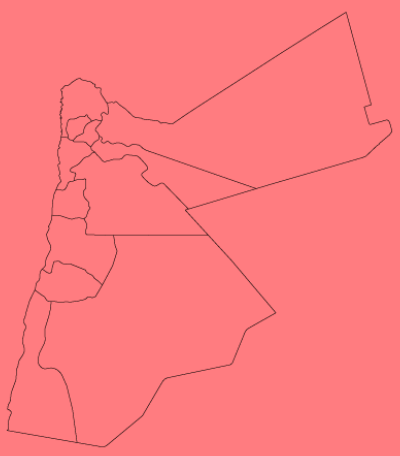
Ministry of Health
The Hashemite Kingdom of Jordan

World Health Organization

NATIONAL **AMR SURVEILLANCE** REPORT

Jordan
Surveillance of Antimicrobial Resistance
Annual Report 2022



Nov 2023

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Document ref. number: MOH/AMR/NAMRSR2022
Document owner: Jordan Ministry of Health
Document classification: ⊙ Public ○ Restricted ○ Internal ○ Confidential
Document version number: 1.0 (.11.2023)

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- **National committee of strengthening the knowledge and evidence through surveillance and research.**
- **National Reference Laboratory for AMR (NRL-AMR).**
- **Jordanian Royal Medical Services.**
- **King Abdullah University Hospital.**
- **Jordan University Hospital.**
- **Amman Surgical Hospital.**
- **Speciality Hospital.**
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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.

Jordanian Ministry of Health has in 2017 launched an initiative to combat antimicrobial resistance and established a Jordanian Committee for AMR. A network of 42 clinical surveillance sites across the country are key to generating, collecting, and reporting AMR surveillance data, and the AMR data from these hospitals across all governorates of Jordan form the basis of this report.

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 Committee for AMR, the AMR focal points in participating surveillance sites and laboratories, and other experts, to strengthen the Jordanian 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 Jordan, and to guide Jordanian 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 Committee, and the pool of experts, for their efforts, support and dedication to the Jordanian National AMR surveillance network and contributions to this report.

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Acknowledgements

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

1. Executive Summary

The **Jordan National AMR Surveillance System** has been established in 2017 by the Jordanian Ministry of Health. It is a lab-based surveillance system and relies on a network of currently 42 clinical microbiology laboratories across all twelve governorates, providing microbiology services for 42 surveillance sites (**Figure 2.3.2, Table 2.3.1, Annex 5.5, Annex 5.6**).

This is the second report of the Jordan National AMR surveillance program, presenting AMR data on 49,044 patients from 42 surveillance sites (public, RMS, University and private sectors), over a 5-year reporting period (2018-2022). Data for the reporting year 2022 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 Jordan. Based on the number of surveillance sites and reported isolates from all regions and sectors in Jordan, and the distribution of pathogens, there is no indication of selective sampling. As such, the data is considered sufficiently representative for the Jordanian patient population; however, it should still be interpreted with caution.

Table 1.1 provides a summary overview of current (2022) levels of antimicrobial resistance (AMR) among relevant and priority pathogens in Jordan (percent resistant isolates, %R):

Table 1.1 Current levels of antimicrobial resistance (AMR) among relevant and priority pathogens in Jordan, Percentage resistant isolates (%R), Jordan, 2022

Priority[a]	Organism	Antibiotic or antibiotic class	N (isolates)	% Resistant isolates
Priority 1: Critical	*Acinetobacter* spp.	Carbapenems (IPM or MEM)	784	**87.1**
	Pseudomonas aeruginosa	Carbapenems (IPM or MEM)	1179	**29.8**
	Enterobacterales (all)	Carbapenems (IPM or MEM)	6745	**10.5**
	Escherichia coli	Carbapenems (IPM or MEM)	4254	**4.2**
	Klebsiella pneumoniae	Carbapenems (IPM or MEM)	1331	**21.3**
	Enterobacterales (all)	Ceftriaxone/Cefotaxime	2795	**44.6**
	Escherichia coli	Ceftriaxone/Cefotaxime	2011	**44.7**
	Klebsiella pneumoniae	Ceftriaxone/Cefotaxime	446	**50.9**
Priority 2: High	*Enterococcus faecium*[b]	Vancomycin (VRE)[c]	290	**46.1**
	Staphylococcus aureus	Oxacillin (MRSA)[d]	1725	**62.0**
	Salmonella spp. (non-typh.)	Fluoroquinolones (ciprofloxacin)	17	**-**
	Neisseria gonorrhoeae	3rd-generation cephalosporins	8	**-**
	Neisseria gonorrhoeae	Fluoroquinolones (ciprofloxacin)	8	**-**
Priority 3: Medium	*Streptococcus pneumoniae*	Penicillin (oral)	120	**36.7**
	Streptococcus pneumoniae	Penicillin (meningitis)	120	**42.5**
	Streptococcus pneumoniae	Penicillin (non-meningitis)	120	**33.3**
	Haemophilus influenzae	Ampicillin	12	**-**
	Shigella spp.	Fluoroquinolones (ciprofloxacin)	12	**-**

[a] Based on: (WHO, 2017), (Tacconelli, et al., 2018),[b] based on combined(MIC+ disk diffusion) results, [c]VRE: Vancomycin-resistant *Enterococcus faecium*, [d]MRSA: Methicillin (oxacillin)-resistant *S. aureus*, (-): small number of isolates tested (<30).

In conclusion, the information contained in this report provides evidence that antimicrobial resistance is widespread and, overall, increasing in clinical settings in Jordan. This AMR surveillance data provides evidence and serves as a basis for acting to control AMR in Jordan.

Tables 1.2 to 1.3 provide a summary overview of antimicrobial resistance trends observed for Gram-negative bacteria and Gram-positive bacteria in Jordan during the period 2017-2022:

Table 1.2 Antimicrobial resistance trends, Jordan, 2017-2022 – Gram-negative bacteria

Antibiotic class/substance	*Escherichia coli*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Acinetobacter* spp.
Aminopenicillins (Ampicillin)	↑	n/a	R	R
Amoxicillin/Clavulanic acid	↓	↑	R	R
Piperacillin/Tazobactam	↑	↑↑	↑↑	↑↑
3rd-/4th-gen. cephalosporins	↓/↓	↓↓/↓↓	↓	↑↑/↓↓
Meropenem	↑	↑↑	↑↑	↑↑
Fluoroquinolones (Ciprofloxacin)	↑↑	↑↑	↑	↑↑
Aminoglycosides (Gentamicin)	↓	↓	↓↓	↓↓
Trimethoprim/sulfamethoxazole	↓	↓↓	R	↓↓
Multidrug resistance (≥ 3 classes)	↓	↓	↑	↑↑

↓/↑: decreasing/increasing trend of percentage resistant isolates (%R), R: intrinsically resistant, n/a: not applicable

Table 1.3 Antimicrobial resistance trends, Jordan, 2017-2022 – Gram-positive bacteria

Antibiotic class/substance	*Staphylococcus aureus*	*Enterococcus faecalis*
Beta-lactam antibiotics	↑↑(OXA)	-
Macrolides (Erythromycin)	↓↓	n/a
Lincosamides (Clindamycin)	↓↓	n/a
Aminoglycosides (Gentamicin)	↓	↑↑ (n.s)
Moxifloxacin	↑↑	↑↑
Glycopeptides	↓	↑↑
Trimethoprim/sulfamethoxazole	↓↓	R
Multidrug resistance (≥ 3 classes)	↑↑	↑

↓/↑ decreasing/increasing trend of percentage resistant isolates (%R), R: intrinsically resistant, n/a: not applicable, n.s.: not significant, OXA: oxacillin

2. Introduction

2.1. Antimicrobial resistance

Antimicrobial resistance (AMR) has become a major threat to public health worldwide, including the Eastern Mediterranean Region. AMR impacts on human health due to increased length of stay, treatment failures, and significant human suffering and deaths, and is leading to increased healthcare costs and indirect costs. Globally, an estimated 700,000 deaths annually are currently attributable to antimicrobial resistance, and this number is expected to increase to 10,000,000 deaths by 2050, with an associated estimated loss to global gross domestic product of up to 100 trillion US dollar per year (Jim O'Neill, 2014). Without effective antibiotics, the success of major surgery and cancer chemotherapy would be compromised (WHO, 2021).

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 Jordan National AMR surveillance system (JARSS)

Jordan started developing and implementing a national AMR surveillance system since May 2018. Based upon ministerial decrees, MOH defined the governance structure by developing a National Coordinating Centre (NCC) to oversee the surveillance activities and the Central Public Health Laboratory (CPHL), Amman. was designated as the National Reference Laboratory (NRL) for AMR surveillance.

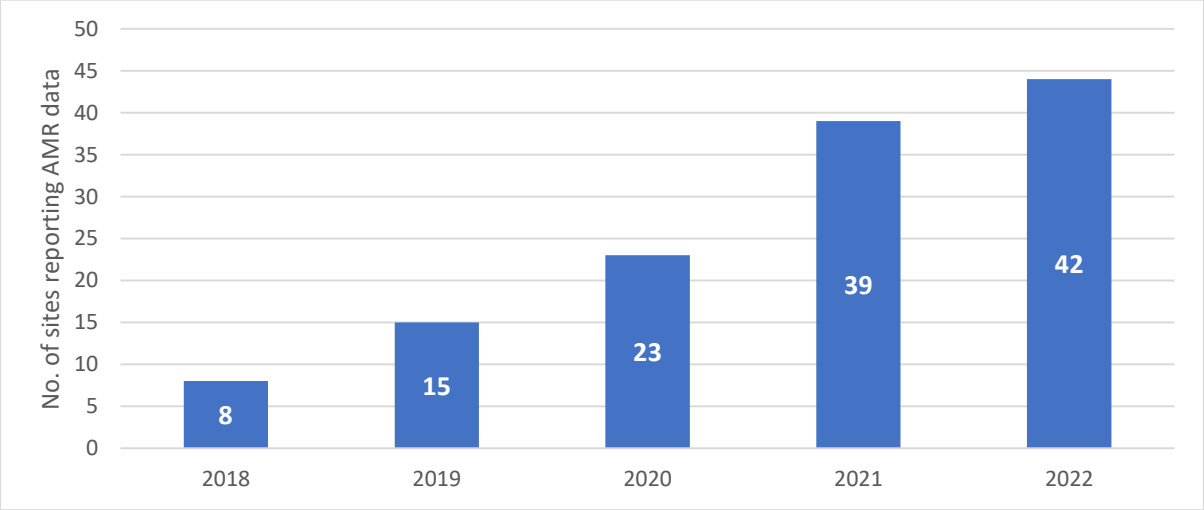
In 2019, the strategy of the "Jordan National Antimicrobial Resistance Surveillance System (JARSS)" was officially endorsed and launched. This surveillance strategy includes goals, objectives, selection criteria of the surveillance sites, mapping and expansion of the surveillance sites, priority pathogens, and drug-bug combinations, the monitoring strategy of antibiotic use and consumption, and the One Health integrated AMR surveillance among humans, animals and the environment (Tricycle project).

Since 2019, the Jordanian National AMR surveillance system has been participating in the Global AMR Surveillance System (GLASS), established by the World Health Organization (WHO) in 2015 (WHO-GLASS, 2015).

As of 2022, the Jordanian AMR surveillance system relies on a network of **42 surveillance sites** (tertiary hospitals), in all 12 governorates of Jordan (**Figure 2.3.1**)

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

Figure 2.3.1 Jordan National AMR Surveillance Network: Number of AMR Surveillance Sites 2018-2022.



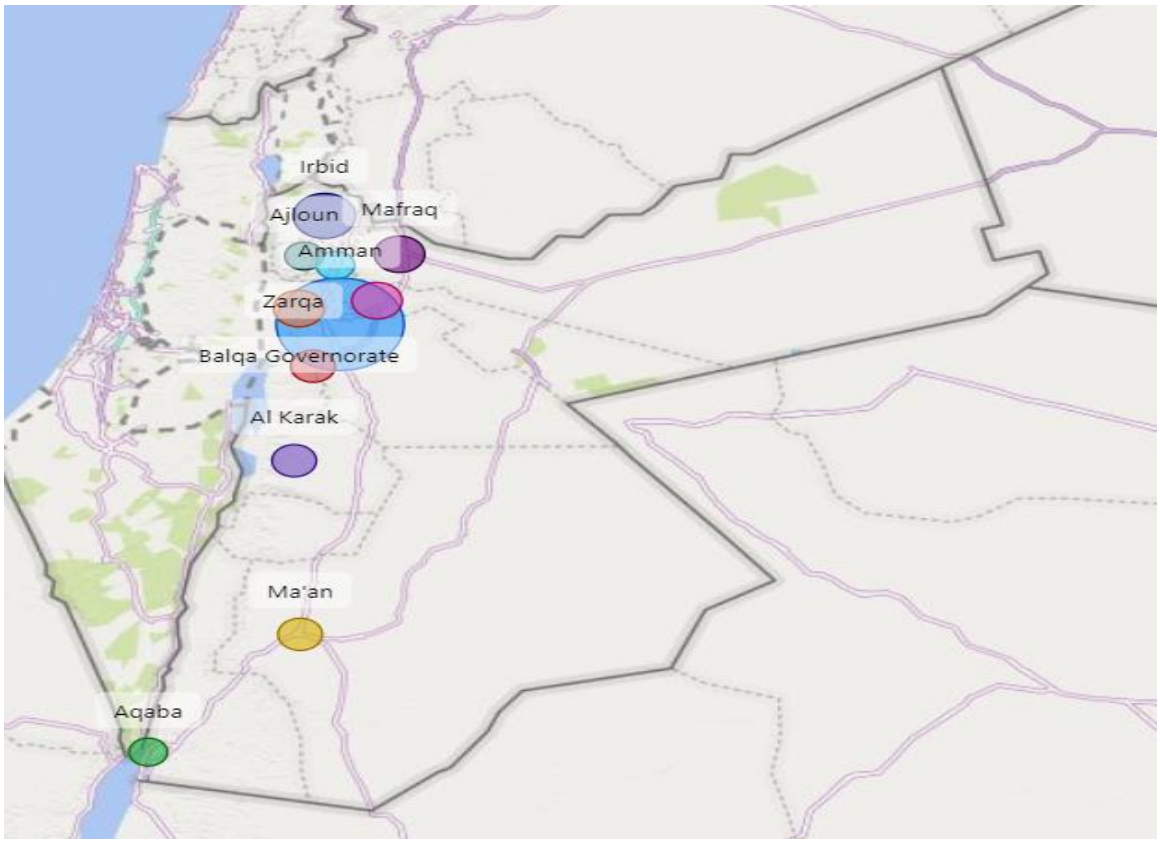
The AMR data submitted includes routine clinical and antibiotic susceptibility testing data from both, governmental, Royal Medical Services (RMS), University hospitals as well as 3 private hospitals. Central confirmatory testing or central repository of isolates is conducted at the Central Public Health Laboratory (CPHL)/National Reference Laboratory for Surveillance of Antimicrobial Resistance (NRL-AMR), Amman, Jordan.

Surveillance sites are sited in all 12 following governorates of Jordan (**Figure 2.3.2, Table 2.3.1**). Since the start of the national AMR surveillance program, the number of healthcare facilities participating in AMR surveillance has increased significantly. **Figure 2.3.3** shows the number of participating public hospitals, private hospitals.

Table 2.3.1 AMR surveillance sites by Governorate 2023

Facility Type	Surveillance sites
Amman	17
Irbid	6
Zarqa	2
Jarash	1
Ajloun	2
Mafraq	3
Balqa	3
Madaba	2
Tafileh	1
Karak	2
Maan	2
Aqaba	1
Total	**42**

Figure 2.3.2 Jordan National AMR surveillance sites, by location (2023).



3. Methods

Hospitals 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 Governorate- and/or country level).

3.1 Data generation

Identification and selection of surveillance sites: Surveillance sites in this report included public and RMS sites available on AMR electronic surveillance system (Health Data Analytics program "HDA"), as well as selected private sites.

Private sites (university hospitals and 3 private hospitals) were identified based on their location, facility type and size, availability of data, and readiness and willingness to participate.

Identification of organisms: 27 out of 42 (64.2%) participating microbiology laboratories use at least one commercial, automated system for identification of bacteria and/or yeast, including VITEK-2[1] (n=27, 64.2%). Only 15 lab(s) (n=15, 35.7%) relies on manual (API) systems only for identification[2]. Unusual test results are confirmed at the CPHL/NRL-AMR.

Antimicrobial susceptibility testing (AST): 27 out of 42 (64.2%) microbiology laboratories use at least one commercial, automated system for routine antimicrobial susceptibility testing, the remaining laboratories (n=15, 35.7%), use manual testing methods only (disc diffusion/Kirby Bauer). Selected organisms (*Haemophilus, Neisseria*) are routinely tested by manual methods (disc diffusion), as per CLSI guideline recommendations. All labs follow CLSI guidelines for antimicrobial susceptibility testing of bacteria (CLSI-M100) and fungi (CLSI-M60) (CLSI, 2022). Unusual antibiotic susceptibility testing results are confirmed locally.

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

AST data submitted to the national AMR surveillance 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[3] AST result is collected and used for analysis (n=17, labs, 40.4%), otherwise the locally interpreted AST result (S/I/R[4]) is collected (n=25 labs, 59.5%).

Clinical and demographic data for each isolate is automatically extracted from the HDA system wherever available. 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.

[1] VITEK® 2. BioMérieux SA, Craponne, France. https://www.biomerieux.com/

[2] API® test system. Analytical Profile Index. BioMérieux SA, Craponne, France. https://www.biomerieux.com/

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

[4] SIR, susceptible/intermediate/resistant

3.2 Data collection

The HDA program was developed and established by EHS (Hakeem) in public and RMS hospitals to facilitate the process of extracting reliable information on AMR data from hospital electronic medical records (EMR). Moreover, nominated focal points at participating surveillance sites in private and University hospitals are submitting AMR data on annual basis to the national AMR Surveillance data management department at MOH. AMR data submitted includes microbiology data and, where available and technically feasible, clinical and demographic data. The reporting protocol is in line with Jordan 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.

For the reporting period 2022, a total of n=148,243 isolates were reported by surveillance sites. Only the non-duplicate diagnostic isolates (n=49,044; 33.1%) are included in the analysis and presented in this report Copy strains (duplicate isolates) were routinely excluded from the analysis (see **section 3.3** for details on inclusion, exclusion, and deduplication criteria).

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

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

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

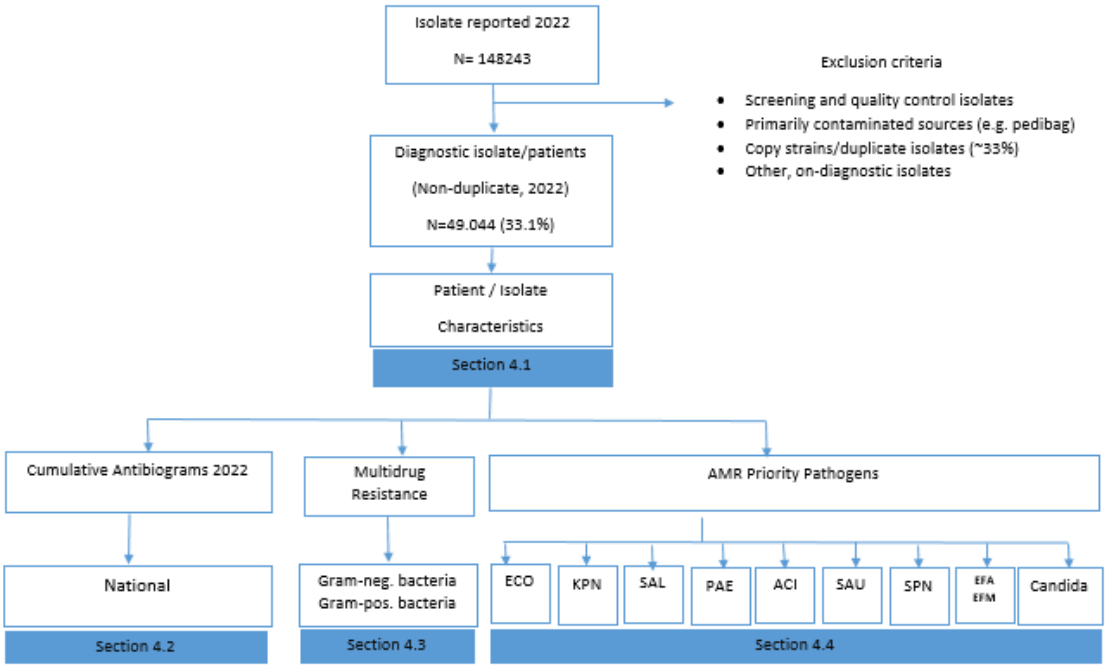
Data submission: At facility level, AMR data is collected and automatically exported from EMR to HDA wherever possible or semi-automated where authorized AMR focal points are submitting data from commercial AST systems or from EMR data by E-Mail attachment.

Data cleaning: After submission of AMR data to the national AMR Surveillance data management department, 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[5]).

Finally, all WHONET AMR data files are added to the national AMR surveillance database (WHONET, 2023). **Figure 3.1.1** presents details on isolates reported and AMR surveillance reports available.

Figure 3.2.1 Number of isolates reported, and AMR surveillance reports available, 2022

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



For the reporting period 2022, the surveillance sites submitted AMR data on 148,243 isolates. After data cleaning and applying exclusion criteria (**Figure 3.1.1**, and section 3.2), a total of n=49,044 (33.1%) non-duplicate diagnostic patient isolates remained for analysis.

Results are presented in this report in section four:

- **Section 4.1 (patient/isolate characteristics)** presents the patient characteristics of isolates reported from all surveillance sites in Jordan during the 2022 reporting period.
- **Section 4.2 (cumulative antibiograms)** presents the national cumulative antibiogram 2022, for Gram-negative and Gram-positive bacteria.
- **Section 4.3 (multidrug resistance)** presents annual trends of multidrug resistance (% MDR) for Gram-negative and Gram-positive bacteria.
- **Section 4.4 (AMR priority pathogens)** presents percent resistant/intermediate/susceptible (% RIS) statistics, and long-term AMR trends for Jordan (2017-2022) for AMR priority pathogens.

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

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

3.3 Data analysis

Data analysis was conducted with the WHONET 2023 Software for Antimicrobial Resistance Surveillance (WHONET, 2023).

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

- Quality control isolates
- 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)
- Species for which less than 30 isolates were available for analysis
- Isolates tested using disc diffusion were excluded in AST analysis, except for *Haemophilus spp.* and *Neisseria spp..*

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), 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 interpreted at either the local or central level. Percent RIS interpretations were based on the CLSI interpretation standard CLSI M100 (ED33: 2023) for bacterial isolates and CLSI interpretation standard M60 ED1:2017 for yeast. For amphotericin B (AMB) and tigecycline, EUCAST v12.0:2022 was used (EUCAST, 2022). For *Candida auris*, tentative breakpoints from U.S. CDC were used (CDC C. auris, 2020).

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

Definitions used:

- **MRSA** was defined as *Staphylococcus aureus*, resistant to oxacillin (OXA).
- **VRE** was defined as *Enterococcus faecalis* or *Enterococcus faecium*, resistant to vancomycin (VAN).
- **CRE** was defined as Enterobacterales, non-susceptible to any carbapenem (imipenem, meropenem, or ertapenem), or found to produce a carbapenemase.
- **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).
- **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).

  - Access group antibiotics: This group includes antibiotics that have activity against a wide range of commonly encountered susceptible pathogens while also showing lower resistance potential than antibiotics in the other groups. Selected Access group antibiotics are recommended as essential first or second choice empiric treatment options for infectious syndromes reviewed by an expert committee and are listed as individual medicines on the Model Lists of Essential Medicines to improve access and promote appropriate use.

