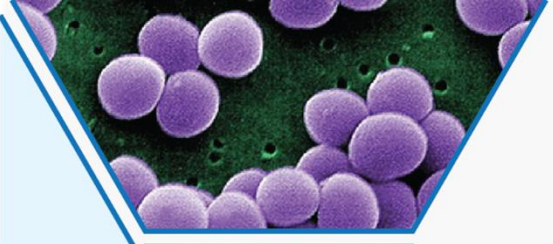

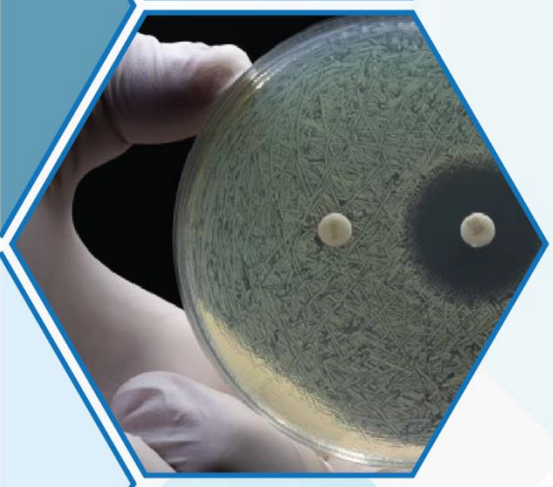

National AMR Surveillance Report

2024

Patient-based Surveillance of Antimicrobial Resistance in the Maldives

Ministry of Health
Republic of Maldives

World Health Organization
Maldives

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FOREWORD

Antimicrobial resistance (AMR) has become a major threat to public health worldwide, including the South-East Asian region, and the Maldives. AMR impacts on human health due to increased length of patient hospitalization, treatment failures, and significant human suffering and deaths, and is increasing healthcare costs, as well as indirect costs to the nation.

In 2024, the Maldives Ministry of Health, in collaboration with WHO and relevant stakeholders, developed the National AMR Surveillance Framework. Following the implementation of this framework, the national AMR surveillance program and network of laboratories was established, with the aim to collect, analyse, and report national data on the levels and trends of antimicrobial resistance in the human health sector.

This national effort aligns with the vision of H.E. President Dr. Mohamed Muizzu to strengthen national systems through evidence-based governance and to safeguard essential public services for future generations.

The national AMR surveillance laboratories network currently consists of twenty-seven (27) surveillance sites (hospitals, centers, clinics) and clinical microbiology laboratories, representing all administrative regions, atolls and inhabited islands of the Maldives. These laboratories and surveillance sites are key to generating, collecting, and reporting AMR surveillance data to the Ministry of Health, which is subsequently published to showcase the antimicrobial resistance in the country.

The Maldives have also since 2024 been contributing AMR data to the Global AMR Surveillance System (GLASS), which was established in 2015 by the World Health Organization (WHO-GLASS, 2025).

AMR surveillance data serves as local evidence and benchmark to assess the national epidemiology of antimicrobial resistance. Sharing this surveillance information enables an open dialogue about challenges and allows tracking progress and effectiveness of antimicrobial stewardship programs, and policies in place and action over time, as the surveillance system and antibiotic stewardship initiatives mature in the country.

In this regard, significant efforts have been made by the Ministry of Health with the collaborating surveillance sites and other local and international experts to strengthen the Maldives national AMR surveillance program, to increase awareness for AMR, and to enhance the technical capacities for AMR surveillance.

It remains our goal to monitor AMR levels and trends in the Maldives and to guide national AMR control policies through robust evidence, enabling effective implementation of the National AMR Action Plan and achievement of its targets.

I sincerely thank all partners and focal points across the participating surveillance sites and laboratories, the National AMR Coordination Committee, and the pool of experts for their continued efforts, support, and dedication to the Maldives National AMR Surveillance Network, and for their valuable contributions to this report.

Abdulla Nazim Ibrahim

Minister of Health

Malé, Maldives

Foreword by WHO Representative for Maldives

Antimicrobial resistance (AMR) remains one of the most significant and complex public health challenges of our time, threatening to undermine decades of progress in modern medicine. In the South-East Asia Region and specifically in the Maldives, the rise of multidrug-resistant organisms poses a direct threat to patient safety, healthcare outcomes, and the sustainability of our health systems.

The World Health Organization (WHO) is honoured to have served as a primary technical partner in this national effort. Our collaboration with the Ministry of Health and the Maldives Food and Drug Authority was central to providing the technical expert assistance required to develop the National AMR Surveillance Framework 2025-2027. Recognizing that a framework is only as strong as its implementation, WHO also led extensive training programs at multiple levels of the health system. These capacity-building initiatives have empowered laboratory and clinical staff to generate the high-quality data that forms the basis of this inaugural report.

This report marks a transformative milestone. With a network of 27 surveillance sites now established across all atolls and the successful submission of national data to the Global AMR Surveillance System (GLASS), the Maldives is demonstrating an unwavering commitment to evidence-based action. While the findings reveal high levels of resistance that mirror concerning global trends, they also provide a clear roadmap for targeted interventions.

Looking ahead, WHO remains a steadfast partner to the Maldives. We are committed to continuing our support to expand surveillance capabilities, moving beyond the laboratory level to encompass the entire health system. This will include a focus on antimicrobial consumption data—both at the national and facility levels—to ensure that surveillance information is integrated into a holistic approach for antimicrobial stewardship. By strengthening these systems today, we safeguard the effectiveness of our medicines for future generations.

I wish to commend the Ministry of Health, the National AMR Coordination Committee, and the dedicated healthcare professionals whose hard work and technical dedication have made this foundational report possible.

Ms Payden,
WHO Representative to Maldives

1. EXECUTIVE SUMMARY

The Maldives has established its first comprehensive national framework for the surveillance of antimicrobial resistance (AMR) in 2025 (MFDA, 2025), marking a major milestone in strengthening public health capacity and evidence-based decision-making. This inaugural National AMR Surveillance Report presents data from 56,005 patients and their diagnostic isolates, collected between 2016 and 2024 from 196 healthcare facilities and 27 clinical microbiology laboratories across all administrative regions, atolls, and inhabited islands. The breadth of participating sites - spanning primary care centers, regional hospitals, tertiary institutions, and both public and private laboratories - provides a robust and geographically representative picture of the AMR situation in the Maldives.

The report includes national cumulative antibiograms, multidrug-resistance (MDR/XDR/PDR) statistics, and detailed resistance trends for key AMR priority pathogens. Overall, the data reveal high, and in several cases increasing levels of antimicrobial resistance. In 2024, 32.5% of all isolates met the definition of multidrug resistance (MDR), while 8.8% and 2.4% were classified as possible extensive drug resistance (XDR) and possible pan-drug resistance (PDR), respectively. *Escherichia coli* and *Staphylococcus aureus* accounted for the largest absolute burden of MDR, with MDR rates of 40.4% and 38.4%. Particularly concerning are the extreme resistance patterns observed in *Acinetobacter* spp., with 30.6% possible XDR and 13.8% possible PDR, and in *Klebsiella pneumoniae*, with 15.2% possible XDR and 4.0% possible PDR. *Pseudomonas aeruginosa* also shows notable levels of extreme resistance, including 6.5% possible PDR.

Figures 1.1 and 1.2 provide an overview of current (2024) levels and trends of antimicrobial resistance for selected AMR priority pathogens and key antimicrobials used for treatment of human infectious diseases.

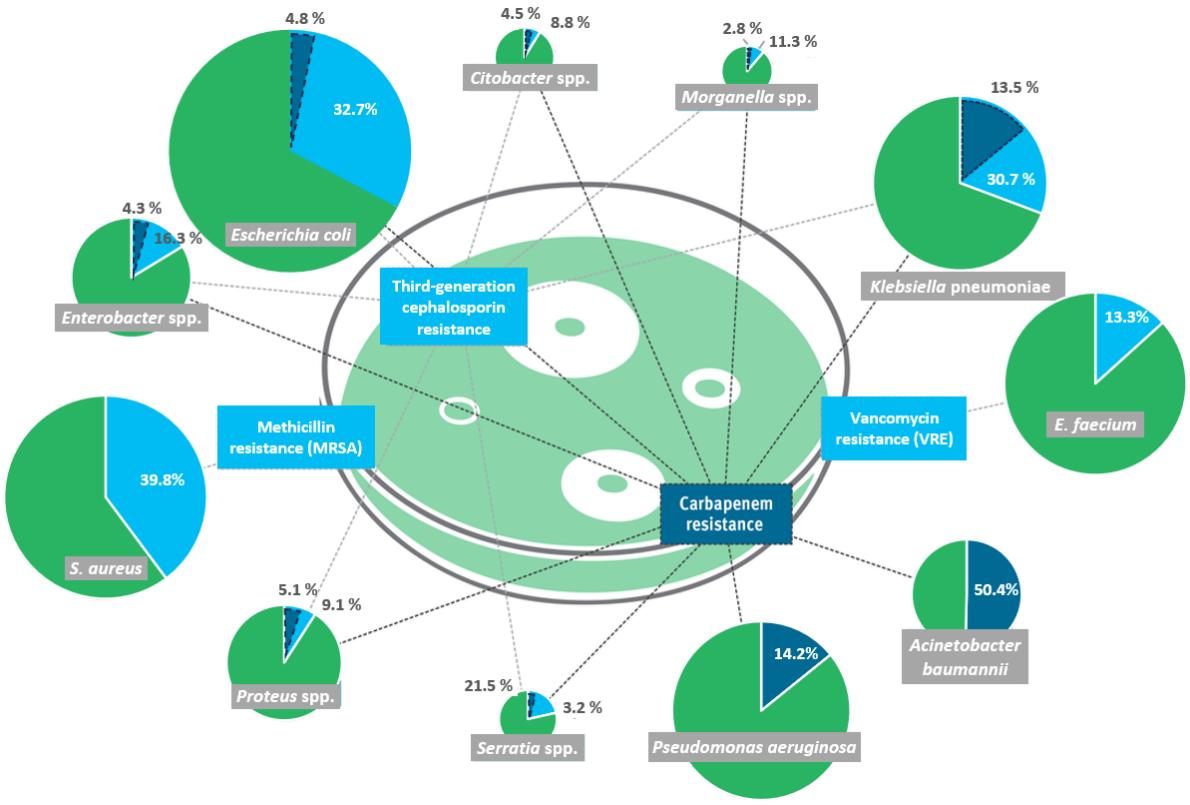


Figure 1.1. Percent of Isolates resistant (%R) to third-generation cephalosporins, carbapenems, methicillin, and vancomycin, Maldives, 2024

Resistance to third-generation cephalosporins, fluoroquinolones, and carbapenems among Enterobacterales is high, and has risen steadily since 2019, increasing reliance on last-line antibiotics and narrowing treatment options. Methicillin-resistant *Staphylococcus aureus* (MRSA) rates have also escalated, reaching nearly 40% in 2024. These trends mirror global and regional patterns and highlight the growing clinical and public-health burden posed by resistant pathogens.

The establishment of the national AMR surveillance system - aligned with WHO GLASS standards and supported by the Ministry of Health, Maldives Food and Drug Authority (MFDA) , Health Protection Agency (HPA), National Reference Laboratory for AMR (NRL-AMR), and international partners - provides the Maldives with a critical platform for monitoring resistance trends, guiding clinical treatment decisions, informing national policy, and evaluating the impact of stewardship and infection prevention and control (IPC) interventions. The system also strengthens the Maldives' contribution to global AMR monitoring efforts, with national data submitted to WHO GLASS for the first time in 2024.

This report represents a foundational milestone in building a sustainable, high-quality AMR surveillance system for the Maldives. Continued collaboration across the health sector, investment in laboratory capacity, and systematic data reporting will be essential to mitigate the growing threat of AMR.

The findings underscore the urgent need to strengthen antimicrobial stewardship, enhance IPC practices, and ensure the responsible use of antimicrobials to safeguard their effectiveness for future generations.

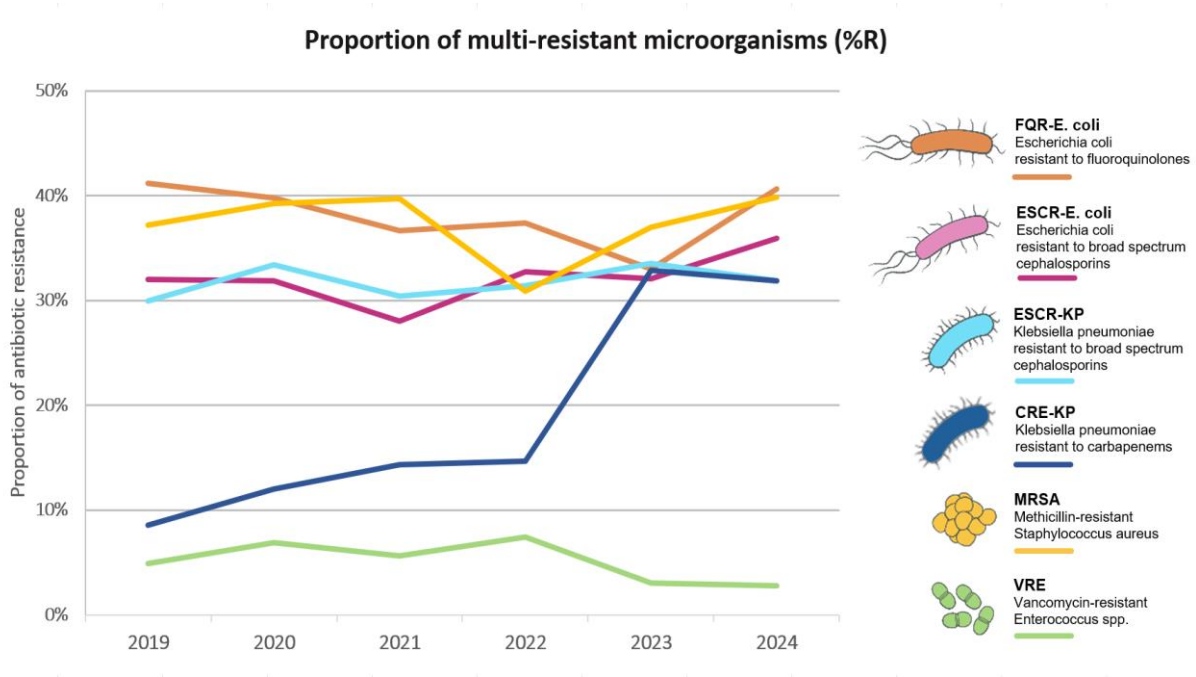


Figure 1.2. Antimicrobial resistance among major pathogens in human medicine: percentages of bacteria resistant to specific antibiotics, Maldives, 2019-2024

The Maldives has successfully established a foundational AMR surveillance system that provides critical insights into national resistance patterns. The findings reveal high, and in some cases increasing levels of AMR, consistent with regional and global trends.

Strengthening laboratory capacity, expanding surveillance coverage, standardizing testing practices, and enhancing stewardship and IPC programs will be essential to mitigate the growing threat of AMR and safeguard the effectiveness of antimicrobial therapy in the Maldives.

2. INTRODUCTION

2.1 Antimicrobial resistance

Antimicrobial resistance (AMR) is the ability of a microorganism to resist the action of one or more antimicrobial agents. AMR threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria, fungi, viruses, and parasites.

AMR occurs when bacteria, fungi, viruses, and parasites change over time and no longer respond to medicines, making infections harder to treat and increasing the risk of diseases spread, severe illness and death. AMR impacts on human health due to increased length of hospitalization, treatment failures, and significant human suffering and deaths, as well as leading to increased healthcare costs and indirect costs.

The consequences of AMR can be severe, as prompt treatment with effective antimicrobials is the most important intervention to reduce the risk of poor outcome of serious infections. In fact, AMR has become a major threat to public health worldwide, including South Asia, and the Maldives.

In 2021, an estimated 4.71 million deaths globally were associated with bacterial AMR, with an estimated 1.14 million deaths directly attributed to bacterial AMR. By 2050, global deaths associated with AMR are projected to increase to 8.22 million, including 1.91 million deaths directly attributed to AMR.

Moreover, it is estimated that by 2050 South-East Asia will have the highest all-age AMR mortality rate. The estimated number of deaths associated with AMR in this region was 1.26 million in 2021, including 335,000 deaths attributable to AMR. These numbers are expected to increase by 2050 to 2.4 million deaths associated with AMR, including 604,000 deaths attributable to AMR (GBD, 2024).

The major drivers behind the occurrence and spread of AMR are the overuse and misuse of antimicrobial agents in human health, as well as in animal health. Poor implementation of infection prevention and control strategies, and low vaccination rates, are further contributing to the spread of multidrug-resistant pathogens. The emergence and spread of AMR are driven by the overuse and misuse of antimicrobials in human and animal health, weak infection prevention and control practices, and low vaccination coverage. In the Maldivian context, geographical dispersion across islands and limited diagnostic capacity and access to medicines further contribute to the spread of multidrug-resistant pathogens.

2.2 Surveillance of antimicrobial resistance

Surveillance includes the continuous and systematic collection, analysis, and interpretation of health data, and the dissemination of such data to those who need to know, particularly to those who are in a position to take action (WHO-S, 2025).

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 AMR is an important cornerstone of the local and national response to AMR. AMR surveillance enables the concerned public health and health authorities to monitor, document and report on patterns, levels and trends of antibiotic resistance. AMR surveillance data is needed for the planning, implementation, and evaluation of AMR prevention and control strategies and activities.

Local and national AMR surveillance data serves as local evidence and benchmark data for the antimicrobial resistance situation in health facilities and 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.

Upon request of Member States, the World Health Organization has in 2015 established the Global AMR Surveillance System (GLASS). The Maldives have enrolled in the Global AMR Surveillance program (GLASS) in 2018 and are since 2024 submitting national AMR data to GLASS.

2.3 Maldives National AMR Surveillance Framework and System

In September 2025, the Ministry of Health published the Maldives National AMR Surveillance Framework 2025-2027, which outlines the strategic approach that the government is taking to establish patient-based surveillance of antimicrobial resistance in the Maldives (MFDA, 2025). The national AMR surveillance framework establishes the national AMR Surveillance program and describes the goals, objectives, methods, standards, as well as the roles and responsibilities of concerned stakeholders for national AMR surveillance and provides a roadmap for implementation.

The National AMR surveillance program allows, for the first time, the Maldivian government, national and local committees, healthcare and public health professionals, academia and researchers, international agencies, and other stakeholders, to:

- better understand the epidemiology of AMR in the Maldives
- generate local, regional, and national AMR data, and cumulative antibiograms
- analyse and predict patterns and trends of antimicrobial resistance
- detect and characterize newly emerging antimicrobial resistant organisms
- identify clusters and potential outbreaks of community- and healthcare-associated infections
- help to develop antimicrobial treatment guidelines for empiric treatment of common infections
- inform, guide, and monitor the effectiveness of antimicrobial stewardship programs, and
- contribute to the scientific body of literature on AMR in South Asia.

