93	98	96		82	26	98				95	96	95	68
Enterococcus gallinarum	50	98							31		70	31	61			26	100				94	92					43	65
Enterococcus avium	47	59							10		86	54				98	96				93						26	82
Streptococcus salivarius	47				89		42		41						93	96			86		100						87	
Streptococcus sanguinis	38				100		72		50						76	100			80		100						75	
Streptococcus parasanguinis	30				79		27									100			87		100						37	



		Beta Lactams						Macrolides		Aminoglycosides			Fluroquinolones			Glycopeptides		Others										
Organism	No of patients	AMP	CTX	FOX	CRO	OXA	PEN	AZM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	FUS	LNZ	NIT	PNV	QDA	RIF	SXT	TCY	TGC
Streptococcus dysgalactiae ss.	28						100		30							100			42							67	35	
Streptococcus sp.	28													75													52	
Bacillus sp.	26															100												
Enterococcus raffinosus	25	44							18		75	20				96					100						30	
Staphylococcus caprae	22					57	5		46	59						100			91		100				95	96	96	
Streptococcus intermedius	21															100			70									

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

Table 4.2.2.2 Abu Dhabi Emirate Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-negative bacteria (isolates from all sources, N=60,359)

		Beta lactams																Macrolides		Aminoglycosides			Fluroquinolones			Carbapenems									
Organism	**No of Patients**	**AMC**	**AMP**	**CZO**	**CFM**	**CTX**	**FEP**	**CRO**	**FOX**	**CAZ**	**CZA**	**CZT**	**CXM**	**PIP**	**TZP**	**TIC**	**TCC**	**AZM**	**ERY**	**AMK**	**GEN**	**TOB**	**CIP**	**LVX**	**NOR**	**ETP**	**IPM**	**MEM**	**CLI**	**COL**	**FOS**	**LNZ**	**NIT**	**SXT**	**TCY**
Escherichia coli	26,841	75	34	44		65	74	64		70			58		93					96	90		56		71	99	99	99			98		95	63	
Klebsiella pneumoniae	11,258	79	0	58		76	85	76		77			69		85					97	94		74		92	97	95	98			77		34	81	
Pseudomonas aeruginosa	6,390						88			85	90	89		79	88	78	80			96	91	92	84	78			82	85		56					
Serratia marcescens	1,341	1	0	0		90	96	86	12	94			4		90					96	96	78	83		97	98	88	98			87		0	98	60
Citrobacter koseri	1,285	93	0	85		90	96	91		95			79		94					98	98		95		100	100	97	100			86		77	96	
Proteus mirabilis	1,205	81	56	60		85	91	88	89	90			83		98					90	69	77	64		81	94	27	97			76		1	63	
Haemophilus influenzae	1,153	87	58					97					80					86					90	92										57	68
Klebsiella aerogenes	1,113	3	0	10		78	94	77	15	77			43		84					98	97		90		97	98	76	98			78		21	94	
Salmonella sp.	978	73	86	0		96	72	98		65					62					6	4		81		94	100	100	100			81		62	97	
Enterobacter sp.	877	1	1	0			87								94						92		77			98		99					66	80	
Enterobacter cloacae	837	1	2	1		82	91	76		80			22		85					98	95		82		94	96	91	98			58		41	87	
Stenotrophomonas maltophilia	636																							83										92	
Morganella morganii	604	1	1	0		76	97	84	44	85			4		95					96	85	82	53		86	99	24	99			10		0	68	
Acinetobacter baumannii	569			1			91	70		89				85	90	89	92			95	94	94	86				94	94						94	
Klebsiella oxytoca	522	77	0	55		93	89	81		86			73		91					95	93		81		94	96	95	97			79		76	84	
Acinetobacter sp.	441						85			80					89					96	89		90	94			94	94						94	

		Beta lactams																Macrolides		Aminoglycosides			Fluroquinolones			Carbapenems									
Organism	No of Patients	AMC	AMP	CZO	CFM	CTX	FEP	CRO	FOX	CAZ	CZA	CZT	CXM	PIP	TZP	TIC	TCC	AZM	ERY	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	CLI	COL	FOS	LNZ	NIT	SXT	TCY
Moraxella catarrhalis	439	86																92	84															78	79
Citrobacter freundii	262	7	0	4		74	91	75		81			34		83					96	94		75		93	96	94	98			84		92	82	
Enterobacter cloacae complex	240	9		4			94	84	4	87			33		84					98	95	88	79			96	98	99					40	87	
Neisseria gonorrhoeae	223				99			100										93					12												16
Enterobacter hormaechei	222	0				79	94			80					82					99	94		84		98	95	94	98			81		29	85	
Klebsiella pneumoniae ss. ozaenae	175	72	1	41			81	72		78			65		88					88	94		82			96	98	98			68		52	87	
Pseudomonas sp.	136						83			81					86					89	80		81	81			92	87						62	
Acinetobacter calcoaceticus-baumannii	132			0			88	55		82					87					96	94	90	92	100			100	97						97	
Klebsiella sp.	130	11	0	0		74	96			76					85					95	97		91		95	99	75	98			86		30	95	
Citrobacter sp.	119	65	1	41			87	74		77			59		97						88		74	8		100	98	100					86	77	
Providencia rettgeri	104	4	7	3		89	94	74		91			65		96					92	81		77		96	95	67	99			72		6	76	
Achromobacter xylosoxidans	103						16			83				80	83	76	85			15	7	12	4				70	83		46				91	
Moraxella sp.	96	79																84	85				92											78	69
Haemophilus parainfluenzae	91	77	45					91					73					80					75	82										54	41
Salmonella Typhi	91	72	72			70	61	81		49					60			90		0	0		6		76	100	95	100			79		65	80	

		Beta lactams																Macrolides		Aminoglycosides			Fluroquinolones			Carbapenems									
Organism	No of Patients	AMC	AMP	CZO	CFM	CTX	FEP	CRO	FOX	CAZ	CZA	CZT	CXM	PIP	TZP	TIC	TCC	AZM	ERY	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	CLI	COL	FOS	LNZ	NIT	SXT	TCY
Burkholderia cepacia	75						25			85					28					15	10	10	37	65			8	92		0				83	
Salmonella Paratyphi C	67	96	89					100															92											100	
Providencia stuartii	66		5			87	96		95	92			75		98					96	22	20	64		88	96	39	98			76		0	88	
Pseudomonas putida	61						92			83				68	72	6	6			98	96	85	86				88	83						20	
Acinetobacter lwoffii	55						95			76				75	70	55				98	98	100	94				100	100						75	
Serratia sp.	52	2	0	0			78	52					0		94						90		71			90	91	94						90	
Pseudomonas stutzeri	50						100			98				94	96	82	91			92	96	95	96				98	98						93	
Enterobacter gergoviae	48	73	21	52			87	73		82			53		96					90	88		89			100	94	100					85	89	
Proteus vulgaris	43	68	0				92	46		83			4		100						86		76			94	21	97					0	71	
Aeromonas hydrophila	42						100			95					64					100	100		100				52	70						84	
Sphingomonas paucimobilis	39						88			78					85					80	83		67				92	97						89	
Vibrio cholerae	36	92	72				100			91					100					91	91		86				91	100						94	97
Pantoea sp.	34	79					97			94					100					100	100		91			96	93	97			43		31	88	
Acinetobacter junii	33						100			97					78					100	94		81				100	100						94	
Salmonella Paratyphi B	33	97	81					100															79											81	
Acinetobacter nosocomialis	32						94			81				66	87	83	97			97	100	100	100				97	97						100	

		Beta lactams																Macrolides		Aminoglycosides			Fluroquinolones			Carbapenems									
Organism	No of Patients	AMC	AMP	CZO	CFM	CTX	FEP	CRO	FOX	CAZ	CZA	CZT	CXM	PIP	TZP	TIC	TCC	AZM	ERY	AMK	GEN	TOB	CIP	LVX	NOR	ETP	IPM	MEM	CLI	COL	FOS	LNZ	NIT	SXT	TCY
Citrobacter braakii	31	3				92	100			93					84					96	94		76		84	100	89	100			100		93	80	
Citrobacter farmeri	31	68	0	52			69	59					50		100						87		68			100	100	100					100	77	
Pantoea agglomerans	31	67	26				93	86					27		100						94		90			95		100					45	100	
Neisseria meningitidis	31							100															89					100						0	
Pseudomonas fluorescens	29						79			96					83					74			76				84	82						59	
Achromobacter denitrificans	28						15			82					86					15	11		4					85						89	
Proteus hauseri	28	52	5							89					100						100		96			95	29	100					0	85	
Proteus sp.	28	84	39				100	80					46		100						69		76					100						85	
Raoultella ornithinolytica	27	64					96			89					100					100	100		81			100	92	100			55		56	77	
Achromobacter sp.	23						26			64					74						10		22				85							95	
Salmonella Group D (D1, D2, D3)	22	100	100					100															96											100	
Salmonella Paratyphi A	22																						5											100	
Providencia sp.	21	10					85								90													85						65	
Serratia liquefaciens	21														76						81														
Elizabethkingia meningoseptica	20														15						5		85					0						80	