  - Watch group antibiotics: This group includes antibiotic classes that have higher resistance potential and includes most of the highest priority agents among the Critically Important Antimicrobials for Human

Medicine and/or antibiotics that are at relatively high risk of selection of bacterial resistance. These medicines should be prioritized as key targets of stewardship programs and monitoring. Selected Watch group antibiotics are recommended as essential first or second choice empiric treatment options for a limited number of specific infectious syndromes and are listed as individual medicines on the WHO Model Lists of Essential Medicines.

- Reserve group antibiotics: This group includes antibiotics and antibiotic classes that should be reserved for treatment of confirmed or suspected infections due to multi-drug-resistant organisms. Reserve group antibiotics should be treated as "last resort" options. Selected Reserve group antibiotics are listed as individual medicines on the WHO Model Lists of Essential Medicines when they have a favourable risk-benefit profile and proven activity against "Critical Priority" or "High Priority" pathogens identified by the WHO Priority Pathogens List1, notably carbapenem resistant Enterobacteriaceae. These antibiotics should be accessible, but their use should be tailored to highly specific patients and settings, when all alternatives have failed or are not suitable. These medicines could be protected and prioritized as key targets of national and international stewardship programs involving monitoring and utilization reporting, to preserve their effectiveness.
- Occurrence and significance of resistance and actions to take following confirmation of results:
  Category I (S1): not reported or rarely reported to date.
  Category II (S2): uncommon in most institutions.

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 2023. For additional statistical analysis the following software packages are used:

- IBM SPSS Statistics, version 28.0.0.0 (IBM, 2022) for statistical significance of proportion trends over time.

If fewer than 30 AST results for a specific pathogen-antibiotic combination were available for analysis, then the table data are presented, but marked with a footnote, indicating that results should be interpreted with caution. If fewer than 10 AST results for a specific pathogen-antibiotic combination were submitted, then percentage 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. 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). Error bars in graphs represent the upper limit of the 95% confidence interval.

4. Results

4.1 Patient/isolate characteristics

For the reporting period 2022 (one year), n=49,044 non-duplicate diagnostic isolates from n=42 surveillance sites are available for analysis. For 2022, most frequently reported pathogens were *E. coli* (38.4%), followed by *K. pneumoniae* (10.8%), *S. aureus* (8.7%), and *P. aeruginosa* (6.7). All AMR priority pathogens together accounted for 68.8% of all reported isolates (**Figure 4.1.1**).

Figure 4.1.1 Distribution of reported AMR priority pathogens, Jordan, 2022, by pathogen (n=49,044)

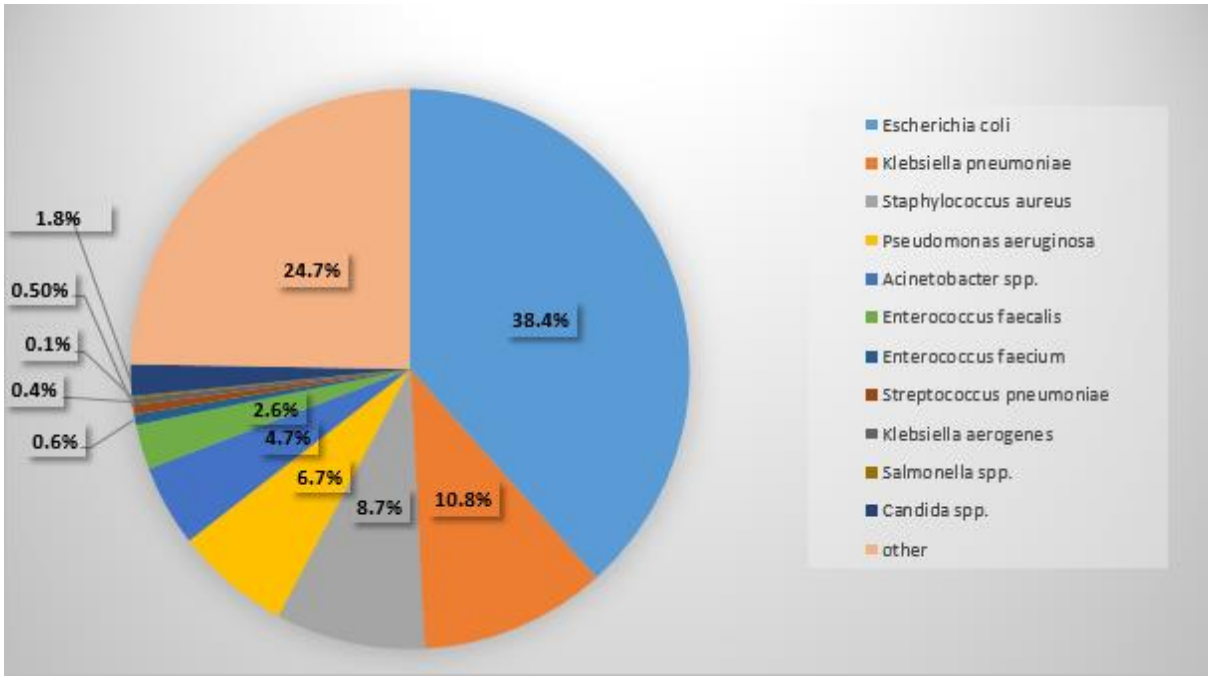
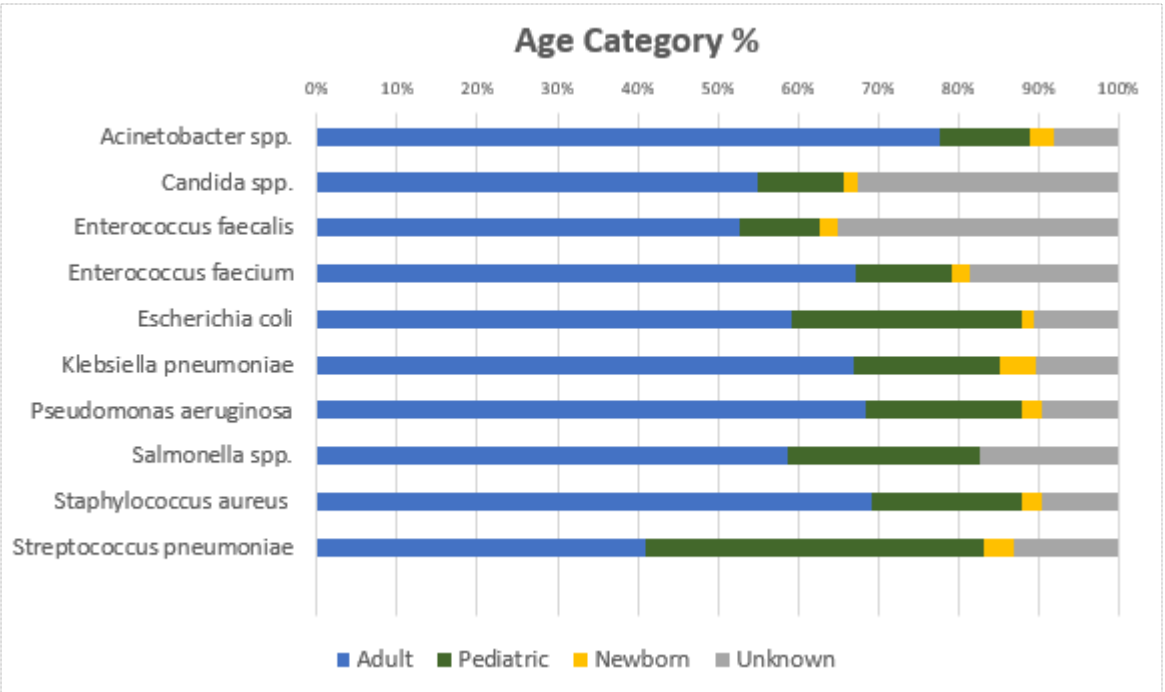


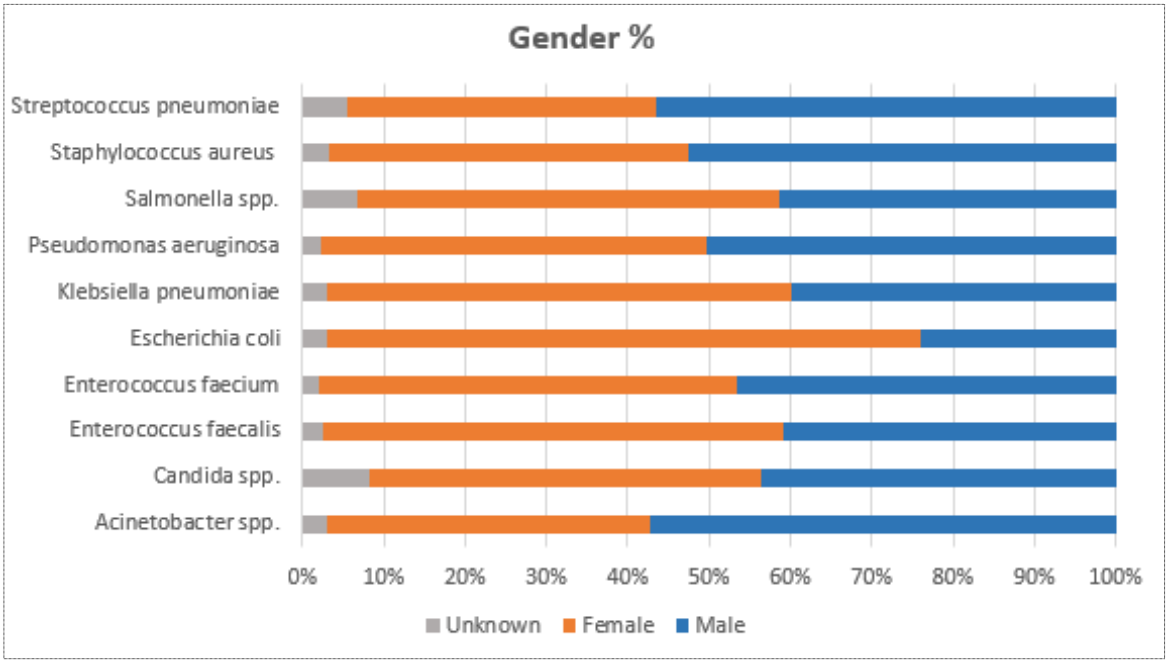
Figure 4.1.2 (next page) presents the distribution of reported patients/isolates by age category, gender, isolate source, location type, and clinical specialty/department. These figures also give a good indication on the availability of Meta data, i.e. the completeness of data reporting.

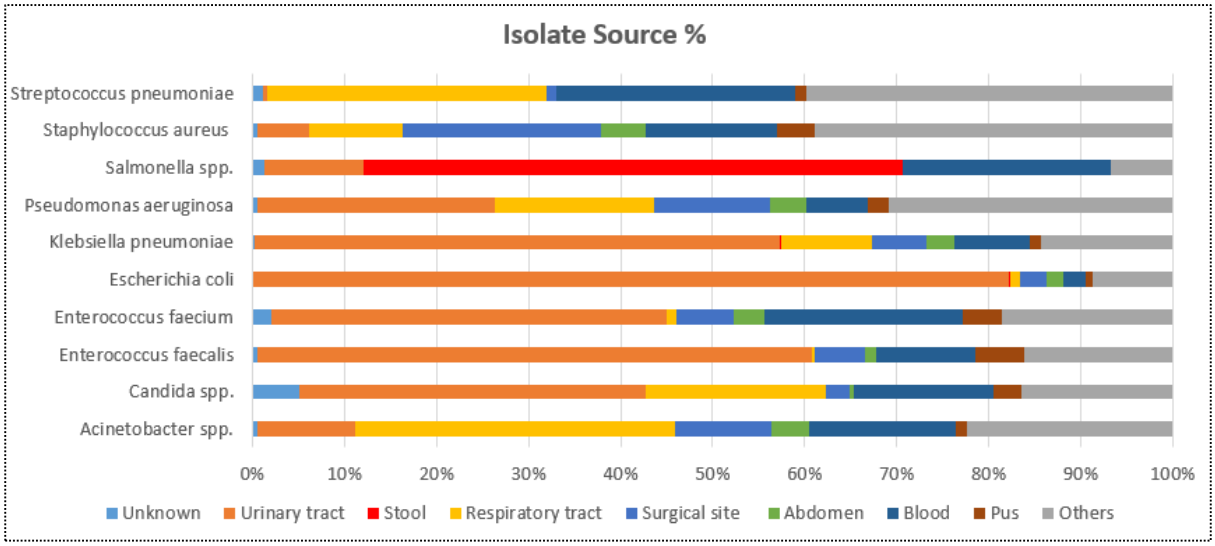
- **Age:** the data shows that the adult age group was the most reported category, *Acinetobacter* spp, affects predominantly adults as compared to other age categories, however, adult and paediatric categories were equally affected by *S. pneumoniae.*
- **Gender:** 61% of reported isolates are in females, with predominance of *E. coli*, *K. pneumoniae* and Enterococci , which is due to the higher prevalence of urinary tract infections in females (*E. coli*, *K. pneumoniae* and Enterococci are commonly isolated from the urinary tract), while *S. pneumoniae* and *Acinetobacter spp.* are more prevalent in males.
- **Isolate source:** Distribution by isolate source shows the typical and expected patterns of specimen sources: *E. coli*, *K. pneumoniae* and Enterococci are predominantly isolated from urine, *Salmonella spp*. from stool, Pneumococci from respiratory tract and blood, *S. aureus* from surgical site and blood, whereas *P. aeruginosa* is mostly found in urine, respiratory tract, and surgical site, *Acinetobacter spp.* is mostly found in respiratory tract and blood. *Candida* spp. is isolated mostly from urine, respiratory tract and blood.
- **Location type:** Distribution by location type shows that *Acinetobacter spp.* is prominent in ICU. All relevant location types are included in good numbers (outpatients, emergency, inpatient (non-ICU), and intensive care).
- **Clinical specialty/department:** Distribution by clinical speciality/department specialty shows that all relevant clinical specialties are represented in the data, including internal medicine, surgery, emergency & intensive care, neonatology & paediatrics, obstetrics & gynaecology, etc.

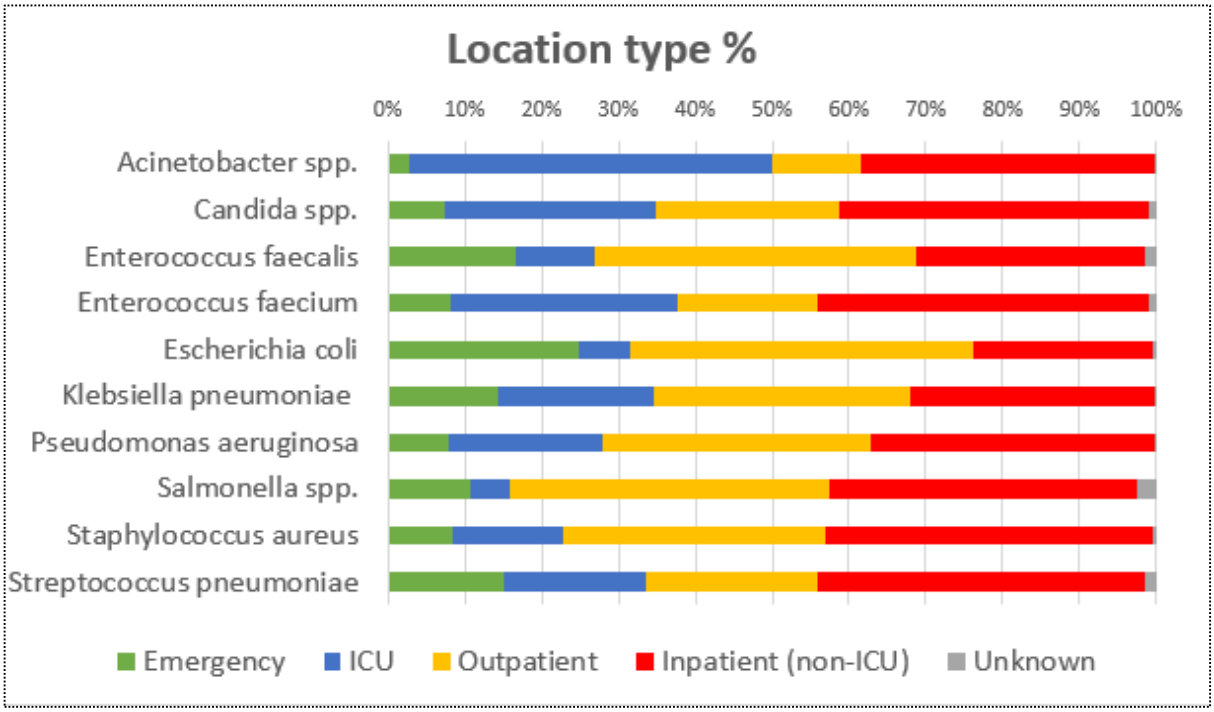
Figure 4.1.2 Distribution of reported pathogens, Jordan, 2022, by age category, gender, isolate source, location type, and department

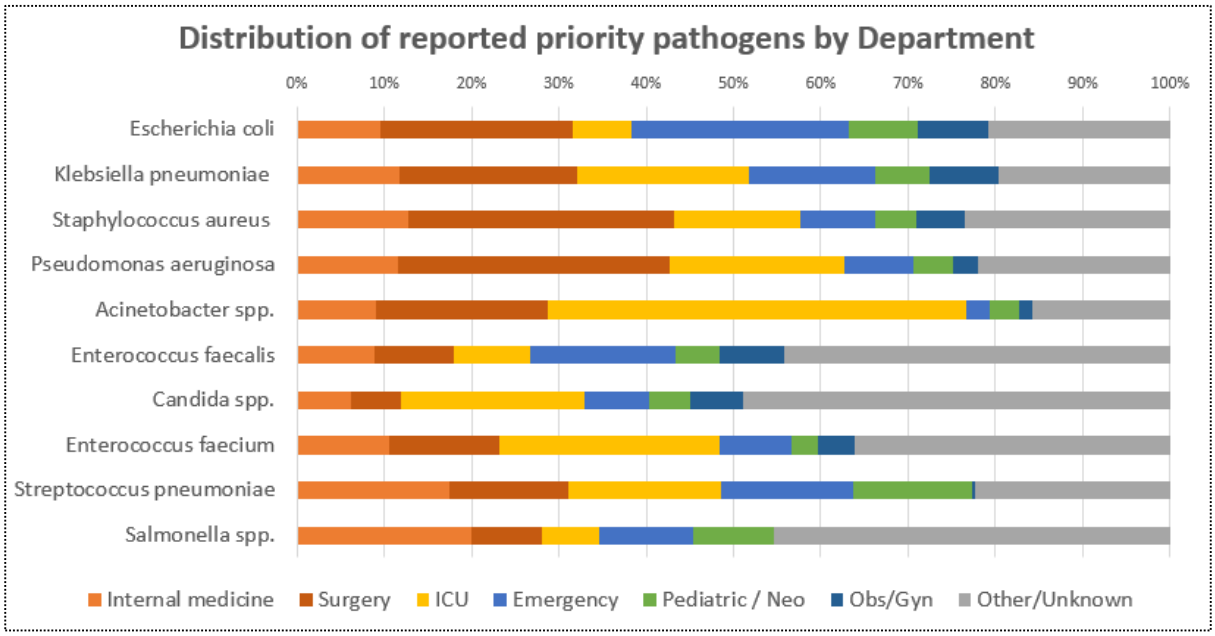


Note: Newborn: 0-30 days, Pediatric: 1 month to 18 years, Adult: 19+ years




Isolate Source %
Streptococcus pneumoniae
Staphylococcus aureus
Salmonella spp.
Pseudomonas aeruginosa
Klebsiella pneumoniae
Escherichia coli
Enterococcus faecium
Enterococcus faecalis
Candida spp.
Acinetobacter spp.
0%
10%
20%
30%
40%
50%
60%
70%
80%
90%
100%
Unknown
Urinary tract
Stool
Respiratory tract
Surgical site
Abdomen
Blood
Pus
Others


Location type %
0%
10%
20%
30%
40%
50%
60%
70%
80%
90%
100%
Acinetobacter spp.
Candida spp.
Enterococcus faecalis
Enterococcus faecium
Escherichia coli
Klebsiella pneumoniae
Pseudomonas aeruginosa
Salmonella spp.
Staphylococcus aureus
Streptococcus pneumoniae
Emergency
ICU
Outpatient
Inpatient (non-ICU)
Unknown


Distribution of reported priority pathogens by Department
0%
10%
20%
30%
40%
50%
60%
70%
80%
90%
100%
Escherichia coli
Klebsiella pneumoniae
Staphylococcus aureus
Pseudomonas aeruginosa
Acinetobacter spp.
Enterococcus faecalis
Candida spp.
Enterococcus faecium
Streptococcus pneumoniae
Salmonella spp.
Internal medicine
Surgery
ICU
Emergency
Pediatric / Neo
Obs/Gyn
Other/Unknown

Representativeness of the data for the Jordan population:

The data is largely representative of the whole Jordanian population, with a few important limitations. This report presents the, by far, largest data set and best currently available non-duplicate AMR data on a very large number of patients from all health sectors. The data includes all relevant governorates and regions, location types and age groups, representing a wide range of medical conditions, disease severities, and clinical specialties.

The data presented in this report is:

- **fully representative for public sector healthcare facilities in Jordan (100% sample size for hospitals, centers, and clinics);**
- **highly representative for inpatients, outpatient, emergency and ICU patients.**

The data is still slightly skewed towards Amman governorate, because most of the participating hospitals are located in Amman, serving a considerable proportion of the Jordanian population. However, the balancing of data will further improve over time, as new surveillance sites are now preferably and increasingly selected from other governorates, in particular from hospitals that are newly establishing HDA for their EMR.

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 Jordan, within the few limitations as described above.

4.2 Cumulative Antibiograms (2022)

4.2.1 Jordan National Cumulative Antibiogram

Table 4.2.1.1 National Cumulative Antibiogram (2022): Percent susceptible isolates (%S[a]) – Gram-neg. bacteria (isolates from all sources, N=35,009)

Gram-negative Bacteria	Isolates	Access							Watch												Reserved					
	N	AMP	AMC	CZO	AMK	GEN	SXT	NIT[b]	TZP	CXM	CRO	CTX	CAZ	FEP	IPM	MEM	ETP	TOB	CIP	LVX	ATM	CZA	CZT	COL	TGC	FOS
Gram-negative bacteria (all)	35009	14	53	35	86	77	45	78	75	41	49	49	55	62	S2	S2	S2	64	48	54	61	S2	77	S1	77	90
Enterobacterales	28681	14	53	37	92	81	45	79	82	42	52	53	57	66	S2	S2	S2	58	48	54	65	S2	78	S1	80	90
Enterobacter cloacae	989	R	R	R	93	81	69	51	74	16	56	61	64	75	S2	S2	S2	-	65	67	69	S2	79	S1	83	63
Klebsiella aerogenes	196	R	R	R	83	75	55	38	65	17	44	56	48	71	S2	S2	S2	-	56	-	-	S2	-	S1	-	-
Escherichia coli [c]	18823	15	55	39	95	83	41	88	86	43	53	53	58	66	S2	S2	S2	69	46	48	66	S2	88	S1	94	95
Klebsiella pneumoniae	5289	R	52	34	85	77	49	42	68	38	43	44	45	56	S2	S2	S2	-	50	57	57	S2	63	S1	72	77
Klebsiella oxytoca	602	R	59	42	92	82	60	66	77	R	49	59	58	71	S2	S2	S2	-	50	79	50	S2	-	S1	-	-
Morganella morganii	252	R	R	R	92	65	37	R	94	R	66	61	68	88	S2	S2	S2	-	26	46	81	S2	-	S1	-	-
Proteus mirabilis	887	36	90	61	94	66	38	R	93	68	72	75	81	88	S2	S2	S2	-	51	58	68	S2	90	R	R	-
Proteus vulgaris	63	R	-	-	96	81	-	R	94	R	77	-	87	-	S2	S2	S2	-	50	-	-	S2	-	S1	-	-
Serratia marcescens	242	R	R	R	89	88	76	R	79	R	64	65	75	85	S2	S2	S2	-	67	86	77	S2	-	R	70	-
Citrobacter freundii	226	R	R	R	94	81	63	86	82	R	60	59	62	82	S2	S2	S2	-	54	74	83	S2	-	S1	-	-
Non-fermenting Gram-neg. rods	6071	R	R	5	61	57	47	14	48	12	19	16	47	46	50	50	R	65	47	54	51	79	75	97	67	-
Acinetobacter baumannii	2091	R	R	3	25	29	42	8	9	10	9	4	10	11	12	11	R	29	10	9	R	-	-	S1	73	R
Pseudomonas aeruginosa	3275	R	R	4	85	78	R	14	75	10	R	R	70	71	75	74	R	75	69	73	67	81	76	S1	R	-
Stenotrophomonas maltophilia	232	R	R	-	R	R	78	-	R	-	R	R	51	-	R	R	R	R	70	88	R	-	-	-	-	-

[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-duplicate). [b] NIT: Nitrofurantoin data from urine isolates only. [c] E. coli (urinary tract isolates): FOS 95 %S.