Key to the success of the national AMR surveillance program is the generation, collection, analysis and reporting of high-quality clinical AMR data by participating surveillance sites and laboratories, the National Reference Laboratory for AMR (NRL-AMR), and the central level unit at Maldives Food and Drug Authority (designated by MOH by as the national AMR secretariate). An overview of the AMR surveillance data flow is provided in **Figure 2.3.1**:

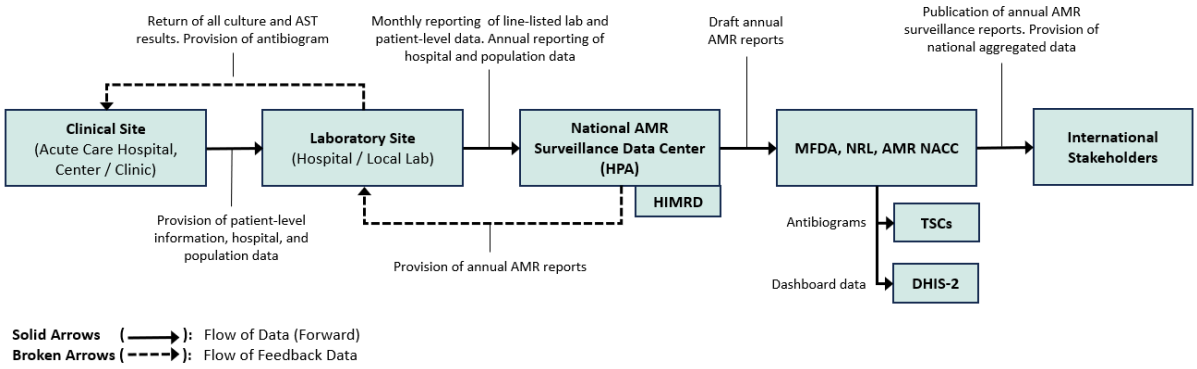


Figure 2.3.1. Diagram of antimicrobial resistance (AMR) surveillance data flow within the Maldives AMR Surveillance System

In 2025, a network of 27 hospitals and microbiology laboratories has been enrolled, geographically representative of all administrative regions, atolls and inhabited islands of the country, serving inpatient and outpatient healthcare facilities, from both the government and the private sector (**Table 2.3.1**). Surveillance sites and laboratories were identified and selected based on the following criteria:

- Demographic, socioeconomic and geographic representativeness
- Representation of different levels (primary, secondary, tertiary) and types (outpatient, inpatient, intensive care) of healthcare, including all clinical specialties
- Quality laboratory capacity for identification of relevant pathogens, antimicrobial susceptibility testing, and interpretation of results

- Ability to generate, manage, and report clinical and microbiological AMR surveillance data
- Support from facility staff and management to participate in AMR surveillance and to comply with applicable protocols
- Facility staff participated in technical training on AMR surveillance and data management.

The participating AMR surveillance sites and microbiology laboratories are key to generating and collecting AMR surveillance data and reporting it to the Maldives National AMR Program, and the AMR clinical and microbiology data collected from these surveillance sites and laboratories form the basis of this surveillance report.

Table 2.3.1. National AMR surveillance sites: hospitals and laboratories – by atoll and island

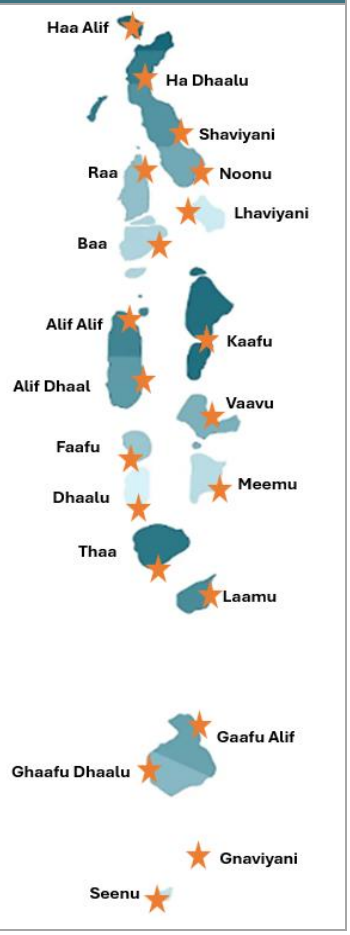
Nr.	Hospital / Laboratory Name	Atoll / Island	Location
1	Addu Equatorial Hospital	S. Hithadhoo	
2	Dr. Abdul Samadh Memorial Hospital	G.Dh. Thinadhoo	
3	Baa Atoll Hospital	B. Eydhafushi	
4	Faafu Atoll Hospital	F. Nilandhoo	
5	Fuvamulah Atoll Hospital	Gn. Fuvamulah	
6	Gaaf Alifu Atoll Hospital	GA. Villingili	
7	ADK Hospital	K. Malé	
8	Hulhumale Hospital	K. Hulhumalé	
9	IGMH/DH	K. Malé	
10	Medica Hospital	K. Malé	
11	Senahiya Military Hospital	K. Malé	
12	Treetop Hospital	K. Hulhumalé	
13	Gaamu Regional Hospital	L. Gan	
14	Haa Alif Atoll Hospital	H.A. Dhidhdhoo	
15	Kulhudhuffushi Regional Hospital	H.Dh. Kulhudhuffushi	
16	Meemu Regional Hospital	M. Muli	
17	Thaa Atoll Hospital	Th. Veymandoo	
18	Ungoofaaru Regional Hospital	R. Ungoofaaru	
19	Alif Alif Atoll Hospital	AA. Rasdhoo	
20	Alif Dhaal Atoll Hospital	A.Dh. Mahibadhoo	
21	Dhaal Atoll Hospital	Dh. Kudahuvadhoo	
22	Lhaviyani Atoll Hospital	Lh. Naifaru	
23	Medlab Diagnostics	K. Malé	
24	Mediflex Laboratories	K. Malé	
25	Noonu Atoll Hospital	N. Manadhoo	
26	Shaviyani Atoll Hospital	Sh. Funadhoo	
27	Vaavu Atoll Hospital	V. Felidhoo	

Table 2.3.2. National AMR surveillance sites and laboratories – by administrative region and ownership

Facility Type	North	North Central	Central	South-Central	South	Total
Surveillance sites						
Hospitals (public)	3	4	8	5	4	**24**
Hospitals (private)	-	-	3	-	-	**3**
Centers/Clinics (public)	38	41	33	37	20	**169**
Centers/Clinics (private)	-	-	-	-	-	**0**
Laboratories						
Laboratories (public)	3	4	6	5	4	**22**
Laboratories (private)	-	-	5	-	-	**5**

3. METHODS

Hospitals, centers, clinics and microbiology laboratories 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 subnational (island, atoll) and country level.

3.1. Data generation

Identification of organisms (ID):

Five out of 27 (18.5%) participating microbiology laboratories use at least one commercial, automated system for identification of bacteria and/or yeast, including MALDI-ToF (n=1), VITEK® 2 (n=4), and Autobio AutoMic-i600 (n=1), the remaining 22 laboratories (81.5%) rely on manual systems only for identification of organisms (e.g., biochemical tests). Unusual test results are usually confirmed locally. Forwarding isolates to the NRL-AMRS for ID confirmation and further characterisation (e.g. typing/subtyping, toxin-production) is currently not done on a routine basis but planned to be established.

Antimicrobial susceptibility testing (AST):

Five out of 27 (18.5%) microbiology laboratories use at least one commercial, automated system for routine antimicrobial susceptibility testing, including Vitek® 2 (n=4), and AutoMic-i600 (n=1), the remaining 22 laboratories use manual testing methods as a primary method (disc diffusion/Kirby Bauer). All laboratories follow the Clinical and Laboratory Standards Institute (CLSI) guidelines for antimicrobial susceptibility testing of bacteria and fungi (CLSI, 2025). Unusual antibiotic susceptibility testing results are usually confirmed locally. Forwarding isolates with suspected important antimicrobial resistance (e.g. carbapenemase-producing organisms) to the NRL-AMRS is currently not done on a routine basis but planned to be established.

Interpretation of susceptibility testing results:

For interpretation of susceptibility testing results for fungi and yeast, all participating laboratories routinely apply the CLSI guidelines. If CLSI has not set breakpoints for certain pathogen-antimicrobial combinations, then other guidelines are applied, including the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines (EUCAST, 2025), for tigecycline and amphotericin B, and the Center for Disease Control and Prevention (CDC) tentative guidelines (CDC C. auris, 2024), for *Candida auris*.

Quality control:

All participating microbiology laboratories are:

- operated by an MoH-licensed healthcare provider
- headed by a licensed clinical microbiologist or clinical pathologist
- must comply with the National Standard for Clinical Laboratories (MoH-Lab, 2022)
- Two laboratories (2/27; 7.4%) are routinely participating in external quality assurance (EQAS) programs (IGMH: EQuAsia-Chulalongkorn University Veterinary School (CUVET), Treetop Hospital: MHL EQAS (MI001).

Currently, none of the participating microbiology laboratories is laboratory-accredited, however this is planned.

3.2 Data collection

AMR surveillance data files are collected at the surveillance site/laboratory by trained healthcare professionals on a monthly, quarterly or annual basis. AMR surveillance raw data files are either extracted from HIS/LIS systems or from ID/AST machines in the microbiology laboratory. Alternatively, some surveillance sites are entering the AMR raw data manually into either the WHONET (WHONET, 2025) database software, or into a Microsoft Excel spreadsheet.

AMR surveillance data collected includes microbiology laboratory data (including specimen type, specimen collection date, organism name, antibiotics tested, AST test method, AST test result). Where available, the measured AST result (MIC or disk diffusion diameter) is collected and used for interpretation and analysis (n=5/19 laboratories, 26.3%), otherwise the locally interpreted AST categorical result (S/I/R) is collected (n=14/19 laboratories, 73.7%).

Clinical and demographic data was available for 15 out of 19 laboratories (79.0%) in 2024. This includes information on e.g., patient date of birth, age, gender, nationality, patient location (clinic/ward), location type, clinical specialty/department, date of admission/discharge, and health outcome.

AMR data for trends over time is available for the period 2016 to 2024 for the following healthcare facilities only: IGMH/DH, ADK, TTH.

Data submission:

For the reporting period 2024, eighteen surveillance sites/laboratories (18/27; 66.7%) submitted AMR surveillance data to the central level at AMR Surveillance Data Center at Health Protection Agency (HPA).

Data cleaning:

After submission of AMR data to the national AMR Surveillance Unit at MoH/MFDA, 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 the central level, any remaining identifiable quality control 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[1]). Finally, all WHONET AMR data files are added to the national AMR surveillance database.

Details on the number of isolates reported, selected for analysis, exclusion criteria, and analysis reports available are presented in **Figure 3.2.1**:

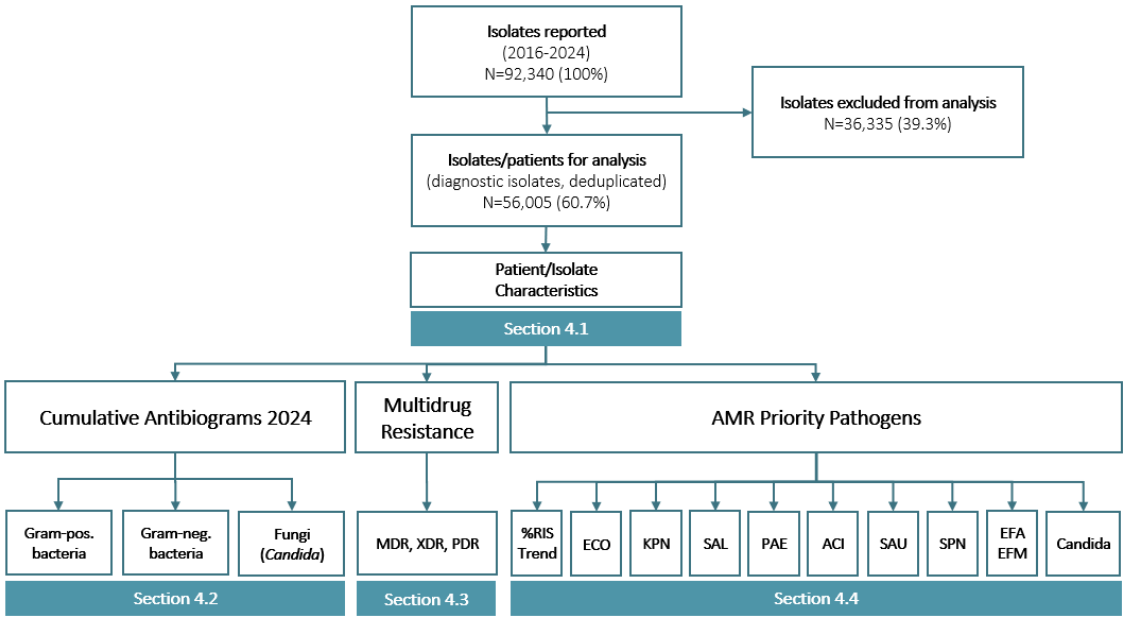


Figure 3.2.1. Number of isolates reported and selected for analysis, exclusion criteria, and analysis reports available.

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

3.3 Data analysis

Data analysis was mainly conducted with the WHONET microbiology laboratory database software (WHONET, 2025).

Exclusion criteria:

The following data was excluded from analysis, if technically feasible:

- Internal quality control isolates (e.g., weekly ATCC QC strains)
- External quality control isolates (EQAS, i.e., CAP-Pt, ACP-MLE, RCPA, REQAS)
- Isolates labelled as 'screening', 'validation', 'verification', 'proficiency testing', or similar
- Suspected screening isolates (e.g., *S. aureus* isolates from axilla, nose, and groin).
- Duplicate isolates (copy strains), i.e., only the first isolate per patient, specimen type and species during the reporting period (one year) was included
- Isolates from primarily contaminated specimen types (e.g., pedibag)
- Other non-diagnostic isolates (e.g., from environmental sampling, infection control)
- Species for which less than 10 isolates are available for analysis
- Antimicrobial agents that are selectively/not routinely tested (i.e., less than 70% of isolates were tested)

De-duplication:

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

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

The percentage resistant, intermediate, and susceptible (%RIS) isolates were either interpreted at the national AMR Surveillance Center, or, if this was technically not feasible, obtained from laboratories in form of already locally interpreted (S/I/R) results. Percent RIS interpretations were based on the CLSI interpretation standard CLSI M100 (ED35:2025) for bacterial isolates and CLSI interpretation standard M60-Ed2:2020 for yeast. For amphotericin B (AMB) and tigecycline, EUCAST v15.0:2025 was used (EUCAST, 2025). For *Candida auris*, tentative breakpoints from U.S. CDC were used (CDC C. auris, 2024).

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), cefoxitin (FOX), methicillin (MET), and/or flucloxacillin (FLC).
- **VRE** was defined as Enterococci (*E. faecalis*, *E. faecium*), resistant to vancomycin (VAN).
- **CRE** was defined as Enterobacterales, non-susceptible to carbapenems (imipenem, meropenem, and/or ertapenem).
- **FQR-E. coli** was defined as fluoroquinolone-resistant *Escherichia coli* (norfloxacin and/or ciprofloxacin)
- **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 laboratory. 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 laboratories* 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 laboratories* in all antimicrobial categories (i.e. no agents tested as susceptible for that organism).

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

Statistical considerations:

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

- IBM SPSS Statistics, version 31, or CDC Epi Info™ for Windows v7.2, for statistical significance of proportion trends over time,
- Online calculation tool, for calculation of Wilson confidence intervals (95% C.I.) (AUSVET, 2018).

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

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

Confidence intervals: For %RIS analyses, a 95% confidence interval is determined for the percentage of resistance (%R) and percentage of susceptibility (%S), based on the Wilson Score Interval with or without continuity correction method for calculating confidence intervals for a sample proportion (normal approximation to a binomial distribution) (Agresti & Coull, 1998). Confidence interval calculations were obtained either from WHONET (which uses the Wilson Score Interval with continuity correction method), or calculated using an online calculator tool, using the Wilson Score Interval (without continuity correction) method. Error bars in graphs represent the upper limit of the 95% confidence interval

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4. RESULTS

4.1 Patient/Isolate Characteristics

A total of n=92'340 isolates were reported for the reporting period 2016 to 2024:

- For the reporting period 2016 to 2022 (7 years), n=50'389 isolates were reported from ADK, IGMH and Treetop Hospital.
- For the reporting period 2023 to 2024, these sites plus an additional 15 surveillance sites reported data (n=41'951).

After removal of non-diagnostic (e.g., screening, quality control), and duplicate isolates, a total of n=56'005 (60.7 %) non-duplicate isolates/patients remained for analysis. A breakdown of the number of reported non-duplicate isolates/patients by year is shown in **Figure 4.1.1.**

For the reporting period 2024 (one year), a total of n=21'158 isolates were reported by 18 surveillance sites/labs, located on 30 islands of 13 atolls. After removal of non-diagnostic and duplicate isolates, a total of n=15'380 (72.7 %) non-duplicate isolates/patients remained for analysis.

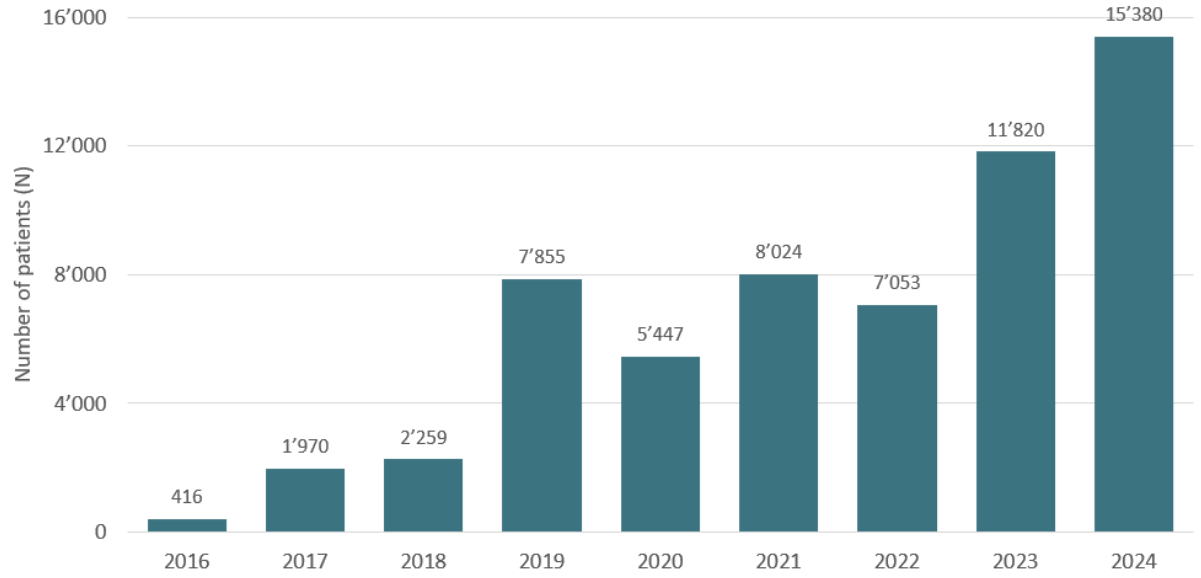


Figure 4.1.1. Distribution of isolates/patients, Maldives, 2016-2024, by year (n=56'005)

Distribution of isolates/patients by atoll, island and facility:

The bulk of the AMR surveillance data received was from the capital city of the country located in Kaafu Atoll, where four major hospitals operate. From the rest of the country, Haa Dhaalu atoll contributed the most, and seven atolls did not yet submit any AMR surveillance data (**Table 4.1.1**).

Most of the isolates were received from Male' with a total of 11'148 (52.7%) followed by Hulhumale' with 6,793 (32.1%) isolates. Both Male' and Hulhumale are part of the capital city of Greater Male Region with several major hospitals and clinics contributing to the large number of isolates. Within the islands in the atolls, Kulhudhuffushi submitted data for 1'029 (4.9%) isolates, while the submissions from other islands remained below 400 isolates (see **Table 4.1.2 in Annex 7.5**).

From the 18 surveillance sites reporting data for 2024, IGMH/DH reported the largest number of isolates (n=7'869), followed by Treetop Hospital and Hulhumale Hospital. Within the islands, Kulhudhuffushi regional hospital reported the highest number of isolates (n=1'178) (**Table 4.1.2, Table 4.1.3**).