Code	Antibiotic	Code	Antibiotic
AMC	Amoxicillin/Clavulanic acid	FEP	Cefepime
AMK	Amikacin	FOS	Fosfomycin
AMP	Ampicillin	FOX	Cefoxitin
AZM	Azithromycin	GEN	Gentamicin
CAZ	Ceftazidime	IPM	Imipenem
CFM	Cefixime	LNZ	Linezolid
CIP	Ciprofloxacin	LVX	Levofloxacin
CLI	Clindamycin	MEM	Meropenem
COL	Colistin	NIT	Nitrofurantoin
CRO	Ceftriaxone	NOR	Norfloxacin
CTX	Cefotaxime	PIP	Piperacillin
CXM	Cefuroxime	SXT	Trimethoprim/Sulfamethoxazole
CZA	Ceftazidime/Avibactam	TCC	Ticarcillin/Clavulanic acid
CZO	Cefazolin	TCY	Tetracycline
CZT	Ceftolozane/Tazobactam	TIC	Ticarcillin
ERY	Erythromycin	TOB	Tobramycin
ETP	Ertapenem	TZP	Piperacillin/Tazobactam

4.2.3 Dubai Emirate

Table 4.2.3.1 Dubai Emirate Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-pos. bacteria (isolates from all sources, N=24,596)

		Betalactams											Macrolides	Aminoglycosides			Fluroquinolones			Glycopeptides		Others												
Organism	No of patients	AMX	AMC	AMP	CTX	CPT	CRO	CXM	FEP	FOX	OXA	PEN	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CHL	CLI	DAP	FUS	LNZ	MEM	MTR	NIT	QDA	RIF	SXT	TCY	TGC
Staphylococcus aureus	9,088					100				64	66	16	63	89			66	68	68	100	100		80	100	31	100			99	82	100	82	88	100
Streptococcus pyogenes	4,209			96	97		97					98	68					90		100		99	82			100							86	
Streptococcus agalactiae	4,017			100	99			100				100	33					86		99			40			99			53				17	
Enterococcus faecalis	1,613		99	100				0		0		98	10	18	75	60	66	72		100	100					97			98	0			25	100
Streptococcus pneumoniae	1,098				95		96					92	41					95	98	100		94	67			100	75				100	61	50	100
Staphylococcus saprophyticus	807									40	36	4	40	100			98	99	99	99	98		77	100	0	98			100	5	100	92	90	24
Staphylococcus epidermidis	626		25					24		27	32	10	26	75			60	67	62	100	89		59	100	15	99			99	15	96	74	80	48
Staphylococcus haemolyticus	408			7	24					12	20	6	20	74			44	49	48	98	98		54	99	13	97			98	6	90	71	56	27
Staphylococcus hominis	311		39				40	36		30	34	12	21	95			72	74	72	99	96		62		9	97			96	16	99	83	70	51
Streptococcus, beta-haem. Group A	282			99	100		99					98	58					92	0	99		98	80			99						0	81	98
Streptococcus, beta-haem. Group B	252			100								100											69											
Enterococcus faecium	205		15	23			0	0		0		25	13		75	55	16	25		86	84					87			32	83			36	74
Staphylococcus capitis	165		25				36	23		26	30	10	31	53			40	51	39	100	87		44		15	97			100	2	88	93	98	63
Staphylococcus lugdunensis	157		81							73	77	46	74	96			94	96	89	100	100		77		47	100			100	0	100	100	91	25
Streptococcus dysgalactiae	143	100		100	100		100		100			100	35					97	0	100		98	71	100		100						5	43	97
Streptococcus mitis	135			75	89		94		92			59	33					90	0	100		96	84			100							47	100

		Betalactams											Macrolides	Aminoglycosides			Fluroquinolones			Glycopeptides		Others												
Organism	**No of patients**	**AMX**	**AMC**	**AMP**	**CTX**	**CPT**	**CRO**	**CXM**	**FEP**	**FOX**	**OXA**	**PEN**	**ERY**	**GEN**	**GEH**	**STH**	**CIP**	**LVX**	**MFX**	**VAN**	**TEC**	**CHL**	**CLI**	**DAP**	**FUS**	**LNZ**	**MEM**	**MTR**	**NIT**	**QDA**	**RIF**	**SXT**	**TCY**	**TGC**
Streptococcus anginosus	123			89	96		93		98			95	60					96	0	94		74	74			89							47	96
Staphylococcus, coagulase negative	85									27	17	13	35	93			61	55	60	92			47			93			86	0	85	85	71	0
Streptococcus salivarius	73			92			98		98			83	53							100			80			100							62	
Streptococcus dysgalactiae ss.	72			94	93		95					93	36					91	0	100		98	62			100						0	37	98
Staphylococcus warneri	67									48	51	20	46	87			82	86	84	97			75			98			98	10	98	96	84	25
Streptococcus sp.	47			46			59		95			61	33					19		62			50			52							25	
Gardnerella vaginalis	44																						95					14						
Enterococcus avium	39			62								62	14		97	61	91			97	100					97							22	83
Enterococcus sp.	38			89								86			90					97						95								
Micrococcus luteus	34											90	44							100			91											
Streptococcus constellatus	28			87	88		90					82	38					96		87		50				87							54	
Streptococcus intermedius	28						96					96	54							92			68											
Streptococcus, beta-haem. Group G	27				100		100					100	19					95		100			70			100							30	
Corynebacterium striatum	25																			100														
Streptococcus sanguinis	23						90					65								96														
Streptococcus, beta-haemolytic	21											86	29										48										29	

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

Table 4.2.3.2 Dubai Emirate Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-neg. bacteria (isolates from all sources, N=36,255)

		Beta lactams														Macrolides			Aminoglycosides			Fluroquinolones				Carbapenems			Others						
Organism	No of patients	AMC	AMP	CZO	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	FEP	PEN	TZP	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	COL	FOS	NIT	SXT	TCY	TGC	TMP
Escherichia coli	17,787	77	36	57	60	60	65			63	59	9	70		93				98	90		47	67			98	98	98		98	96	62		99	
Klebsiella pneumoniae	6,063	79	1	68	72	67	70			74	69	11	78		86				97	94		69	82			95	92	96		34	27	79		89	
Pseudomonas aeruginosa	3,597			1			91	93	94				92		88				97		96	88	89				84	88	33						
Proteus mirabilis	1,015	82	70	78	89	80	87			87	87	10	88		99				89	80		70	72			97	36	97		40	1	68			
Klebsiella aerogenes	767	10	4	16		71	82			81	67	8	93		81				99	98		89	94			97	89	98		24	18	95			
Citrobacter koseri	701	96	0	90		94	95			93	81	12	98		96				99	99		95	97			98	98	99		33	76	98		96	
Serratia marcescens	590	5		0		80	91			88	1	0	95		92				98	98		92	93			95	86	96		37	0	97			
Haemophilus influenzae	551	83	69		95	98				97	78					89	84					92	90					95				62	54		0
Enterobacter cloacae complex	450	5		3		48	69			70	23	0	89		69				99	95		78			94	96	95	99		35	25	87			
Salmonella sp.	436	49	84	17			50			93	24	1	52		53	84			24	21		80	85			100	99	100		33	35	95		93	
Enterobacter cloacae	399	8	11	4	70	74	73		92	70	41	19	83		85				99	95		83	84			87	89	95		11	34	88		90	
Stenotrophomonas maltophilia	318																						89									91			
Klebsiella oxytoca	282	82	2	54	79		86			84	81	10	87		93				99	95		85	86			91	95	95		20	76	87		83	
Morganella morganii	276	2	2	2		62	80			74	3	0	93		90				97	86		60	65		82	95	12	98		2	1	75			
Acinetobacter baumannii	249			1		47	85			66			83		80				87	85		82	84				88	87				86			
Acinetobacter calcoaceticus-	245			0		62	90			69			90		84				95	92		87	91				96	96				94			

		Beta lactams														Macrolides			Aminoglycosides			Fluroquinolones				Carbapenems			Others						
Organism	No of patients	AMC	AMP	CZO	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	FEP	PEN	TZP	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	COL	FOS	NIT	SXT	TCY	TGC	TMP
Moraxella sp.	213	99				98	98			99	96							77				96	96					100				74			
Moraxella catarrhalis	196	96					97			94						96	97	100				97	98									88	33		
Haemophilus sp.	148	63	51				91			91	71					88						96	96	96				99				60			
Citrobacter freundii	126	40		18			83			85	75	0	94		89				99	98		80	93			98	93	98		28	95	88			
Haemophilus parainfluenzae	90		73		97	97											49					60						100					27		0
Neisseria gonorrhoeae	81									100			100	23		93						14											21		
Salmonella enterica ss. enterica (Subgroup	79	3		0			3			90	0		3		3				1	0		71				100	100	100		3	3	95			
Citrobacter braakii	72	77		73	96		79			93	77		89		94				100	99		89				100	85	100		45	96	92			
Burkholderia cepacia	65			0			93			60			21		21				33	22		49	84				13	88				94			
Achromobacter xylosoxidans	61						87			0			14		86				7	6		7					74	96				96			
Acinetobacter sp.	55						70			52			80		86				92	86		86	90				78	87				85			
Pseudomonas putida	54						96			64			96		87				100	100		82	88				93	88				42			
Klebsiella pneumoniae ss.	47	77	12	57			65			65	71		74		91				100	95		76	89			86	85	91		38	58	84		85	
Acinetobacter lwoffii	45			0			91			79			97		62				97	95		91					95	96				86			
Salmonella Typhi	45	51	57				30			73	4		32		50				11	5		11	19			100	100	100		48	41	68			
Pseudomonas stutzeri	43						100						100		100				100			95					97	97				97			