AMC=Amoxicillin/Clavulanic acid, **AMK**=Amikacin, **AMP**=Ampicillin, **ATM**=Aztreonam, **CAZ**=Ceftazidime, **CIP**=Ciprofloxacin, **CRO**=Ceftriaxone **CTX**=Cefotaxime, **CXM**=Cefuroxime, **CZA**= Ceftazidime + Avib, **COL**=Colistin, **CZO**=Cefazolin, **CZT**= ceftolozane/tazobactam **ETP**=Ertapenem, **FEP**=Cefepime, **FOS**=Fosfomycin, **GEN**=Gentamicin, **IPM**=Imipenem, **LVX**=Levofloxacin, **MEM**=Meropenem, **NIT**=Nitrofurantoin, **SXT**=Trimethoprim/Sulfamethoxazole, **TOB**=Tobramycin, **TGC**= Tigecycline, **TZP**=Piperacillin/Tazobactam.

%S=Percent of isolates susceptible, 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, S1= intrinsically susceptible (100%), S2= intrinsically susceptible (99%), (-) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED33:2023. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2023.

Number of H. influenza isolates =52, however, the number tested for each antibiotic <30.

Data source: Jordan Antimicrobial Resistance Surveillance System. Data shown is from 42 surveillance sites from all health sector (Jordan). Version 1.0 (20 Aug 2023).

Table 4.2.1.2 National Cumulative Antibiogram (2022): Percent susceptible isolates (%S[a]) – Gram-pos. bacteria (isolates from all sources, N=14425)

Gram-positive Bacteria	Isolates	ACCESS										WATCH									RESERVED		
	N	AMP	PEN	AMC	OXA	CLI	GEN	TCY	RIF	SXT	NIT	CRO	CTX	ERY	STH	LVX	MFX	VAN	TEC	FLC	TGC	LNZ	QDA
Gram-positive organisms (all)	14425	59	24	53	30	57	78	64	89	78	90	56	51	42	98	69	74	95	94	31	89	99	75
Enterococcus spp.	2744	70	53	90	_	29	51	22	15	27	82	34	20	15	98	47	_	86	91	_	91	S2	24
Enterococcus faecalis	1272	92	79	_	_	R	R	16	_	R	95	R	R	10	97	55	_	93	97	_	87	S2	R
Enterococcus faecium	302	21	15	_	_	R	R	31	0	R	35	R	R	7	_	11	_	55	66	_	90	S2	_
Staphylococcus aureus	4297	6	4	38[b]	38	62	88	67	93	88	98	40	41	55	_	77	79	S1	98	37	97	S2	S2
MSSA	687	_	_	100	100	62	93	81	89	95	100	_	98	57	_	82	76	99	99	0	96	100	_
MRSA	1068	_	_	0	0	60	82	61	93	85	99	_	0	57	_	76	78	98	98	99	96	100	100
Coagulase-neg. staphylococci (CNS)	4228	_	_	18[b]	18	54	76	82	91	67	96	37	30	22	_	72	72	99	94	14	81	99	98
Staphylococcus epidermidis	586	_	_	18[b]	18	50	87	78	100	87	_	_	_	19	_	_	54	S2	89	_	4	S2	_
Staphylococcus saprophyticus	66	_	_	_	_	68	_	_	_	81	_	_	_	20	_	_	_	S2	93	_	_	S2	_
Streptococcus pneumoniae	257	59	63	72	_	52	68	47	S2	_	_	83	80	34	_	S2	S2	100	66	_	_	S1	S2
Streptococcus pyogenes	123	S1	S1	_	_	69	_	71	_	_	_	S1	S1	65	_	_	_	S1	S1	_	_	S1	S2
Streptococcus agalactiae	1177	S1	S1	91	_	21	47	32	_	41	96	S1	S1	39	_	73	58	S1	S1	_	74	S1	S2
Streptococcus spp. (viridans group)	948	68	49	86	27	56	59	70	_	41	78	76	59	50	_	82	_	S1	77	_	_	S1	S1

[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] Extrapolated, based on Oxacillin.

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **FLC**= Flucloxacillin, **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, **TGC**= Tigecycline **, VAN**=Vancomycin.

%S=Percent of isolates susceptible, 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, S1= intrinsically susceptible (100%), S2= intrinsically susceptible (99%), (-) =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 ED33:2023. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2023.

Number of *Staphylococcus aureus isolate tested for cephalexin <30*

Data source: Jordan Antimicrobial Resistance Surveillance System. Data shown is from surveillance sites from all health sector (Jordan). Version 1.0 (20 Aug 2023).

4.3 Multidrug resistance

4.3.1 MDR, XDR, PDR Summary

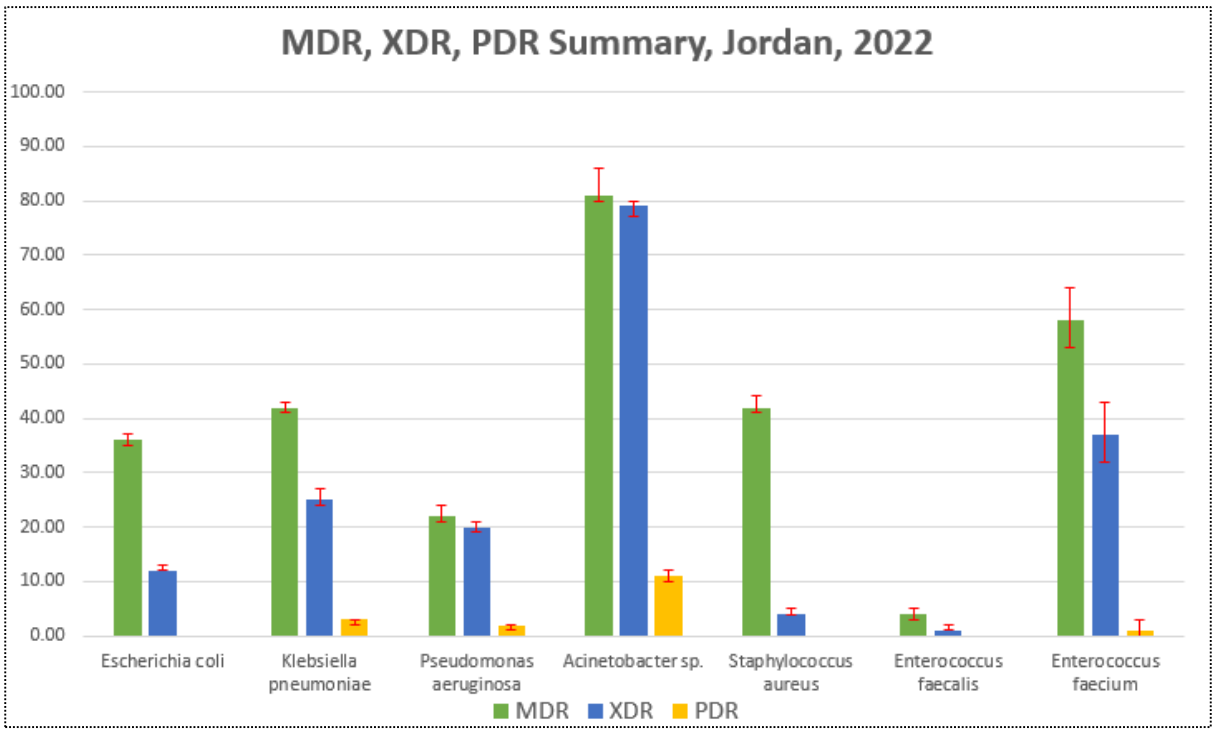
In a 2012 publication, the European Centre for Disease Prevention and Control (ECDC) proposed definitions for common bacterial pathogens resistant to multiple antimicrobials (Magiorakos, et al., 2012). MDR/XDR/PDR results are summarized below.

Table 4.3.1 MDR, XDR, PDR Summary, Jordan, 2022

Organism	Number of isolates	MDR	Possible XDR	Possible PDR
Escherichia coli	18,823	6,799 (36%)	2,302 (12%)	70 (0%)
Klebsiella pneumoniae	5,289	2,230 (42%)	1,344 (25%)	140 (3%)
Pseudomonas aeruginosa	3,275	730 (22%)	651 (20%)	59 (2%)
Acinetobacter sp.	2,309	1,874 (81%)	1,817 (79%)	252 (11%)
Staphylococcus aureus	4,247	1,787 (42%)	187 (4%)	5 (0%)
Enterococcus faecalis	1,271	47 (4%)	16 (1%)	
Enterococcus faecium	302	176 (58%)	112 (37%)	3 (1%)
Total	35,516	13643 43.3%)	6429 (34.6%)	529(6.2%)

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

Figure 4.3.1 MDR, XDR, PDR Summary, Jordan, 2022

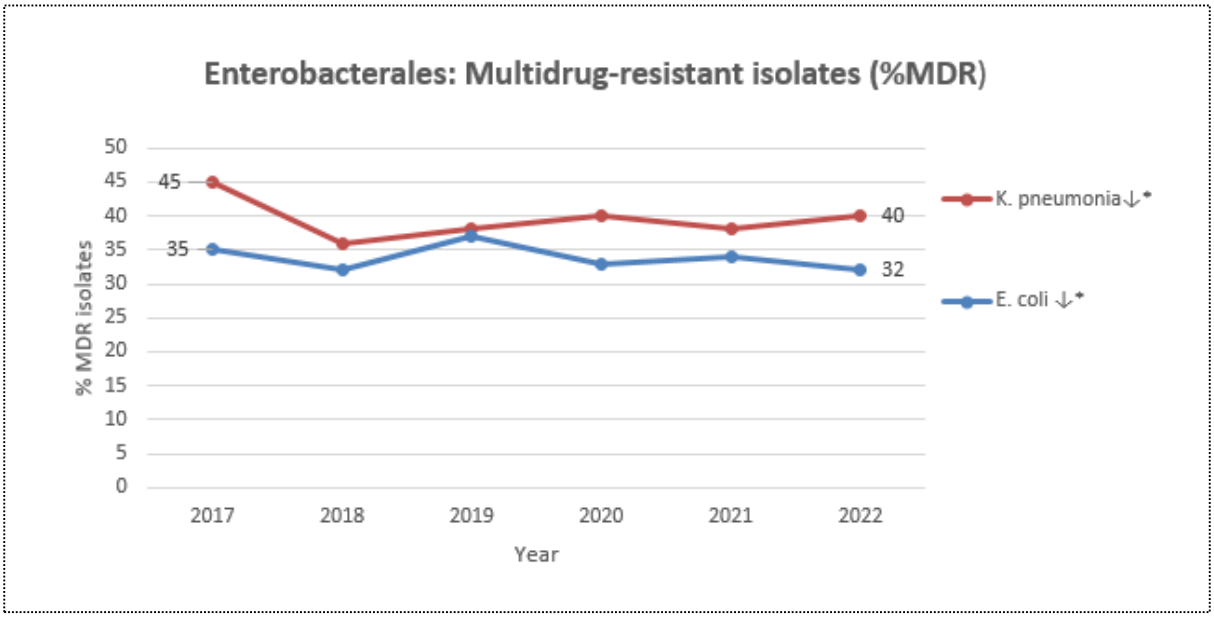


MDR, XDR, PDR Trends

Between 2017 and 2022, multidrug resistance has, overall, decreased for Enterobacterales (*E. coli*, *K. pneumoniae*), and increased for non-fermenting Gram-negative rods (*P. aeruginosa*, *Acinetobacter* spp.), and Gram-positive bacteria (*S. aureus*, *E. faecium*, *E. faecalis*).

4.3.2 Multidrug resistance in Gram-negative Bacteria: Enterobacterales

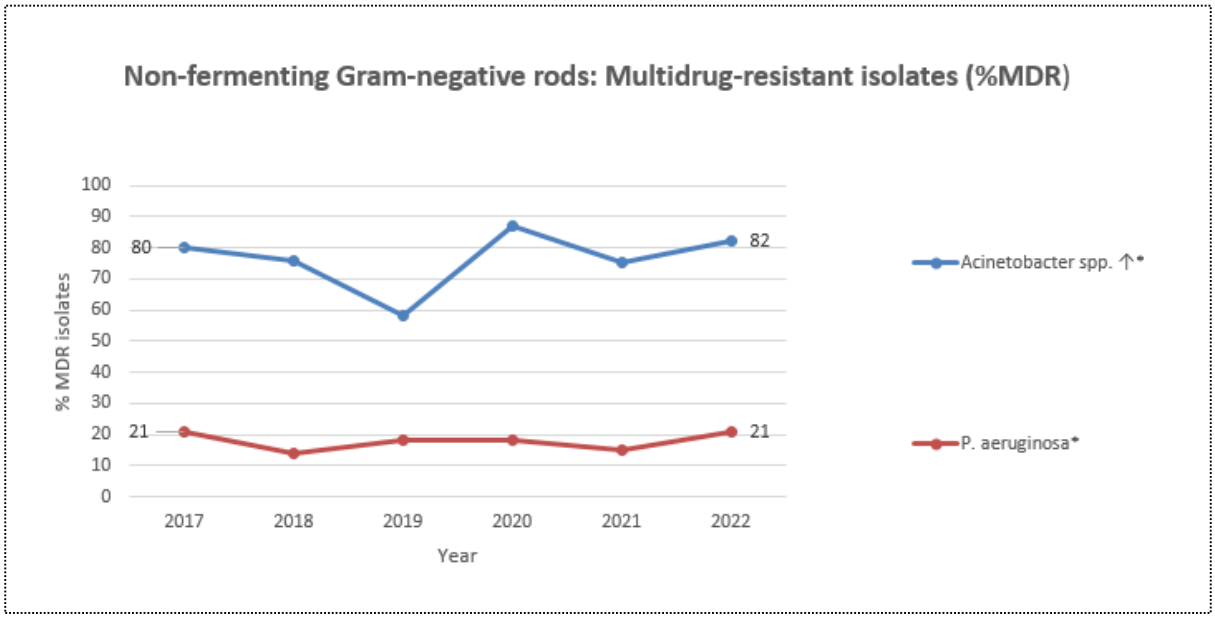
Figure 4.3.2 Annual trends for percentage of isolates multidrug resistant (%MDR) for *E. coli*, *K. pneumoniae*, and *Salmonella* spp. (non-typhoid), Jordan, 2017-2022



*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

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

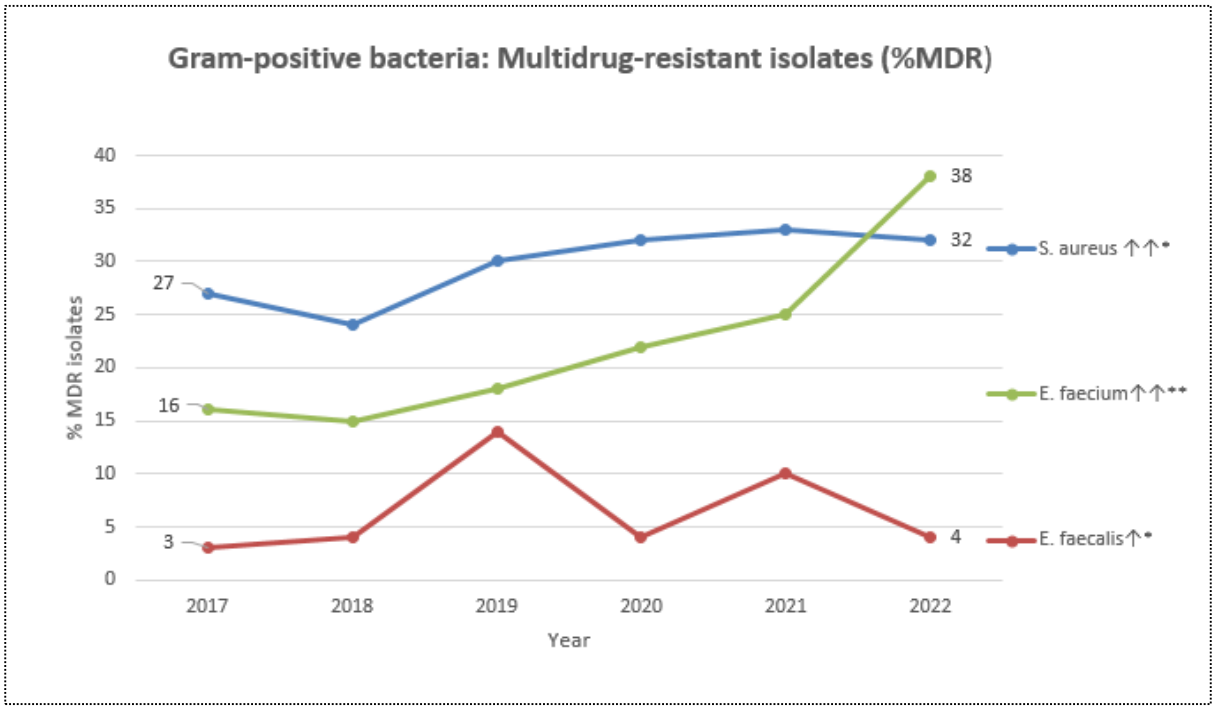
Figure 4.3.3 Annual trends for percentage of isolates multidrug resistant (%MDR) for non-fermenting Gram-negative rods, Jordan, 2017-2022



*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

4.3.4 Multidrug-resistance in Gram-positive Bacteria

Figure 4.3.4 Annual trends for percentage of isolates multidrug resistant (%MDR) for Gram-positive bacteria, Jordan, 2017-2022



*Trend is statistically significant (p<0.001)
**Trend is statistically significant (p<0.05)
Data source: HDA only (public and RMS sites).

4.4 AMR priority pathogens

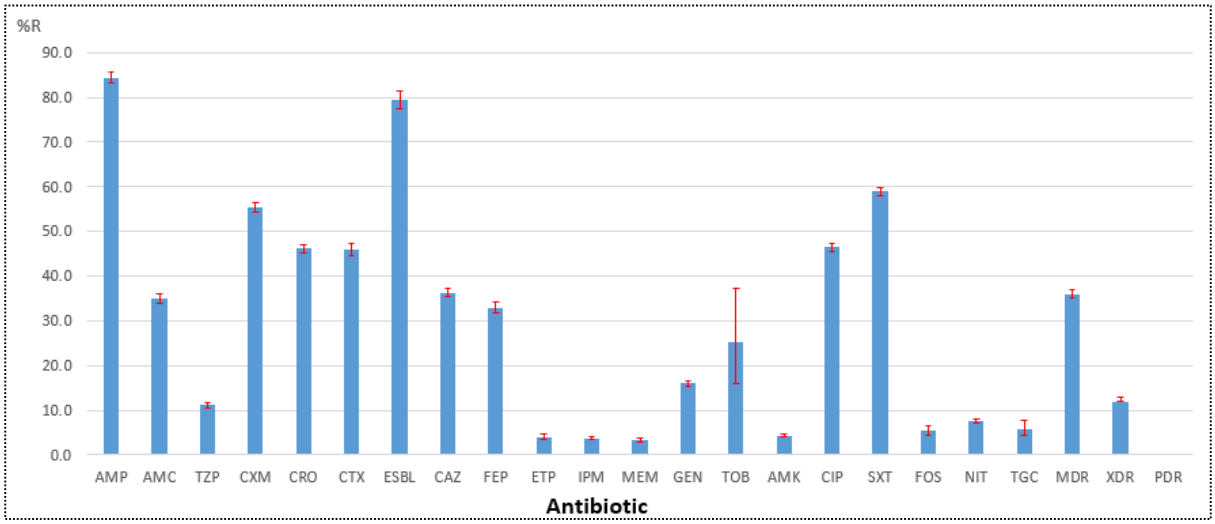
4.4.1 Escherichia coli

Table 4.4.1.1 Percentages of resistant, intermediate, and susceptible isolates for *Escherichia coli*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Escherichia coli* (N=18,823)			
		Isolates (N)	% R	% I	% S
Ampicillin	AMP	4,229	84.4	0.9	14.7
Amoxicillin/clavulanic acid	AMC	7,778	35.0	9.6	55.3
Piperacillin/tazobactam	TZP	8,833	11.1	3.1	85.7
Cefuroxime (oral)	CXM	7,550	55.4	1.8	42.8
Ceftriaxone	CRO	9,718	46.1	0.8	53.1
Cefotaxime	CTX	5,250	45.8	1.4	52.8
Extended-spectrum β-lactamase	ESBL	1,692	79.4		20.6
Ceftazidime	CAZ	9,875	36.3	6.1	57.5
Cefepime	FEP	6,017	32.9	0.9	66.2
Ertapenem	ETP	5,996	4.0	0.6	95.3
Imipenem	IPM	10,600	3.8	0.4	95.8
Meropenem	MEM	5,056	3.2	0.4	96.4
Gentamicin	GEN	11,956	16.0	0.6	83.4
Tobramycin	TOB	71	25.4	5.6	69.0
Amikacin	AMK	11,103	4.4	1.0	94.6
Ciprofloxacin	CIP	10,119	46.4	7.6	46.0
Trimethoprim/sulfamethoxazole	SXT	8,715	58.9	0.1	41.0
Fosfomycin[a]	FOS	1,952	5.5	0.0	94.5
Nitrofurantoin[a]	NIT	9,751	7.6	3.7	88.7
Tigecycline[b]	TGC	893	5.8	0.2	94.0
Multidrug-resistance (≥3 classes NS)[c]	MDR	6,799	36.0	_	_
Extensive drug resistance (possible)	XDR	2,302	12.0	_	_
Pan-drug resistance (possible)	PDR	70	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).

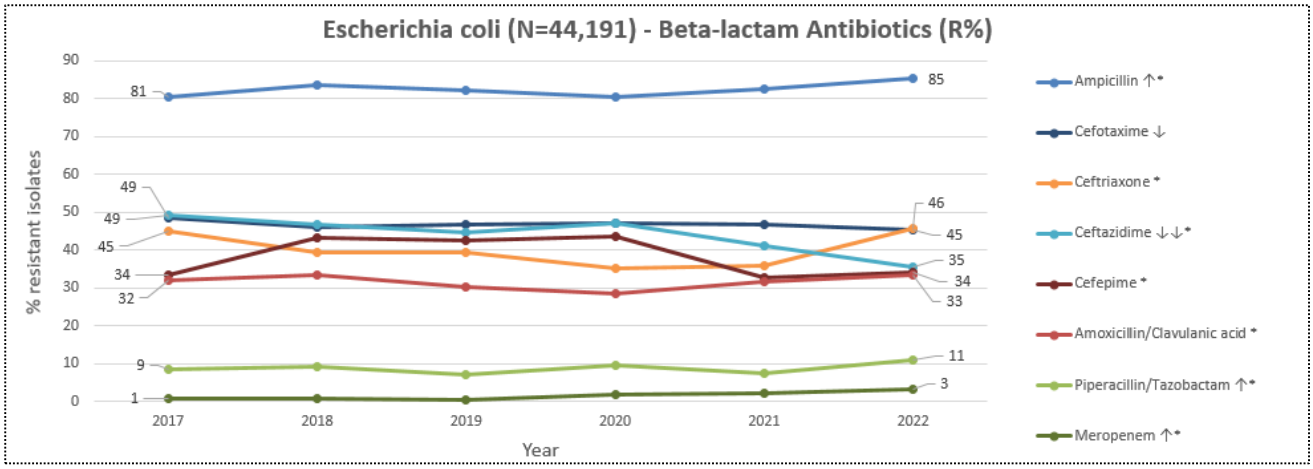
Figure 4.4.1.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Escherichia coli*, isolates from all sources, Jordan, 2022



For 2020, resistance in *Escherichia coli* ranged from 0% for glycylcyclines (tigecycline) to 84.4% for aminopenicillins (ampicillin).