Atoll	Isolates (N)	Isolates (%)	Patients (N)	Patients (N)
Kaafu	17'941	84.8	12'750	
Haa Dhaalu	1'178	5.6	989	
Seenu	399	1.9	314	
Gaafu Dhaalu	360	1.7	295	
Raa	314	1.5	196	
Gnaviyani	258	1.2	212	
Laamu	190	0.9	161	
Baa	141	0.7	141	
Haa Alif	120	0.6	92	
Thaa	118	0.6	106	
Gaafu Alif	65	0.3	51	
Faafu	58	0.3	58	
Meemu	16	0.1	15	
Shaviyani	0	0	0	
Noonu	0	0.0	0	
Lhaviyani	0	0.0	0	
Alif Alif	0	0.0	0	
Alif Dhaal	0	0.0	0	
Vaavu	0	0.0	0	
Dhaalu	0	0.0	0	
Total	**21'158**	**100**	**15'380**	

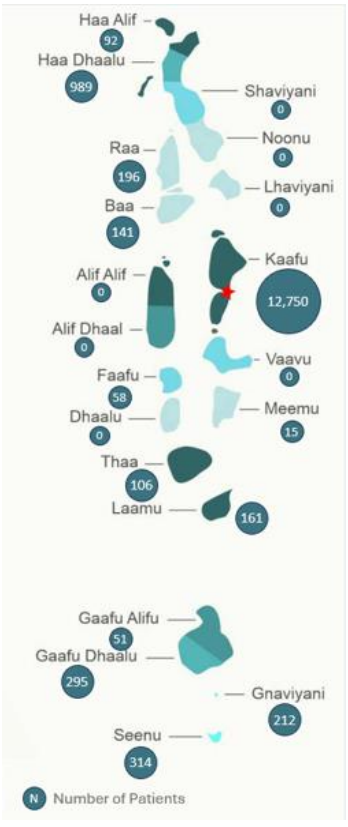


Table 4.1.1. Distribution of isolates/patients, Maldives, 2024, by atoll

Distribution of isolates/patients by age, gender and nationality:

For patients reported for the year 2024, gender and age were known for 55.4% of isolates/patients. For those patients with known gender, the majority were females (71.7%), predominantly of younger age (25 to 44 years). For males, the largest number of isolates were from either very young patients (age < 1 year) or from elderly patients (age 65+ years) (**Figure 4.1.2**).

Nationality was known for 18.9 % of isolates/patients only. For those with known nationality, the vast majority were Maldivians (98.5%), followed by Indians (0.5%) and Bangladeshi (0.3%). See also **Table 4.1.4** in **Annex 7.6** for more details on nationality.

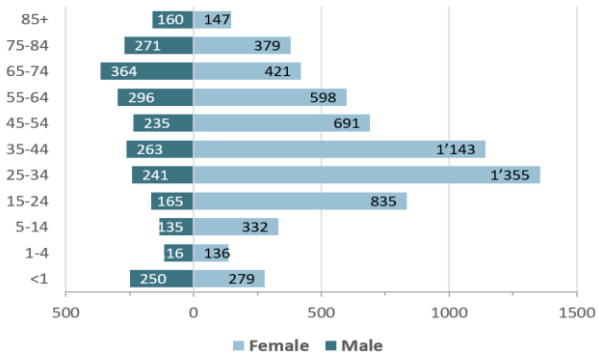


Figure 4.1.2. Distribution of patients, Maldives, 2024, by age and gender

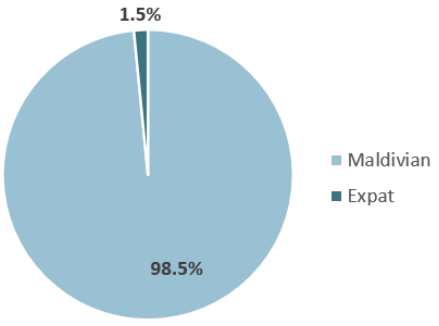


Figure 4.1.3. Distribution of patients, Maldives, 2024, by nationality group (%)

Table 4.1.3. Distribution of isolates/patients, Maldives, 2024, by facility

Facility	Isolates (N)	Isolates (%)	Patients (N)	Isolates per patient
IGMH/DH	7'869	37.2	4'781	1.6
Treetop Hospital	4'160	19.7	2'805	1.5
Hulhumalé Hospital	2'633	12.4	2'585	1.0
ADK Hospital	1'804	8.5	1'221	1.5
Kulhudhuffushi Regional Hospital	1'178	5.6	989	1.2
Senahiya Military Hospital	914	4.3	847	1.1
Medica	561	2.7	511	1.1
Addu Equatorial Hospital	399	1.9	314	1.3
Dr. Abdul Samad Memorial Hospital	360	1.7	295	1.2
Ungoofaaru Regional Hospital	314	1.5	196	1.6
Fuvamulah Hospital	258	1.2	212	1.2
Laamu Gamu Regional Hospital	190	0.9	161	1.2
Baa Atoll Hospital	141	0.7	141	1.0
Ha Alif Atoll Hospital	120	0.6	92	1.3
Thaa Atoll Hospital	118	0.6	106	1.1
G.A. Atoll Hospital	65	0.3	51	1.3
Faafu Atoll Hospital	58	0.3	58	1.0
Meemu Regional Hospital	16	0.1	15	1.1
Total	**21'158**	**100.0**	**15'380**	**1.4**

Table 4.1.4. Distribution of patients, Maldives, 2024, by department/specialty

By Department/Specialty	Isolates (N)	Isolates (%)	Patients (N)
Outpatient	8'919	42.2	7'098
Mix	3'141	14.8	2'553
Emergency	374	1.8	300
Medicine	710	3.4	294
Surgery	478	2.3	269
ICU	321	1.5	124
Paediatrics	155	0.7	118
Other hospital	144	0.7	87
Haematology & Oncology	57	0.3	24
Obstetrics & Gynaecology	20	0.1	20
Neonatal ICU	23	0.1	18
Critical Care Unit	10	0.0	6
Unknown	6'806	32.2	5'111
Total	**14'352**	**100**	**10'911**

Figure 4.1.5. Distribution of patients, Maldives, 2024, by patient location type

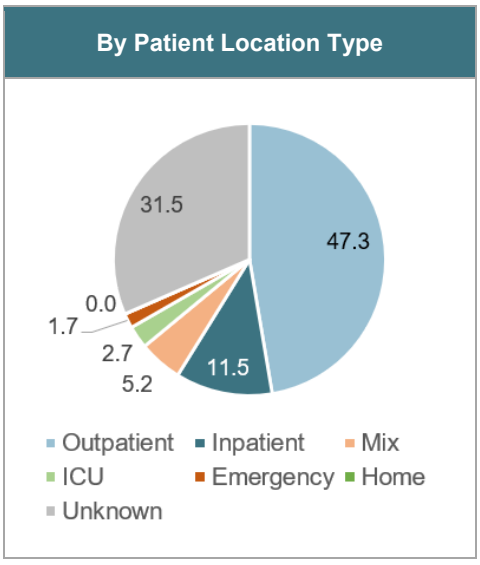
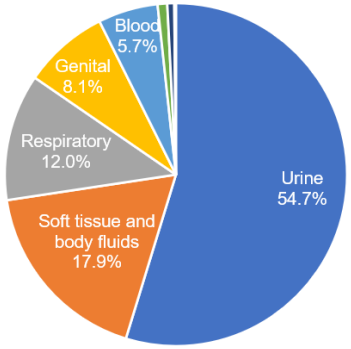


Table 4.1.7. Distribution of isolates/patients, Maldives, 2024, by specimen type

Specimen type	Isolates (N)	Isolates (%)	Patients (N)	Isolates (%)
Urine	11’579	54.7	9’231	
Soft tissue and body fluids	3’785	17.9	2’861	
Respiratory	2’529	12.0	2’181	
Genital	1’705	8.1	1’505	
Blood	1’197	5.7	816	
Stool	192	0.9	177	
Unknown	139	0.7	98	
Other	32	0.2	30	
Total	21’158	100	16’899	



Distribution of isolates/patients by organism:

For 2024, most frequently reported pathogens were *E. coli* (n=5’575; 26.3 %), followed by *K. pneumoniae* (n=3’363; 15.9 %), *P. aeruginosa* (n=1,414; 6.7 %), and *S. aureus* (n=1’387; 6.6 %) (**Figure 4.1.6.**). See **Figure 4.1.7** in **Appendix 5.7** for a more detailed breakdown of reported organisms by genus and species.

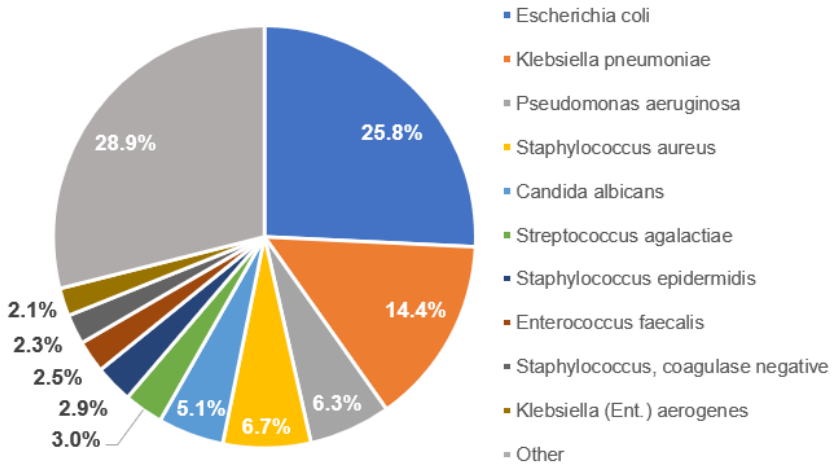


Figure 4.1.6. Distribution of isolates, Maldives, 2024, by organism, Top 10

4.2 Cumulative Antibiograms

4.2.1 Maldives National Cumulative Antibiogram

Table 4.2.1.1. National Cumulative Antibiogram (2024): Percent susceptible isolates (%S, %SDD[&]) – Gramnegative bacteria (isolates from all sources)

Gramnegative Bacteria	Isolates	Penicillins				β-Lactams Cephalosporins				Carbapenems			Aminoglycosides			FQ	Other		
	N	AMP	AMC	TZP	CZO	CXM[a]	CRO	CAZ	FEP	IPM	MEM	ETP	AMK	GEN	TOB	CIP	ATM	SXT	NIT[b]
Gramnegative bacteria (all)	11'692	32	68	87	-	67/60	70	-	77	82	87	93	87	86	78	68	76	77	69
Haemophilus influenzae	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Moraxella catarrhalis	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Enterobacterales	9'272	32	70	89	67	67/61	71	-	77	85	89	93	88	87	78	66	81	77	71
Citrobacter spp.	302	R	76	95	-	-/62	88	-	95	96	96	97	92	97	57	92	75	95	82
Enterobacter spp. (other)	354	R	R	88	R	49/64	82	-	91	93	95	93	90	92	80	83	94	90	42
Klebsiella aerogenes[c]	386	R	R	92	R	R	86	-	96	94	95	95	94	95	-	90	94	94	18
Escherichia coli[d]	4'646	42	76	93	71	49/56	65	-	77	96	96	98	90	88	76	55	77	71	94
Klebsiella pneumoniae	2'607	R	74	83	75	66/68	72	-	72	76	78	85	86	84	77	71	87	79	34
Klebsiella oxytoca	47	R	85	94	-	69/71*	88	-	77*	91*	95*	88*	83	94	-	86	-	86	-
Morganella morganii	139	R	R	100	R	R	85	-	100*	0*	97	94	99	98	-	86	95*	93	R
Proteus mirabilis	283	75	75	99	-	83/86	92	-	100	26	95	82	93	92	-	85	100*	80	R
Proteus vulgaris	55	R	53*	100	R	R	82*	-	93*	-	-	-	84*	91*	-	91	-	83*	R
Providencia spp.	16*	R	R	81*	R	-	-	-	-	-	-	-	69*	70*	-	81*	-	81*	R
Salmonella spp. (non-typhoid)	95	69*	-	-	-	-	92	-	-	-	-	-	-	-	-	61	-	95	-
Salmonella Typhi/Paratyphi	11*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	18*	-	100*	-
Serratia marcescens	176	R	R	-	R	R	78	-	96	94	97	90	96	85	-	83	-	99	R
Shigella spp.	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Non-ferm. gramnegative rods	1'503	R	R	83	-	-	-	82	82	81	85	R	85	87	89	80	63	58	-
Acinetobacter baumannii	209	R	R	57	-	R	-	56	54	48	50	R	62	58	-	53	R	79	-
Pseudomonas aeruginosa	1'125	R	R	85	-	R	R	83	84	83	87	R	87	94	89	83	71	R	R
Stenotrophomonas maltophilia[f]	54	R	R	R	-	-	R	-	-	R	R	R	R	R	R	-	R	76	-

[&]The percent susceptible (%S) and percent susceptible dose dependant (%SDD) 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).

[*]A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution.

[a]Cefuroxime: oral/parenteral breakpoints. [b]NIT: Nitrofurantoin data from urine isolates only. [c]*Klebsiella aerogenes*: formerly *known as Enterobacter aerogenes.* [d]*E. coli* (urinary tract isolates): FOS 99 %S. [f]*S. maltophilia*: LVX 88 %S, MNO 79 %S.

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

%S=Percent of isolates susceptible, FQ=Fluoroquinolones, N=Number, R=intrinsically resistant, spp.=species, (–) =No data available, small number of isolates tested (N<30), antimicrobial agent is not indicated, or not effective clinically. Interpretation standard: CLSI M100 ED35:2025. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2025.

Data source: Maldives National Antimicrobial Resistance Surveillance System. Data shown is from 18 surveillance sites from public and private sector (Maldives), including 13 Atolls and 30 islands. Version 1.0 (15 December 2025).

Table 4.2.1.2. National Cumulative Antibiogram (2024): Percent susceptible isolates (%S, %SDD[&]) – Grampositive bacteria (isolates from all sources)

Grampositive Bacteria	Isolates	β-Lactams							MLS		AG	Fluoroquinolones			Glycopept.		Other				
	N	PEN	AMP	OXA	FOX	AMC	CRO	CTX	ERY	CLI	GEN	CIP	LVX	NOR	VAN	TEC	SXT	NIT[a]	LNZ	TCY	RIF
Grampositive bacteria (all)	4'644	40	69	46	-	84	83	81	38	68	77	68	70	69	98	93	78	76	98	-	-
Staphylococcus aureus	1'208	23	-	63	62	62[b]	-	-	60	84	84	59	56	65	100	100	83	84	99	92	98
MSSA[c]	880	35	-	100	100	100	-	-	64	89	88	67	67	63	100	100	86	83	100	94	100
MRSA[d]	363	-	-	0	0	0	-	-	50	76	75	45	36	-	100	100	77	85	96	89	95
Coagulase-neg. staphylococci	2'033	17	-	36	41	41[b]	-	-	31	60	78	71	71	72	99	91	80	90	97	77	92
Staphylococcus epidermidis	520	17	-	37	46	46[b]	-	-	32	60	66	66	68	-	99	81	74	85	100	75	92
Staphylococcus saprophyticus[g]	356	9	-	32	38	38[b]	-	-	21	60	95	93	93	-	99	96	91	91	96	87	99
Staphylococcus haemolyticus	314	14	-	24	28	28[b]	-	-	21	55	73	54	56	-	99	98	71	99	98	66	94
Staphylococcus lugdunensis	58	27	-	52	54	54[b]	-	-	83	88	93	93	93	-	100	98	98	100*	100	71	98
***Enterococcus* spp.**	611	82	75	-	-	-	R	R	-	R	R	66	67	70	96	96	R	89	97	-	-
Enterococcus faecalis	427	94	90*	-	-	-	R	R	-	R	R	69	72	-	99	99	R	97	98	-	-
Enterococcus faecium	48	9	-	-	-	-	R	R	-	R	R	6	7	-	84	87	R	23	81*	-	-
***Streptococcus* spp.**	729	93	89	-	-	-	96	93	49	66	-	-	90	-	98	-	-	-	99	47	-
Streptococcus pneumoniae	22*	41[e]	-	-	-	-	94[f]	94[f]	30	65	-	-	95	-	100	-	50	-	100	50	100
Streptococcus pyogenes (GAS)	52	100	100	-	-	-	98	100	51	53	-	-	85	-	100	-	-	100	100	58	-
Streptococcus agalactiae (GBS)[g]	378	100	100	-	-	-	98	95	59	73	-	-	92	-	98	-	-	-	99	41	-
Streptococcus (viridans group)	25*	52*	64*	-	-	-	88*	88*	39*	71*	-	-	76*	-	92*	-	-	-	88*	64*	-

[&]The percent susceptible (%S) and percent susceptible dose dependant (%SDD) 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).

*A small number of isolates were tested (N<30), and the percentage susceptible should be interpreted with caution.

[a]NIT: Nitrofurantoin data from urine isolates only. [b]inferred from Cefoxitin. [c]MSSA=Oxacillin-susceptible *S. aureus*. [d]MRSA=Oxacillin-resistant *S. aureus*. [e]Data shown is based on breakpoints for oral penicillin (penicillin V). Penicillin G (parenteral): 100 %S. [f]Data shown for CRO and CTX is based on non-meningitis breakpoints. [g]excludes isolates from vagina.

AMP=Ampicillin, **AMC**=Amoxicillin/Clavulanic acid, **CLI**=Clindamycin, **CIP**=Ciprofloxacin, **CRO**=Ceftriaxone, **CTX**=Cefotaxime, **ERY**=Erythromycin, **FOX**=Cefoxitin, **GEN**=Gentamicin, **LNZ**=Linezolid, **LVX**=Levofloxacin, **NIT**=Nitrofurantoin, **NOR**=Norfloxacin, **OXA**=Oxacillin, **PEN**=Penicillin G, **QDA**=Quinupristin/Dalfopristin, **RIF**=Rifampin, **SXT**=Trimethoprim/Sulfamethoxazole, **TEC**=Teicoplanin, **TCY**=Tetracycline, **VAN**=Vancomycin.

%S=Percent of isolates susceptible, AG=Aminoglycosides, GAS=Group A streptococci, GBS=Group B streptococci, Glycopept.=Glycopeptides, MLS=Macrolides, Lincosamides, and Streptogramins, N=Number, R=intrinsically resistant, spp.=species, (-) =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 ED35:2025. Presentation standard: CLSI M39-A5:2022. Data analysis: WHONET 2025.

Data source: Maldives National Antimicrobial Resistance Surveillance System. Data shown is from 18 surveillance sites from public and private sector (Maldives), including 13 Atolls and 30 islands. Version 1.0 (15 December 2025).

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 in **Table 4.3.1.1** and **Figure 4.3.1.1**.

The antimicrobial resistance profile from 10,128 isolates in the Maldives shows a considerable burden of multidrug-resistant (MDR) organisms, with 32.5% of all isolates classified as MDR. *Escherichia coli*, the most frequently isolated organism, contributes the largest number of MDR cases (1,838), representing 40.4% of its isolates. *Staphylococcus aureus* also shows a high MDR proportion at 38.4%, while *Acinetobacter* spp. demonstrates a similarly elevated MDR rate of 35.1%. *Klebsiella pneumoniae* presents a moderate MDR burden at 27.3%.

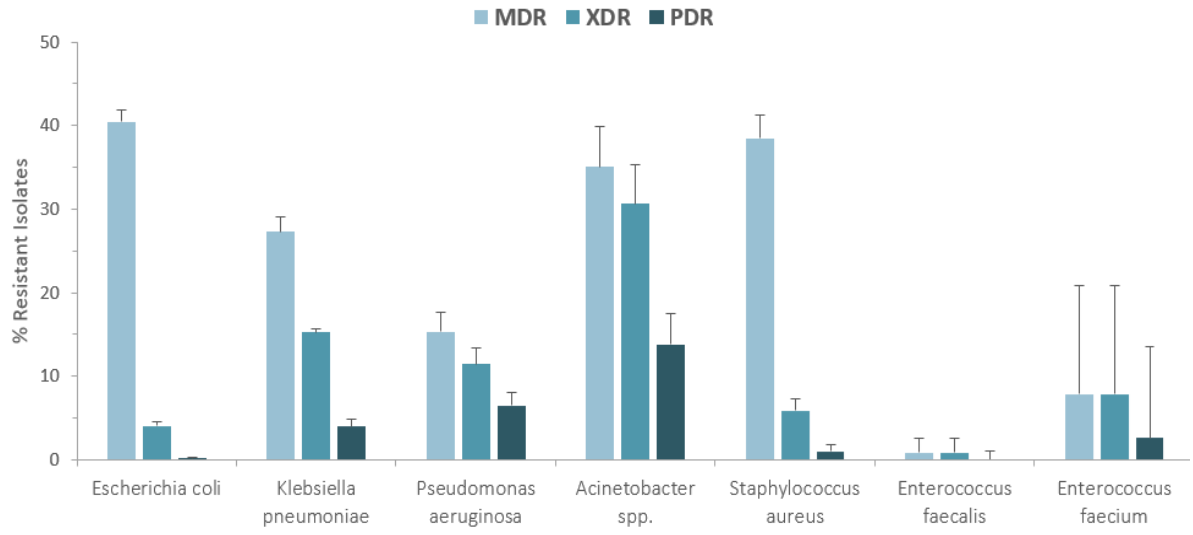
Possible XDR and PDR patterns, although less common overall, highlight critical resistance threats. Across all organisms, 8.8% of isolates meet possible XDR criteria and 2.4% meet possible PDR criteria. *Acinetobacter* spp. stands out with particularly severe resistance levels (30.6% XDR; 13.8% PDR) underscoring its role as a high-risk pathogen in the Maldives. *K. pneumoniae* also shows concerning rates, with 15.2% XDR and 4.0% PDR. *Pseudomonas aeruginosa* exhibits notable extreme resistance as well (11.4% XDR; 6.5% PDR).