		Beta lactams														Macrolides			Aminoglycosides			Fluroquinolones				Carbapenems			Others						
Organism	No of patients	AMC	AMP	CZO	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	FEP	PEN	TZP	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	COL	FOS	NIT	SXT	TCY	TGC	TMP
Providencia stuartii	36						94			90			88		89				94	51		64				96	36	91		20	0	91			
Citrobacter sp.	35	36					65			55	24		82		71				100	100		62				93	89	94			90	82			
Klebsiella sp.	35			21			59			67	56		71		91				97	83		76	87			76		75				77			
Sphingomonas paucimobilis	35						82			88			85		90				81	81		71					86	91				71			
Proteus vulgaris	31	90	8				86			93	15		97		100				100	97		93				92	17	96			4	90			
Vibrio cholerae	30		85																													79	96		
Enterobacter hormaechei	29	8		4			64			74	19		88		78				100	92		65				96	100	100		0	31	95			
Providencia rettgeri	28						80			77			82		82				96	93		85				89	50	85		46	8	89			
Campylobacter jejuni	25																	83																	
Enterobacter gergoviae	25	91					96			95	70		96		100				100	96		92				100	100	100				92			
Aeromonas hydrophila	24						74						83		50				91	83		74					54					83			
Enterobacter sp.	24	18											82		65				91	90		71				86		86				85			
Shigella sonnei	24									26												29					100	100				21			
Haemophilus parahaemolyticus	23		0			0																0													
Neisseria meningitidis	23									100												80						100							

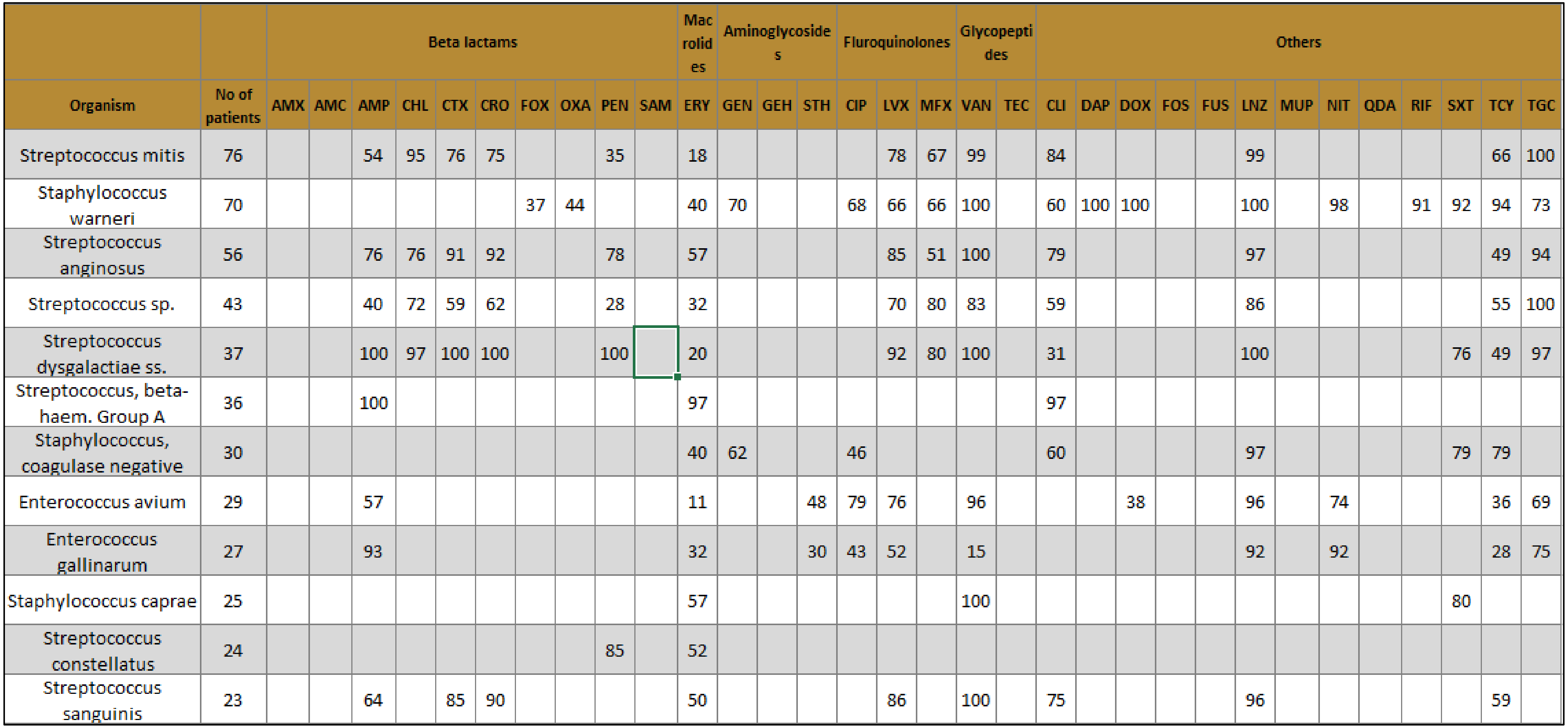
		Beta lactams														Macrolides			Aminoglycosides			Fluroquinolones				Carbapenems			Others						
Organism	No of patients	AMC	AMP	CZO	CFM	CTX	CAZ	CZA	CZT	CRO	CXM	CXA	FEP	PEN	TZP	AZM	CLR	ERY	AMK	GEN	TOB	CIP	LVX	MFX	NOR	ETP	IPM	MEM	COL	FOS	NIT	SXT	TCY	TGC	TMP
Pseudomonas fluorescens	23						100						90		85							70										32			
Pseudomonas sp.	23						86						91		90							77						96							
Citrobacter farmeri	22	77					76			76			77		96				100	86		52				100	100	95				82			
Pantoea agglomerans	22	76								81			81		96				95	95		91				80						90			
Pseudomonas luteola	21						75						100		90				100			81					100	100							

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

4.2.4 Northern Emirates

Table 4.2.4.1 Northern Emirates Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-pos. bacteria (isolates from all sources, N=12,074)

		Beta lactams										Macrolides	Aminoglycosides			Fluroquinolones			Glycopeptides		Others												
Organism	No of patients	AMX	AMC	AMP	CHL	CTX	CRO	FOX	OXA	PEN	SAM	ERY	GEN	GEH	STH	CIP	LVX	MFX	VAN	TEC	CLI	DAP	DOX	FOS	FUS	LNZ	MUP	NIT	QDA	RIF	SXT	TCY	TGC
Staphylococcus aureus	4,352							42	48	9		58	87			58	60	61	98	99	80	100	98		0	100		100		99	82	84	100
Streptococcus agalactiae	2,252			99	97	100	100			98		36					88	69	100		49					100					77	16	99
Enterococcus faecalis	1,170			99						96		13	21	76	65	68	72		99			97	36			96		98				28	100
Staphylococcus epidermidis	752							23	25	12		26	65			48	48	48	99	77	51	99	88			100		99		92	62	80	72
Streptococcus pyogenes	613	99		100	98	100	100			99		70					86	81	100		88					100					82	84	100
Staphylococcus hominis	482							34	37			23	95			66	67	67	99		65	100	93			100		94		98	76	68	78
Staphylococcus haemolyticus	325							7	12			13	60			36	37	37	99		46	99	71			99		99		77	76	57	68
Streptococcus pneumoniae	286				91	94	97			94		37					91	96	100		58					100				100	62	45	100
Staphylococcus capitis	270							32	29			33	39			29	32	32	100		32	100	99			100		99		71	79	98	77
Streptococcus, beta-haem. Group B	258			100						100											69												
Staphylococcus saprophyticus	244							54	42	15		31	97			96	94	96	98	99	76	100	98		0	100		98		98	94	90	61
Enterococcus sp.	142	100	99	98						78	100			95		82	81		99				87	86		98		97				45	
Enterococcus faecium	120			22						22		4	19		47	16	18		92				15			89		20	90			25	66
Streptococcus dysgalactiae	82	100				100				96		38									65												
Staphylococcus lugdunensis	78							59	70	26		81	95			90	92	93	100	100	81	100	97		0	100	0	96		100	99	94	59



		Beta lactams										Macrolides	Aminoglycosides			Fluroquinolones			Glycopeptides		Others												
Organism	**No of patients**	**AMX**	**AMC**	**AMP**	**CHL**	**CTX**	**CRO**	**FOX**	**OXA**	**PEN**	**SAM**	**ERY**	**GEN**	**GEH**	**STH**	**CIP**	**LVX**	**MFX**	**VAN**	**TEC**	**CLI**	**DAP**	**DOX**	**FOS**	**FUS**	**LNZ**	**MUP**	**NIT**	**QDA**	**RIF**	**SXT**	**TCY**	**TGC**
Streptococcus mitis	76			54	95	76	75			35		18					78	67	99		84					99						66	100
Staphylococcus warneri	70							37	44			40	70			68	66	66	100		60	100	100			100		98		91	92	94	73
Streptococcus anginosus	56			76	76	91	92			78		57					85	51	100		79					97						49	94
Streptococcus sp.	43			40	72	59	62			28		32					70	80	83		59					86						55	100
Streptococcus dysgalactiae ss.	37			100	97	100	100			100		20					92	80	100		31					100					76	49	97
Streptococcus, beta-haem. Group A	36			100								97									97												
Staphylococcus, coagulase negative	30											40	62			46					60					97					79	79	
Enterococcus avium	29			57								11			48	79	76		96				38			96		74				36	69
Enterococcus gallinarum	27			93								32			30	43	52		15							92		92				28	75
Staphylococcus caprae	25											57							100												80		
Streptococcus constellatus	24									85		52																					
Streptococcus sanguinis	23			64		85	90					50					86		100		75					96						59	