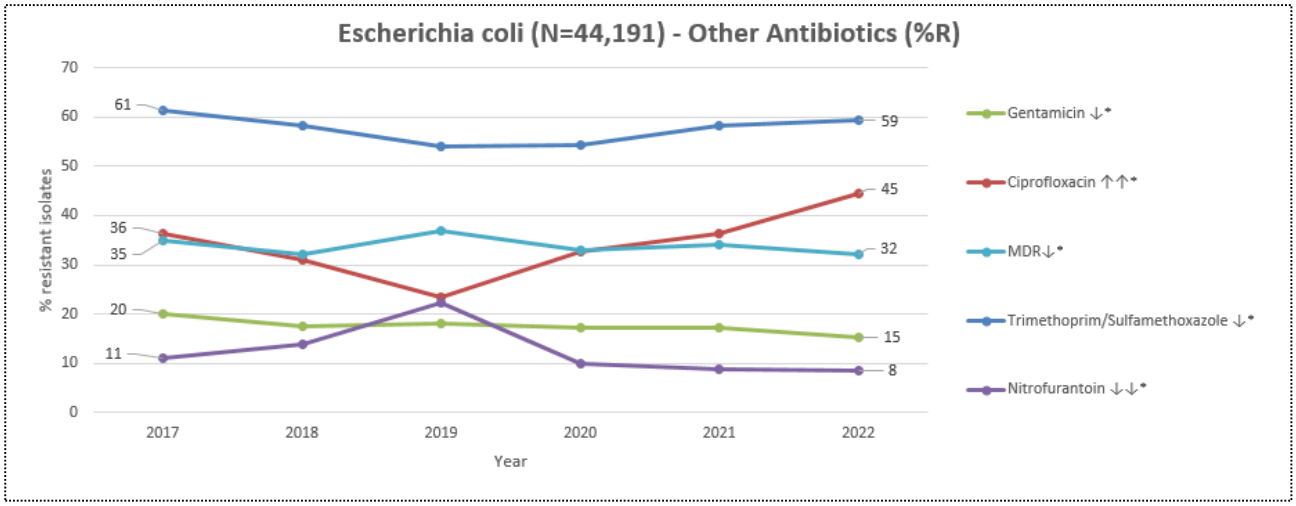
- Susceptibility of urinary tract isolates of *E. coli* to fluoroquinolones (ciprofloxacin) was 46%
- Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *E. coli* was 36%, 12 %, and 0%, respectively.

Figure 4.4.1.2 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, Jordan, 2017-2022 – Beta-lactam Antibiotics



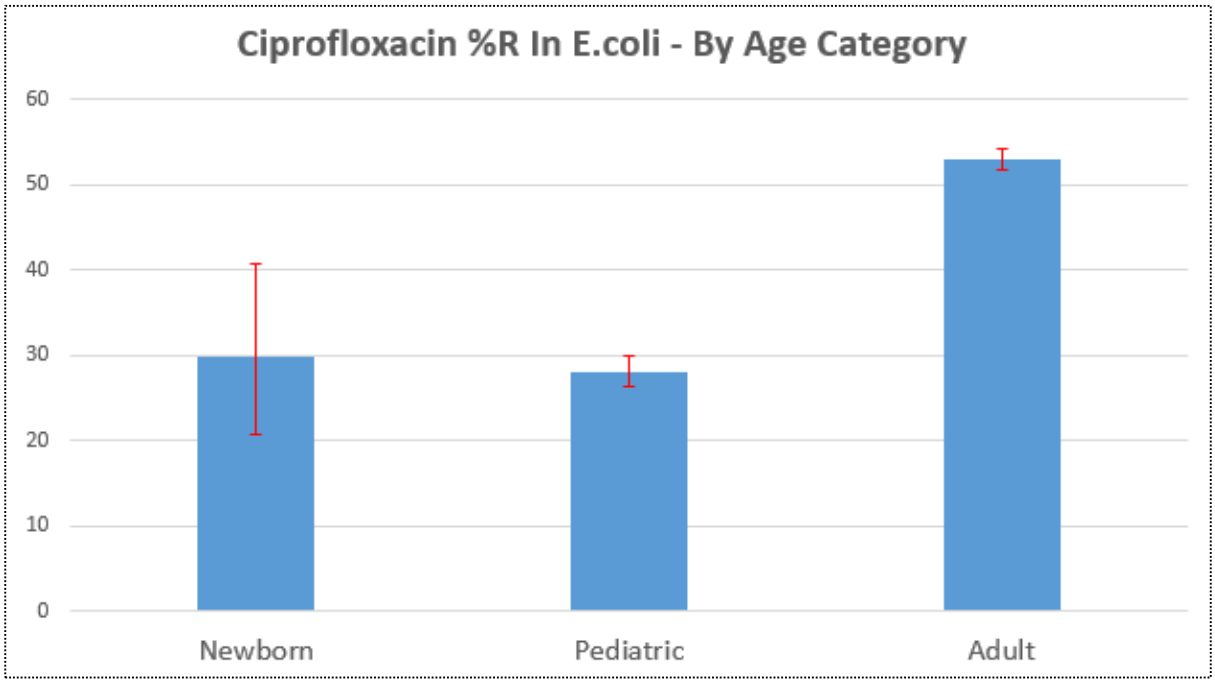
*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

Figure 4.4.1.3 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, Jordan, 2017-2022 – Other Antibiotics



*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

Figure 4.4.1.4 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, Jordan, 2022 – By age category and age group



Note: Newborn: 0-30 days, Pediatric: 1 month to 18 years, Adult: 19+ years

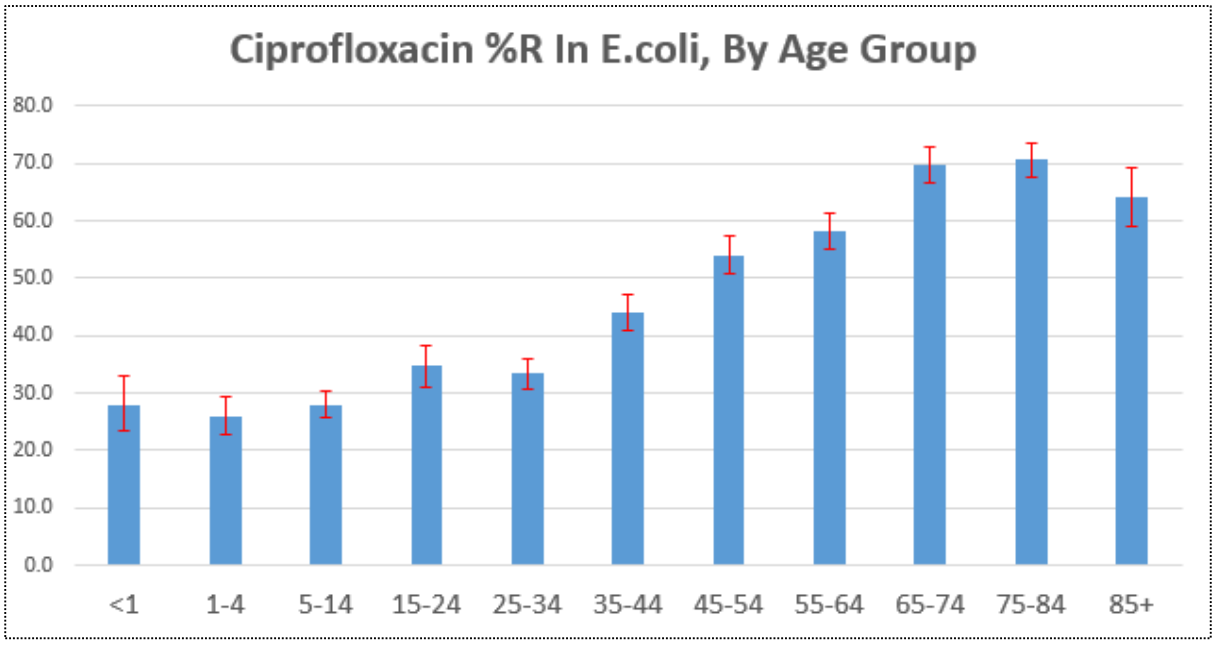


Figure 4.4.1.5 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, Jordan, 2022 – By gender.

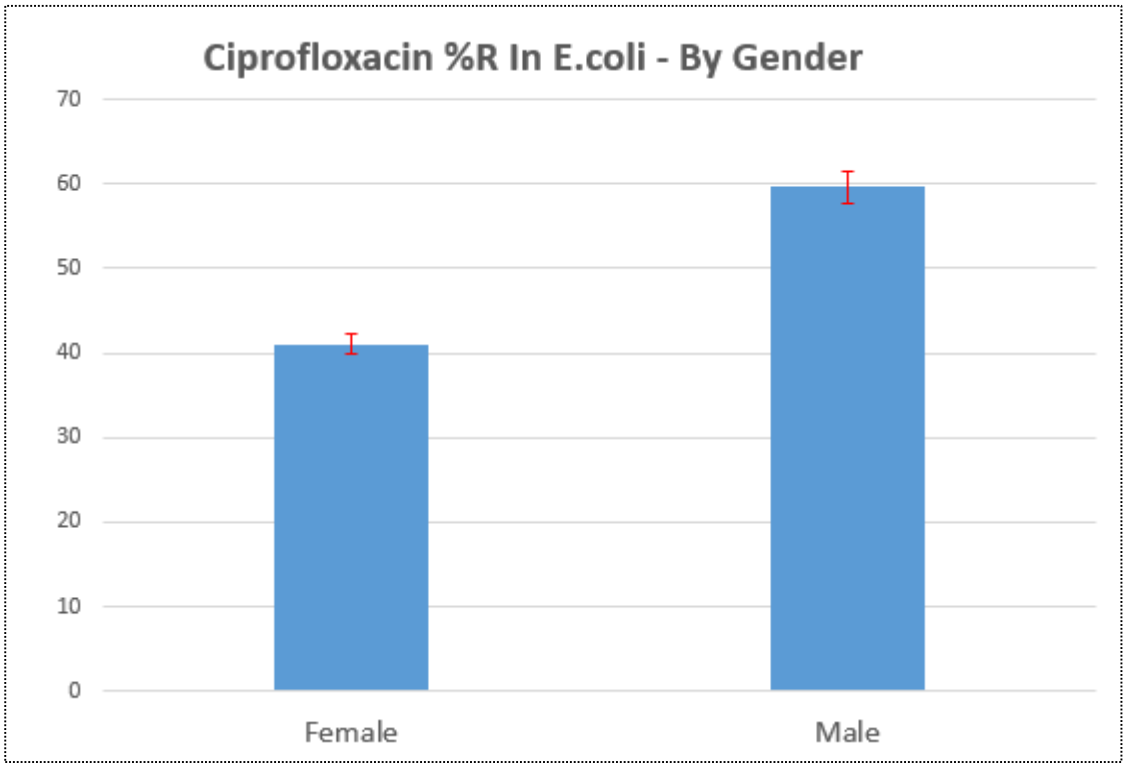
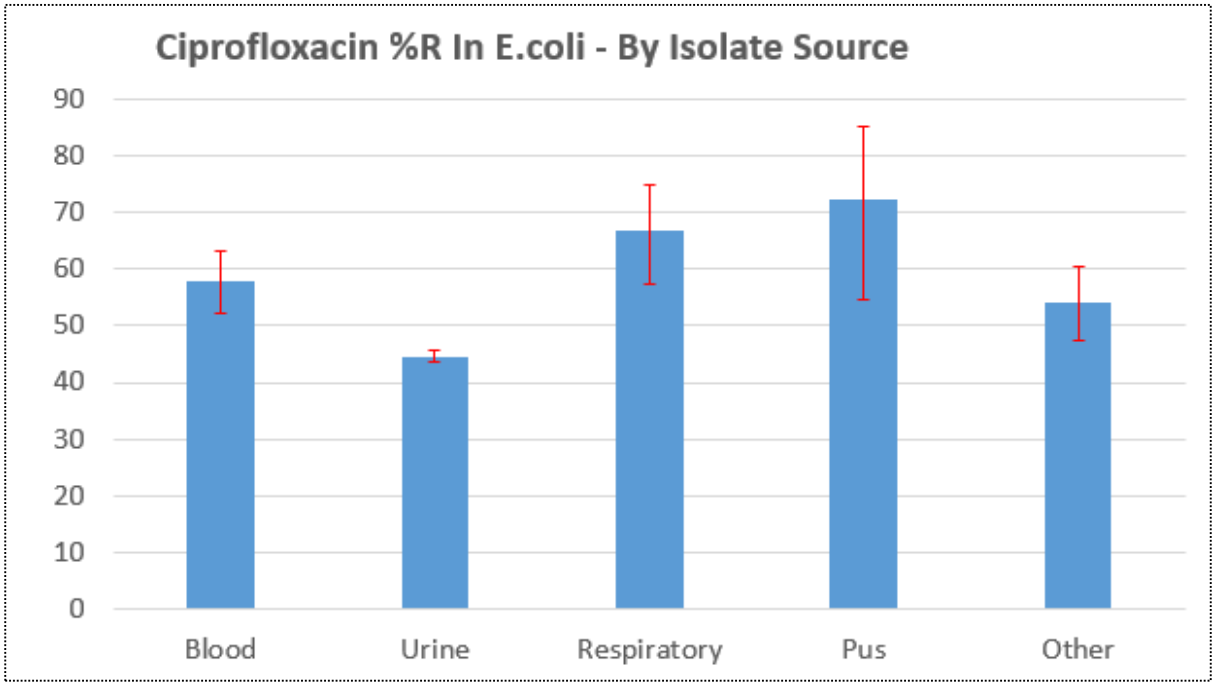


Figure 4.4.1.6 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, Jordan, 2022 – By isolate source and patient location type



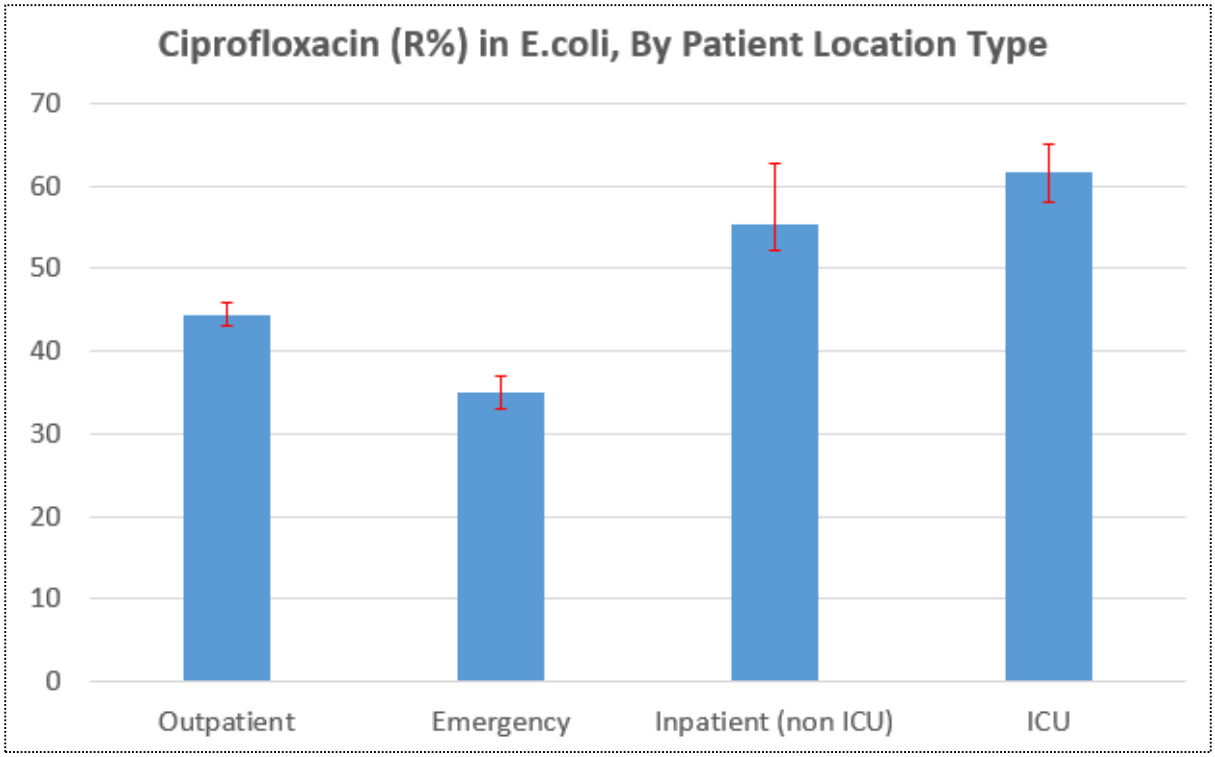
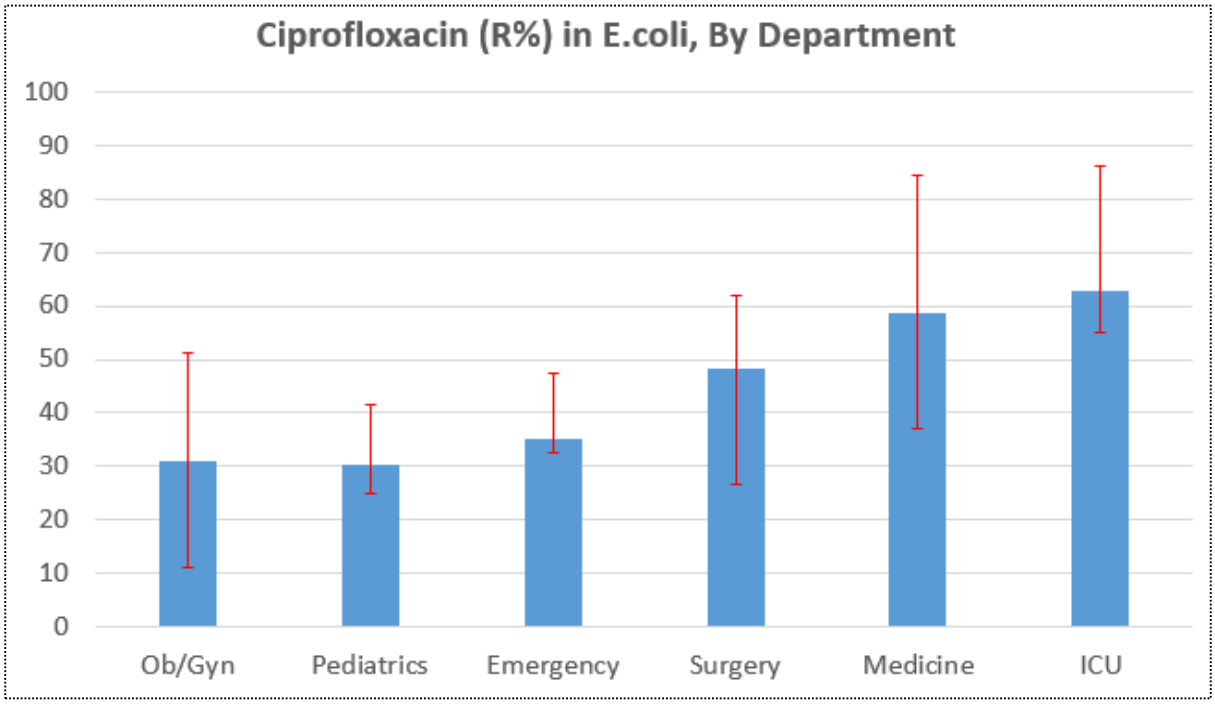


Figure 4.4.1.7 Percentage of isolates resistant (%R) to fluoroquinolones (ciprofloxacin) for *Escherichia coli*, Jordan, 2022 – By department



4.4.2 Klebsiella pneumoniae

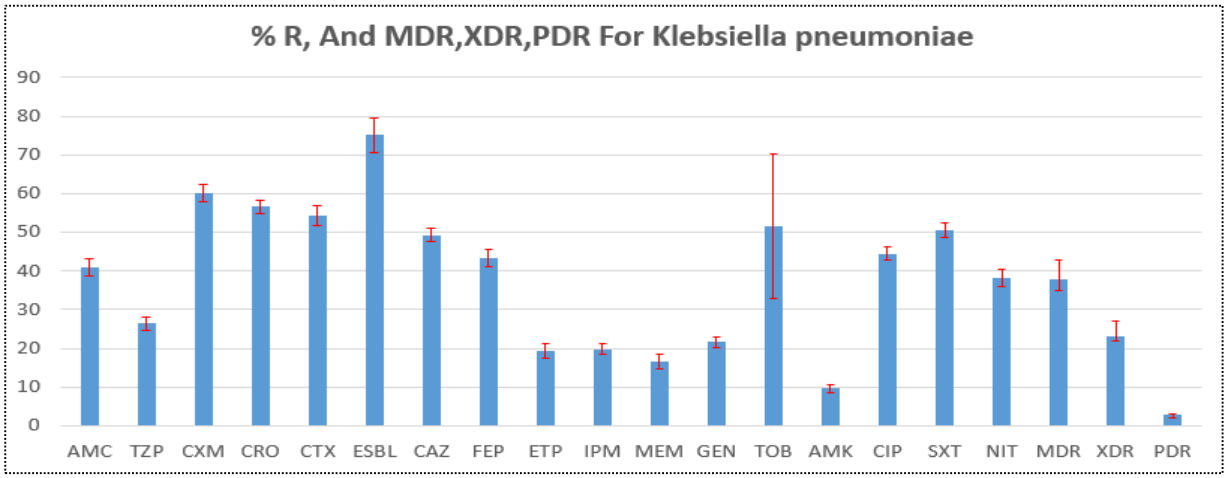
Table 4.4.2.1 Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Klebsiella pneumoniae* (N= 5,289)			
		Isolates (N)	% R	% I	% S
Amoxicillin/clavulanic acid	AMC	2,054	41.0	7.4	51.7
Piperacillin/tazobactam	TZP	2,688	26.5	5.6	67.9
Cefuroxime (oral)	CXM	1,926	60.1	1.6	38.3
Ceftriaxone	CRO	2,818	56.6	0.7	42.7
Cefotaxime	CTX	1,428	54.2	1.6	44.2
Extended-spectrum β-lactamase	ESBL	383	75.2		24.8
Ceftazidime	CAZ	2,980	49.3	5.9	44.7
Cefepime	FEP	1,988	43.3	0.4	56.3
Ertapenem	ETP	1,734	19.3	1.2	79.5
Imipenem	IPM	3,185	19.7	2.0	78.2
Meropenem	MEM	1,604	16.7	0.6	82.7
Gentamicin	GEN	3,286	21.6	1.0	77.4
Tobramycin	TOB	29	51.7	3.4	44.8
Amikacin	AMK	3,441	9.6	5.0	85.4
Ciprofloxacin	CIP	3,042	44.4	6.0	49.6
Trimethoprim/sulfamethoxazole	SXT	2,486	50.6	0.2	49.3
Nitrofurantoin[a]	NIT	1,825	38.1	20.3	41.6
Multidrug-resistance (≥3 classes NS)[b]	MDR	2230[a]	42.0	_	_
Extensive drug resistance (possible)	XDR	1344[a]	25.0	_	_
Pan-drug resistance (possible)	PDR	140[a]	3.0	_	_

[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, Jordan, 2022

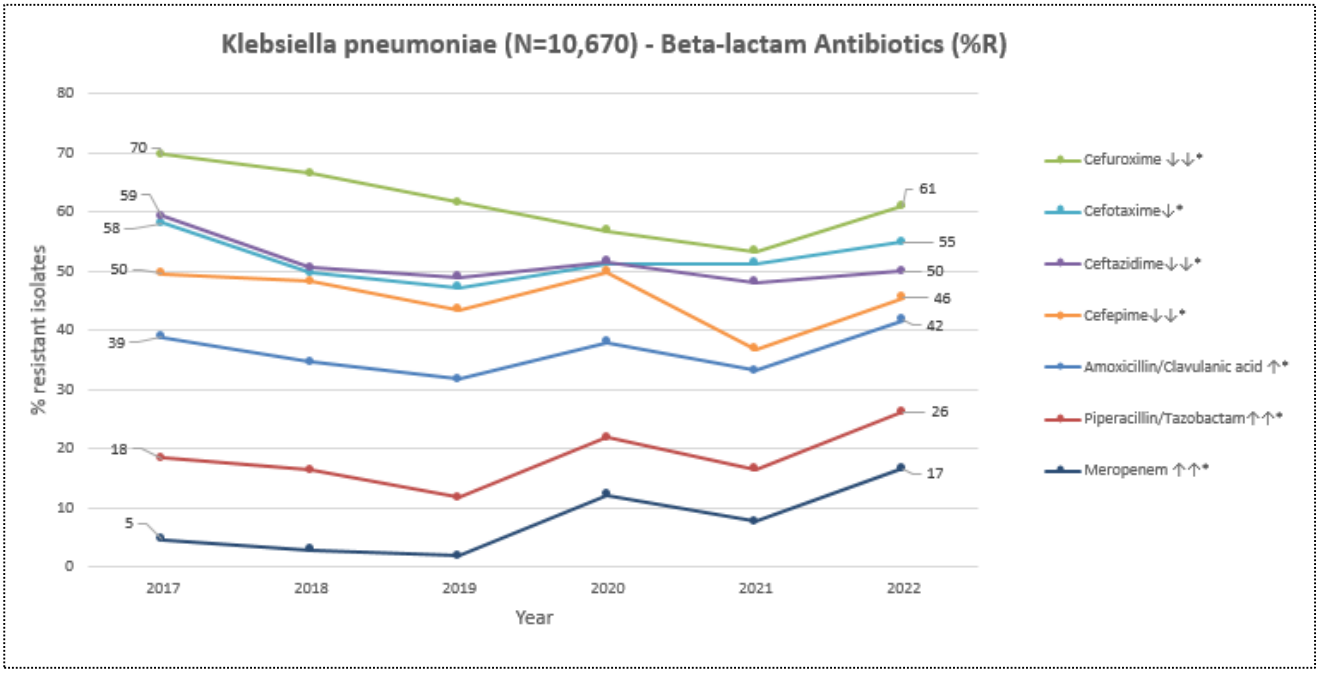


For 2022, resistance in *Klebsiella pneumoniae* ranged from 9.6 %R for amikacin (aminoglycosides), to 75.2 %R for ESBL and 60.1, 56.6 %R for cefuroxime (CXM) and ceftriaxone (CRO) Respectively.