Table 4.3.1.1. MDR, XDR, PDR Summary, Maldives, 2024

Organism	Isolates (N)	MDR	Possible XDR	Possible PDR
Escherichia coli	4’547	1’838 (40.4 %)	183 (4.0 %)	6 (0.1 %)
Klebsiella pneumoniae	2’575	702 (27.3 %)	392 (15.2 %)	103 (4.0 %)
Pseudomonas aeruginosa	1’096	168 (15.3 %)	125 (11.4 %)	71 (6.5 %)
Acinetobacter spp.	405	142 (35.1 %)	124 (30.6 %)	56 (13.8 %)
Staphylococcus aureus	1’129	434 (38.4 %)	66 (5.8 %)	11 (1.0 %)
Enterococcus faecalis	338	3 (0.9 %)	3 (0.9 %)	0 (0 %)
Enterococcus faecium	38	3 (7.9 %)	3 (7.9 %)	1 (2.6 %)
Total	**10’128**	**3’290 (32.5 %)**	**896 (8.8 %)**	**248 (2.4 %)**

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

Figure 4.3.1.1. MDR, XDR, PDR Summary, Maldives, 2024



4.4 AMR Priority Pathogens

4.4.1 Summary (%RIS and annual trends)

Table 4.4.1.1. Antimicrobial resistance (AMR) among AMR priority pathogens, Percentage resistant isolates (%R), Maldives, 2024

Group[a]	Pathogen	Antibiotic or antibiotic class	Isolates (N)	Percent resistant isolates (%R)
Critical group	*Acinetobacter baumannii*	Carbapenem-resistant (imipenem)	139	**50.4**
	Enterobacterales	3rd-generation cephalosporin-resistant	7'258	**27.9**
	Enterobacterales	Carbapenem-resistant	2'165	**13.5**
High group	*Salmonella* Typhi/Paratyphi	Fluoroquinolone-resistant (ciprofloxacin)	11	**54.5**
	Shigella spp.	Fluoroquinolone-resistant (ciprofloxacin)	3	-
	Enterococcus faecium	Vancomycin-resistant (VRE)	45	**13.3**
	Pseudomonas aeruginosa	Carbapenem-resistant (imipenem)	761	**14.2**
	Non-typhoidal *Salmonella*	Fluoroquinolone-resistant (ciprofloxacin)	94	**12.8**
	Neisseria gonorrhoeae	3rd-generation cephalosporin-resistant	0	-
	Neisseria gonorrhoeae	Fluoroquinolon-resistant (ciprofloxacin9	0	-
	Staphylococcus aureus	Methicillin-resistant (MRSA)	960	**36.0**
Medium group	Group A Streptococci	Macrolide-resistant (erythromycin)	49	**46.9**
	Streptococcus pneumoniae	Macrolide-resistant (erythromycin)	20	**70.0**
	Haemophilus influenzae	Ampicillin-resistant	1	-
	Group B streptococci	Penicillin-resistant	510	**0.0**
Fungi	*Candida albicans*	Fluconazole-resistant	765	**2.5**

[a]Based on WHO Bacterial Priority Pathogen list (WHO, 2024).

Annual Trends of Resistance: Table 4.4.1.2 and **Table 4.4.1.3** present AMR data on annual trends of resistance (%R) for gram-negative and gram-positive bacteria for the reporting period 2016 to 2024.

Table 4.4.1.2. Antimicrobial resistance trends, Maldives, 2016-2024 – Gram-negative bacteria

Antibiotic class/substance	*Escherichia coli*	*Klebsiella pneumoniae*	*Salmonella* spp. (non-typhoid)	*Pseudomonas aeruginosa*	*Acinetobacter* spp.
Ampicillin	↓	n/a	↑	R	R
Amoxicillin/Clavulanic acid	↓	↑	→ (< 1%R)	R	R
Piperacillin/Tazobactam	→	↑	→ (< 1%R)	→	↓
3rd-/4th-gen. Cephalosporins	↑	↑	↑	→	↓
Carbapenems	↑	↑	→	↑	↑
Fluoroquinolones	↑	↑	↑	↓	↑
Aminoglycosides	↓	↑	→	→	↑
Trimethoprim/Sulfamethoxazole	→	↑	↓	R	↑

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

Table 4.4.1.3. Antimicrobial resistance trends, Maldives, 2016-2024 – Gram-positive bacteria

Antibiotic class/substance	*Staphylococcus aureus*	*Streptococcus pneumoniae*	*Enterococcus faecalis*	*Enterococcus faecium*
Beta-lactam antibiotics	↑	No data	↓	→ (> 90 %R)
Macrolides	↓	No data	R	R
Lincosamides	↓	No data	R	R
Aminoglycosides	↑	No data	R*	R*
Fluoroquinolones	↑	No data	↓	
Glycopeptides	→ (0 %R)	No data	→ (0 %R)	↑
Trimethoprim/Sulfamethoxazole	↓	No data	R	R

↓/↑/→: decreasing/increasing/horizontal trend of percentage resistant isolates (%R), R: intrinsically resistant. R*: Enterococci are resistant to aminoglycosides when used in monotherapy. However, synergy with beta-lactams or glycopeptides is still likely if the isolate does not express an acquired aminoglycoside-modifying enzyme.

4.4.2 Escherichia coli

Table 4.4.2.1. Percentages of resistant, intermediate, and susceptible isolates for *Escherichia coli*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*Escherichia coli* (n=4'646)			
		Isolates (N)	%R	%I	%S[a]
Ampicillin	AMP	3'032	56.4	1.8	41.8
Amoxicillin/Clavulanic acid	AMC	3'766	15.9	8.2	75.9
Piperacillin/Tazobactam	TZP	3'710	7.1	0.2	92.7
Cefazolin	CZO	88	27.3	2.3	70.5
Cefuroxime (oral)	CXM	791	42.4	8.5	49.2
Ceftriaxone	CRO	3'691	34.1	0.8	65.2
Cefotaxime	CTX	790	19.4	4.1	76.6
Ceftazidime	CAZ	2'422	17.1	3.6	79.4
Cefepime	FEP	1'234	21.7	1.7	76.5
Ertapenem	ETP	2'071	2.1	0.3	97.6
Imipenem	IPM	933	3.5	0.6	95.8
Meropenem	MEM	1'106	3.2	0.8	96.0
Amikacin	AMK	3'939	5.6	4.4	90.0
Gentamicin	GEN	3'992	10.5	1.6	87.8
Ciprofloxacin	CIP	4'327	35.7	9.2	55.0
Norfloxacin	NOR	3'120	30.0	1.6	68.5
Trimethoprim/Sulfamethoxazole	SXT	4'068	28.3	0.3	71.3
Fosfomycin[b]	FOS	2'764	1.3	0.1	98.6
Nitrofurantoin[b]	NIT	3'187	2.8	3.1	94.1
Tigecycline[c]	TGC	746	0	0	100
Multidrug-resistance (≥3 classes NS)[d]	MDR	4'547	40.4	–	–
Extensive drug resistance (possible)	XDR	4'547	4.0	–	–
Pan-drug resistance (possible)	PDR	4'547	0.1	–	–

[a] %S includes %SDD (susceptible, dose-dependent).
[b] Fosfomycin and Nitrofurantoin: Isolates from urinary tract only.
[c] Tigecycline: FDA breakpoints (S≤2, R≥8)
[d] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

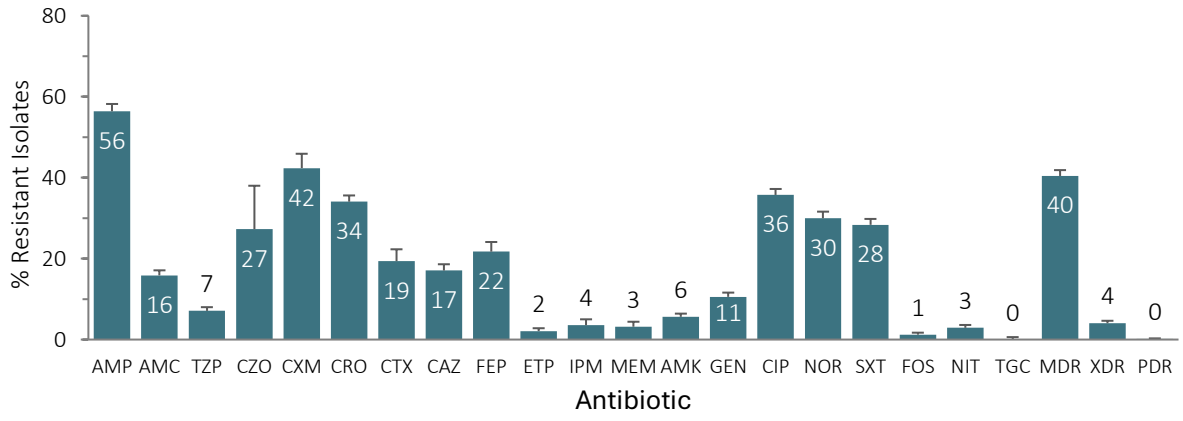
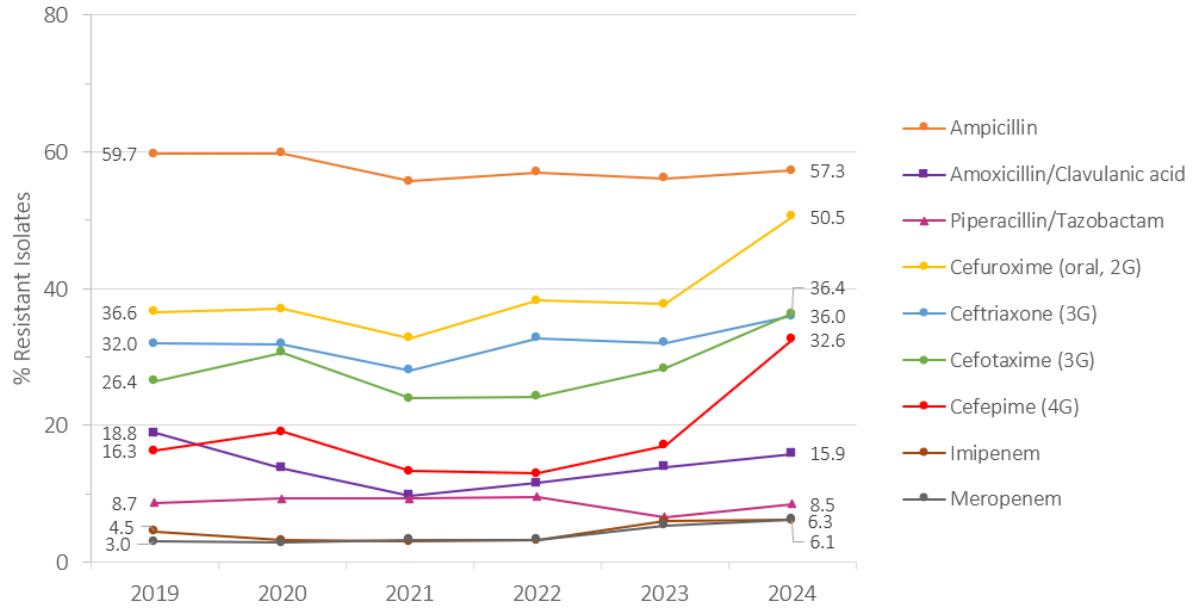


Figure 4.4.2.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Escherichia coli*, isolates from all sources, Maldives, 2024 (n=4'646)

For 2024, antibiotic resistance rates (%R) for *E. coli* ranged from 0 % for tigecycline, to 56 % for aminopenicillins (ampicillin).

Prevalence of multidrug resistance (%MDR, possible XDR, possible PDR) in *E. coli* was 40.4 %, 4.0 %, and 0.1 %, respectively.

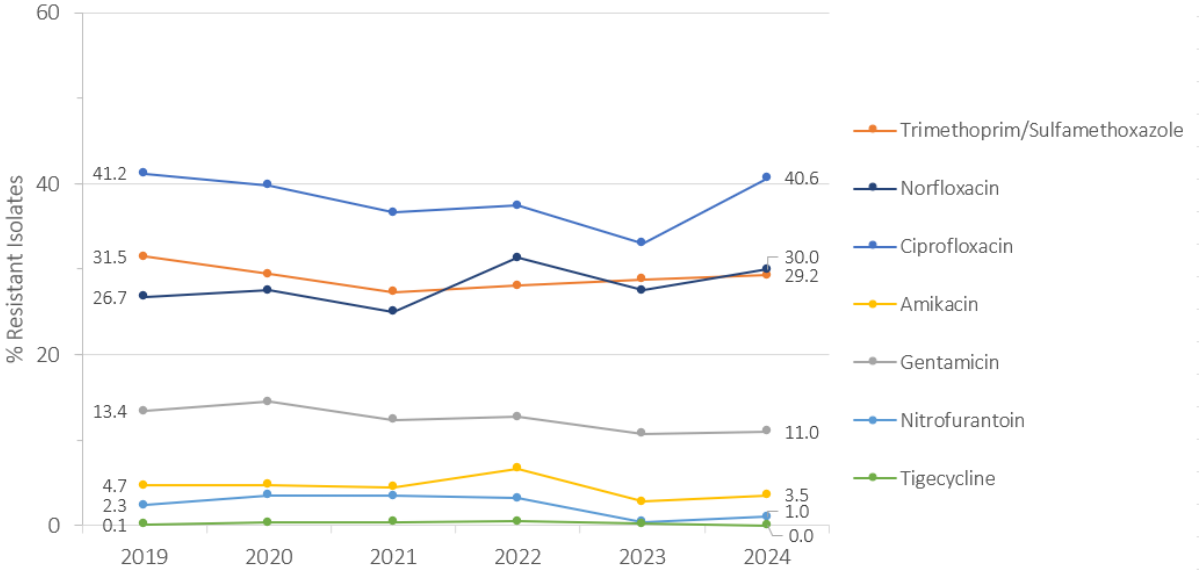
Figure 4.4.2.2 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, Maldives, 2019-2024, beta-lactam antibiotics



Escherichia coli shows increasing trends of resistance (%R) for

- 2nd- to 4th-generation cephalosporins (cefuroxime, cefotaxime, ceftriaxone, cefepime), and
- carbapenems (imipenem, meropenem).

Figure 4.4.2.3 Annual trends for percentage of isolates resistant (%R) for *Escherichia coli*, Maldives, 2019-2024, other antibiotics



Escherichia coli shows decreasing or horizontal trends of resistance (%R) for

- trimethoprim/sulfamethoxazole,
- fluoroquinolones (nalidixic acid, ciprofloxacin, levofloxacin and ofloxacin; but not norfloxacin)
- aminoglycosides (amikacin, gentamicin), and
- nitrofurantoin, and
- tigecycline.

4.4.3 Klebsiella pneumoniae

Table 4.4.3.1. Percentages of resistant, intermediate, and susceptible isolates for *Klebsiella pneumoniae*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*Klebsiella pneumoniae* (n=2'607)			
		Isolates (N)	%R	%I	%S[a]
Amoxicillin/Clavulanic acid	AMC	1'992	18.4	7.6	73.9
Piperacillin/Tazobactam	TZP	2'429	16.7	0.4	82.9
Cefazolin	CZO	98	24.5	1.0	74.5
Cefuroxime (oral)	CXM	965	32.6	1.9	65.5
Ceftriaxone	CRO	2'023	27.9	0.3	71.7
Cefotaxime	CTX	442	9.0	3.6	87.3
Ceftazidime	CAZ	956	30.2	5.3	64.4
Cefepime	FEP	1'230	26.8	0.8	72.3
Ertapenem	ETP	1'145	14.8	0.3	85.0
Imipenem	IPM	894	20.8	3.2	76.0
Meropenem	MEM	1'043	21.3	0.6	78.1
Amikacin	AMK	2'112	13.6	0.8	85.7
Gentamicin	GEN	2,163	15.9	0.6	83.6
Ciprofloxacin	CIP	2'413	24.6	4.8	70.7
Norfloxacin	NOR	1'155	12.7	1.6	85.6
Trimethoprim/Sulfamethoxazole	SXT	2'272	20.5	0.2	79.3
Nitrofurantoin[b]	NIT	1'086	18.8	45.1	36.1
Tigecycline[c]	TGC	797	3.4	4.3	92.3
Multidrug-resistance (≥3 classes NS)[d]	MDR	2,575	27.3	–	–
Extensive drug resistance (possible)	XDR	2,575	15.2	–	–
Pan-drug resistance (possible)	PDR	2,575	4.0	–	–

[a] %S includes %SDD (susceptible, dose-dependent).
[b] Nitrofurantoin: Isolates from urinary tract only.
[c] Tigecycline: FDA breakpoints (S≤2, R≥8)
[d] Multidrug resistance (MDR) was defined as acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

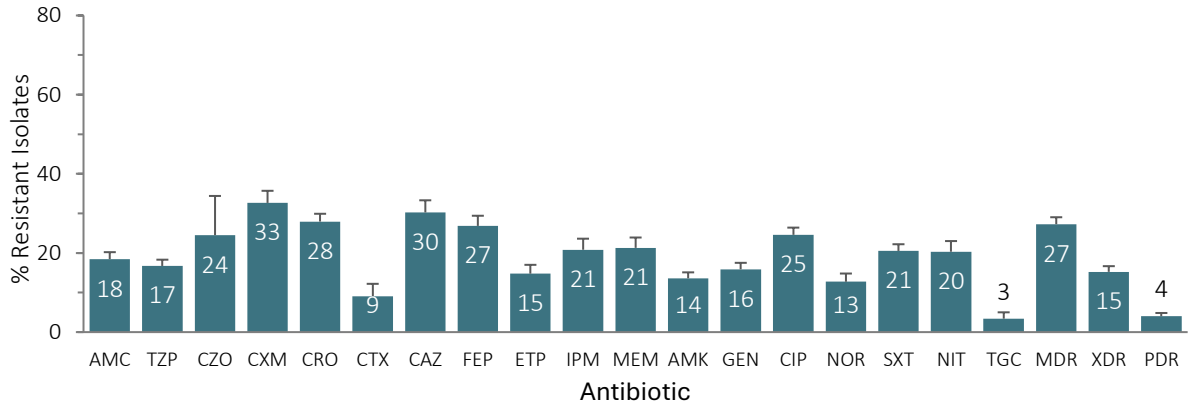
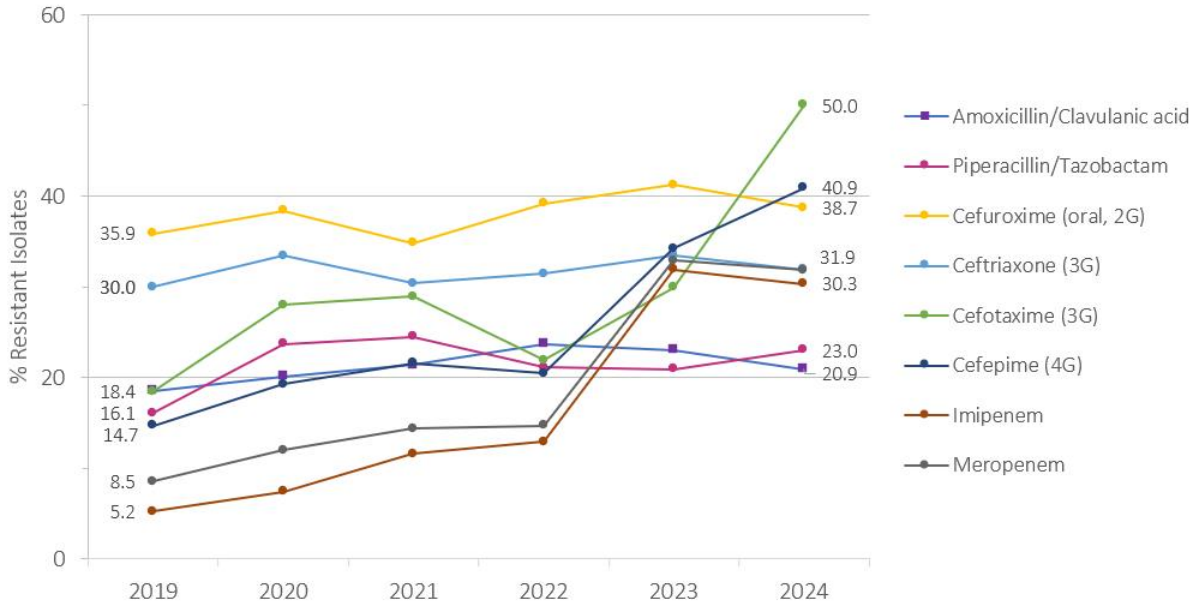


Figure 4.4.3.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Klebsiella pneumoniae*, isolates from all sources, Maldives, 2024 (n=2,607)

For 2024, antibiotic resistance rates (%R) for *K. pneumoniae* ranged from 3.4 % for tigecycline, to 33 % for cefuroxime.