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

Table 4.2.4.2 Northern Emirates Cumulative Antibiogram (2024): Percent susceptible isolates (%S) – Gram-neg. bacteria (isolates from all sources, N=21,823)

		Beta lactams												Aminoglycosides			Fluroquinolones			Carbapenems			Others												
Organism	No of patients	AMC	AMP	CAZ	CFM	CRO	CTX	CXM	CZO	FEP	FOX	SAM	TZP	AMK	GEN	TOB	CIP	LVX	MFX	ETP	IPM	MEM	ATM	CHL	CLR	COL	CZA	CZT	DOX	FOS	NIT	NOR	SXT	TCY	TGC
Escherichia coli	9,288	74	33	60		56	58	49	46	63		53	93	97	89		38	68		98	98	99								98	94		61		99
Klebsiella pneumoniae	4,274	76		67		68	70	62	59	73		64	84	95	92		66	89		92	92	94								59	27		76		95
Pseudomonas aeruginosa	2,635			85					0	85			76	96			81				81	84				48	88	91							
Enterobacter cloacae	641	2	11	73		71	70	18	2	82			84	97	93		75	84		91	94	97								43	31		87		92
Proteus mirabilis	541	68		83		78	76	77	66	84		67	98	84	72		57			96	36	97						95		61	1		58		23
Acinetobacter baumannii	482			89		61	14		0	88		88	86	95	95		86				94	94				67							94		
Serratia marcescens	452	2		92		88	83	0	0	95				98	98		89			95	94	98					99			61	0		99		94
Klebsiella aerogenes	445	7	10	76		77	63	31	5	89	16		83	98	97	96	87	96		95	92	98				0				52	21		91		95
Citrobacter koseri	399	92	1	93		92	88	78	89	94			95	99	98		92	90		97	98	99						98		70	77		96		99
Stenotrophomonas maltophilia	394																	86															92		
Haemophilus influenzae	199	40	38	94		94	91	77							74		85					85		88	72								65		
Morganella morganii	194	2		69		62	61	4	1			7	94	97	79		41			97	7	98					100	96		2	3		63		32
Klebsiella oxytoca	190	76	7	78		80	66	69	53	79	64	40	84	96	91	76	72	79		94	96	96								54	72		72		98
Salmonella sp.	159	51	81	44		91	95	0	0	47		33	47	0	0		77			100	98	100					29	23		52	44		97		96
Klebsiella sp.	132	51			50	73	73	49	49	94	63		100	100	99	100	87	87			100	100							92		91		78		
Citrobacter freundii	111	12	19	71		77	56	32	3	81	12	47	87	95	82	65	64	71		92	89	93	62			0				61	92	69	69		95
Achromobacter xylosoxidans	80			82		5	7		5	20			86	31	28		13				65	87				41							95		

		Beta lactams												Aminoglycosides			Fluroquinolones			Carbapenems			Others												
Organism	No of patients	AMC	AMP	CAZ	CFM	CRO	CTX	CXM	CZO	FEP	FOX	SAM	TZP	AMK	GEN	TOB	CIP	LVX	MFX	ETP	IPM	MEM	ATM	CHL	CLR	COL	CZA	CZT	DOX	FOS	NIT	NOR	SXT	TCY	TGC
Acinetobacter calcoaceticus-	63	4	0	88		82		4		85			83	92	86	88	86	86		0	90	91				0					0		78		
Burkholderia cepacia	60			96		3			3	6			9	6	7		48				11	93				5							82		
Acinetobacter lwoffii	55			90		82			23	93		81	49	98	82		75				91	92											83		
Klebsiella pneumoniae ss.	52	72		78		65		65	56	70			79	81	85		62			80	84	84								37	54		80		
Providencia stuartii	51			96		91	89	74		96		30	100	94	20		59			96	37	96								38	0		86		18
Salmonella enterica ss. enterica	41	0	76	0			89	0	0	0	0	0	0	0	0	0	87	90	0	97	100	100	0								0	0	92		97
Neisseria gonorrhoeae	40				100	100											8																	15	
Pseudomonas stutzeri	37			100					8	100			100	94			88				97	100											84		
Elizabethkingia meningoseptica	36			6						3			3	3	18		33				6	6											85		
Pseudomonas fluorescens	33			84						84			70	100			76				88	90											53		
Pseudomonas putida	33			78						83			50	97			75				81	71											7		
Sphingomonas paucimobilis	32			82		90			57	64			85	90	93		84				93	93											90		
Salmonella Typhi	27	43		25						22			41	0	0		27			100	100	100											58		
Enterobacter cloacae complex	26	8		75				48					83	77	77		65			100	100	100									35				
Moraxella sp.	24			96		100			75					96	100		96					100											91		
Pseudomonas sp.	23			96						100			100				91					100													
Providencia rettgeri	22									95				100	96		100					90											96		
Proteus sp.	21												100		100		95																85		

Code	Antibiotic	Code	Antibiotic
AMC	Amoxicillin/Clavulanic acid	ETP	Ertapenem
AMK	Amikacin	FEP	Cefepime
AMP	Ampicillin	FOS	Fosfomycin
ATM	Aztreonam	FOX	Cefoxitin
CAZ	Ceftazidime	GEN	Gentamicin
CFM	Cefixime	IPM	Imipenem
CHL	Chloramphenicol	LVX	Levofloxacin
CIP	Ciprofloxacin	MEM	Meropenem
CLR	Clarithromycin	MFX	Moxifloxacin
COL	Colistin	NIT	Nitrofurantoin
CRO	Ceftriaxone	NOR	Norfloxacin
CTX	Cefotaxime	SAM	Ampicillin/Sulbactam
CXM	Cefuroxime	SXT	Trimethoprim/Sulfamethoxazole
CZA	Ceftazidime/Avibactam	TCY	Tetracycline
CZO	Cefazolin	TGC	Tigecycline
CZT	Ceftolozane/Tazobactam	TOB	Tobramycin
DOX	Doxycycline	TZP	Piperacillin/Tazobactam

4.3 Multidrug resistance

4.3.1 MDR, XDR, PDR Summary

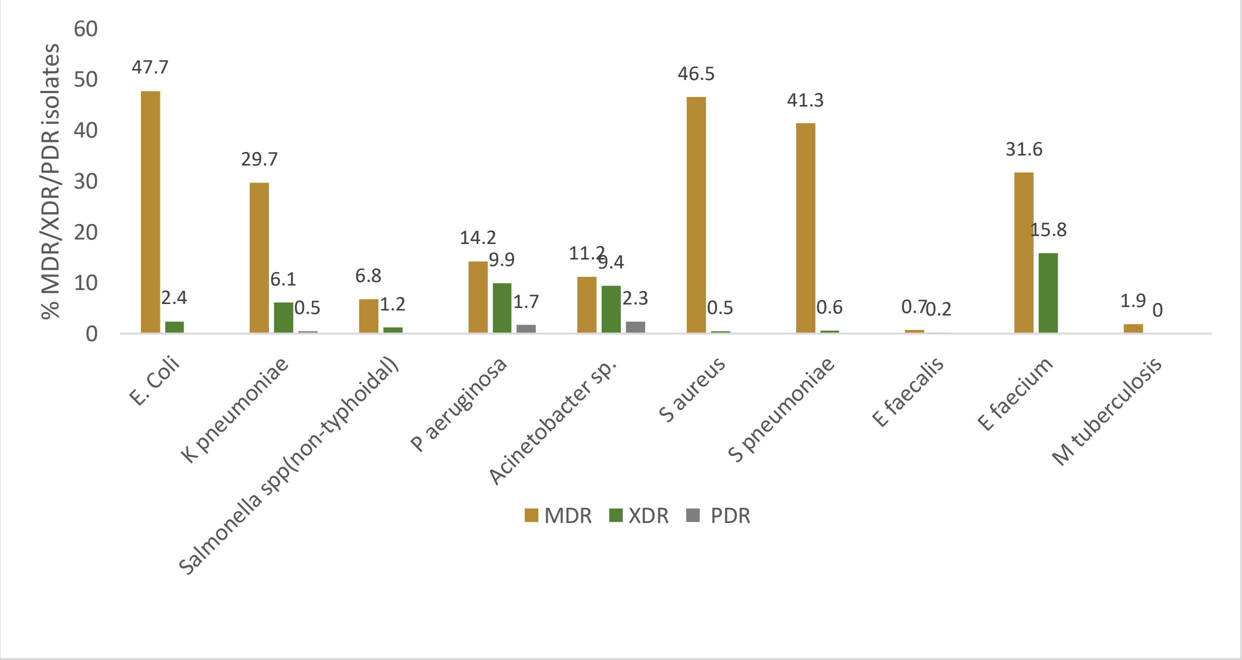
In a 2012 publication, the European Centre for Disease Prevention and Control (ECDC) proposed definitions for common bacterial pathogens resistant to multiple antimicrobials (Magiorakos, et al., 2012). Similar definitions were applied for organisms where these were not available from this publication (*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 4.3.1.1 MDR, XDR, PDR Summary, United Arab Emirates, 2024