- Non-susceptibility (%R+%I) to carbapenems was 19.7%, 16.7%, and 19.3%NS for imipenem, meropenem and ertapenem, respectively.
- Susceptibility of urinary tract isolates of *K. pneumoniae* to fluoroquinolones (ciprofloxacin) was 44.4 %S.
- Prevalence of multidrug resistance (%MDR/XDR/PDR[6]) in *K. pneumoniae* was 42%, 25%, and 3%, respectively.

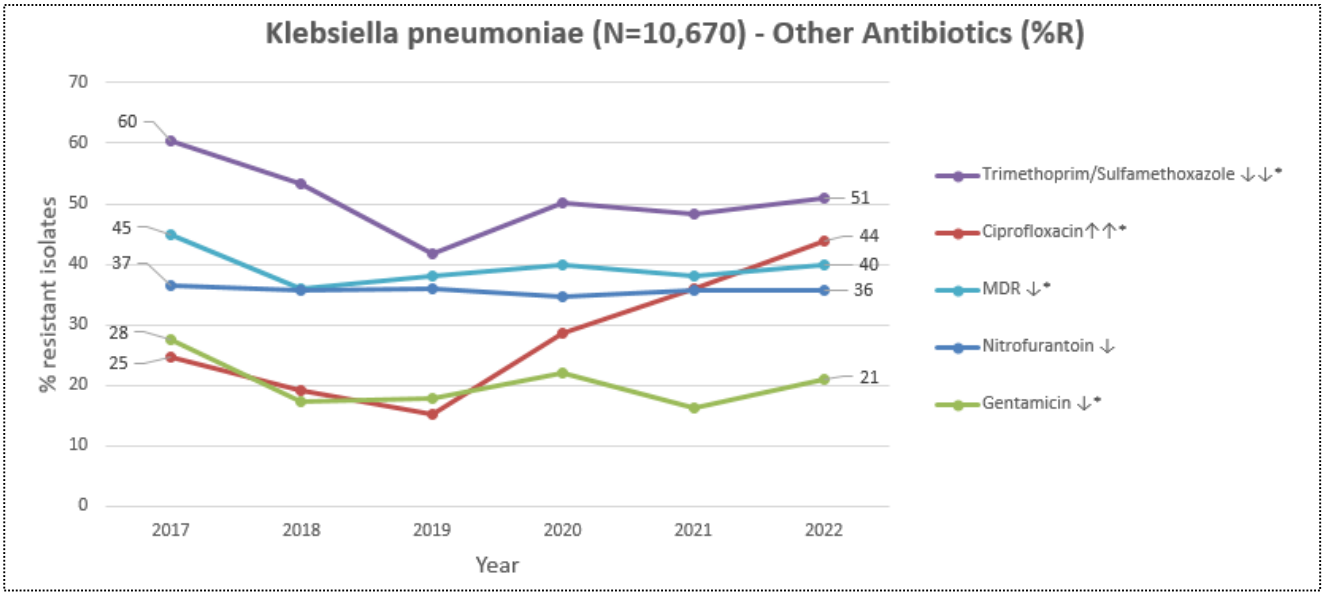
[6] Possible XDR, possible PDR

Figure 4.4.2.2 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, Jordan, 2010-2022 – Beta-lactam Antibiotics



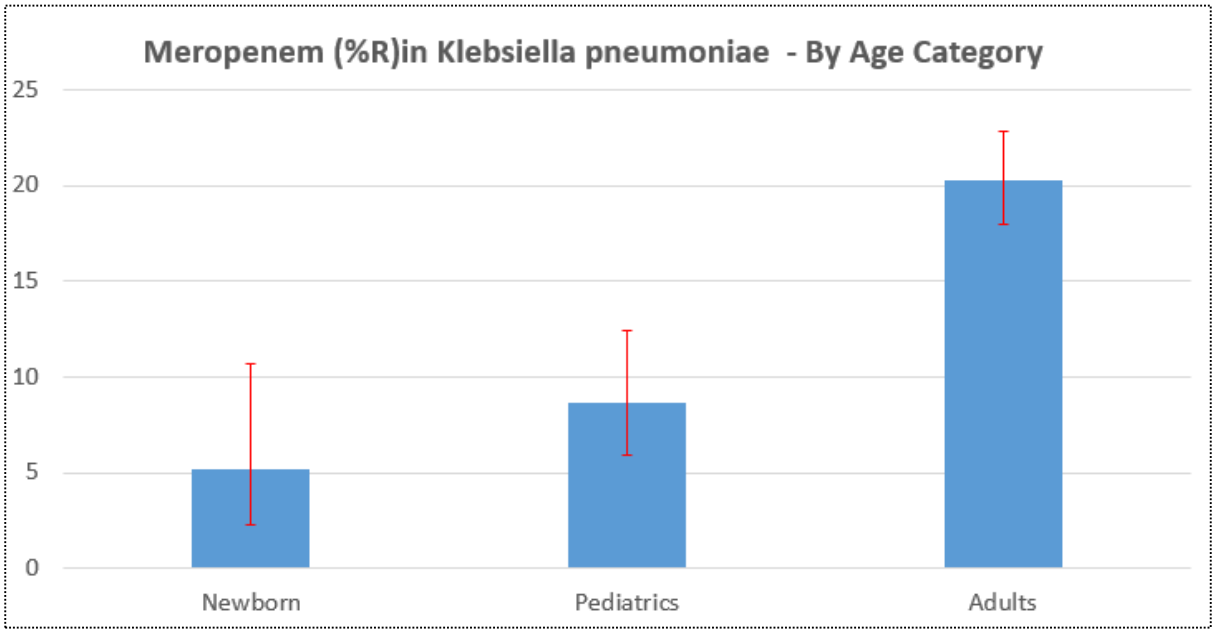
***Trend is statistically significant (p<0.001)**
Data source: HDA only (public and RMS sites).

Figure 4.4.2.3 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, Jordan, 2010-2022 – Other Antibiotics



***Trend is statistically significant (p<0.001)**
Data source: HDA only (public and RMS sites).

Figure 4.4.2.4 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, Jordan, 2022 – By age category and age group



Note: Newborn: 0-30 days, Pediatric: 1 month to 18 years, Adult: 19+ years

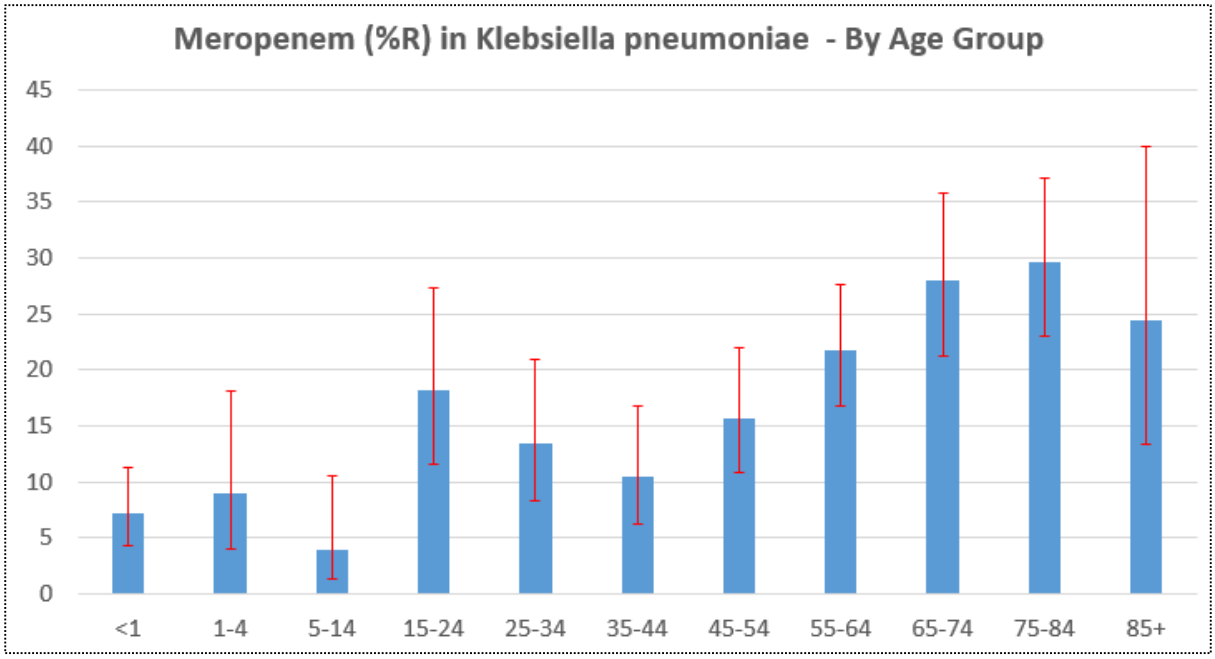


Figure 4.4.2.5 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, Jordan, 2022 – By gender.

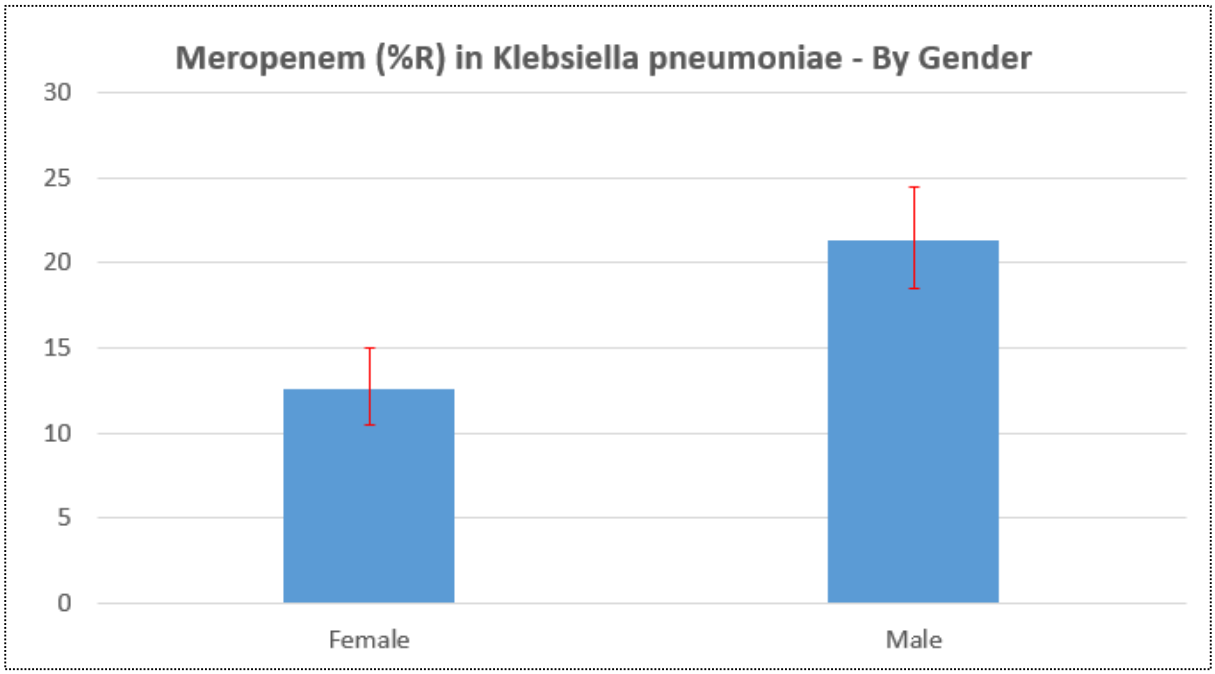
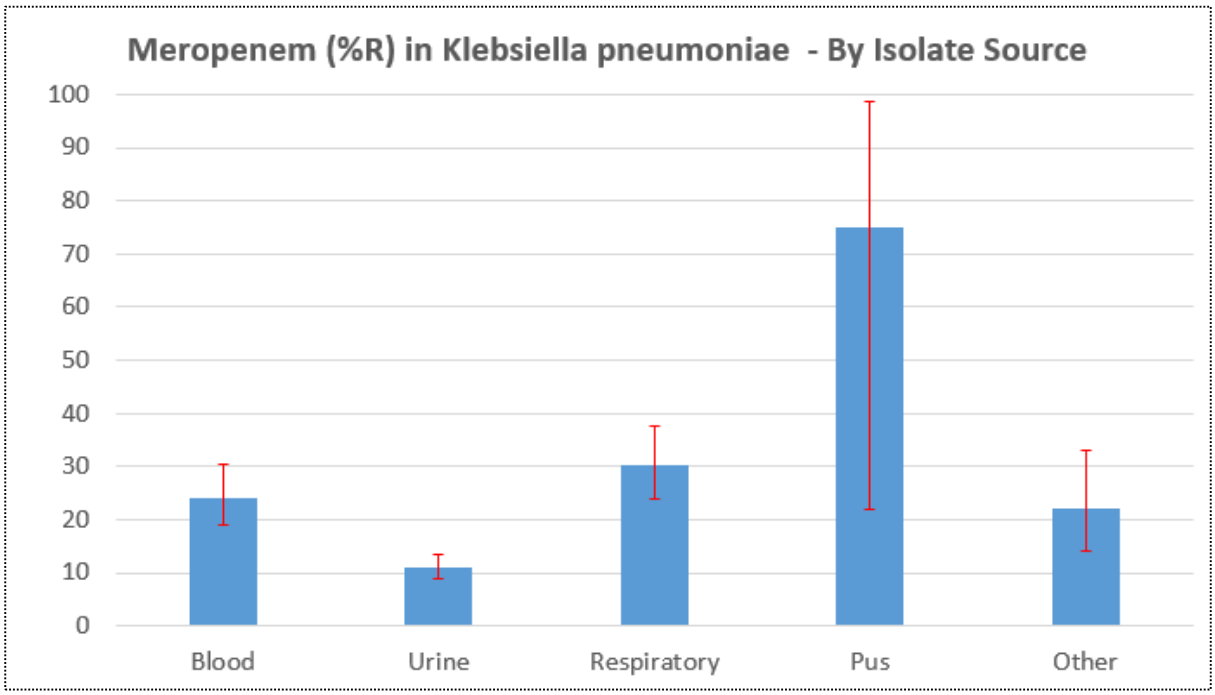


Figure 4.4.2.6 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, Jordan, 2022 – By isolate source and patient location type



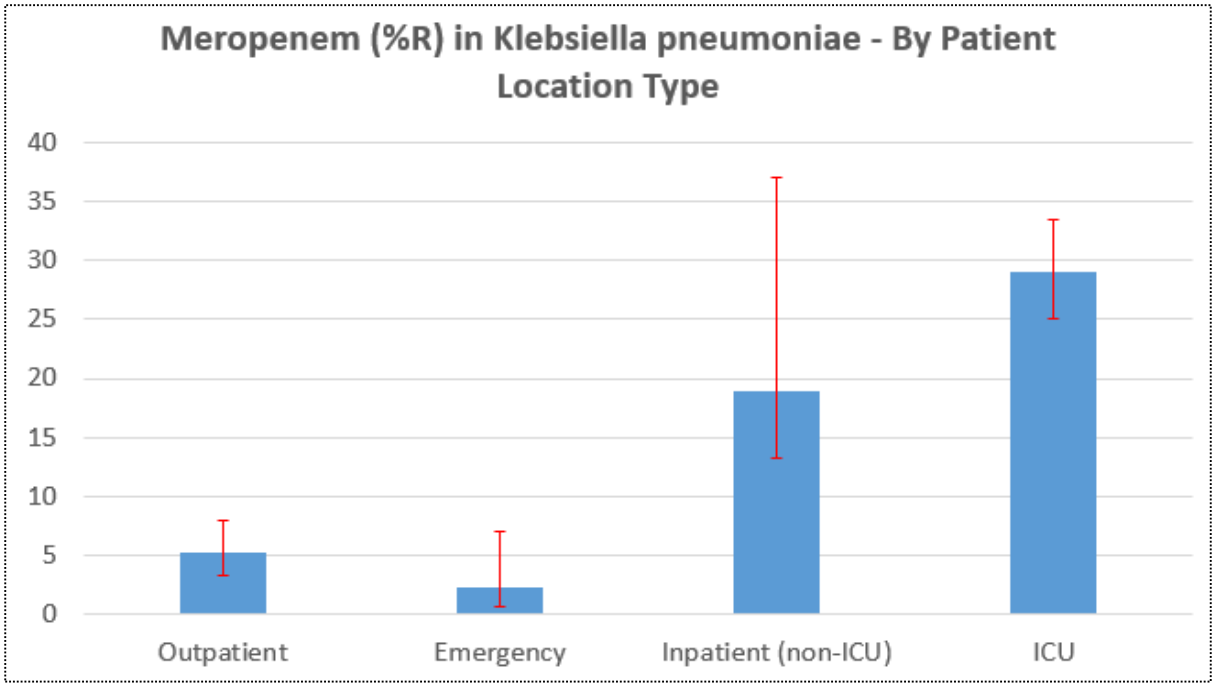
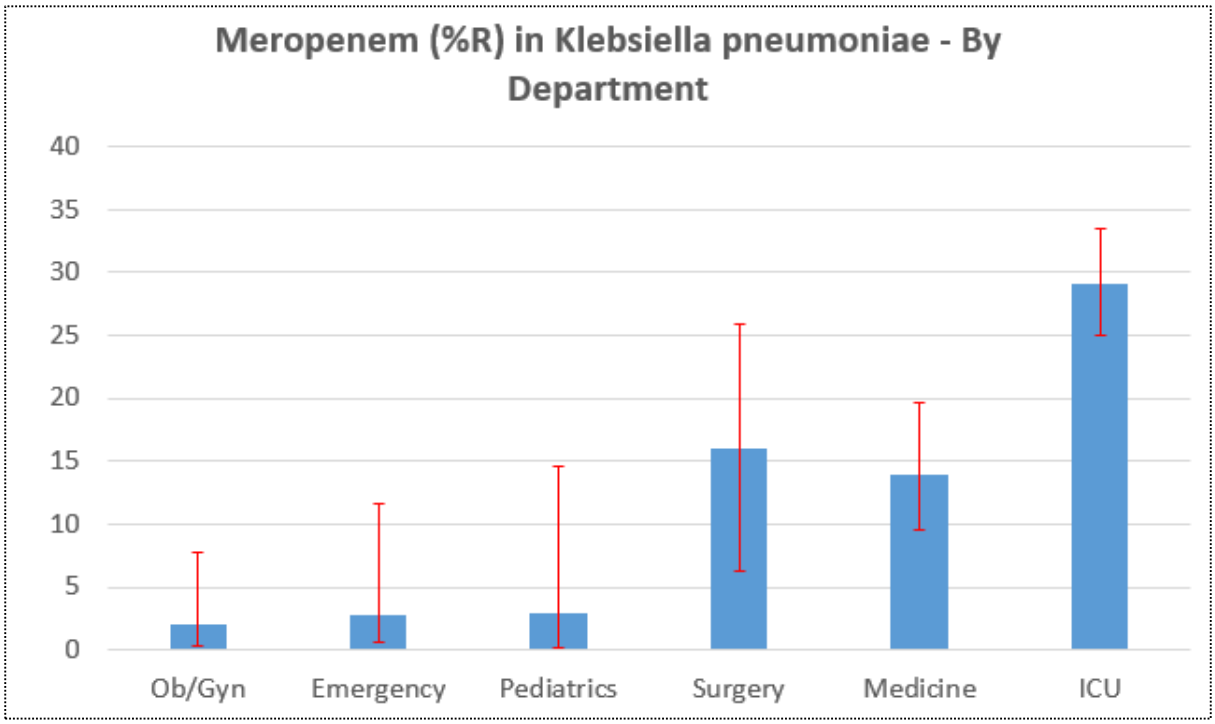


Figure 4.4.2.7 Percentage of isolates resistant (%R) to carbapenems (meropenem) for *Klebsiella pneumoniae*, Jordan, 2022 – By department



4.4.3 Pseudomonas aeruginosa

Table 4.4.3.1 Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Pseudomonas aeruginosa* (N=3,275)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	1,979	23.5	1.7	74.7
Ceftazidime	CAZ	2,335	26.1	4.4	69.5
Cefepime	FEP	1,396	20.2	8.4	71.4
Imipenem	IPM	2,289	23.6	1.5	74.9
Meropenem	MEM	1,359	21.9	4.1	74.0
Gentamicin	GEN	1,998	20.0	1.9	78.1
Tobramycin	TOB	409	24.4	1.0	74.6
Amikacin	AMK	2,448	13.3	1.9	84.8
Ciprofloxacin	CIP	2,200	28.0	3.3	68.7
Multidrug-resistance (≥3 classes NS)[a]	MDR	730	22.0	_	_
Extensive drug resistance (possible)	XDR	651	20.0	_	_
Pan-drug resistance (possible)	PDR	59	2.0	_	_

[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 4.4.3.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Pseudomonas aeruginosa,* isolates from all sources, Jordan, 2022