Prevalence of multidrug resistance (%MDR, possible XDR, possible PDR) in *K. pneumoniae* was 27.3 %, 15.2 %, and 4.0 %, respectively.

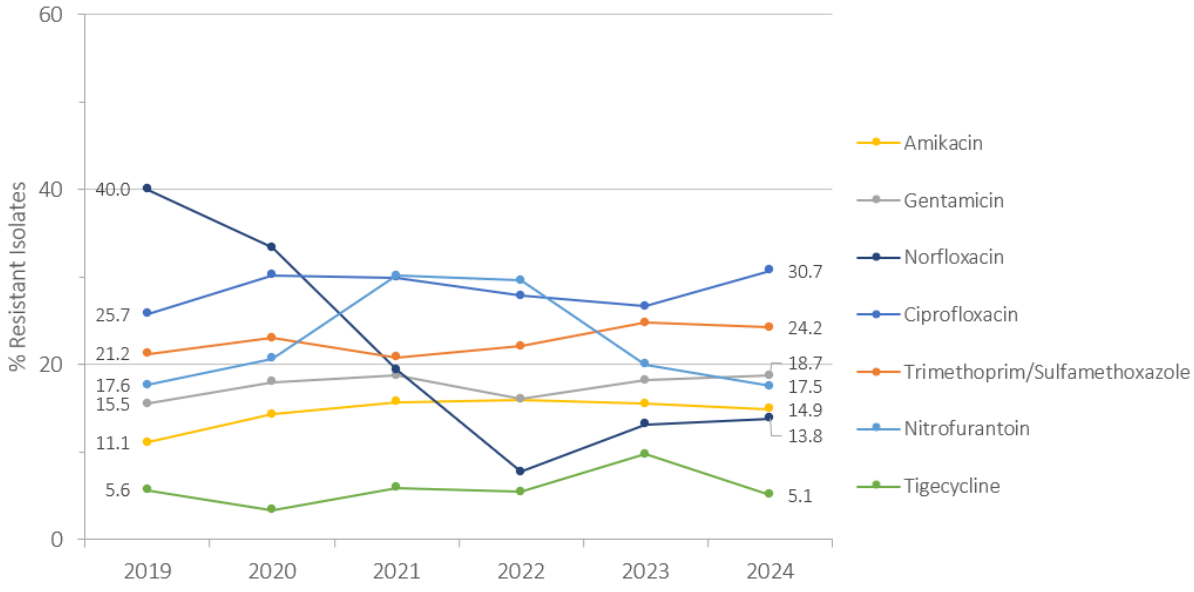
Figure 4.4.3.2 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, Maldives, 2019-2024, beta-lactam antibiotics



Klebsiella pneumoniae shows increasing trends of resistance (%R) for all classes of beta-lactam antibiotics, including:

- broad-spectrum penicillins (amoxicillin/clavulanic acid, piperacillin/tazobactam),
- 2nd-, 3rd- and 4th-generation cephalosporins (cefuroxime, ceftriaxone, cefotaxime, cefepime),
- carbapenems (imipenem, meropenem).

Figure 4.4.3.3 Annual trends for percentage of isolates resistant (%R) for *Klebsiella pneumoniae*, Maldives, 2019-2024, other antibiotics



Klebsiella pneumoniae shows increasing trends of resistance (%R) for

- aminoglycosides (amikacin, gentamicin)
- ciprofloxacin (but not norfloxacin), and
- trimethoprim/sulfamethoxazole.

Figure 4.4.3.4 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by region

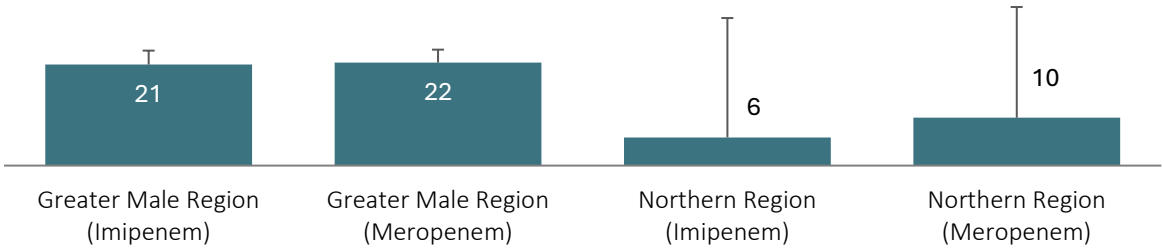


Figure 4.4.3.5 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by atoll

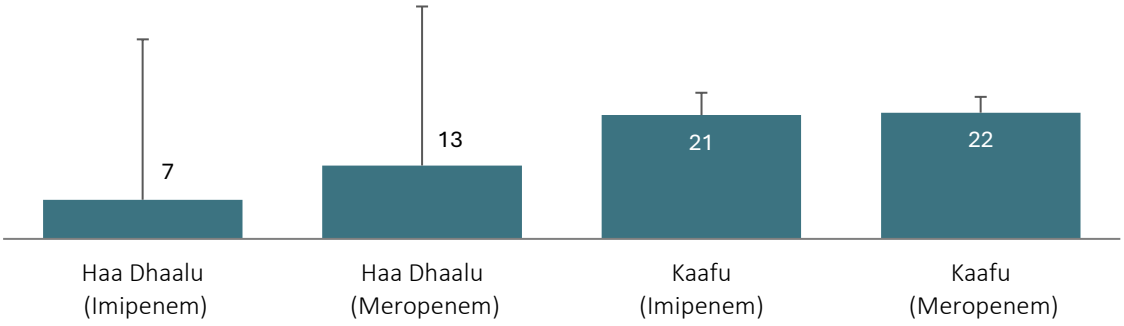


Figure 4.4.3.6 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by island

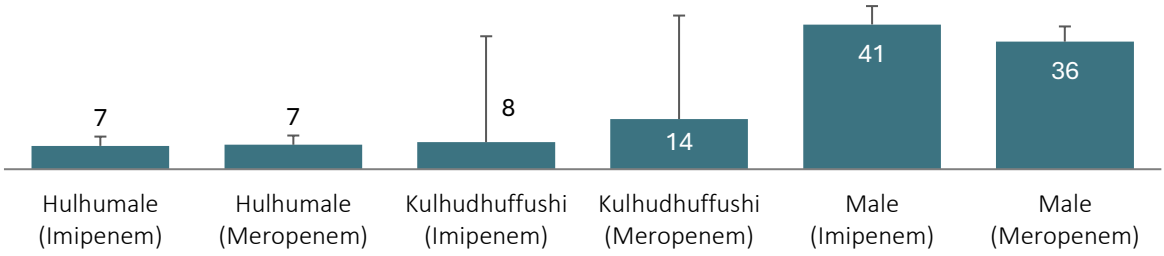


Figure 4.4.3.7 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by age category

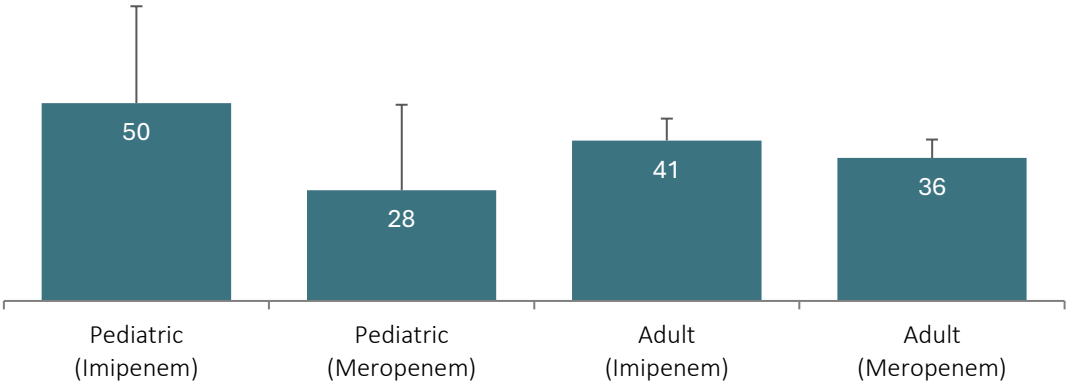


Figure 4.4.3.8 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by gender

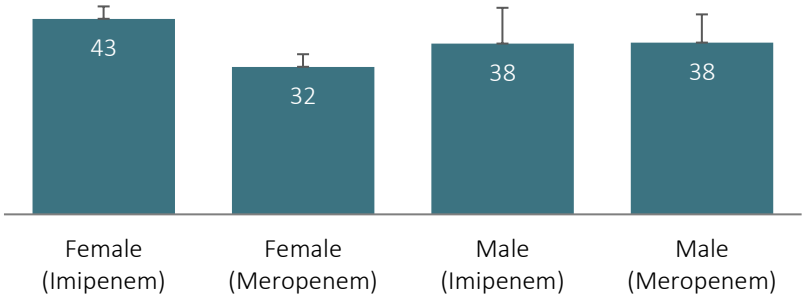


Figure 4.4.3.9 Percentage of isolates resistant to carbapenems (Meropenem) for *Klebsiella pneumoniae*, Maldives, 2024, by isolate source

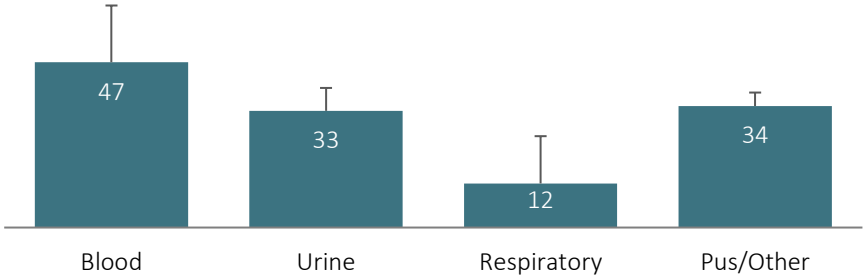


Figure 4.4.3.10 Percentage of isolates resistant to carbapenems (Meropenem) for *Klebsiella pneumoniae*, Maldives, 2024, by patient location type

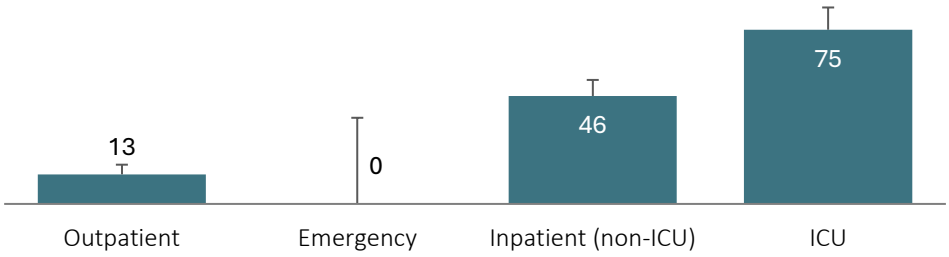
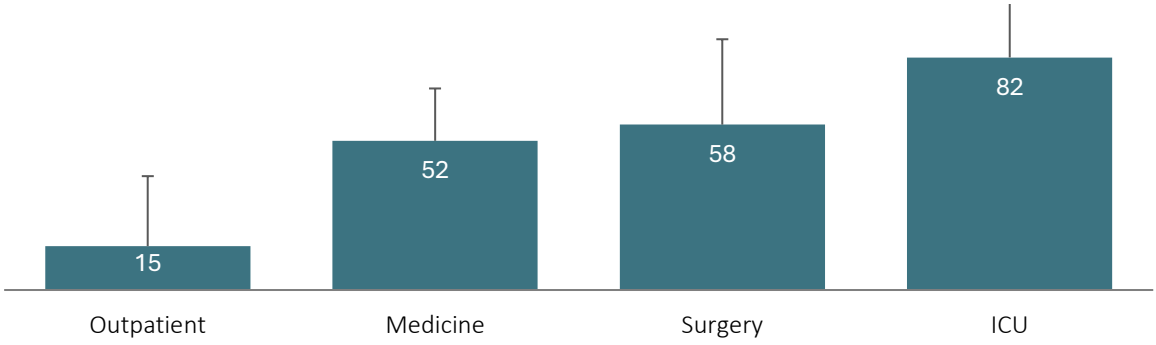


Figure 4.4.3.11 Percentage of isolates resistant to carbapenems for *Klebsiella pneumoniae*, Maldives, 2024, by clinical specialty/department



4.4.4 Salmonella spp. (non-typhoid)

Table 4.4.4.1. Number of *Salmonella* spp. Isolates, Maldives, 2024, by species

Organism	Isolates (N)	Isolates (%)	Patients (N)
Salmonella sp.	53	50.0	53
Salmonella enterica ss. *enterica* (Subgroup I)	41	38.7	41
Salmonella Paratyphi A	5	4.7	5
Salmonella Typhi	5	4.7	5
Salmonella Paratyphi	1	0.9	1
Salmonella enterica ss. *arizonae* (Subgroup IIIa)	1	0.9	1

Table 4.4.4.2. Percentages of resistant, intermediate, and susceptible isolates for *Salmonella* spp., isolates from all sources, Maldives, 2024

Antibiotic	Code	*Salmonella* spp. (non-typhoid) (n=106)			
		Isolates (N)	%R	%I	%S
Ampicillin	AMP	15*	26.7*	0*	73.3*
Ceftriaxone	CRO	92	7.6	0	92.4
Ertapenem	ETP	60	1.7	0	98.3
Imipenem	IPM	64	0	0	100
Meropenem	MEM	69	0	1.4	98.6
Ciprofloxacin	CIP	105	17.1	26.7	56.2
Levofloxacin	LVX	14*	14.3*	35.7*	50.0*
Trimethoprim/Sulfamethoxazole	SXT	104	4.8	0	95.2

*A small number of isolates were tested (N<30), and the results should be interpreted with caution.

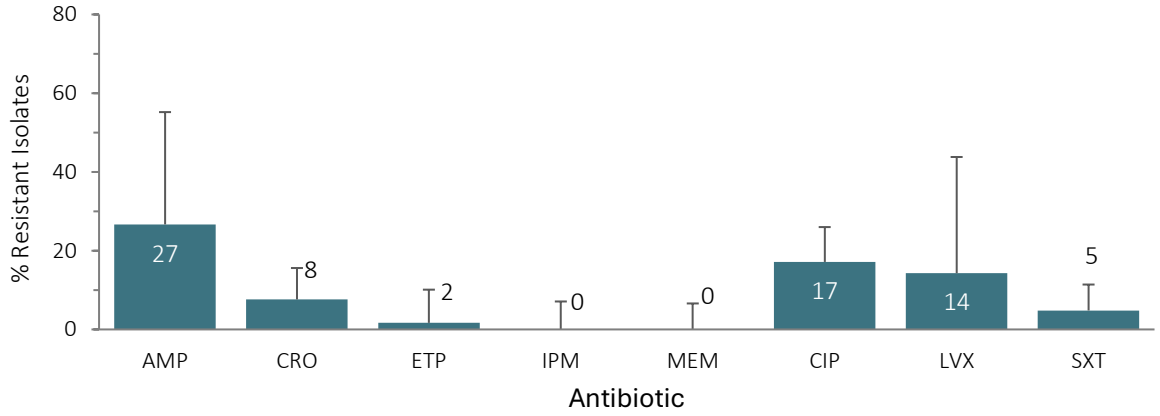
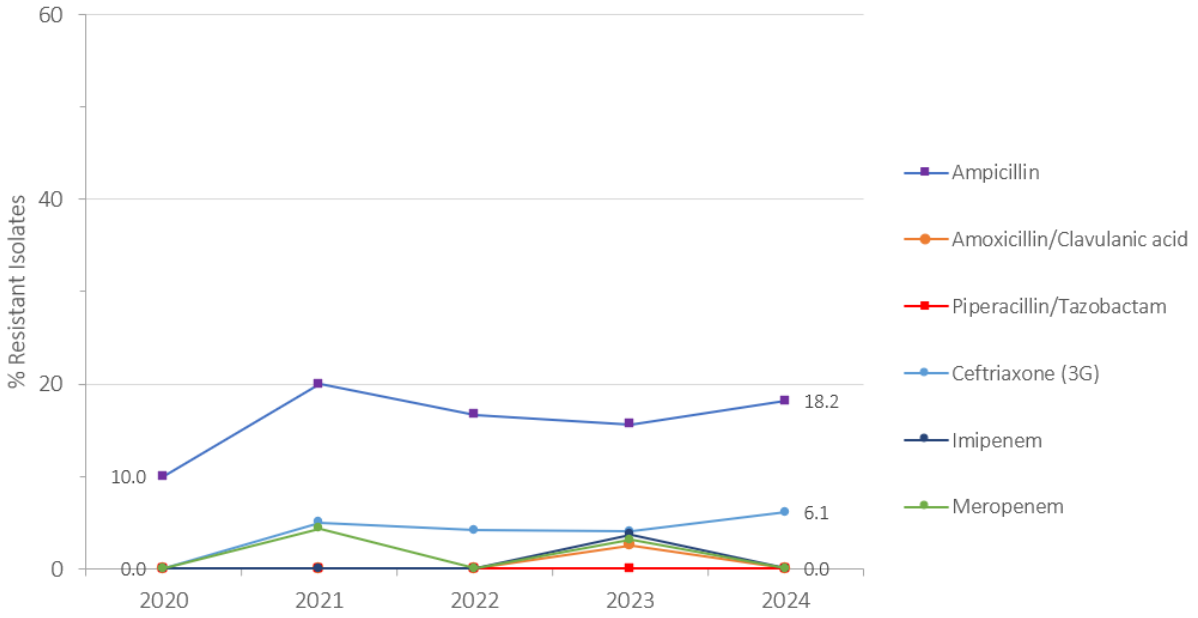


Figure 4.4.4.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Salmonella* spp., isolates from all sources, Maldives, 2024 (n=106)

For 2024, antibiotic resistance rates (%R) for *Salmonella* spp. ranged from 0-2 % for carbapenems (ertapenem, imipenem, meropenem), to 30.8 % for ampicillin.