Organism	Number of isolates	MDR	Possible XDR	Possible PDR
Escherichia coli	42,478	20,280 (47.7%)	1,035 (2.4%)	9 (0%)
Klebsiella pneumoniae	16,597	4,923 (29.7%)	1,015 (6.1%)	85 (0.5%)
Salmonella spp. (non-typhoidal)	1,299	89 (6.8%)	16 (1.2%)	1 (0%)
Pseudomonas aeruginosa	9,429	1,336 (14.2%)	930 (9.9%)	158 (1.7%)
Acinetobacter sp.	1,836	206 (11.2%)	172 (9.4%)	42 (2.3%)
Staphylococcus aureus	18,659	8,684 (46.5%)	95 (0.5%)	3 (0%)
Streptococcus pneumoniae	2,198	907 (41.3%)	14 (0.6%)	3 (0.1%)
Enterococcus faecalis	5,261	39 (0.7%)	11 (0.2%)	0 (0%)
Enterococcus faecium	507	160 (31.6%)	80 (15.8%)	4 (0%)
Mycobacterium tuberculosis	1,369	26 (1.9 %)	No data	No data
Total	**99,633**	**36.650 (36.8 %)**	**3,368 (3.3 %)**	**305 (0.3 %)**

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

Figure 4.3.1.1 MDR, XDR, PDR Summary, United Arab Emirates, 2024



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, 2024

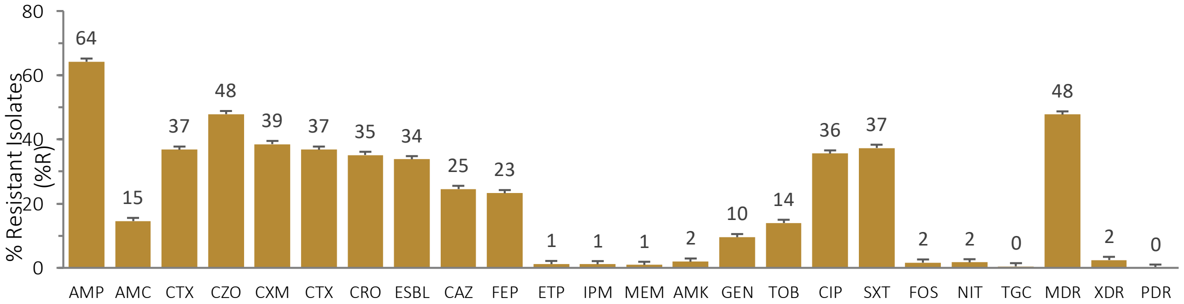
Antibiotic	Code	***Escherichia coli*** (N=53,918)			
		Isolates (N)	**% R**	**% I**	**% S**
Ampicillin	AMP	23,947	64.2	1.1	34.7
Amoxicillin/clavulanic acid	AMC	39,624	14.6	9.1	76.3
Piperacillin/tazobactam	TZP	41,921	6.0	0.4	89.7
Cefuroxime (oral)	CXM	29,635	38.5	5.0	55.7
Ceftriaxone	CRO	27,524	35.2	0.1	64.7
Cefotaxime	CTX	14,734	36.8	0.8	62.1
Extended-spectrum β-lactamase	ESBL	7,192	33.8	–	66.2
Ceftazidime	CAZ	37,077	24.6	24.6	69.0
Cefepime	FEP	39,497	23.2	0.4	72.6
Ertapenem	ETP	37,195	1.2	0.2	98.6
Imipenem	IPM	38,022	1.1	0.5	97.4
Meropenem	MEM	39,699	0.9	0.1	99.0
Gentamicin	GEN	41,982	9.5	0.4	87.5
Tobramycin	TOB	4,385	14.0	0.6	61.4
Amikacin	AMK	33,208	1.9	1.3	91.6
Ciprofloxacin	CIP	41,649	35.6	12.8	48.8
Trimethoprim/sulfamethoxazole	SXT	41,357	37.4	0.0	54.7
Fosfomycin[a]	FOS	28,701	1.6	0.2	98.1
Nitrofurantoin[a]	NIT	39,007	1.7	3.1	95.2
Tigecycline[b]	TGC	5,400	0.5	0.4	98.9
Multidrug-resistance (≥3 classes NS)[c]	MDR	42,478	47.7	–	–
Extensive drug resistance (possible)	XDR	42,478	2.4	–	–
Pan-drug resistance (possible)	PDR	42,478	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, 2024



For 2024, resistance in *Escherichia coli* ranged from 1.0% for carbapenems (Meropenem) to 64% for aminopenicillins (ampicillin). Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *E. coli* was 47.7%, 2.4%, and 0%, respectively.

4.4.2 *Klebsiella pneumoniae*

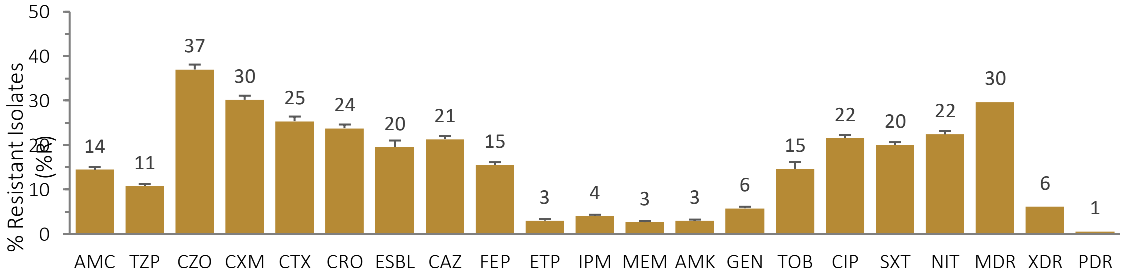
Table 4.4.2.1 Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae*, isolates from all sources, United Arab Emirates, 2024

Antibiotic	Code	***Klebsiella pneumoniae*** (N=21,594)			
		Isolates (N)	**% R**	**% I**	**% S**
Amoxicillin/clavulanic acid	AMC	14,956	14.4	6.4	79.2
Piperacillin/tazobactam	TZP	16,307	10.7	1.6	81.5
Cefuroxime (oral)	CXM	10,580	30.2	2.2	66.5
Ceftriaxone	CRO	9,910	23.8	0.6	75.6
Cefotaxime	CTX	6,361	25.3	1.5	72.9
Extended-spectrum β-lactamase	ESBL	3,167	19.5	–	80.5
Ceftazidime	CAZ	14,302	21.3	4.0	74.6
Cefepime	FEP	15,311	15.5	0.2	81.8
Ertapenem	ETP	14,098	3.0	0.4	96.5
Imipenem	IPM	14,388	3.9	1.9	93.8
Meropenem	MEM	15,327	2.6	0.2	97.2
Gentamicin	GEN	16,381	5.7	0.1	91.5
Tobramycin	TOB	2,103	14.6	0.7	64.9
Amikacin	AMK	12,782	2.9	0.3	91.8
Ciprofloxacin	CIP	16,206	21.5	6.8	68.2
Trimethoprim/sulfamethoxazole	SXT	16,065	20.0	0.0	72.7
Nitrofurantoin[a]	NIT	14,007	22.4	46.2	31.4
Multidrug-resistance (≥3 classes NS)[b]	MDR	16,597	29.7	–	–
Extensive drug resistance (possible)	XDR	16,597	6.1	–	–
Pan-drug resistance (possible)	PDR	16,597	0.5	–	–

[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 , 2024



For 2024, resistance in *Klebsiella pneumoniae* ranged from 3.0 %R for meropenem (Carbapenems), to 30 %R for cefuroxime (CXM).

Non-susceptibility (%R+%I) to carbapenems was 4.0%, 3.0%, and 3.0 %NS for imipenem, meropenem and ertapenem, respectively.

Prevalence of multidrug resistance (%MDR/XDR/PDR[8]) in *K. pneumoniae* was 29.7 %, 6.1%, and 0.5%, respectively.