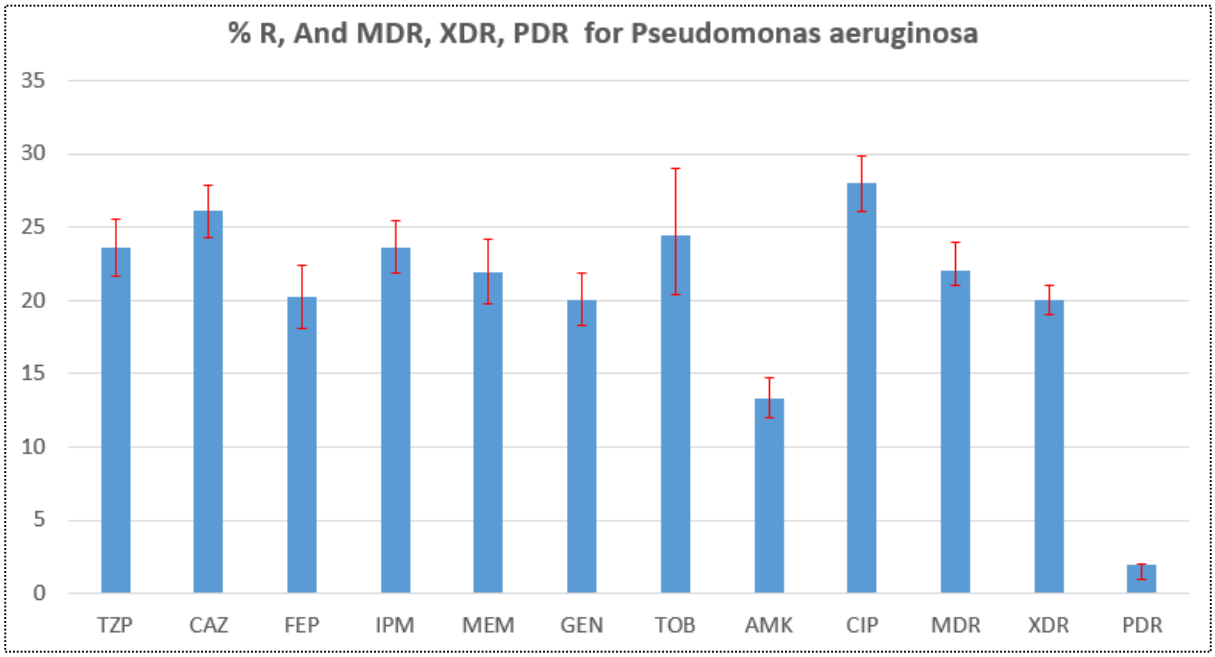
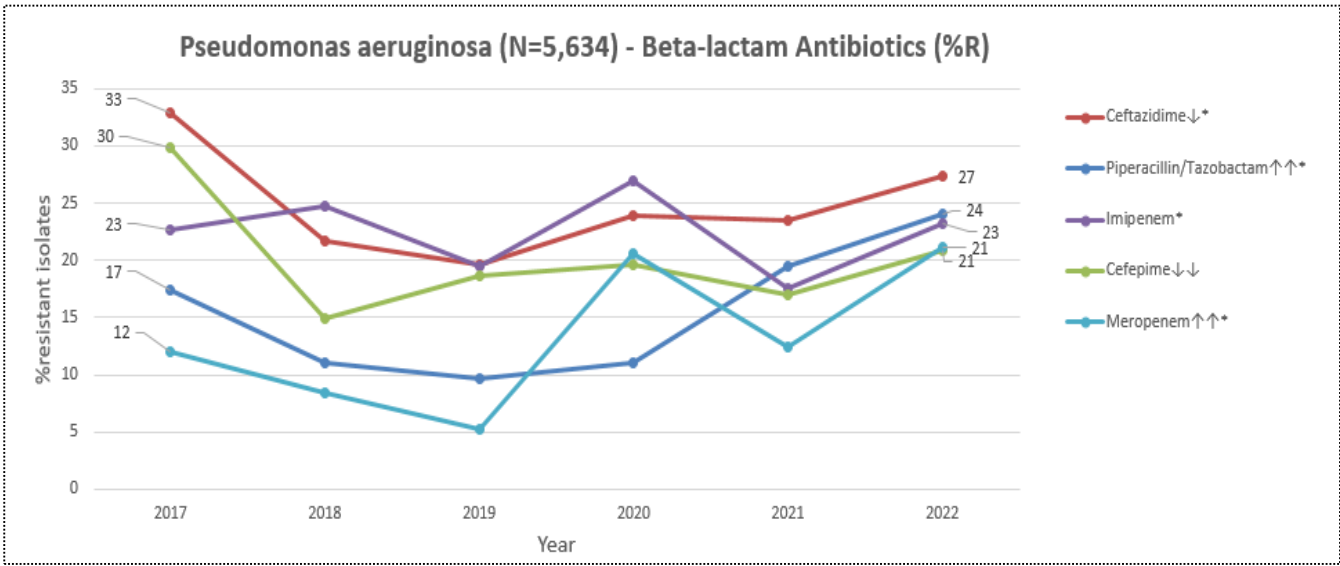
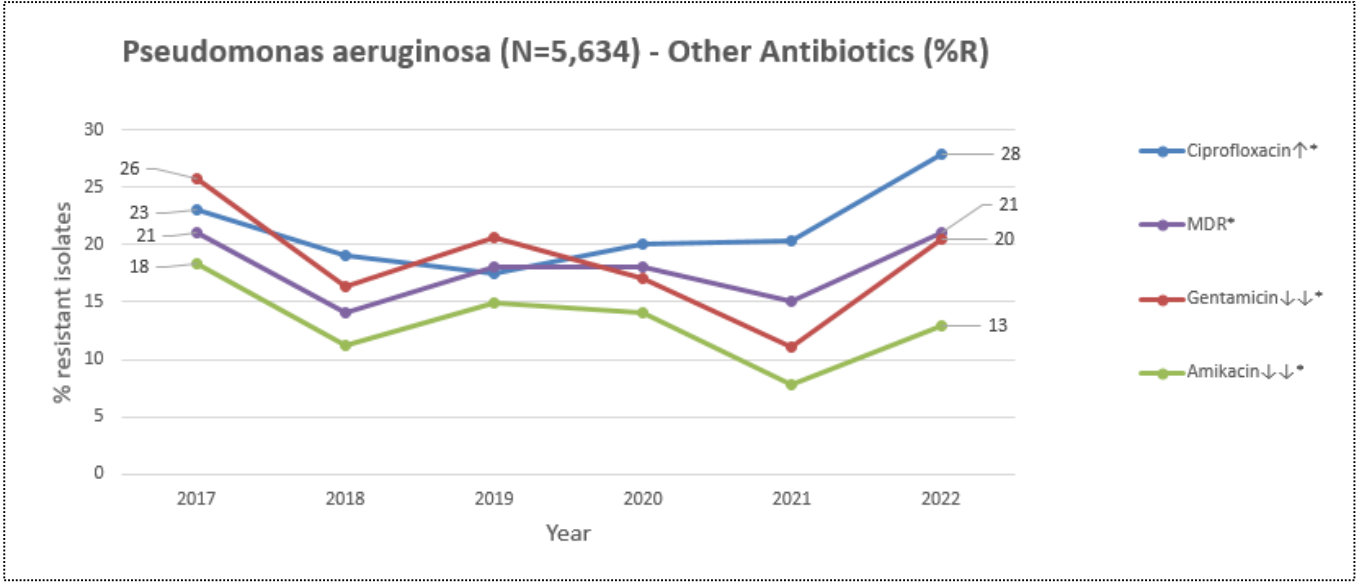


Figure 4.4.3.2 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, Jordan, 2010-2022 – Beta-lactam Antibiotics



*****Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

Figure 4.4.3.3 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, Jordan, 2010-2022 – Other Antibiotics



*****Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

4.4.4 Acinetobacter spp.

Table 4.4.4.1 Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp., isolates from all sources, Jordan, 2022

Antibiotic	Code	*Acinetobacter* spp. (N=2,309)			
		Isolates (N)	% R	% I	% S
Piperacillin/tazobactam	TZP	1,428	88.9	0.7	10.4
Ceftazidime	CAZ	1,590	86.5	0.8	12.6
Cefepime	FEP	1,092	76.8	9.6	13.6
Imipenem	IPM	1,649	85.0	0.3	14.7
Meropenem	MEM	951	85.5	0.8	13.7
Gentamicin	GEN	1,443	67.0	2.5	30.5
Tobramycin	TOB	106	71.7	0.0	28.3
Amikacin	AMK	1,609	67.1	5.5	27.3
Ciprofloxacin	CIP	1,415	86.5	0.5	13.0
Trimethoprim/Sulfamethoxazole	SXT	1,132	57.5	0.4	42.0
Minocycline	MNO	74	62.2	12.2	25.7
Tetracycline	TCY	115	71.3	15.7	13.0
Multidrug-resistance (≥3 classes NS)[a]	MDR	1874	81.0	_	_
Extensive drug resistance (possible)	XDR	1817	79.0	_	_
Pan-drug resistance (possible)	PDR	252	11.0	_	_

[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 *Acinetobacter* spp., isolates from all sources, Jordan, 2022

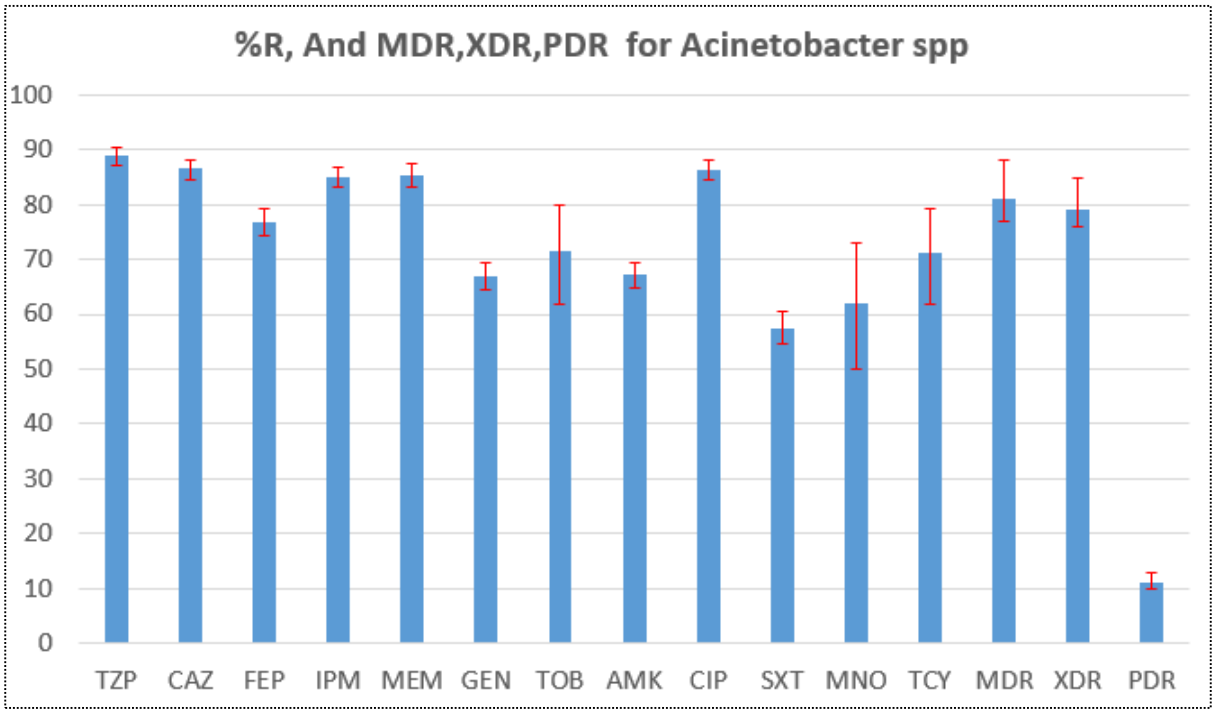
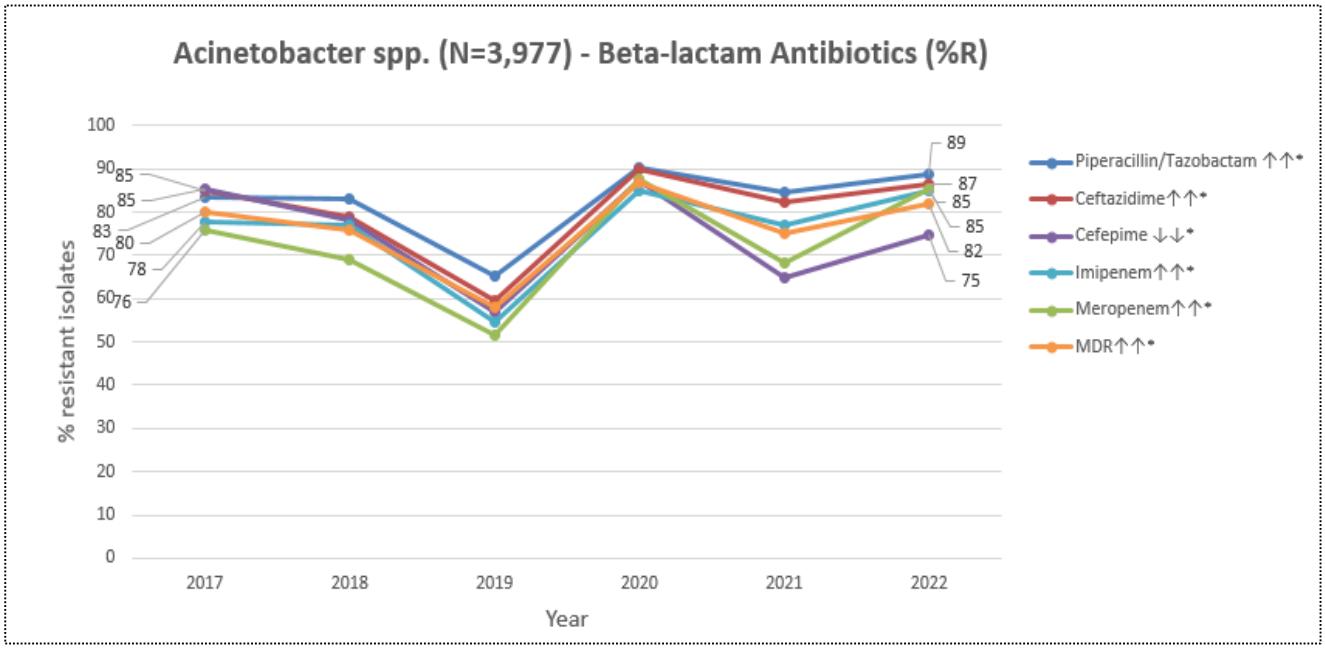


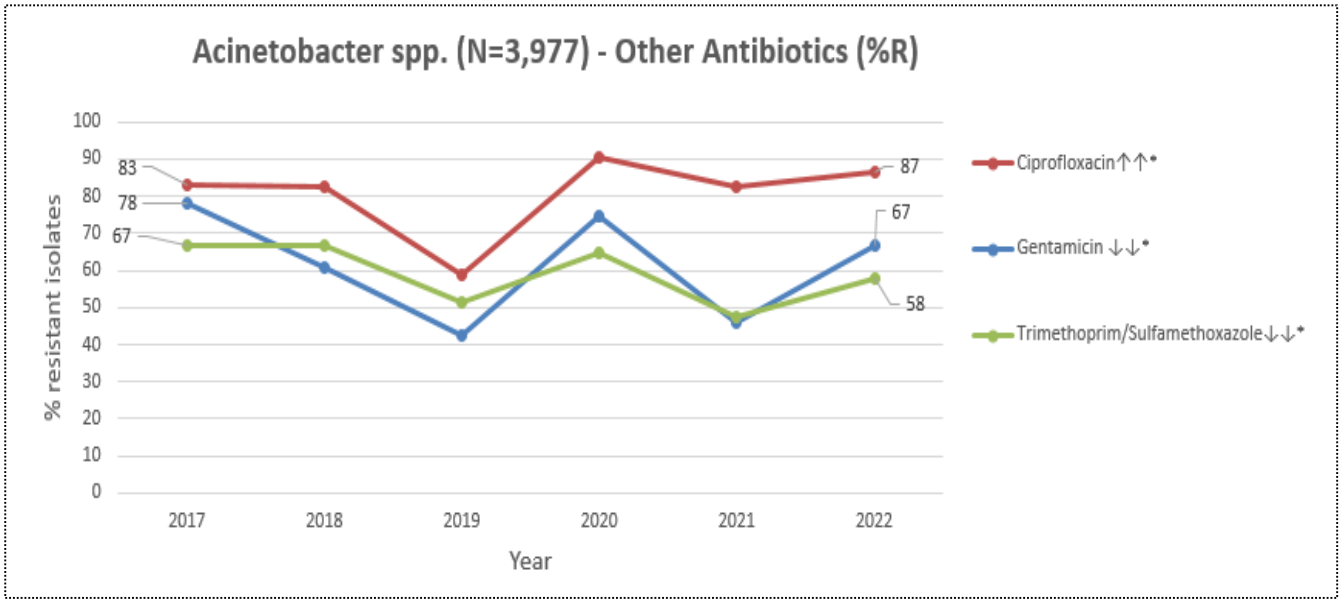
Figure 4.4.4.2 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., Jordan, 2013-2022 – Beta-lactam antibiotics

Between 2017 and 2022, for Acinetobacter, resistance levels are not decreasing.



*Trend is statistically significant (p<0.01)
Data source: HDA only (public and RMS sites).

Figure 4.4.4.3 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., Jordan, 2014-2022 – Other Antibiotics



*Trend is statistically significant (p<0.01)
Data source: HDA only (public and RMS sites).

4.4.5 Staphylococcus aureus

Table 4.4.5.1 Percentages of resistant, intermediate, and susceptible isolates for *Staphylococcus aureus*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Staphylococcus aureus* (n=4,247)			
		Isolates (N)	% R	% I	% S
Oxacillin	OXA	1,725	62.0[a]	0.1	38.0[a]
Gentamicin	GEN	2,318	9.7	2.2	88.1
Rifampicin	RIF	1,075	7.1	0.2	92.7
Ciprofloxacin	CIP	1,027	21.7	3.1	75.2
Levofloxacin	LVX	1,188	22.4	0.3	77.3
Moxifloxacin	MFX	697	15.1	5.9	79.1
Trimethoprim/sulfamethoxazole	SXT	2,012	11.5	0.2	88.2
Clindamycin	CLI	3,118	37.5	0.5	62.0
Erythromycin	ERY	3,219	43.4	1.1	55.5
Linezolid	LNZ	1,323	0.8	0.0	99.2
Vancomycin	VAN	3,522	2.4	0.9	96.8
Quinupristin/Dalfopristin	QDA	94	0.0	0.0	100.0
Tigecycline[b]	TGC	811	1.7	1.4	96.9
Cefazolin	CZO	147	23	5.4	71.4
Multidrug-resistance (≥3 classes NS)[c]	MDR	1787	62.0	_	_
Extensive drug resistance (possible)	XDR	187	4.0	_	_
Pan-drug resistance (possible)	PDR	5	0.0	_	_

[a] MRSA/MSSA is calculated as resistance/susceptibility to oxacillin: %MRSA =62 % and %MSSA =38%
[b] Tigecycline: EUCAST breakpoints (S≤0.5, R>0.5)
[c] Multidrug resistance (MDR) was defined as isolate being MRSA

Figure 4.4.5.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Staphylococcus aureus,* isolates from all sources, Jordan, 2022

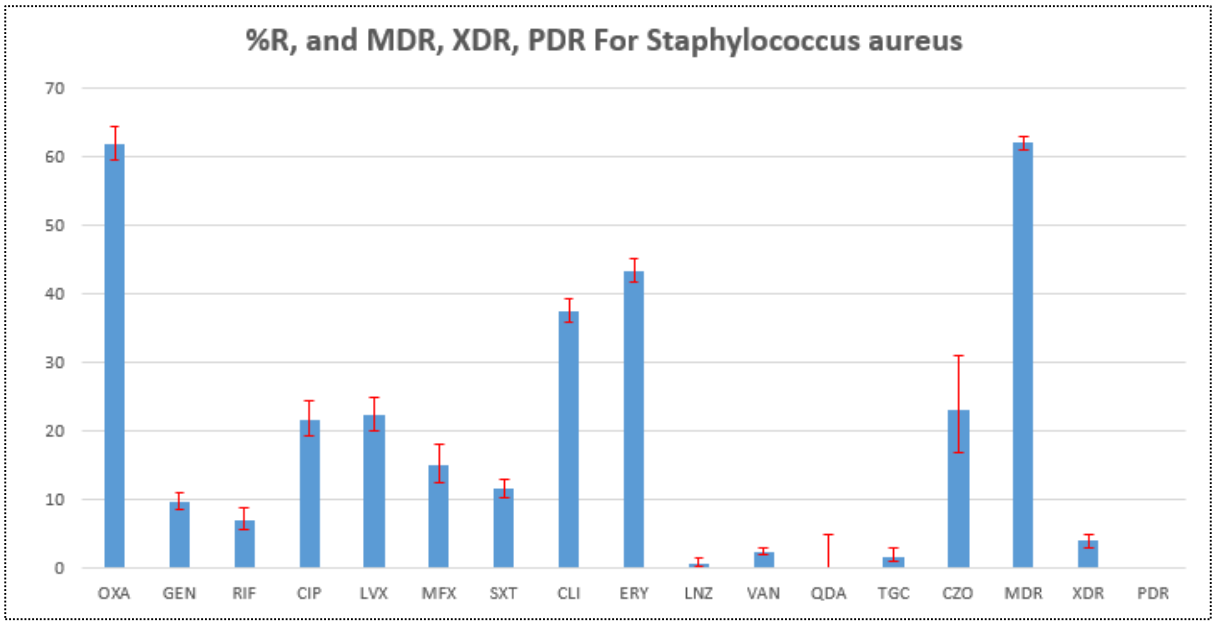
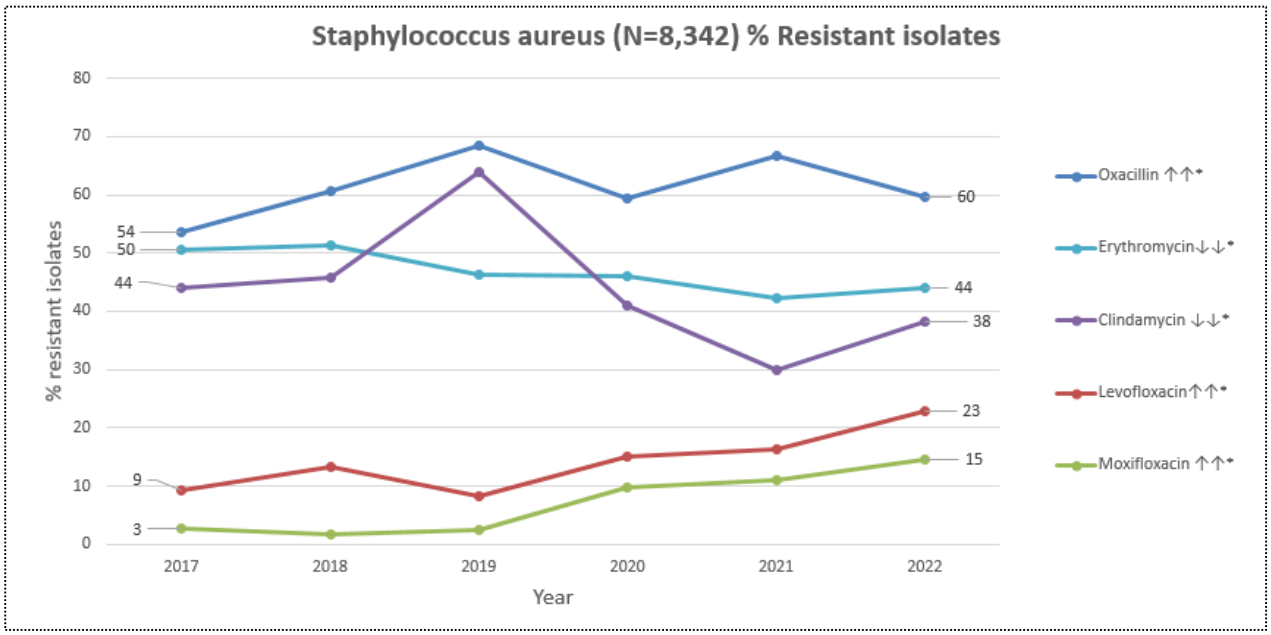
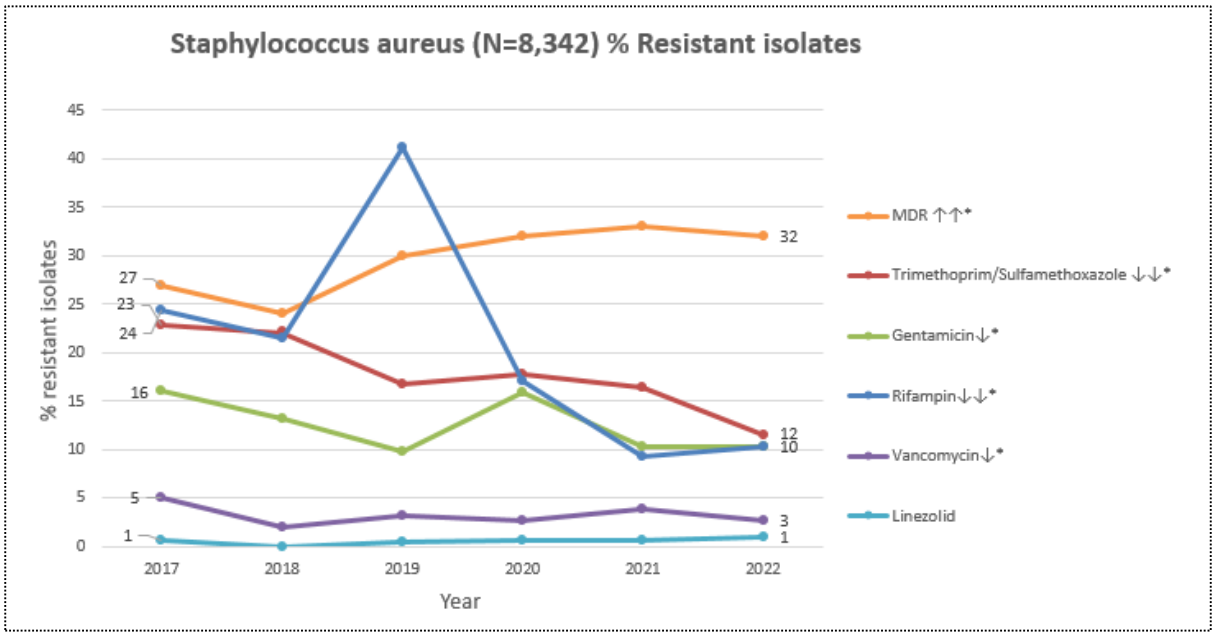