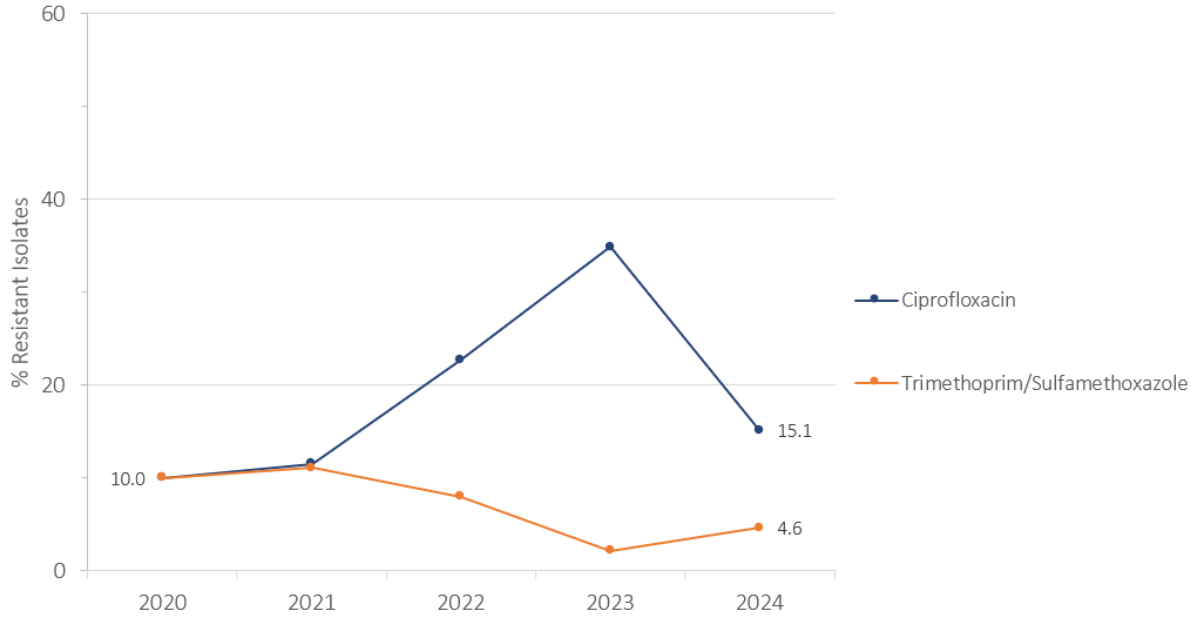
Figure 4.4.4.2 Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp., Maldives, 2019-2024, beta-lactam antibiotics



Salmonella spp. shows increasing trends of resistance (%R) for

- penicillins (ampicillin) and
- 3rd-generation cephalosporins (ceftriaxone).

Figure 4.4.4.3 Annual trends for percentage of isolates resistant (%R) for *Salmonella* spp., Maldives, 2019-2024, other antibiotics



Salmonella spp. shows an increasing trend of resistance for

- fluoroquinolones (ciprofloxacin).

4.4.5 Pseudomonas aeruginosa

Table 4.4.5.1. Percentages of resistant, intermediate, and susceptible isolates for *Pseudomonas aeruginosa*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*Pseudomonas aeruginosa* (n=1'125)			
		Isolates (N)	%R	%I	%S
Piperacillin/Tazobactam	TZP	1'001	12.0	3.3	84.7
Ticarcillin/Clavulanate	TCC	110	10.0	6.4	83.6
Ceftazidime	CAZ	963	15.4	1.7	83.0
Cefepime	FEP	910	11.4	4.9	83.6
Aztreonam	ATM	150	20.0	9.3	70.7
Imipenem	IPM	761	14.2	3.3	82.5
Meropenem	MEM	830	11.6	1.3	87.1
Colistin	COL	577	4.9	74.2	21.0
Tobramycin	TOB	175	8.6	2.3	89.1
Amikacin	AMK	895	11.2	1.7	87.2
Netilmicin	NET	66	13.6	3.0	83.3
Ciprofloxacin	CIP	1'021	14.8	2.7	82.5
Levofloxacin	LVX	923	16.4	2.2	81.5
Multidrug-resistance (≥3 classes NS)[a]	MDR	1'096	15.3	–	–
Extensive drug resistance (possible)	XDR	1'096	11.4	–	–
Pan-drug resistance (possible)	PDR	1'096	6.5	–	–

[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).

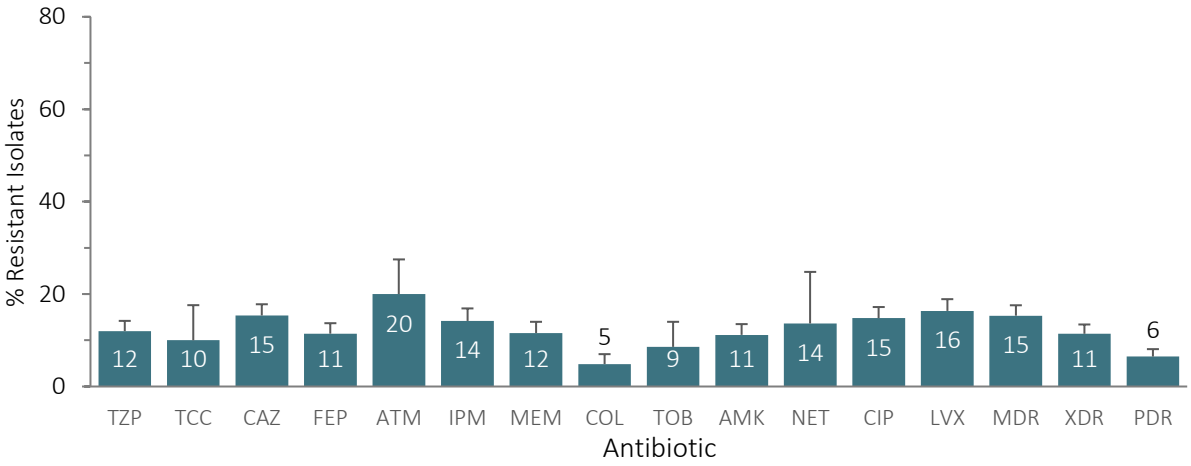
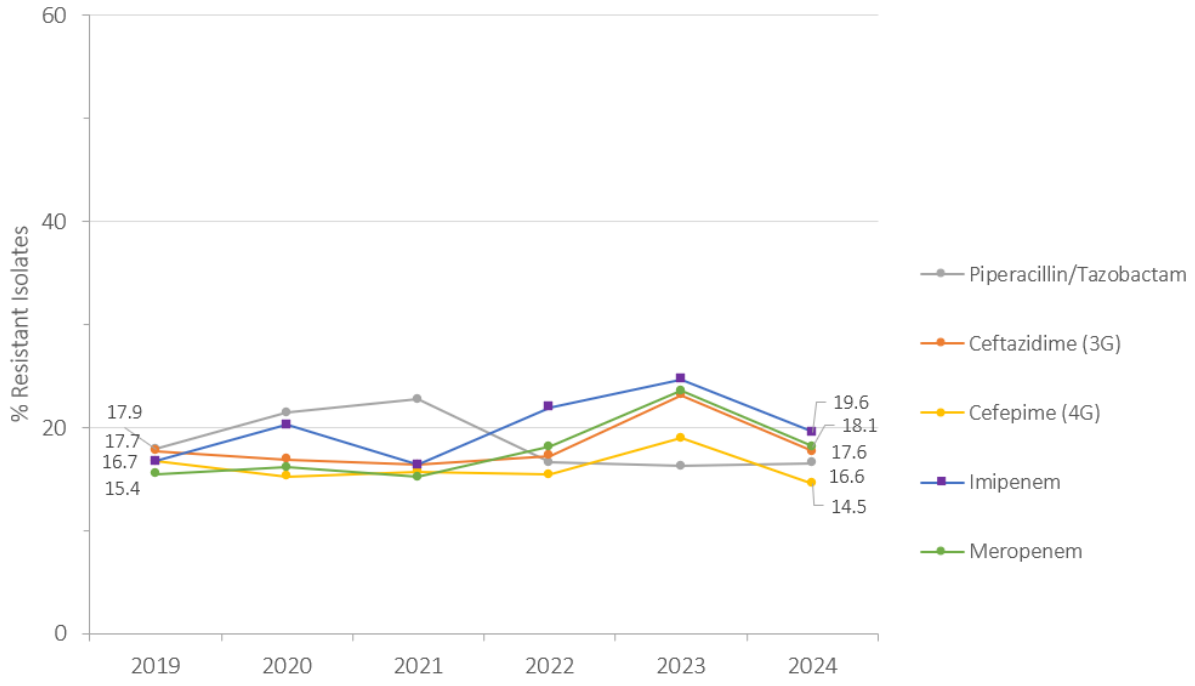


Figure 4.4.5.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Pseudomonas aeruginosa,* isolates from all sources, Maldives, 2024 (n=1'125)

For 2024, antibiotic resistance rates (%R) for *P. aeruginosa* ranged from 4.9 % for colistin to 20.0 % for aztreonam.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) for *Pseudomonas aeruginosa* was 15.3 %, 11.4 %, and 6.5 %, respectively.

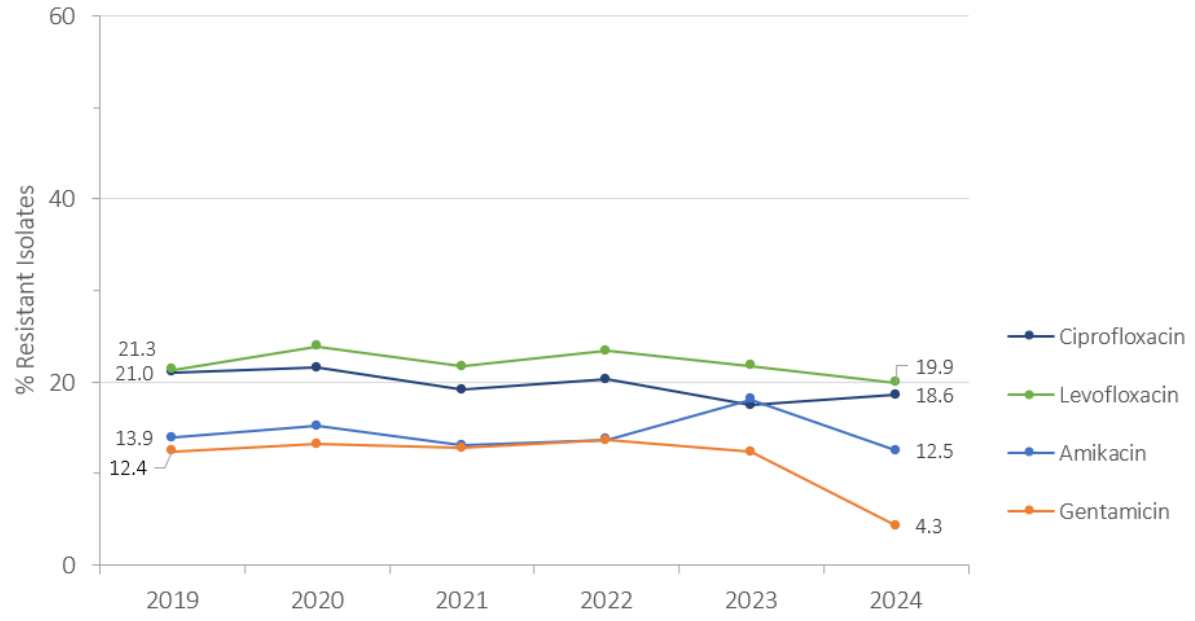
Figure 4.4.5.2 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, Maldives, 2019-2024, beta-lactam antibiotics



Pseudomonas aeruginosa shows increasing trends of resistance (%R) for

- carbapenems (imipenem, meropenem).

Figure 4.4.5.3 Annual trends for percentage of isolates resistant (%R) for *Pseudomonas aeruginosa*, Maldives, 2019-2024, other antibiotics



Pseudomonas aeruginosa shows decreasing trends of resistance for

- fluoroquinolones (ciprofloxacin, levofloxacin), and
- aminoglycosides (amikacin, gentamicin).

4.4.6 Acinetobacter spp.

Table 4.4.6.1. Percentages of resistant, intermediate, and susceptible isolates for *Acinetobacter* spp., isolates from all sources, Maldives, 2024

Antibiotic	Code	*Acinetobacter* spp. (n=406)			
		Isolates (N)	%R	%I	%S
Piperacillin/Tazobactam	TZP	392	36.0	2.0	62.0
Ceftazidime	CAZ	325	30.2	3.7	66.2
Ceftriaxone	CRO	186	15.6	52.7	31.7
Cefepime	FEP	262	37.0	5.0	58.0
Imipenem	IPM	225	42.7	0.9	56.5
Meropenem	MEM	245	40.8	0.8	58.4
Amikacin	AMK	280	27.5	5.0	67.5
Gentamicin	GEN	398	30.4	1.8	67.8
Ciprofloxacin	CIP	401	33.4	5.0	61.6
Levofloxacin	LVX	207	30.4	12.1	57.5
Trimethoprim/Sulfamethoxazole	SXT	396	18.2	0	81.8
Colistin	COL	145	1.4	91.7	0
Minocycline	MNO	35	14.3	2.9	82.9
Multidrug-resistance (≥3 classes NS)[a]	MDR	405	35.1	–	–
Extensive drug resistance (possible)	XDR	405	30.6	–	–
Pan-drug resistance (possible)	PDR	405	13.8	–	–

[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).

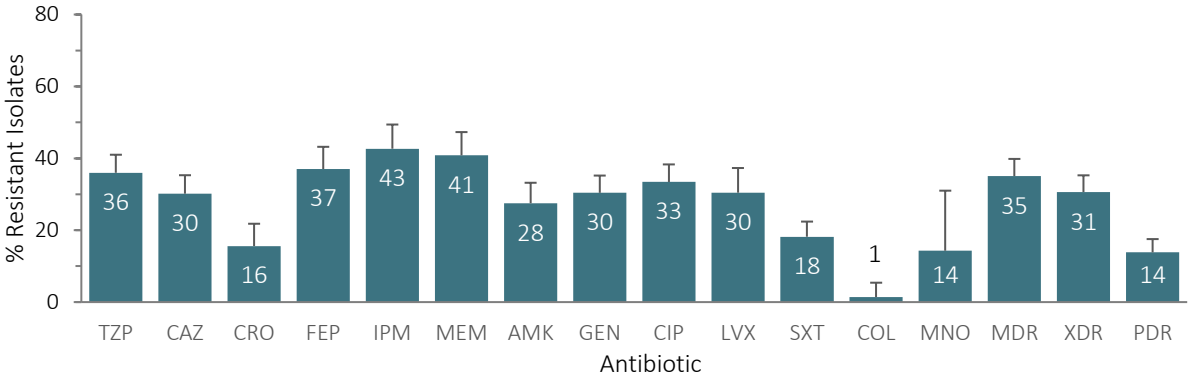
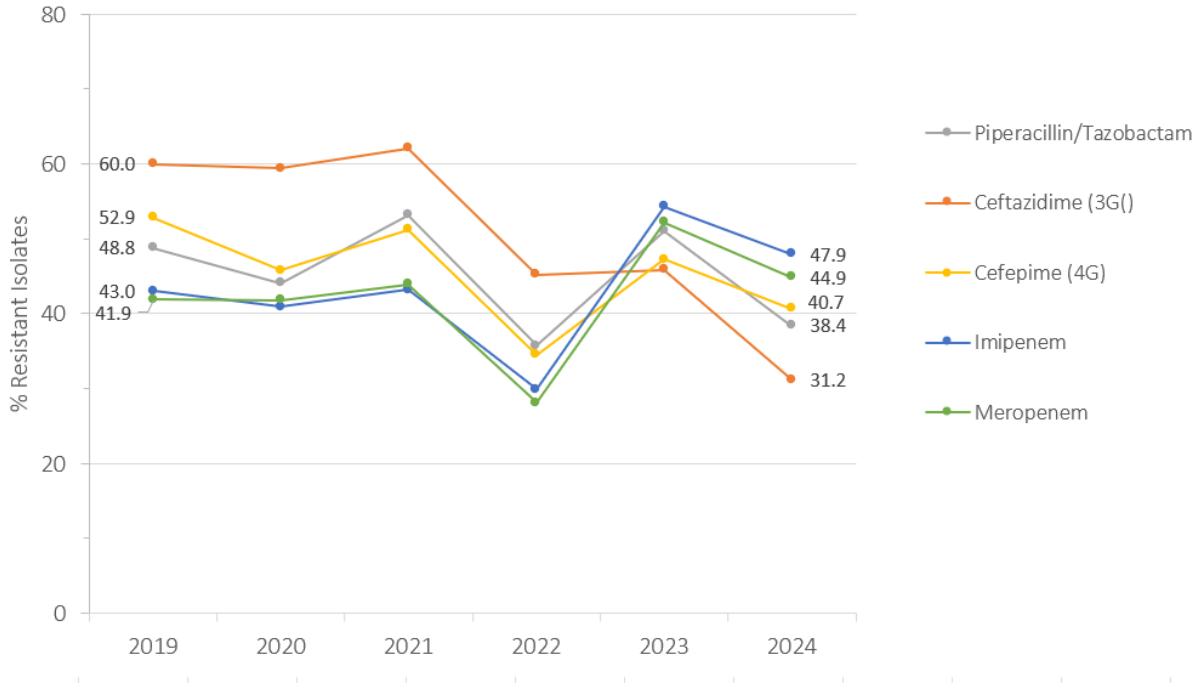


Figure 4.4.6.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Acinetobacter* spp., isolates from all sources, Maldives, 2024 (n=406)

For 2024, antibiotic resistance rates (%R) for *Acinetobacter* spp. ranged from 1.4 % for colistin, to 41-43 % for carbapenems.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) for *Acinetobacter* spp. was 35.1 %, 30.6 %, and 13.8 %, respectively.

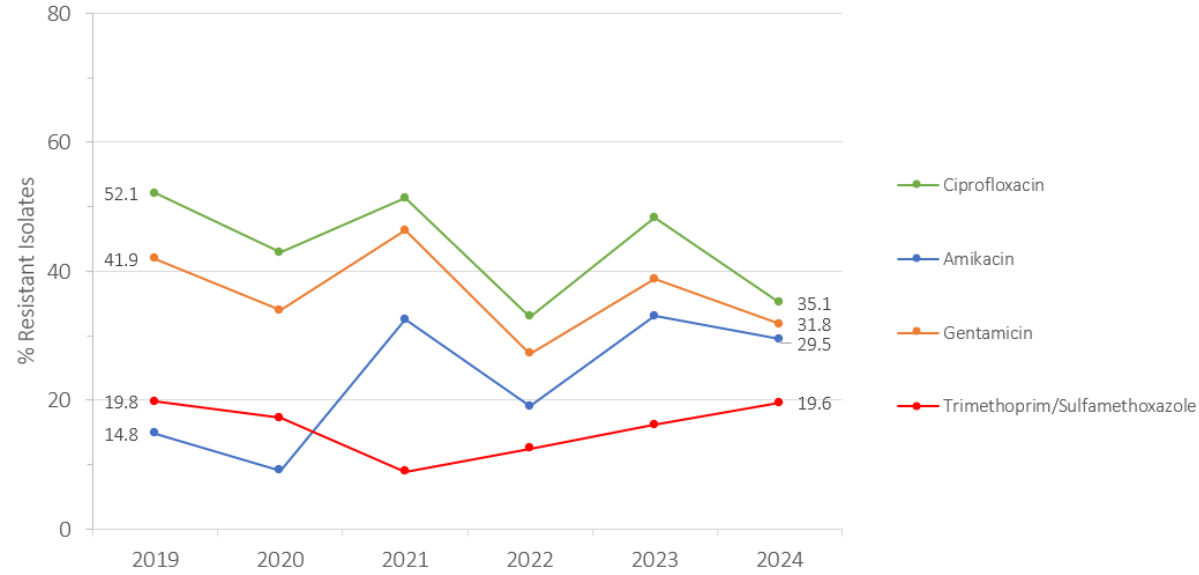
Figure 4.4.6.2 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., Maldives, 2019-2024, beta-lactam antibiotics



Acinetobacter spp. shows decreasing trends of resistance (%R) for all beta-lactam antibiotics, including

- broad-spectrum penicillins (piperacillin/tazobactam),
- 3rd- and 4th generation cephalosporins (ceftazidime, cefepime), and
- carbapenems (imipenem, meropenem).

Figure 4.4.6.3 Annual trends for percentage of isolates resistant (%R) for *Acinetobacter* spp., Maldives, 2019-2024, other antibiotics



Acinetobacter spp. shows decreasing trends of resistance (%R) for

- fluoroquinolones (ciprofloxacin),
- gentamicin, but not amikacin.