4.4.3 *Salmonella spp. (non-typhoidal)*

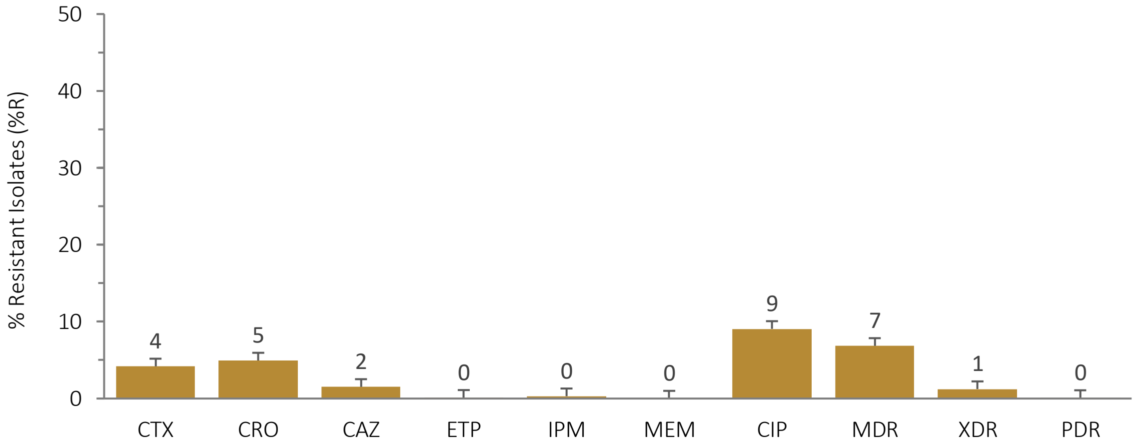
Table 4.4.3.1 Percentages of resistant, intermediate, and susceptible isolates for *Salmonella* spp. (non-typhoidal), isolates from all sources, United Arab Emirates, 2024

Antibiotic	Code	*Salmonella* spp. (non-typhoid) (N=1,773)			
		Isolates (N)	% R	% I	% S
Cefotaxime	CTX	526	4.2	0.4	95.1
Ceftriaxone	CRO	768	4.9	0.0	95.1
Ceftazidime	CAZ	988	1.5	0.2	49.1
Ertapenem	ETP	963	0.1	0.1	99.7
Imipenem	IPM	982	0.3	0.2	99.4
Meropenem	MEM	1,000	0.0	0.0	100.0
Ciprofloxacin[a]	CIP	982	9.1	11.7	73.3
Multidrug-resistance (≥3 classes NS)[b]	MDR	1,299	6.9	–	–
Extensive drug resistance (possible)	XDR	1,299	1.2	–	–
Pan-drug resistance (possible)	PDR	1,299	0.1	–	–

[a] Ciprofloxacin results refer to extra-intestinal (non-stool) isolates only.

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

Figure 4.4.3.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Salmonella* spp. (non-typhoidal), isolates from all sources, United Arab Emirates, 2024



For 2024, resistance in *Salmonella* spp. (non-typhoidal) ranged from 0.0 %R for carbapenems (meropenem), to 9.0 %R for fluoroquinolones (ciprofloxacin, extraintestinal isolates).

Susceptibility of non-typhoidal *Salmonella* spp. (extra-intestinal isolates) to ciprofloxacin was 73.0%.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *Salmonella* spp. (non-typhoidal) was 6.9 %, 1.2% and 0.1%, respectively.

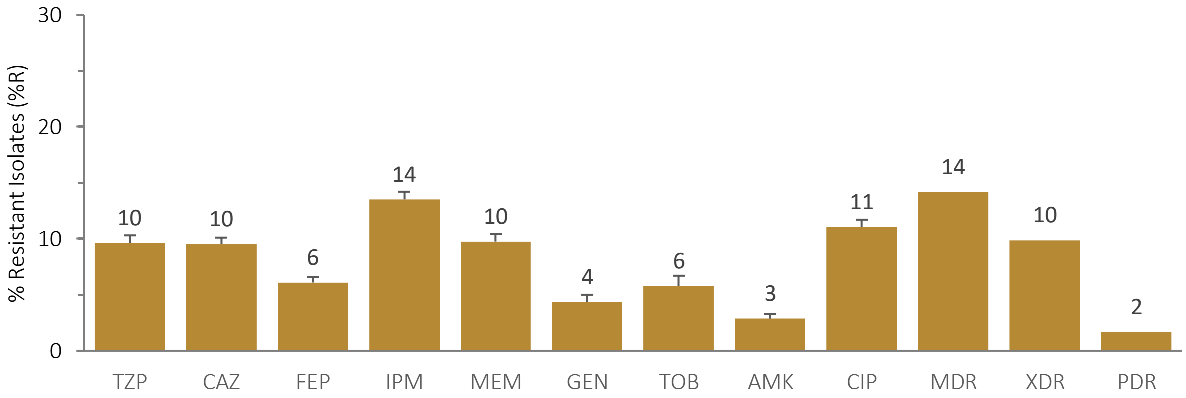
4.4.4 *Pseudomonas aeruginosa*

Table 4.4.4.1 Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa*, isolates from all sources, United Arab Emirates, 2024

Antibiotic	Code	*Pseudomonas aeruginosa* (N=12,625)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	8,590	9.6	2.9	87.5
Ceftazidime	CAZ	9,285	9.5	3.4	87.1
Cefepime	FEP	9,144	6.1	5.1	88.8
Imipenem	IPM	9,112	13.5	3.3	83.1
Meropenem	MEM	9,192	9.7	4.0	86.2
Gentamicin	GEN	4,051	4.3	4.5	91.2
Tobramycin	TOB	2,700	5.8	1.2	87.5
Amikacin	AMK	8,127	2.9	1.0	96.2
Ciprofloxacin	CIP	9,214	11.0	3.0	84.4
Multidrug-resistance (≥3 classes NS)[a]	MDR	9,429	14.2	–	–
Extensive drug resistance (possible)	XDR	9,429	9.9	–	–
Pan-drug resistance (possible)	PDR	9,429	1.7	–	–

[a] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 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, 2024



For 2024, resistance in *Pseudomonas aeruginosa* ranged from 2.9 – 5.8 %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 14.2 %, 9.9%, and 1.7%, respectively.

4.4.5 *Acinetobacter spp.*

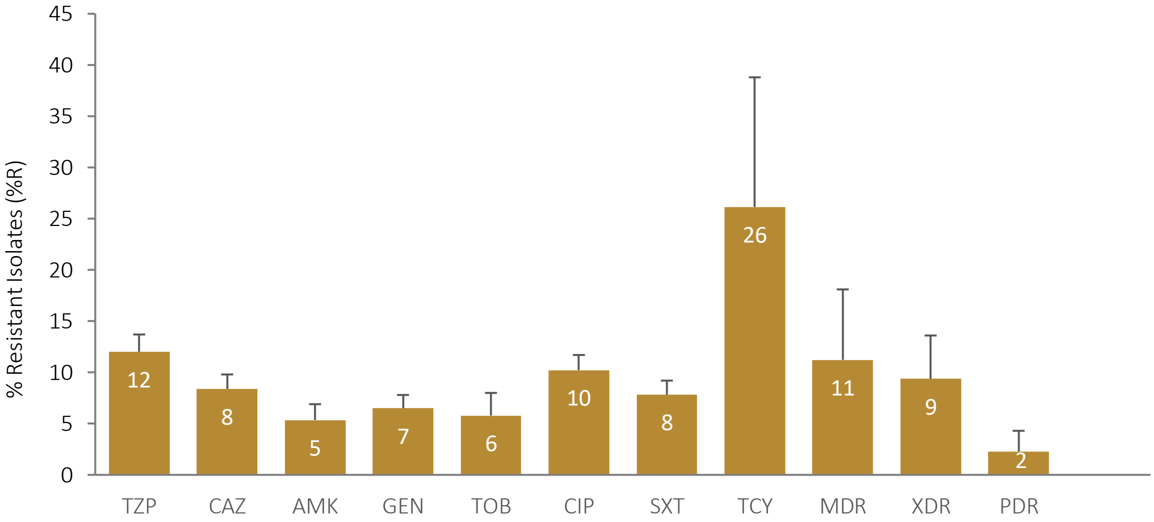
Table 4.4.5.1 Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp., isolates from all sources, United Arab Emirates, 2024

Antibiotic	Code	***Acinetobacter* spp.** (N=2,546)			
		Isolates (N)	**% R**	**% I**	**% S**
Piperacillin/tazobactam	TZP	1,681	12.0	3.1	84.1
Ceftazidime	CAZ	1,788	8.4	5.9	85.7
Cefepime	FEP	1,698	8.1	3.1	88.5
Imipenem	IPM	1,651	5.6	0.6	93.8
Meropenem	MEM	1,764	5.9	0.5	93.6
Gentamicin	GEN	1,799	6.5	1.8	91.6
Tobramycin	TOB	604	5.8	1.0	93.2
Amikacin	AMK	1,121	5.4	1.2	93.4
Ciprofloxacin	CIP	1,781	10.2	2.8	87.0
Trimethoprim/Sulfamethoxazole	SXT	1,763	7.8	0.0	86.6
Tetracycline	TCY	65	26.2	3.1	70.8
Multidrug-resistance (≥3 classes NS)[a]	MDR	1,835	11.2	–	–
Extensive drug resistance (possible)	XDR	1,835	9.4	–	–
Pan-drug resistance (possible)	PDR	1,835	2.3	–	–

[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).

[d] Includes duplicate isolates.