Figure 4.4.5.2 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, Jordan, 2010-2022 – Beta-lactams, fluoroquinolones, macrolides and lincosamides



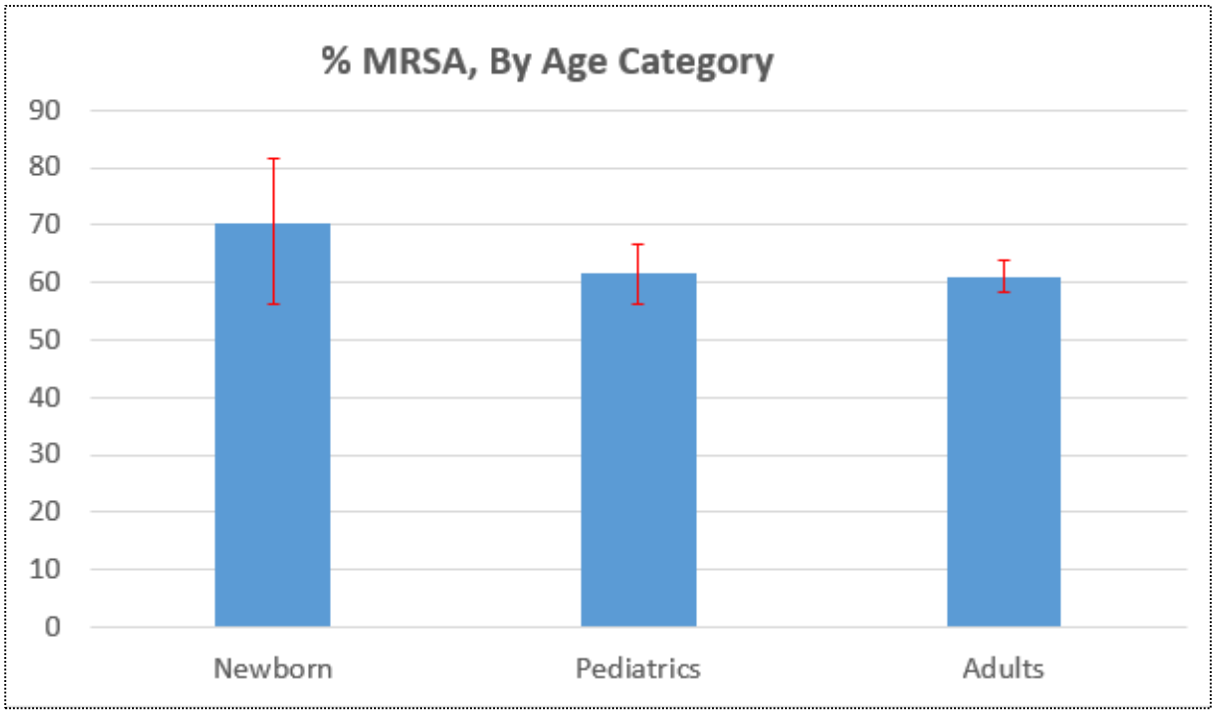
*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

Figure 4.4.5.3 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, Jordan, 2010-2022 – Other Antibiotics



*Trend is statistically significant (p<0.001)
Data source: HDA only (public and RMS sites).

Figure 4.4.5.4 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Jordan, 2022 – By age category and age group (years)



Note: Newborn: 0-30 days, Pediatric: 1 month to 18 years, Adult: 19+ years

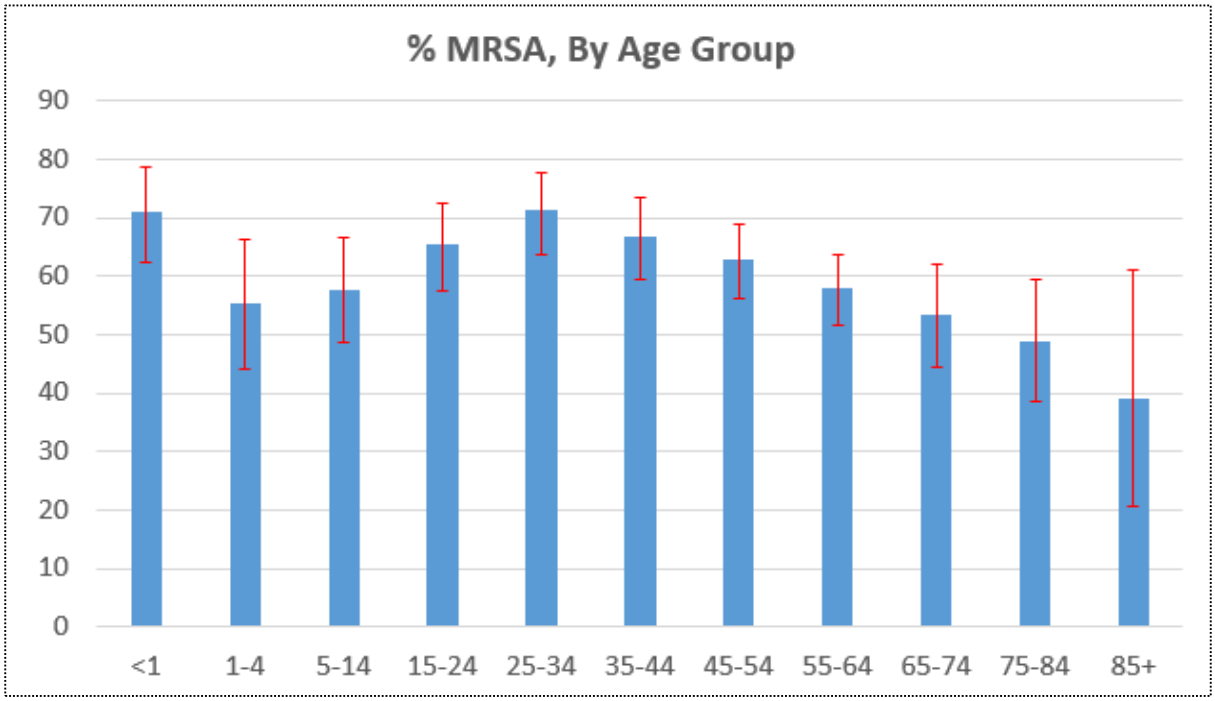


Figure 4.4.5.5 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Jordan, 2022 – By gender

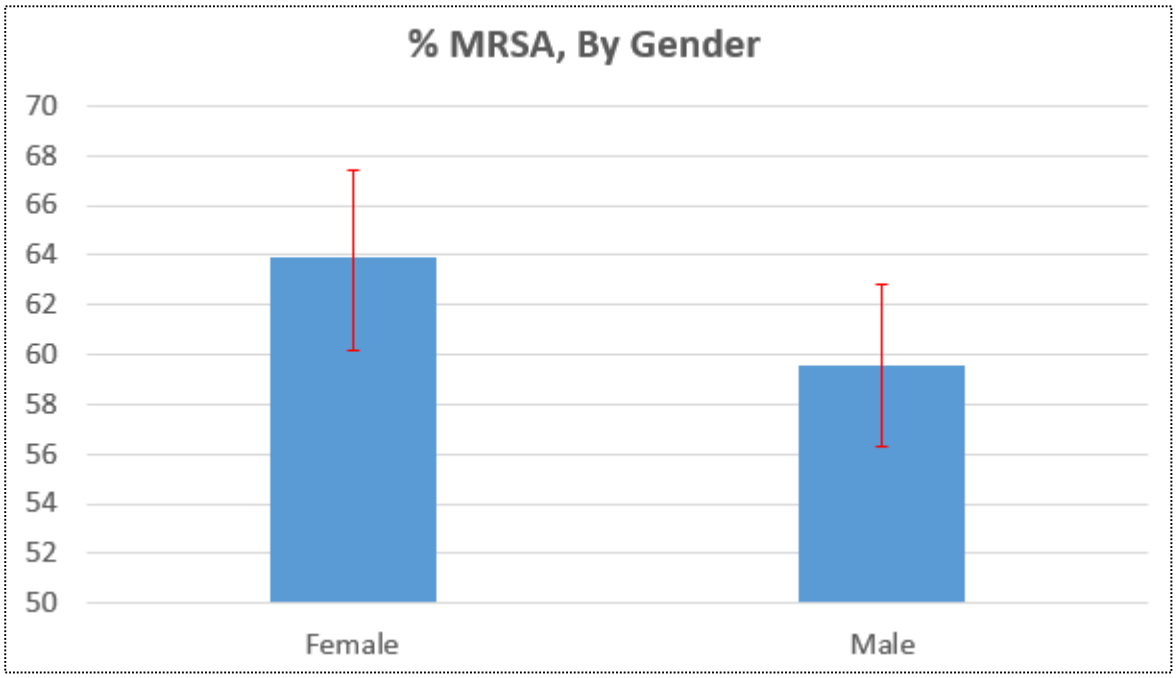
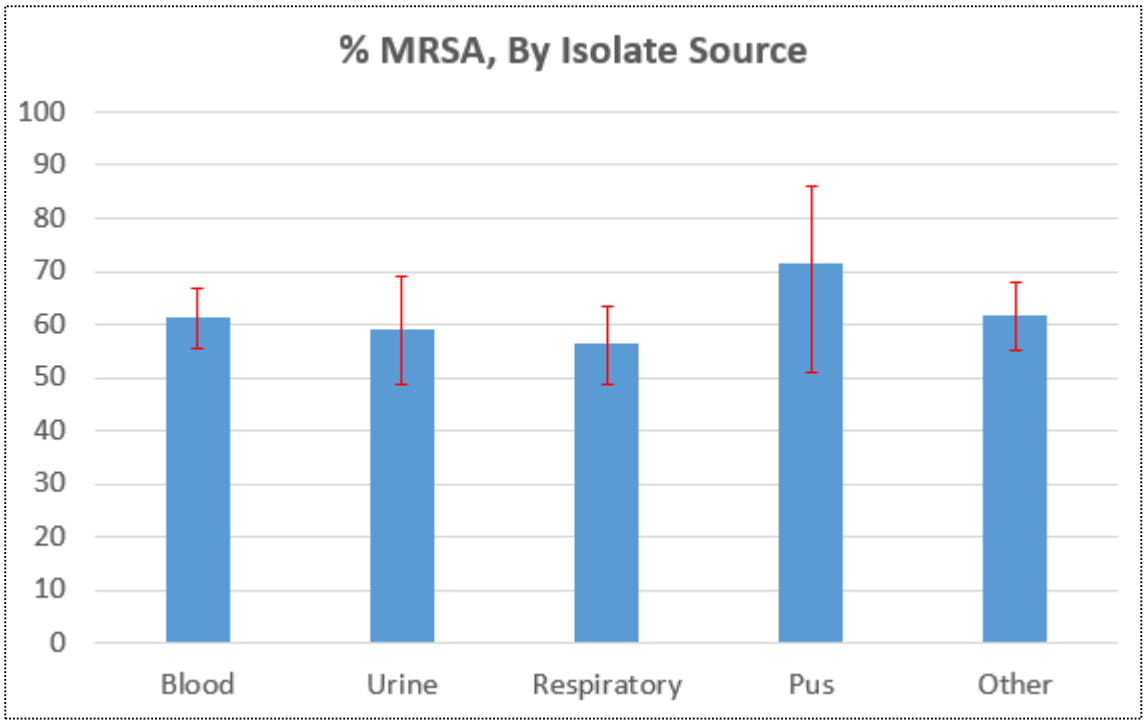


Figure 4.4.5.6 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Jordan, 2022 –By isolate source and patient location type



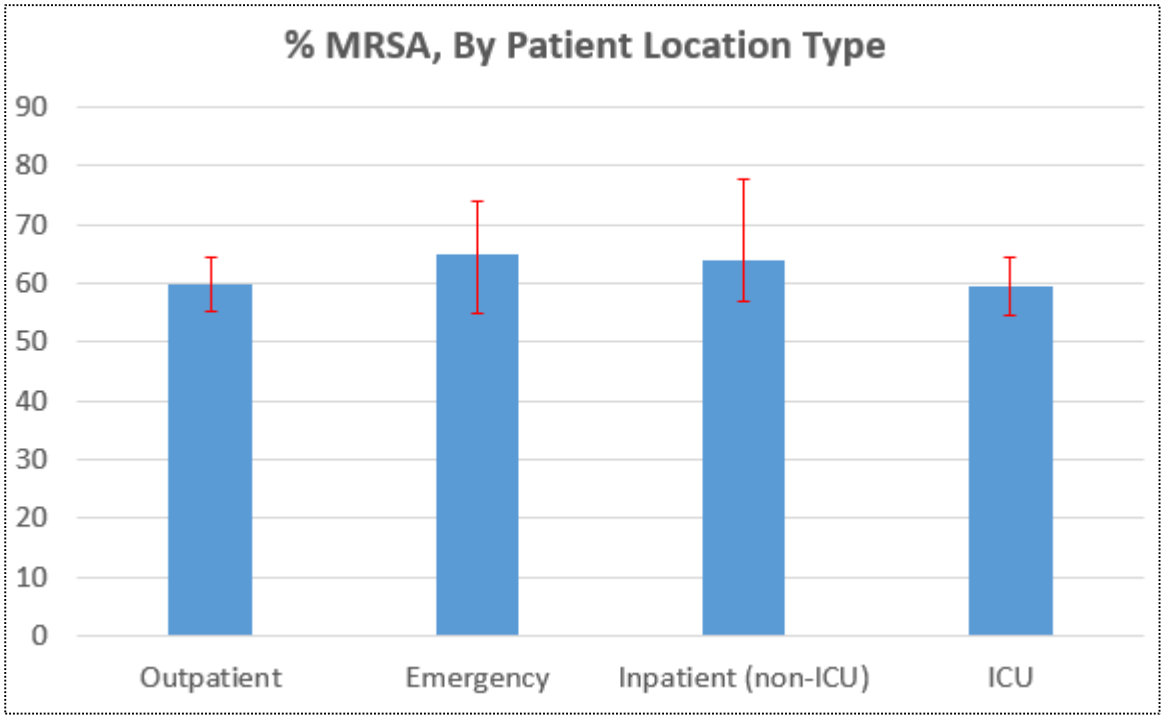
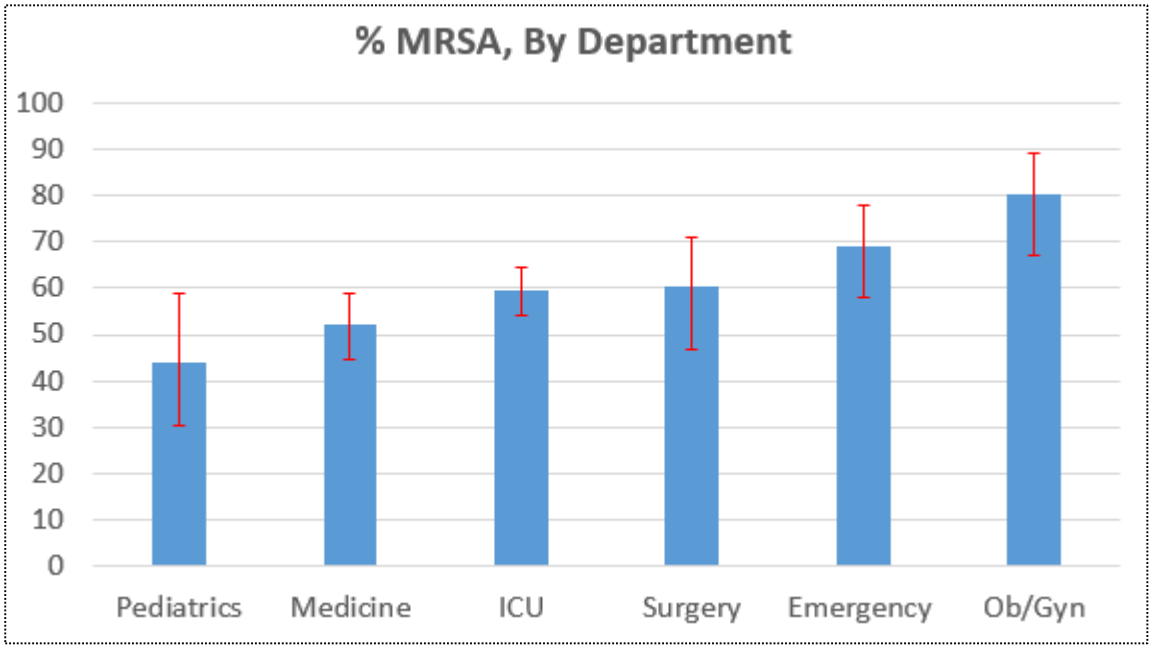


Figure 4.4.5.7 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Jordan, 2022 –By department



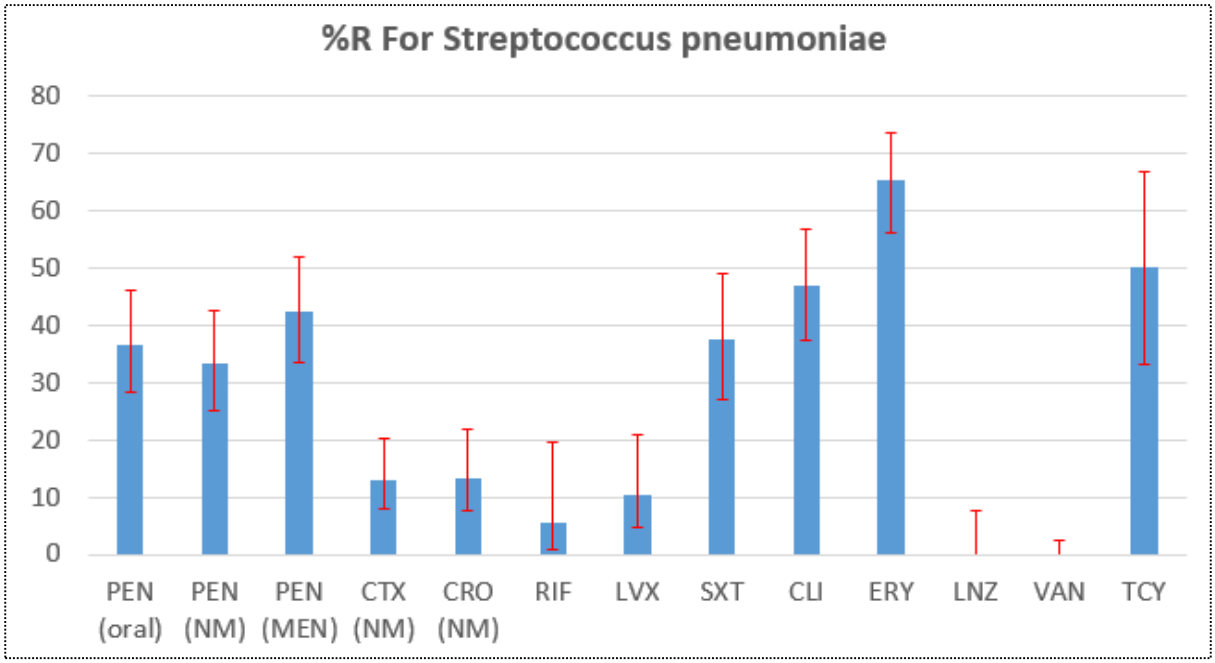
4.4.6 Streptococcus pneumoniae

Table 4.4.6.1 Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Streptococcus pneumoniae* (N=251)			
		Isolates (N)	% R	% I	% S
Penicillin G (oral breakpoints)	PEN (oral)	120	36.7	8.3	55.0
Penicillin G (non-meningitis breakpoints)	PEN (NM)	120	33.3	4.2	62.5
Penicillin G (meningitis breakpoints)	PEN (MEN)	120	42.5	2.5	55.0
Amoxicillin (non-meningitis breakpoints)	AMX (NM)	4	-	-	-
Cefuroxime (oral breakpoints)	CXM (oral)	12	-	-	-
Cefotaxime (non-meningitis breakpoints)	CTX (NM)	132	12.9	6.8	80.3
Ceftriaxone (non-meningitis breakpoints)	CRO (NM)	99	13.1	4.0	82.8
Rifampin	RIF	37	5.4	0.0	94.6
Levofloxacin	LVX	67	10.4	1.5	88.1
Moxifloxacin	MFX	25	-	-	-
Trimethoprim/Sulfamethoxazole	SXT	80	37.5	12.5	50.0
Clindamycin	CLI	109	46.8	0.9	52.3
Erythromycin	ERY	124	65.3	0.8	33.9
Linezolid	LNZ	58	0.0	0.0	100.0
Vancomycin	VAN	187	0.0	0.0	100
Quinupristin/Dalfopristin	QDA	1	-	-	-
Tetracycline	TCY	36	50.0	2.8	47.2

(-) =No data available, small number of isolates tested (N<30)

Figure 4.4.6.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Streptococcus pneumoniae,* isolates from all sources, Jordan, 2022



4.4.7 Enterococcus faecalis and Enterococcus faecium

Table 4.4.7.1 Percentages of resistant, intermediate, and susceptible isolates for *Enterococcus faecalis* and *Enterococcus faecium*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Enterococcus faecalis* (N=1271)				*Enterococcus faecium* (N=302)			
		N	% R	% I	% S	N	% R	% I	% S
Ampicillin	AMP	357	8.4	0.0	91.6	106	79.2	0.0	20.8
Gentamicin (high level)	GEH	195	37.9	0.0	62.1	70	62.9	0.0	37.1
Streptomycin (high level)	STH	18	-	-	-	6	-	-	-
Levofloxacin	LVX	349	41.8	2.9	55.3	93	82.8	6.5	10.8
Moxifloxacin	MFX	-	-	-	-	1	-	-	-
Linezolid	LNZ	372	1.9	0.0	98.1	112	1.8	0.9	97.3
Vancomycin	VAN	506	**6.9**[a]	0.2	92.9	136	**45.6**[a]	0.0	54.4
Teicoplanin	TEC	275	2.9	0.4	96.7	62	35.5	0.0	64.5
Tigecycline[b]	TGC	255	0.4	0.0	87.5	72	1.4	0.0	90.3
Multidrug-resistance (≥3)[c]	MDR	47	4.0	-	-	176	58.0	-	-
Extensive drug resistance	XDR	16	1.0	-	-	112	37.0	-	-
Pan-drug resistance	PDR	-	-	-	-	3	1.0	-	-

(-) =No data available, small number of isolates tested (N<30),

[a] %VRE for *Enterococcus* spp. = 15%.