4.4.7 Staphylococcus aureus

Table 4.4.7.1. Percentages of resistant, intermediate, and susceptible isolates for *Staphylococcus aureus*, isolates from all sources[a], Maldives, 2024

Antibiotic	Code	*Staphylococcus aureus* (n=1'192)			
		Isolates (N)	%R	%I	%S
Oxacillin	OXA	960	36.0	–	62.7
Cefoxitin	FOX	395	**38.0**	–	61.5
Gentamicin	GEN	927	11.2	5.0	83.8
Rifampicin	RIF	628	1.9	0.2	97.9
Ciprofloxacin	CIP	901	34.0	6.9	59.2
Levofloxacin	LVX	835	35.0	9.5	55.6
Trimethoprim/Sulfamethoxazole	SXT	932	16.3	0.8	82.9
Clindamycin	CLI	798	15.5	0.4	84.1
Erythromycin	ERY	1'026	38.1	2.0	59.8
Linezolid	LNZ	460	1.5	0	98.5
Vancomycin	VAN	647	0	0	100
Tigecycline[b]	TGC	465	0	0	99.4
Multidrug-resistance (≥3 classes NS)[c]	MDR	1,129	25.1	–	–
Extensive drug resistance (possible)	XDR	1,129	5.8	–	–
Pan-drug resistance (possible)	PDR	1,129	1.0	–	–

[a] excluding axilla, nose, and groin
[b] Tigecycline: EUCAST breakpoints (S≤0.5, R>0.5)
[c] Multidrug resistance (MDR) was defined as isolate being either a MRSA or having acquired non-susceptibility (NS) to at least one agent in three or more antimicrobial classes (Magiorakos, et al., 2012).

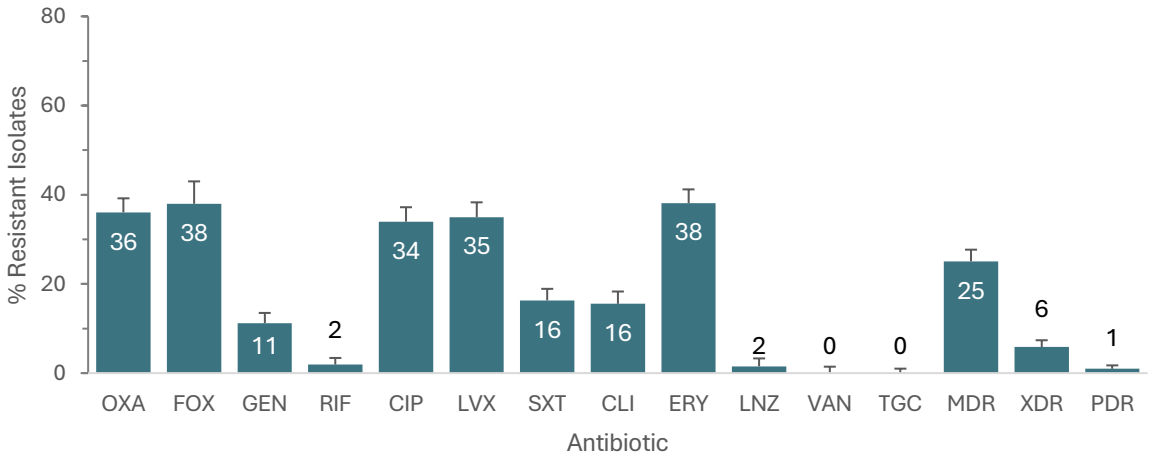


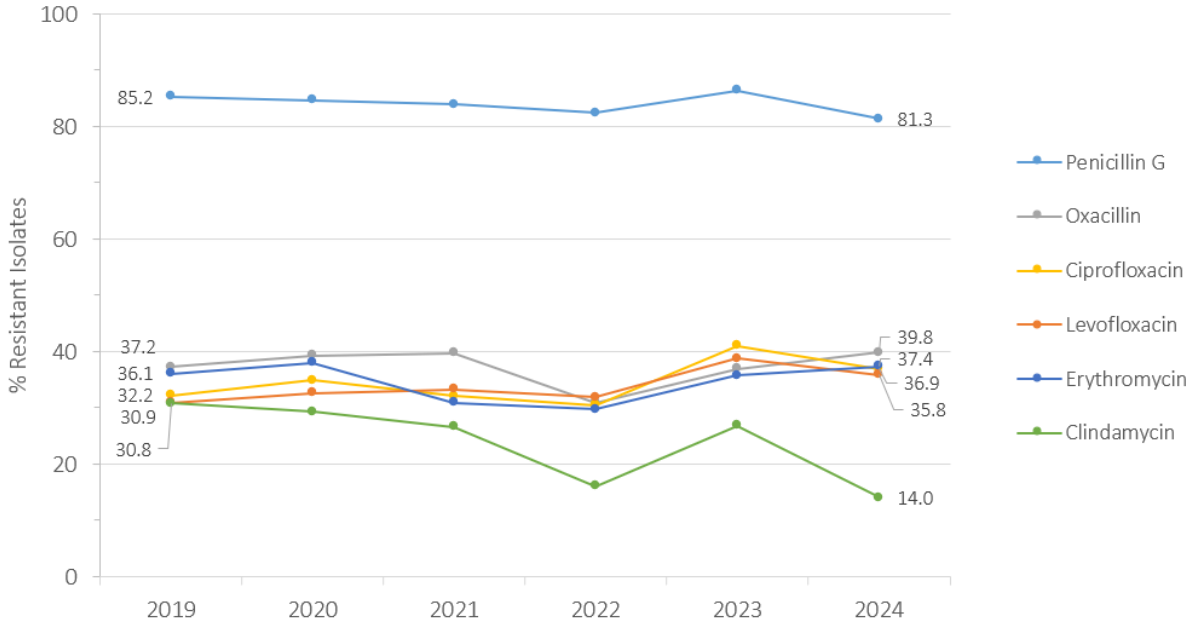
Figure 4.4.7.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Staphylococcus aureus,* isolates from all sources, Maldives, 2024 (n=1'192)

For 2024, antibiotic resistance rates (%R) for *S. aureus* ranged from 0 % for vancomycin and tigecycline, to 34-38 % for beta-lactam antibiotics, fluoroquinolones, and macrolides.

Percentage MRSA was 38.0 % for all isolates (based on cefoxitin), whereas for blood culture isolates, MRSA rate was 69.2 %.

Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) in *S. aureus* was 25.1 %, 5.8 %, and 1.0 %, respectively.

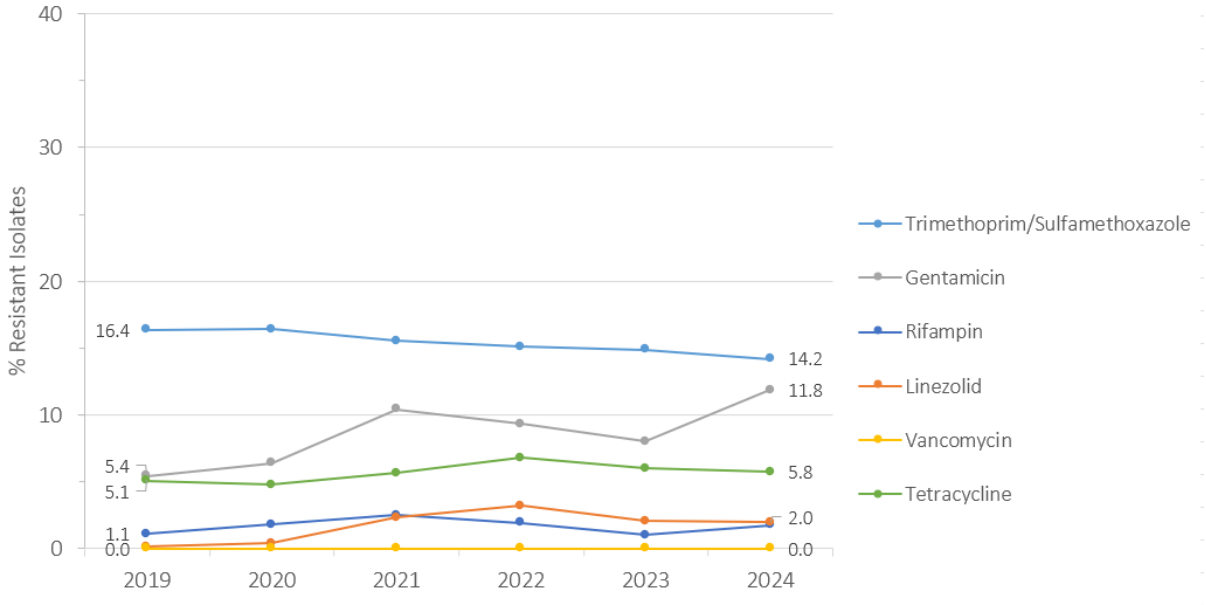
Figure 4.4.7.2 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, Maldives, 2019-2024, beta-lactam antibiotics



Staphylococcus aureus shows increasing trends of resistance (%R) for

- fluoroquinolones (ciprofloxacin, levofloxacin)
- lincosamides (clindamycin).

Figure 4.4.7.3 Annual trends for percentage of isolates resistant (%R) for *Staphylococcus aureus*, Maldives, 2019-2024, other antibiotics



Staphylococcus aureus shows increasing trends of resistance (%R) for

- rifampin, and
- tetracycline.

Figure 4.4.7.4 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by region

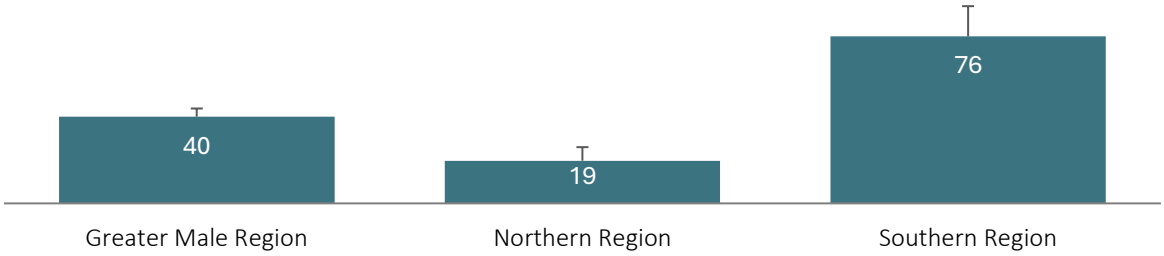


Figure 4.4.7.5 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by atoll

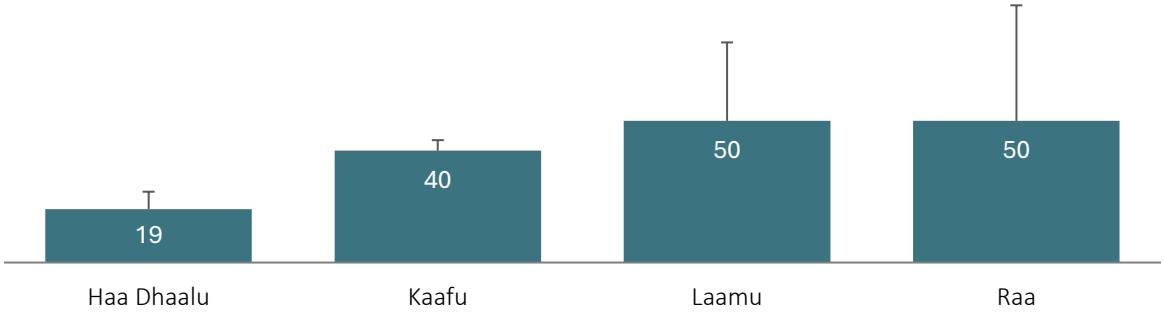


Figure 4.4.7.6 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by island

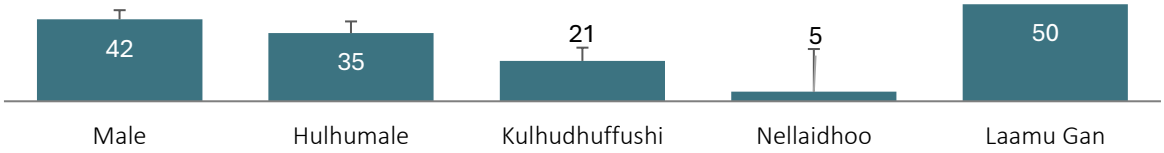


Figure 4.4.7.7 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by age category and age group

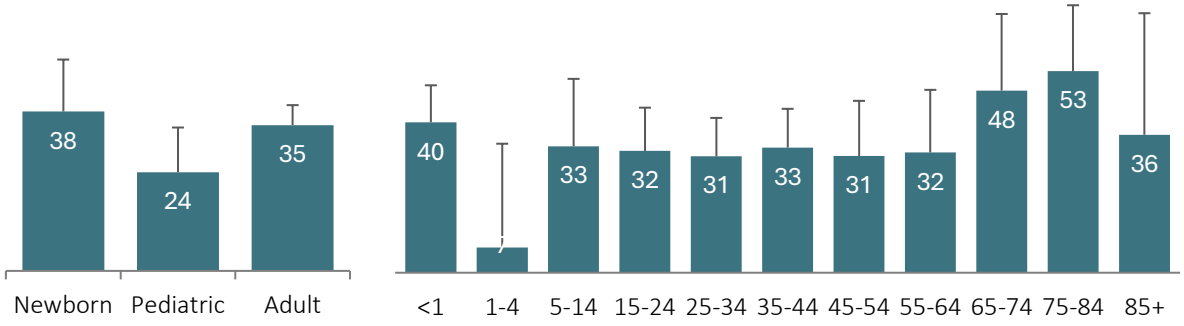


Figure 4.4.7.8 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by gender

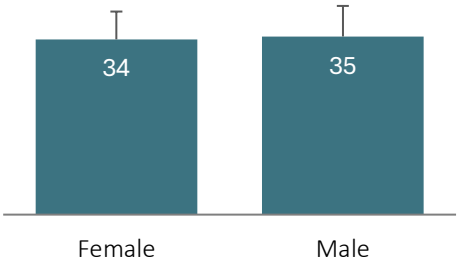


Figure 4.4.7.9 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by isolate source

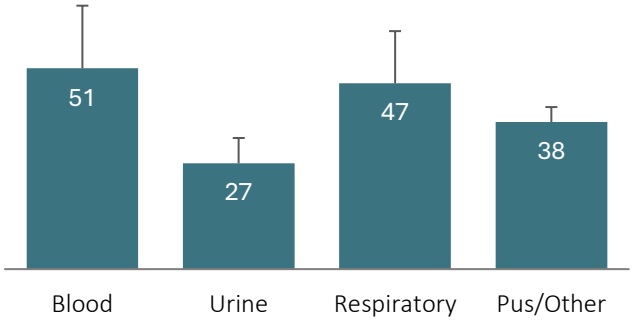


Figure 4.4.7.10 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by patient location type

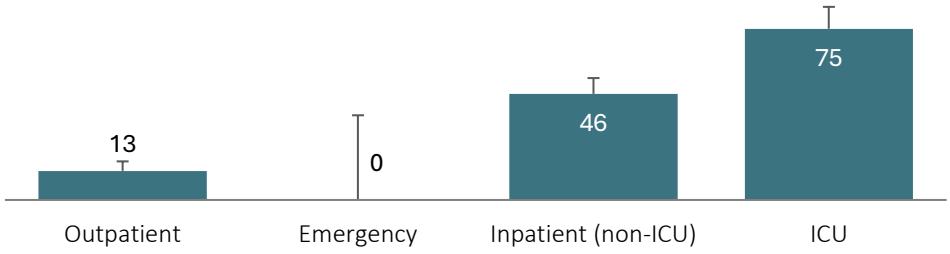
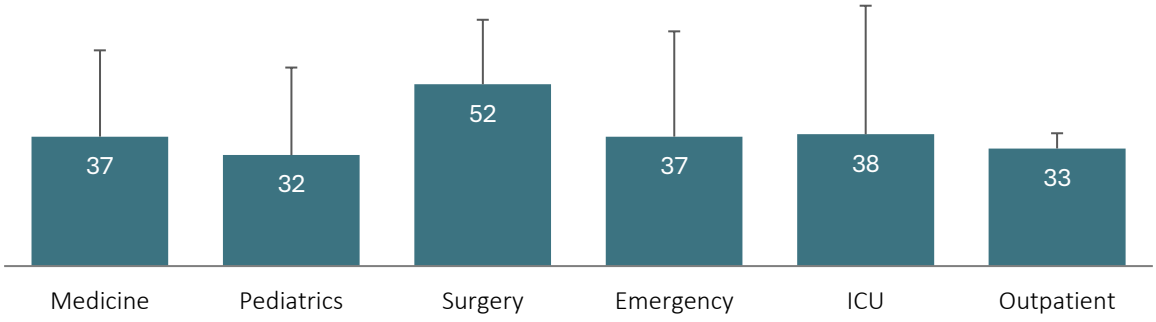


Figure 4.4.7.11 Percentage of isolates resistant to oxacillin (%MRSA) for *Staphylococcus aureus*, Maldives, 2024, by clinical specialty/department



4.4.8 Streptococcus pneumoniae

Table 4.4.8.1. Percentages of resistant, intermediate, and susceptible isolates for *Streptococcus pneumoniae*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*S. pneumoniae* (n=22)			
		Isolates (N)*	%R	%I	%S
Penicillin G	PEN	17	0	0	100
Penicillin G (meningitis breakpoints)	PEN (Men)	17	58.8	0	41.2
Penicillin G (oral breakpoints)	PEN (Oral)	17	5.9	52.9	41.2
Ceftriaxone	CRO	17	5.9	0	94.1
Ceftriaxone (meningitis breakpoints)	CRO (NM)	17	5.9	23.5	70.6
Cefotaxime	CTX	17	0	5.9	94.1
Cefotaxime (meningitis breakpoints)	CTX (NM)	17	5.9	23.5	70.6
Rifampin	RIF	18	0	0	100
Levofloxacin	LVX	21	4.8	0	95.2
Moxifloxacin	MFX	14	0	0	100
Trimethoprim/Sulfamethoxazole	SXT	22	27.3	22.7	50.0
Clindamycin	CLI	20	35.0	0	65.0
Erythromycin	ERY	20	70.0	0	30.0
Linezolid	LNZ	14	0	0	100
Vancomycin	VAN	16	0	0	100
Tetracycline	TCY	20	45.0	5.0	50.0

*A small number of isolates were tested (N<30), and the results should be interpreted with caution.

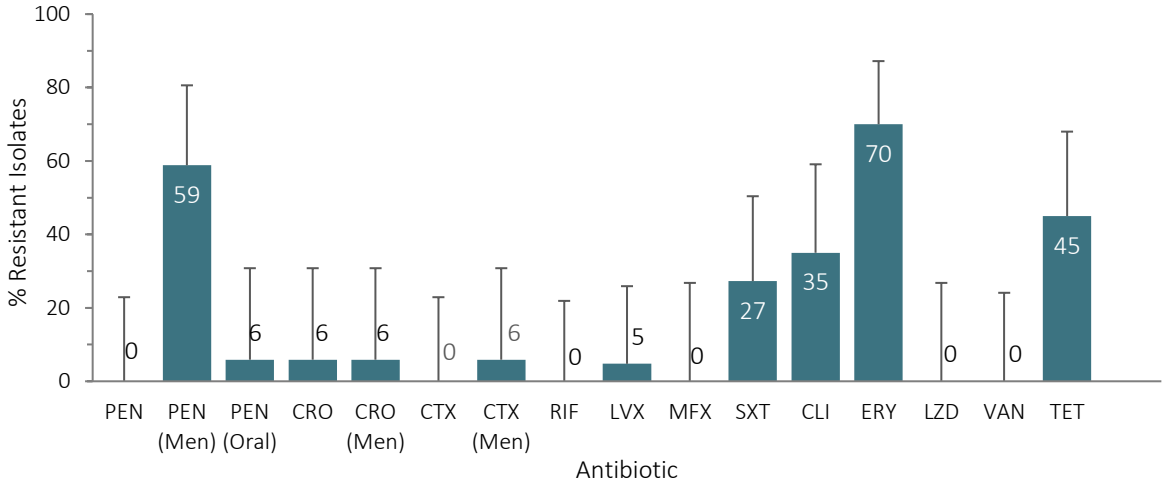


Figure 4.4.8.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *Streptococcus pneumoniae,* isolates from all sources, Maldives, 2024 (n=22)

For 2024, antibiotic resistance rates (%R) for *S. pneumoniae* ranged from 0 % for rifampin, linezolid, and vancomycin, to 70 % for erythromycin.