Figure 4.4.5.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Acinetobacter* spp., isolates from all sources, United Arab Emirates, 2024



For 2024, Prevalence of multidrug resistance (%MDR/XDR/PDR[10]) in *Acinetobacter* spp. was 11.2 %, 9.4%, and 2.3%, 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, 2024

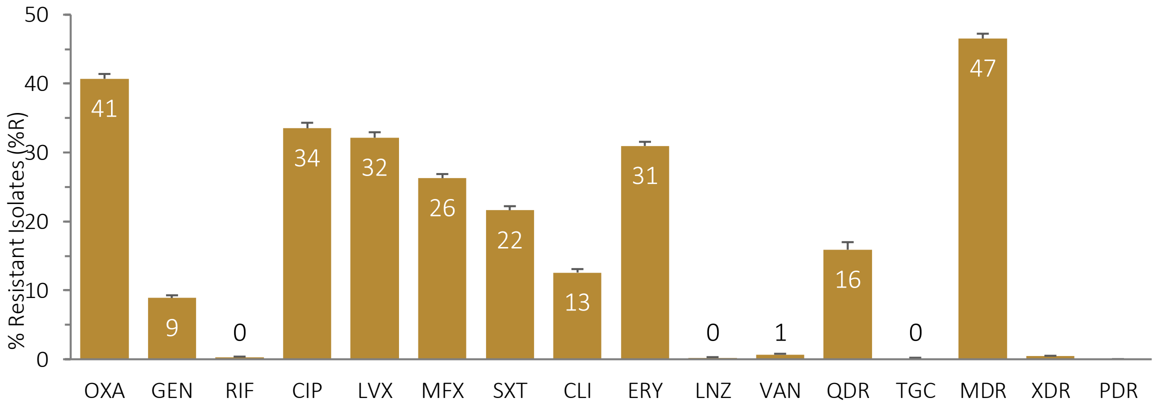
Antibiotic	Code	***Staphylococcus aureus*** (n=24,771)			
		Isolates (N)	**% R**	**% I**	**% S**
Oxacillin	OXA	18,659	40.7[a]	–	59.3[a]
Gentamicin	GEN	20,407	8.9	2.1	88.9
Rifampicin	RIF	17,579	0.3	0.1	99.6
Ciprofloxacin	CIP	14,751	33.5	1.2	65.2
Levofloxacin	LVX	14,543	32.1	1.6	66.3
Moxifloxacin	MFX	17,815	26.3	7.2	66.5
Trimethoprim/sulfamethoxazole	SXT	20,664	21.6	0.0	69.9
Clindamycin	CLI	20,489	12.6	0.2	87.2
Erythromycin	ERY	20,423	31.0	1.4	67.6
Linezolid	LNZ	20,235	0.2	0.0	99.8
Vancomycin	VAN	20,025	0.7	0.1	99.2
Quinupristin/Dalfopristin	QDA	4,259	15.9	0.0	84.1
Tigecycline	TGC	17,953	0.1	0.0	99.9
Multidrug-resistance (≥3 classes NS)[c]	MDR	18,659	46.5	–	–
Extensive drug resistance (possible)	XDR	18,659	0.5	–	–
Pan-drug resistance (possible)	PDR	18,659	0.0	–	–

[a] MRSA/MSSA is calculated as resistance/susceptibility to oxacillin: %MRSA = 40.7% and %MSSA = 59.3%.

[b] Tigecycline: EUCAST breakpoints (S≤0.5, R>0.5)

[c] Multidrug resistance (MDR) was defined as isolate being either a MRSA or having acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

Figure 4.4.6.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Staphylococcus aureus*, isolates from all sources, United Arab Emirates, 2024



For 2024, resistance in *Staphylococcus aureus* ranged from 0% for rifampin, linezolid and tigecycline, to 41% for oxacillin.

Percentage MRSA was 40.7% for all isolates.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *S. aureus* was 46.5%, 0.5%, and 0%, respectively.

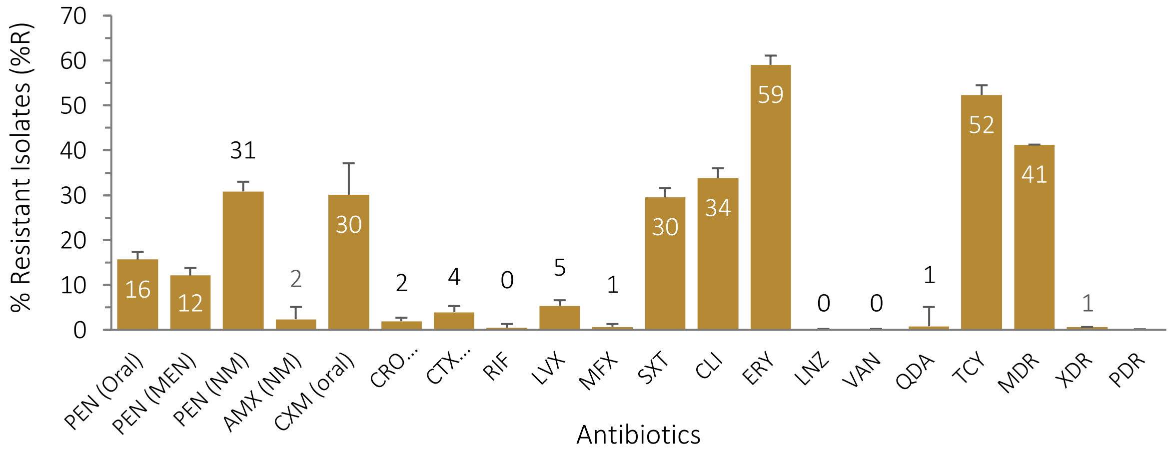
4.4.7 *Streptococcus pneumoniae*

Table 4.4.7.1 Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae*, isolates from all sources, United Arab Emirates, 2024

Antibiotic	Code	***Streptococcus pneumoniae*** (N=2,958)			
		Isolates (N)	**% R**	**% I**	**% S**
Penicillin G (oral breakpoints)	PEN (oral)	1,884	15.7	31.9	52.2
Penicillin G (non-meningitis breakpoints)	PEN (NM)	1,884	12.1	17.8	70.0
Penicillin G (meningitis breakpoints)	PEN (MEN)	1,884	30.8	16.8	52.2
Amoxicillin (non-meningitis breakpoints)	AMX (NM)	294	2.4	6.8	90.8
Cefuroxime (oral breakpoints)	CXM (oral)	196	29.6	2.0	68.4
Cefotaxime (non-meningitis breakpoints)	CTX (NM)	1,088	2.5	2.6	93.5
Ceftriaxone (non-meningitis breakpoints)	CRO (NM)	1,927	1.7	0.8	97.6
Rifampin	RIF	811	0.5	0.0	99.5
Levofloxacin	LVX	1,532	5.4	0.7	94.0
Moxifloxacin	MFX	1,609	0.7	0.7	96.9
Trimethoprim/Sulfamethoxazole	SXT	2,105	29.5	8.3	58.2
Clindamycin	CLI	1,961	33.8	0.7	65.5
Erythromycin	ERY	2,131	59.0	0.4	40.6
Linezolid	LNZ	1,998	0.0	0.2	99.7
Vancomycin	VAN	2,173	0.0	0.0	98.9
Quinupristin/Dalfopristin	QDA	124	0.8	0.0	99.2
Tetracycline	TCY	2,070	52.3	1.1	46.6
Multidrug-resistance (≥3 classes NS)[a]	MDR	2,198	41.3	–	–
Extensive drug resistance (possible)	XDR	2,198	0.6	–	–
Pan-drug resistance (possible)	PDR	2,198	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, 2024



For 2024, resistance in *Streptococcus pneumoniae* ranged from 0% for rifampin, linezolid, and vancomycin, to 59% for erythromycin.

Prevalence of multidrug resistance (%MDR/XDR/PDR) in *S. pneumoniae* was 41.3%, 0.6%, and 0.1%, respectively.

Prevalence of the different pneumococcal serotypes in the UAE is currently unknown (no routine testing of serotypes in participating facilities, no reference lab).

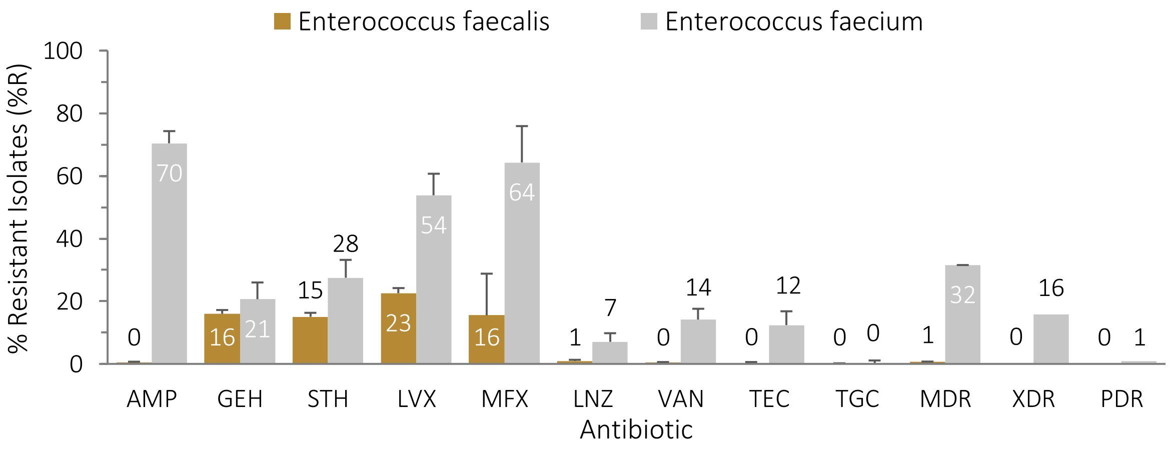
4.4.8 *Enterococcus faecalis and Enterococcus faecium*