[b] Tigecycline: EUCAST breakpoints (S≤0.25, R>0.25).

[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 4.4.7.1 Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Enterococcus faecalis* and *Enterococcus faecium*, isolates from all sources, Jordan, 2022

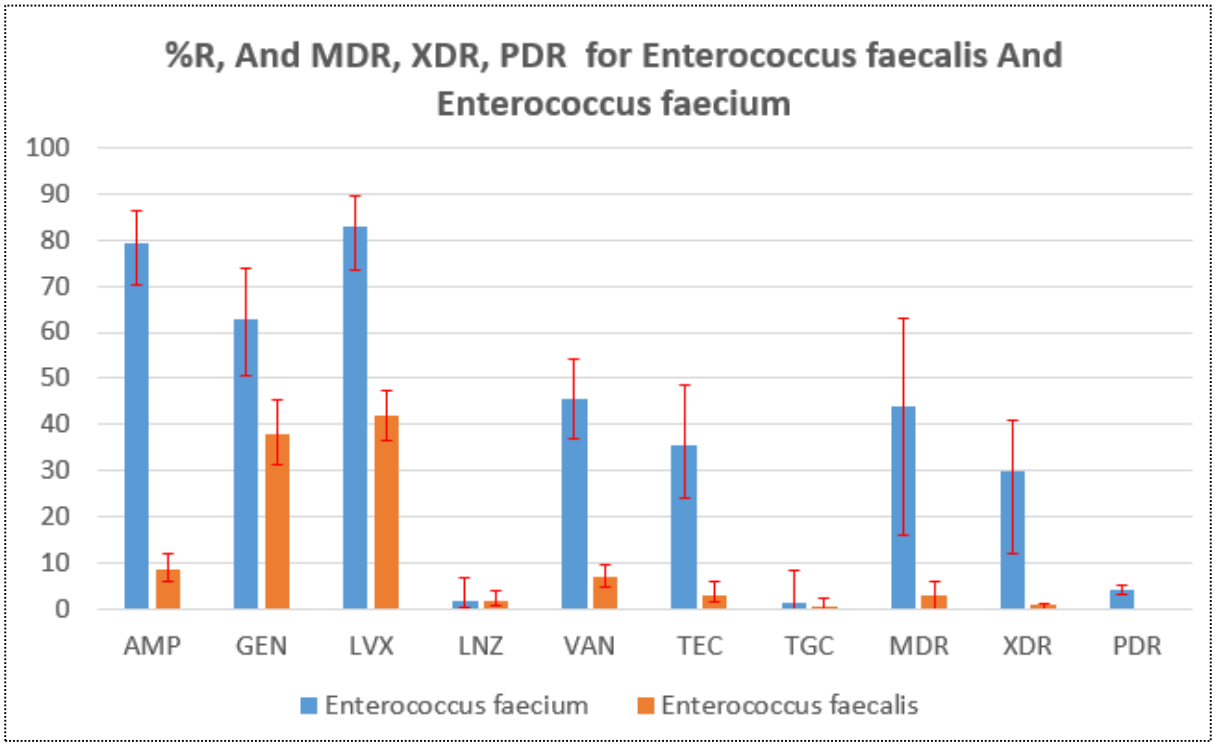
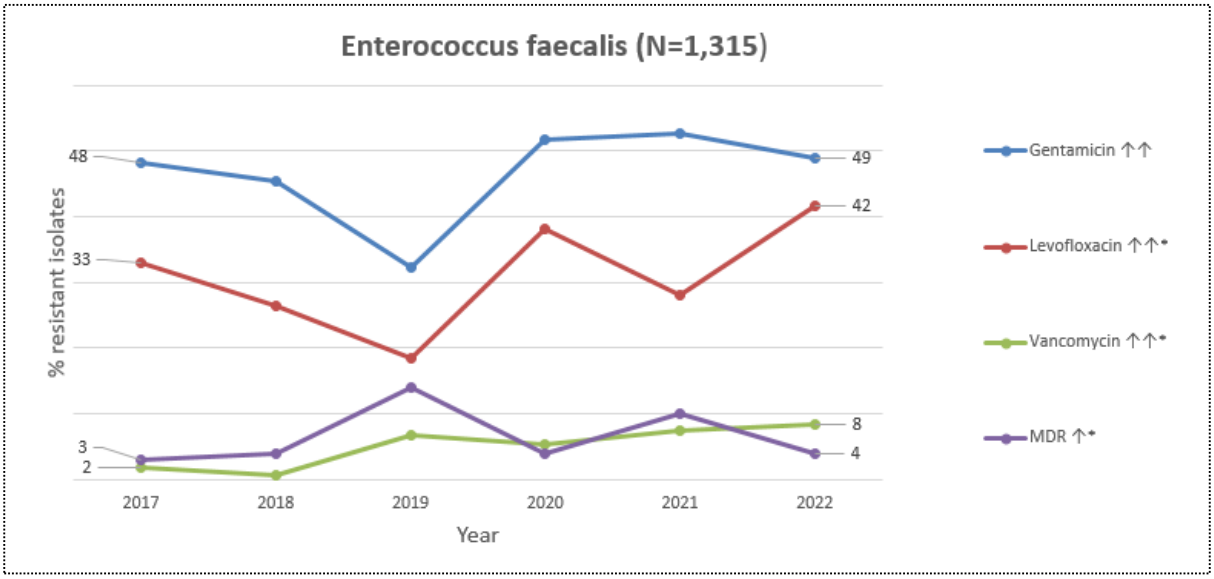


Figure 4.4.7.2 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecalis*, Jordan, 2010-2022



***Trend is statistically significant (p<0.001)**
Data source: HDA only (public and RMS sites).

4.4.8 Candida spp.

Table 4.4.8.1 Percentages of resistant, intermediate, and susceptible isolates for *Candida albicans*, isolates from all sources, Jordan, 2022

Antibiotic	Code	*Candida albicans* (N=538)			
		Isolates (N)	% R	% I	% S
Fluconazole	FLU	108	7.4	0.9	91.7
Voriconazole	VOR	104	1.9	1.9	96.2
Caspofungin	CAS	107	2.8	0.9	96.3
Micafungin	MIC	102	0.0	0.0	100.0
Amphotericin B	AMB	104	11.5	1.0	87.5

Figure 4.4.8.1 Percentages of resistant (%R) isolates for *Candida albicans*, isolates from all sources, Jordan, 2022

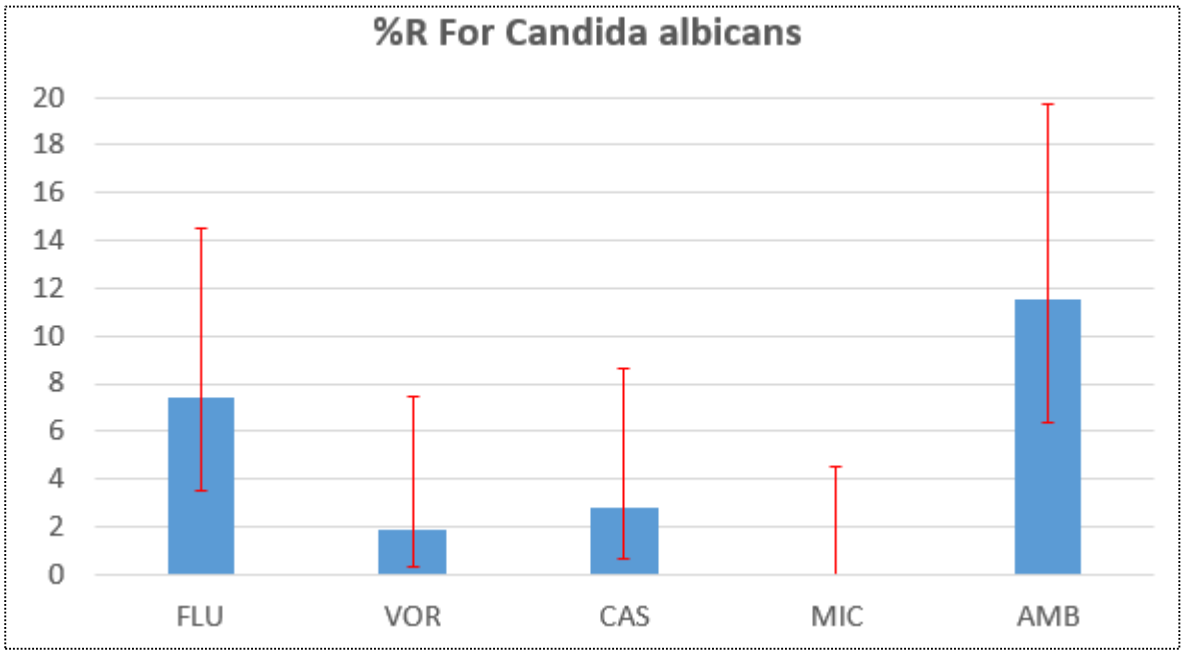
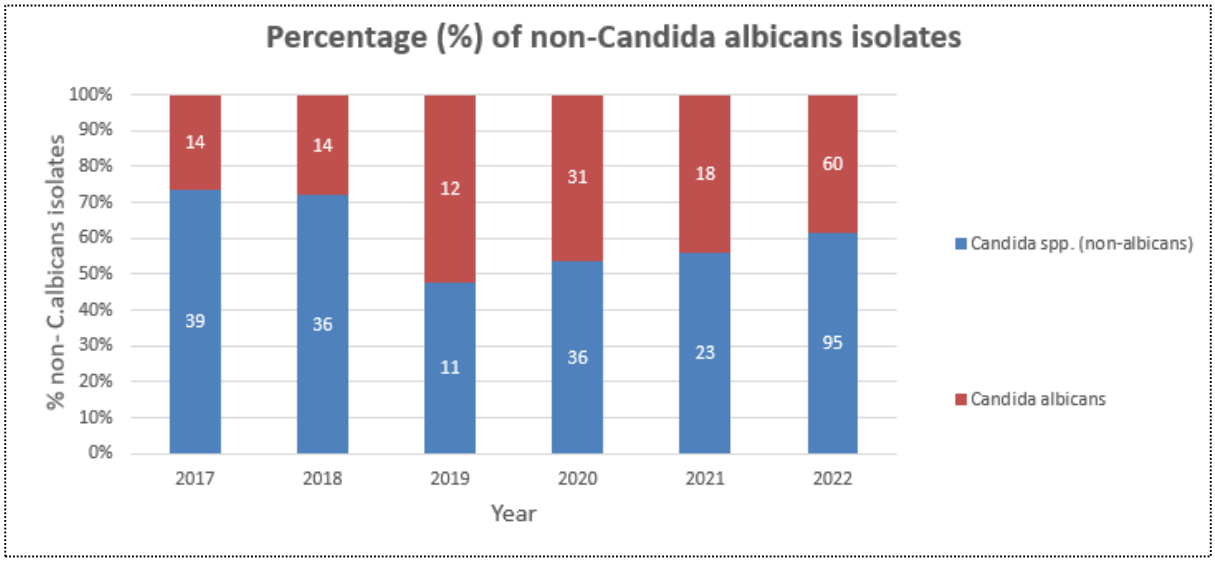


Table 4.4.8.2 Percentage of susceptible isolates for *Candida* spp., isolates from all sources, Jordan, 2022 (Cumulative antibiogram)

	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU[a]	VOR[b]	AMB[c]	CAS[d, e]	MIF[e]
Candida spp.	1038	100.0	91.2	82.5	59.4	85.4	97.9
Candida albicans	538	51.8	91.7	96.2	57.7	96.3	100
C. glabrata[f]	220	21.2	-[g]	13.2	13.2	34.2	92.1
C. tropicalis	131	12.6	88.2	87.9	66.7	100	100
C. parapsilosis	98	9.4	91.7	95.7	78.3	95.7	95.7
Candida krusei[i]	78	-	R	-	-	-	-
Other (C.non-albicans)	41	3.9	-	97.1	84.8	-	-
Candida guilliermondii[i]	22		-	-	-	-	-
C. dubliniensis	9	0.9	-	-	-	-	-
Candida lusitaniae[i]	7	-	-	-	-	-	-
Candida ciferrii[i]	5	-	100	-	-	-	-
C. haemulonii	1	0.1	-	-	-	-	-
Candida spp. (non-albicans)	0	-	-	-	-	-	-
C. auris[h]	0	-	-	-	-	-	-
C. duobushaemulonii	0	-	-	-	-	-	-
Candida famata[i]	0	-	-	-	-	-	-

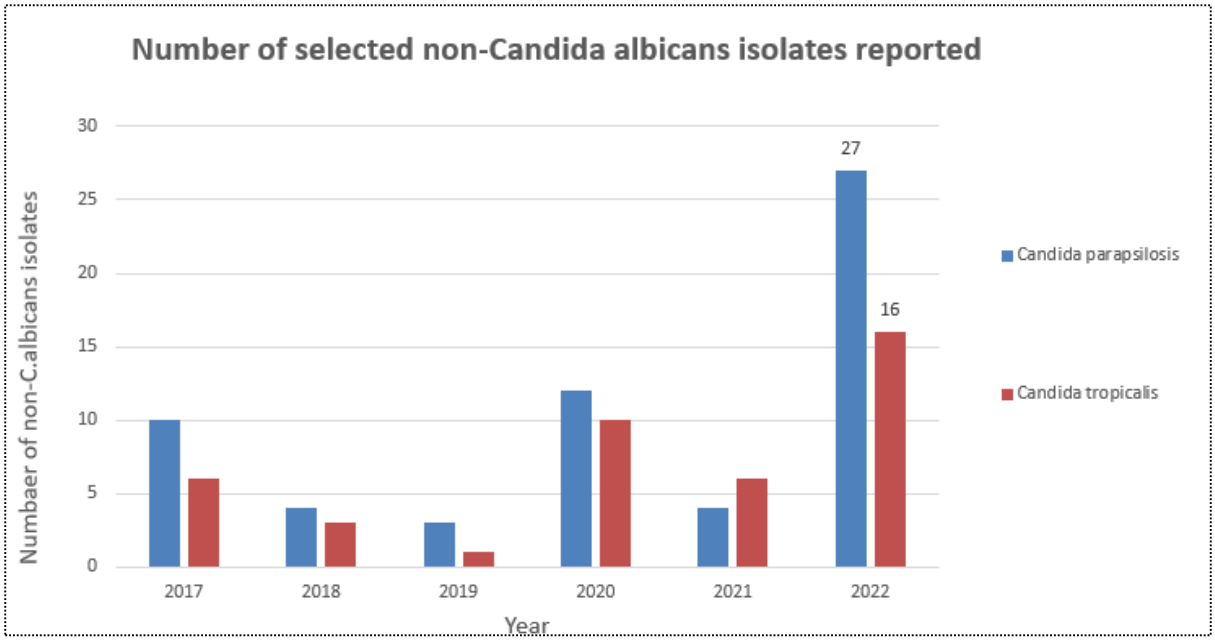
[a]FLU=Fluconazole [b]VOR=Voriconazole [c]AMB=Amphotericin B. EUCAST breakpoints (S≤1, R>1) are used for amphotericin B for *C. albicans, C. glabrata, C. krusei, C. parapsilosis*, and *C. tropicalis* (EUCAST, 2022). Note: some automated systems overcall amphotericin resistance for *Candida* species [d]CAS=Caspofungin.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

Figure 4.4.8.2 Annual trend for percentage of *Candida* (non-albicans) isolates, among all *Candida* isolates (*Candida* spp.), Jordan, 2017-2022



Data source: HDA only (public and RMS sites).

Figure 4.4.8.3 Annual trend for number of selected non-albicans *Candida* spp., Jordan, 2017-2022



Data source: HDA only (public and RMS sites).

5. Annex

Annex 5.1 AMR priority pathogens

The following text on pathogens under Jordan 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.

Jordan 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 Jordan 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.

Candida spp.

- Candida is a genus of yeasts and is the most common cause of fungal infections worldwide.
- It is the largest genus of medically important yeasts.
- The genus *Candida* encompasses about 200 species. Many species are harmless commensals or endosymbionts of hosts including humans; however, when mucosal barriers are disrupted or the immune system is compromised they can invade and cause disease, known as an opportunistic infection. *Candida* is located on most mucosal surfaces and mainly the gastrointestinal tract, along with the skin.
- *Candida albicans* is one of the most commonly isolated species and can cause infections (candidiasis or thrush) in humans and other animals. In winemaking, some species of *Candida* can potentially spoil wines.

- Many species are found in gut flora, including *C. albicans* in mammalian hosts, whereas others live as endosymbionts in insect hosts. Systemic infections of the bloodstream and major organs (candidemia or invasive candidiasis), particularly in patients with an impaired immune system (immunocompromised).
- The genome of several Candida species has been sequenced.
- *Candida auris* is an emerging fungus that presents a serious global health threat. It is often multidrug-resistant. It is difficult to identify with standard laboratory methods, It has caused outbreaks in healthcare settings.

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
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
CDC	Centers for Disease Control and Prevention
CLSI	Clinical and Laboratory Standards Institute
CPHL	Central Public Health Laboratory
CSF	Cerebrospinal fluid
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
EHS	Electronic Health Solutions
EMR	Electronic medical records
EUCAST	European Committee for Antimicrobial Susceptibility Testing
ESBL	Extended spectrum beta-lactamase
E. coli	*Escherichia coli*
E. faecalis	*Enterococcus faecalis*
E. faecium	*Enterococcus faecium*
EQAS	External quality assurance system
JARSS	Jordan Antimicrobial Resistance Surveillance System
GAS	Group A streptococci (*Streptococcus pyogenes*)
GBS	Group B streptococci (*Streptococcus agalactiae*)
GLASS	Global AMR Surveillance System (WHO)
HAI	Healthcare-associated infections
HIS	Hospital information system
HDA	Health Data Analytics program
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
MOH	Ministry of Health
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
NCC	National Coordinating Centre
NM	Non-meningitis
NRL	National Reference Lab
NS	Non-susceptible
P. aeruginosa	*Pseudomonas aeruginosa*
PHC	Primary Healthcare Center
PDR	Pandrug-resistant
R	Intrinsically resistant
RCPAQAP	Royal College of Pathologists of Australasia Quality Assurance Program
REQAS	Regional External Quality Assurance Services (Muscat)
Resp.	Respiratory
RMS	Royal Medical Services
S1	Susceptible 100%
S2	Susceptible 99%
S./Staph. aureus	*Staphylococcus aureus*
S. pneumoniae	*Streptococcus pneumoniae*
sp.. spp.	Species
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.	Hospital name	Governorate	Ownership
1	AL-Shuneh Hospital	South Jordan	MOH
2	Maan Hospital	Maan	MOH
3	Princess Raya Hospital	Irbid	MOH
4	Princess Salma Hospital	Madaba	MOH
5	Queen Rania Hospital	Maan	MOH
6	Jarash Hospital	Jarash	MOH
7	Dr. jamel Al-Totanji Hospital	Amman	MOH
8	AL-Ramtha Hospital	Irbid	MOH
9	Royal Rehabilitation Center (Farah)	Amman	RMS
10	AL-Nadeem Hospital	Madaba	MOH
11	AL-Zarqa Hospital	Zarqa	MOH
12	Al Hussain New Salt Hospital	Al-Salt	MOH
13	Prince Faisal Bin Al-Hussein	Zarqa	MOH
14	AL-Mafraq Hospital	AL-Mafraq	MOH
15	King Talal Hospital	Mafraq	RMS
16	Prince Hussein Hospital	AL-Balqaa	MOH
17	Al-Yarmouk Hospital	Irbid	MOH
18	Prince Hamzah Hospital	Amman	MOH
19	Al-Karak Hospital	AL-Karak	MOH
20	Prince Hashem Bin Abdulla II	Aqapa	RMS
21	Princess Haya Hospital	Ajloun	RMS
22	Prince Ali Bin Al-Hussein Hospital	Alkarak	RMS
23	Prince Hashem Bin Al-Hussein	Zarqa	RMS
24	Al-Basheer Hospital	Amman	MOH
25	Al Iman Hospital	Ajloun	MOS
26	Queen Alia Military Hospital	Amman	RMS
27	Oncology Center - Queen Alia Military hospital	Amman	RMS
28	Al-Mafraq Gynocology and Pediatrics	AL-Mafraq	MOH
29	Princess Rahma Hospital	Irbid	MOH
30	King Hussein Emergency Department	Amman	RMS
31	King Abdullah University Hospital	Irbid	MOH
32	Jordan university Hospital	Amman	MOH
33	Speciality hospital	Amman	Private
34	Amman surgical Hospital	Amman	Private
35	Istishari Hospital	Amman	Private
36	Prince Hussein Center for Urology and Organ Transplantation	Amman	RMS
37	Princess Badea'a Hospital	Irbid	MOH
38	Pricess Iman Research Center	Amman	RMS
39	Queen Alia Center for Heart Diseases	Amman	RMS
40	Queen Rania AlAbdullah Hospital for Children	Amman	RMS
41	Tafilah Govermental Hospital	Al Tafilah	MOH
42	King Hussein Hospital	Amman	RMS

Annex 5.6 Data fields collected for AMR Surveillance

Nr.	Data Field	Description	Format	Classification
1	PATIENT_ID	Patient ID (medical record number)	Required	TEXT
2	LAST_NAME	Patient last name	Desirable	TEXT
3	FIRST_NAME	Patient first name	Desirable	TEXT
4	Date of birth	Patient date of birth (DOB)	Required	DATE (dd/mm/yyyy)
5	Age	Patient age	Required	NUMERICAL
6	Sex	Patient gender	Optional	TEXT
7	NATIONALITY	Patient nationality	Desirable	TEXT
8	Date of admission	Date of patient admission	Required	DATE (dd/mm/yyyy)
9	DATE_DISCH	Date of discharge (for inpatients)	Desirable	DATE (dd/mm/yyyy)
10	Institution	Healthcare facility name	Required	TEXT
11	Governorate	Healthcare facility Governorate	Conditional	TEXT
12	DEPARTMENT	Department/specialty name	Required	TEXT
13	location	Patient location name	Required	TEXT
14	Location type	Patient location type	Desirable	TEXT
15	labaratory	Laboratory name	Required	TEXT
16	Specimen number	Specimen number	Required	TEXT
17	Specimen type	Specimen type	Required	TEXT
18	Specimen date	Specimen collection date	Required	DATE (dd/mm/yyyy)
19	Local specimen code	Specimen code	Required	TEXT
20	Organism	Name of identified organism	Required	TEXT
21	AST_RESULT_CAT	AST result (categorical/interpreted)	Required	TEXT
22	ANTIBIOTIC_NAME	Antimicrobial agent tested	Required	TEXT
23	Clinical outcome	Patient discharge status	Desirable	TEXT
24	Diagnosis	Diagnosis	Desirable	TEXT
25	Test date	Test date	Desirable	DATE (mm/dd/yyyy)

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