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, 2024

Antibiotic	Code	*Enterococcus faecalis* (N=6,760				*Enterococcus faecium* (N=630)			
		N	% R	% I	% S	N	% R	% I	% S
Ampicillin	AMP	5,236	0.5	0.0	99.5	500	70.4	0.0	29.6
Gentamicin (high level)	GEH	3,687	16.0	0.0	74.5	276	20.7	0.0	59.8
Streptomycin (high level)	STH	3,140	15.0	0.0	61.6	280	27.5	0.0	35.0
Levofloxacin	LVX	2,576	22.6	3.8	73.6	210	53.8	8.1	37.6
Moxifloxacin	MFX	184	15.5	1.9	82.4	6	25.0	0.0	75.0
Linezolid	LNZ	5,075	1.0	0.8	98.1	497	7.0	2.6	90.1
Vancomycin	VAN	5,045	0.4	0.0	99.4	495	14.1	0.0	85.9
Teicoplanin	TEC	2,783	0.3	0.0	99.7	299	12.4	0.7	87.0
Tigecycline[c]	TGC	4,064	0.0	0.0	99.9	427	0.0	0.0	65.6
Multidrug-resistance (≥3)[d]	MDR	5,261	0.7	–	–	507	31.6	–	–
Extensive drug resistance	XDR	5,261	0.2	–	–	507	15.8	–	–
Pan-drug resistance	PDR	5,261	0.0	–	–	507	0.8	–	–

[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, 2024



For 2024, Prevalence of multidrug-resistance (%MDR/possible XDR/possible PDR) was 0.7%, 0.2%, and 0% for *E. faecalis*, and 31.6%, 15.8%, and 0.8% 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, 2024 (Cumulative antibiogram)

	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU[a]	VOR[b]	AMB[c]	CAS[d]	MIF[e]
***Candida* spp.**	6,051	100.0	78	77	-	93	96
Candida albicans	3,188	52.7	85	79	88[c]	97	96
Candida spp. (non-albicans)	2,863	47.3	66	77	-	88	96
C. tropicalis	885	15.8	93	96	98	98	98
C. parapsilosis	584	10.4	84	90	94	98	98
C. glabrata[f]	528	9.4	6	-[g]	96	62	94
C. auris[h]	392	7.0	6	-	43	89	94

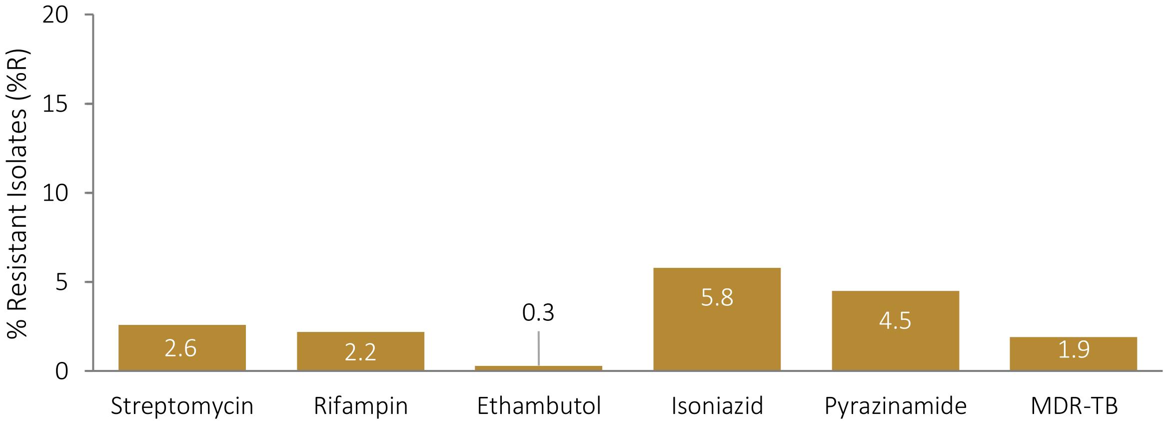
[a]FLU=Fluconazole [b]VOR=Voriconazole [c]AMB=Amphotericin B. EUCAST breakpoints (S≤1, R>1) are used for amphotericin B for *C. albicans, C. glabrata, C. parapsilosis*, and *C. tropicalis* (EUCAST, 2024) Note: Some automated systems overcall amphotericin resistance for *Candida* species [d]CAS=Caspofungin.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

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, 2024

Antibiotic	Code	***M. tuberculosis*** (N=1,375)			
		Isolates (N)	**% R**	**% I**	**% S**
Rifampin	RIF	1,371	2.2 ↓↓	0.0	97.8
Ethambutol	EMB	1,371	0.3 ↓	0.1	99.6
Isoniazid	INH	1,370	5.8 ↓↓	1.4	92.8
Pyrazinamide	PZH	1,033	4.5 ↑	0.0	95.5
Streptomycin	STM	231	2.6 ↑	0.0	97.4
Multidrug-resistance (INH+RIF)	MDR	1,369	1.9 ↓↓	–	–

Figure 4.4.10.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Mycobacterium tuberculosis*, isolates from all sources, United Arab Emirates, 2024



5. Annex

Annex 5.1 AMR priority pathogens

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

E. coli

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

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

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

K. pneumoniae

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

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

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

Salmonella

Salmonella:

- is a major cause of foodborne illness throughout the world,
- is a zoonotic pathogen and can thus be found in the intestines of many food-producing animals such as poultry and pigs, and infection is usually acquired by consumption of contaminated water or food of animal origin such as undercooked meat, poultry, eggs and milk;

- can also contaminate the surface of fruits and vegetables through contact with human or animal faeces, which can lead to foodborne outbreaks; and
- mostly causes gastroenteritis, while some strains, particularly *Salmonella enterica* serotypes Typhi and Paratyphi, are more invasive and typically cause enteric fever – a more serious infection that poses problems for treatment due to antibiotic-resistant strains in many parts of the world.

UAE AMR surveillance focuses on non-typhoidal *Salmonella* because these are the main diarrhoeal pathogens transmitted via the food chain. In many countries, the incidence of non-typhoidal *Salmonella* infections has increased markedly in recent years, for reasons that are unclear. One estimate suggests that there are around 94 million cases, resulting in 155 000 deaths, of non-typhoidal *Salmonella* gastroenteritis each year. The majority of the disease burden, according to this study, is in the WHO South-East Asian Region and the WHO Western Pacific Region (Majowicz, et al., 2010).

P. aeruginosa

Pseudomonas aeruginosa:

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

Acinetobacter spp.

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

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

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

S. aureus

Staphylococcus aureus:

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

Several successful *S. aureus* clones are responsible for most of the international spread and outbreaks in health care and community settings. A recent structured survey showed that the most prevalent clones among methicillin-resistant *S. aureus* (MRSA) in EU countries are ST22 (EMRSA15), ST225 (New York/Japan), ST8 (US300), ST5 (New York/Japan), and ST8 (South German) (Albrecht, Jatzwauck, Slickers, Ehricht, & Monecke, 2011). Among methicillin-susceptible *S. aureus*, the most prevalent clones are ST7, ST15, ST5, ST45 and ST8.

The clonal structure of MRSA and methicillin-susceptible *S. aureus* in the UAE has been assessed by Sonnevend et al., who reported a change in predominance of certain MRSA clones over a 5-year period (2003-2008). In 2003, typical healthcare-associated (HA-MRSA) genotypes (ST239-MRSA-III, ST22-MRSA-IV and ST5-MRSA-II) represented the majority (61.5%) of the isolates. By 2008, this pattern had changed and clonal types considered as community-associated (CA) MRSA comprised 73.1% of the strains, with ST80-MRSA-IV, ST5-MRSA-IV and ST1-MRSA with non-typable SCCmec types being the most frequent (Sonnevend, et al., 2012).

S. pneumoniae

Streptococcus pneumoniae:

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

The clinical burden of pneumococcal infection is concentrated among the oldest and youngest sections of the population. It caused about 826,000 deaths (582,000–926,000) among children 1–59 months old. For HIV-negative children, pneumococcal infection corresponds to 11% of all deaths in this age group (O'Brien, et al., 2009).

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

E. faecium and *E. faecalis*

Enterococci:

- belong to the normal bacterial microbiota of the gastrointestinal tract of both humans and other animals, are usually low-pathogenic but can cause invasive disease under certain circumstances,
- can act as true pathogens and not only as opportunistic commensals, as high-risk clones were recently recognized,
- can cause a variety of infections, including endocarditis, bloodstream and urinary tract infections, and are associated with peritonitis and intra-abdominal abscesses,
- contribute to increasing mortality as well as additional hospital stay,

- emerge as important nosocomial pathogens, as documented in epidemiological data collected over the last two decades and exemplified by the expansion of a major hospital-adapted polyclonal subcluster clonal complex 17 (CC17) in *E. faecium* and by CC2 and CC9 in *E. faecalis*, with the latter clones isolated from farm animals; and
- are highly tenacious and thus easily disseminate in the hospital setting and infections caused by resistant strains are difficult to treat.

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

Annex 5.2 Abbreviations

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

Annex 5.2.1 Abbreviations (antibiotics)

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

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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