Distribution of pneumococcal serotypes in the Maldives is currently unknown (no routine testing of serotypes in participating facilities).

4.4.9 Enterococcus faecalis / Enterococcus faecium

Table 4.4.9.1. Percentages of resistant, intermediate, and susceptible isolates for *Enterococcus faecalis* and *Enterococcus faecium*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*Enterococcus faecalis* (n=427)				*Enterococcus faecium* (n=47)			
		N	%R	%I	%S	N	%R	%I	%S
Penicillin G	PEN	401	6.5	0	93.5	44	90.9	0	9.1
Ampicillin	AMP	10[a]	10.0[a]	0[a]	90.0[a]	1	-	-	-
Ciprofloxacin	CIP	422	27.5	4.0	68.5	47	93.6	0	6.4
Levofloxacin	LVX	413	24.7	3.1	72.2	45	88.9	4.4	6.7
Daptomycin	DAP	306	1.3	35.9	62.7	0	-	-	-
Erythromycin	ERY	416	58.2	33.2	8.7	46	89.1	8.7	2.2
Nitrofurantoin	NIT	246	0.8	2.0	97.2	26	69.2	7.7	23.1
Linezolid	LNZ	281	1.4	0.4	98.2	21	19.0	0	81.0
Vancomycin[c]	VAN	373	**0.5**	0.5	98.9	45	**13.3**	2.2	84.4
Teicoplanin	TEC	372	0.5	0.3	99.2	45	11.1	2.2	86.7
Tetracycline	TCY	366	83.3	0	16.7	45	88.9	0	11.1
Tigecycline[d]	TGC	317	0	0	99.7	36	2.8	0	97.2
Multidrug-resistance (≥3)[e]	MDR	338	0.9	–	–	38[a]	7.9	–	–
Extensive drug resistance	XDR	338	0.9	–	–	38[a]	7.9	–	–
Pan-drug resistance	PDR	338	0	–	–	38[a]	2.6	–	–

[a] A small number of isolates were tested (N<30): percentage resistance should be interpreted with caution.
[b] Nitrofurantoin: Isolates from urinary tract only.
[c] %VRE for *Enterococcus* spp. = 3.6 % (n=611).
[d] Tigecycline: FDA breakpoints for *E. faecalis* (S≤0.25), EUCAST breakpoints for *E. faecium* (S≤0.5, R>0.5).
[e] 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).

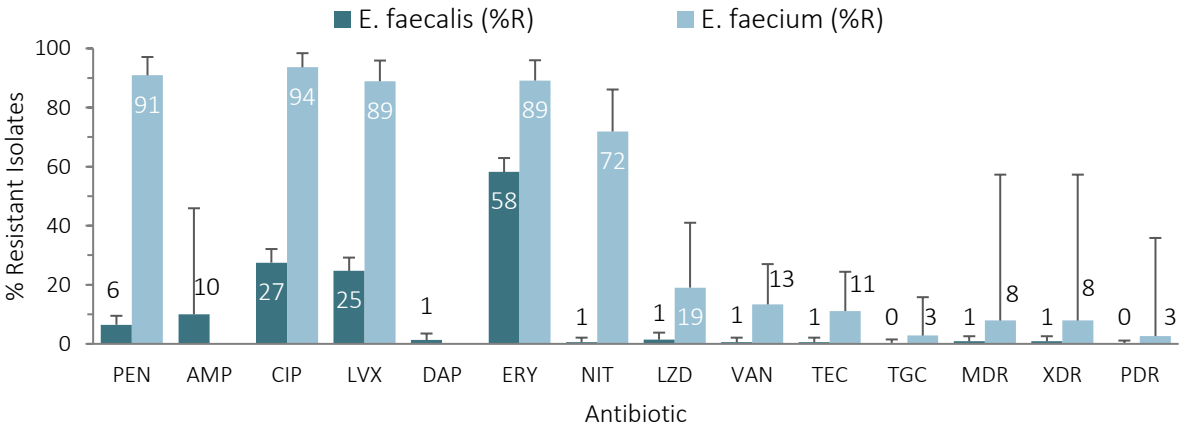
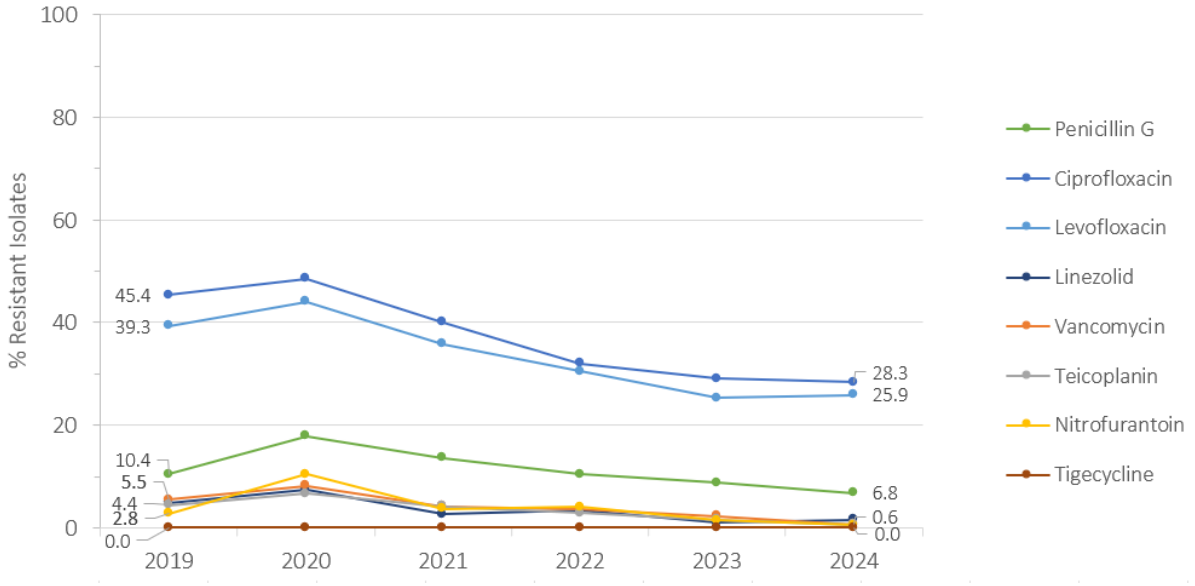


Figure 4.4.9.1. Percentages of resistant (%R), and multidrug-resistant (%MDR/XDR/PDR) isolates for *E. faecalis* and *E. faecium,* isolates from all sources, Maldives, 2024

- For 2024, resistance in *Enterococcus faecalis* ranged from 0-3 % for daptomycin, nitrofurantoin, oxazolidinones (linezolid), glycopeptides (vancomycin, teicoplanin) and tigecycline, to 58.2 % for macrolides (erythromycin).
- For *Enterococcus faecium*, resistance ranged from 3 % for tigecycline, to 89-94 % for fluoroquinolones (levofloxacin, ciprofloxacin) and 89 % for macrolides (erythromycin).
- Vancomycin-resistant Enterococci (VRE) were observed in 0.5 % of *E. faecalis*, and 13.3 % of *E. faecium* isolates, respectively, and in 3.6 % of *Enterococcus* spp. Isolates.
- Prevalence of multidrug resistance (%MDR/possible XDR/possible PDR) was 0.9 %, 0.9 %, and 0 % for *E. faecalis*, and 7.9 %, 7.9 %, and 2.6 % for *E. faecium*, respectively.

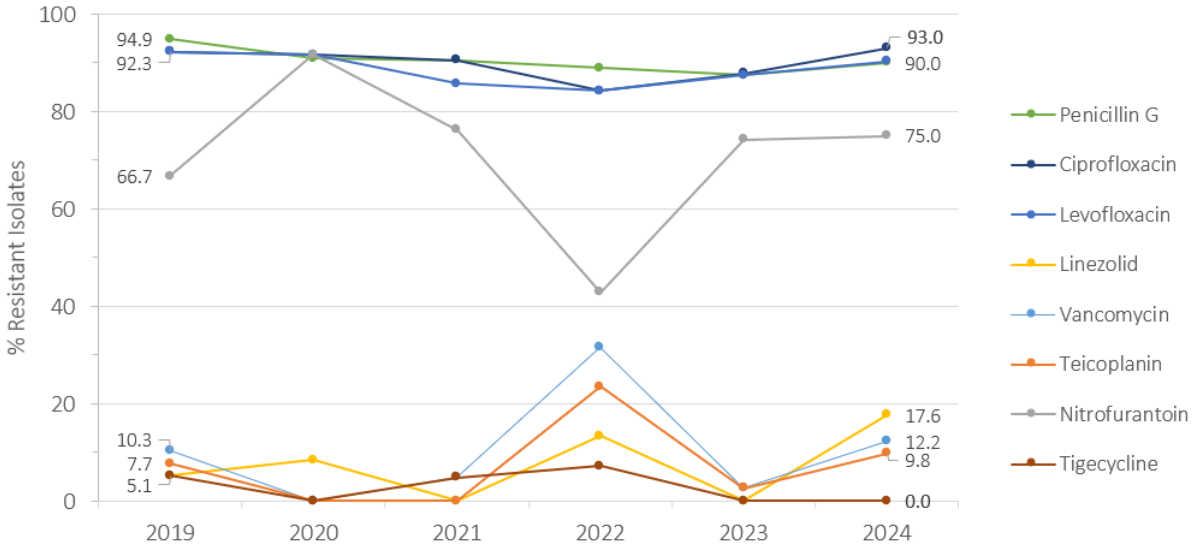
Figure 4.4.9.2 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecalis*, Maldives, 2019-2024



Enterococcus faecalis shows decreasing trends of resistance (%R) for all classes of antibiotics, including

- penicillin,
- fluoroquinolones (ciprofloxacin, levofloxacin),
- linezolid,
- glycopeptides (vancomycin, teicoplanin),
- nitrofurantoin, and
- tigecycline.

Figure 4.4.9.3 Annual trends for percentage of isolates resistant (%R) for *Enterococcus faecium*, Maldives, 2019-2024



Enterococcus faecium shows high levels of resistance (%R) for

- penicillin G,
- fluoroquinolones (ciprofloxacin, levofloxacin), and
- nitrofurantoin.

4.4.10 Candida spp.

Table 4.4.10.1. Percentages of resistant, intermediate, and susceptible isolates for *Candida albicans*, isolates from all sources, Maldives, 2024

Antibiotic	Code	*Candida albicans* (n=769)			
		Isolates (N)	%R	%I	%S
Fluconazole	FLU	765	2.5	0.0	97.5
Voriconazole	VOR	736	1.8	1.4	96.9
Caspofungin	CAS	769	0.4	0.0	99.6
Micafungin	MIC	687	0.1	0.0	99.9
Amphotericin B	AMB	690	2.2	0.0	97.8

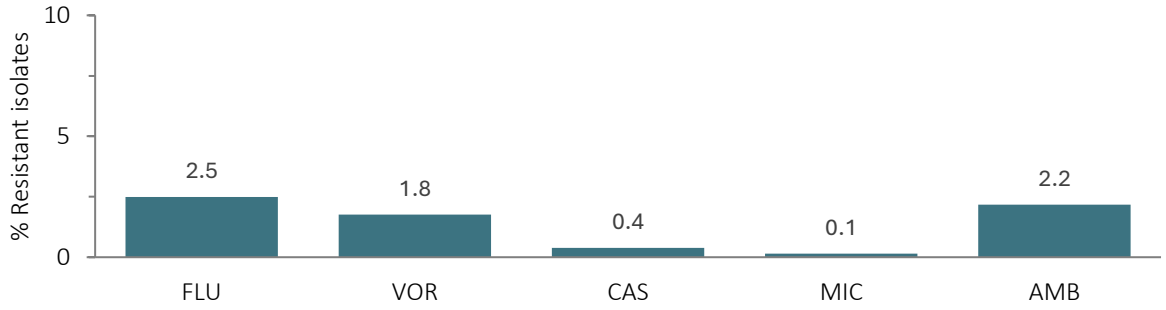
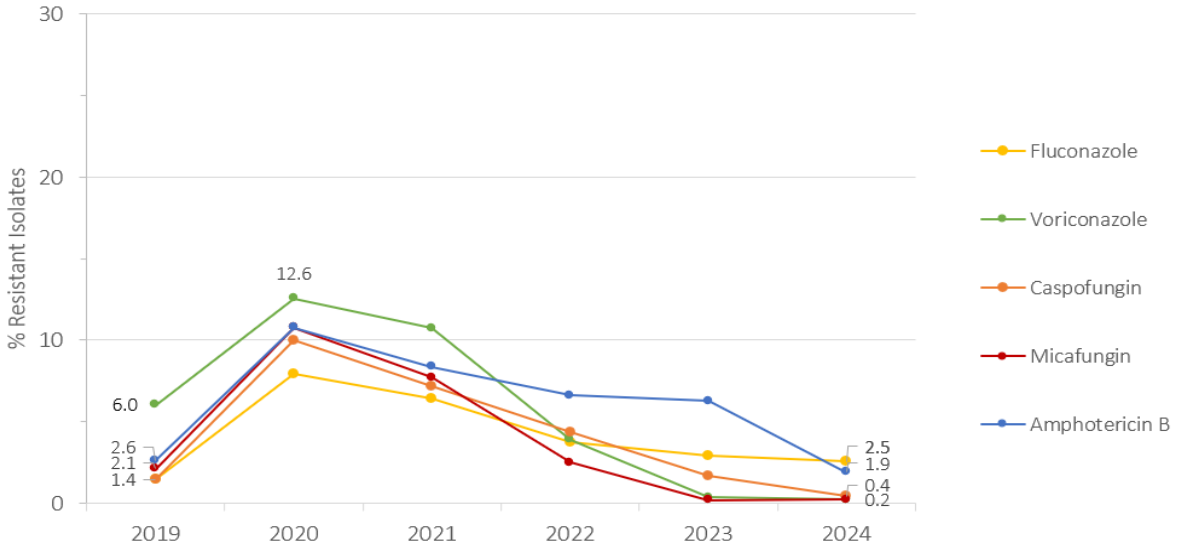


Figure 4.4.10.1. Percentages of resistant (%R) isolates for *Candida albicans*, isolates from all sources, Maldives, 2024

For 2024, resistance in *Candida albicans* ranged from 0.1-0.4 % for echinocandins (caspofungin, micafungin), to 1.8-2.5 % for azoles (fluconazole, voriconazole) and amphotericin B.

Figure 4.4.10.2 Annual trends for percentage of isolates resistant (%R) for *Candida albicans*, Maldives, 2019-2024



Candida albicans shows overall decreasing trends of resistance (%R) for all classes of antifungals, including

- azoles (fluconazole, voriconazole),
- echinocandins (caspofungin, micafungin), and
- amphotericin B

Table 4.4.10.2. Percentage of susceptible isolates for *Candida* spp. and other yeasts, isolates from all sources, Maldives, 2024 (Cumulative antibiogram)

	Isolates (N)	Isolates (%)	Triazoles		Polyenes	Echinocandins	
			FLU[a]	VOR[b]	AMB[c]	CAS[d]	MIF[e]
Yeast (All)	1'254	100.0	94.5	95.0		97.8	99.5
Candida albicans	913	72.8	97.5	96.9	97.8	99.6	99.9
Other yeast (non-*C. albicans*)	270	21.5	85.1	88.0	93.5	92.9	98.5
C. tropicalis	155	12.4	93.8	98.4	97.7	97.7	99.2
Nakaseomyces glabratus[f]	47	3.7	–	–[g]	100	69.6	100
C. parapsilosis	31	2.5	96.6	100	96.7	100	100
Issatchenkia orientalis[h]	11*	0.9	0*	100*	80.0	80.0*	100*
C. auris[i]	5	0.4	–	–	–	–	–
C. dubliniensis	4	0.3	–	–	–	–	–
Trichosporon asahii	4	0.3	–	–	–	–	–
Meyerozyma guilliermondii[k]	3	0.2	–	–	–	–	–
Papiliotrema laurentii[j]	3	0.2	–	–	–	–	–
Trichomonascus ciferrii[l]	3	0.2	–	–	–	–	–
Debaryomyces hansenii[m]	1	0.1	–	–	–	–	–
Saccharomyces spp.	1	0.1	–	–	–	–	–
Trichosporon sp.	1	0.1	–	–	–	–	–
Yarrowia lipolytica[n]	1	0.1	–	–	–	–	–
Candida spp. (not speciated)	71	5.7	–	–	–	–	–

*A small number of isolates were tested (N<30): percentage resistance should be interpreted with caution.

[a]FLU=Fluconazole, [b]VOR=Voriconazole. [c]AMP=Amphotericin B. EUCAST breakpoints (S≤1, R>1) are used for amphotericin B for *C. albicans, C. dubliniensis, C. glabrata, C. krusei, C. parapsilosis*, and *C. tropicalis* (EUCAST, 2025). 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]*Nakaseomyces glabratus*: formerly known as *Candida glabrata*. [g]For *C. glabrata* and voriconazole, current data are insufficient to demonstrate a correlation between in vitro susceptibility testing and clinical outcome. [h]*Issatchenkia orientalis*: formerly known as *Candida krusei.* [i]CDC tentative breakpoints for *Candida auris* (CDC C. auris, 2024). [j]*Papiliotrema laurentii*, formerly known as *Cryptococcus laurentii*. [k]*Meyerozyma guilliermondii*: formerly known as *Candida guilliermondii*. [l]*Trichomonascus ciferrii*: formerly known as *Candida ciferrii*. [m]*Debaryomyces hansenii*: formerly known as *Candida famata.* [n]*Yarrowia lipolytica*: formerly known as *Candida lipolytica*.

5. DISCUSSION

The establishment of a national antimicrobial resistance (AMR) surveillance system in the Maldives represents a major advancement in the country's public-health infrastructure. This first national report provides a comprehensive overview of resistance patterns across a wide range of pathogens and healthcare settings, offering valuable insights into the epidemiology of AMR in the Maldives. When interpreted in the context of global and regional trends, the findings highlight both shared challenges and areas of particular concern for the Maldivian health system.

5.1 Comparison of AMR Levels and Trends with Regional and Global Patterns

The overall burden of multidrug resistance (MDR) in the Maldives - 32.5% of all isolates of AMR priority pathogens - is consistent with levels reported in many low- and middle-income countries (LMICs), particularly in South and Southeast Asia, where AMR prevalence is among the highest globally. The high MDR rates observed in *Escherichia coli* (40.4%) and *Klebsiella pneumoniae* (27.3%) mirror global patterns in which Enterobacterales are major contributors to the AMR burden. Rising resistance to third-generation cephalosporins and fluoroquinolones among Enterobacterales has been widely documented across Asia, driven by widespread antibiotic use, limited stewardship, and high community transmission. The Maldives' increasing resistance trends from 2019 to 2024 align with these regional trajectories.

Carbapenem resistance among Enterobacterales remains a critical global concern, with many countries reporting rapid expansion of carbapenemase-producing organisms. While the Maldives' surveillance system does not yet routinely confirm carbapenemase production, increasing levels of phenotypical resistance to carbapenems, as well as the observed levels of possible XDR in *K. pneumoniae* (15.2%) and *E. coli* (4.0%) strongly suggest that carbapenem resistance is emerging. These values are lower than those reported in some South Asian countries, where carbapenem resistance in *K. pneumoniae* often exceeds 30–50%, but they nonetheless signal a need for strengthened laboratory capacity and early containment strategies.

The situation for non-fermenting gram-negative organisms is particularly concerning. *Acinetobacter* spp. in the Maldives show extremely high levels of resistance, with 35.1% MDR, 30.6% possible XDR, and 13.8% possible PDR. These figures are comparable to some of the highest rates reported globally, including in South and Southeast Asia, where *Acinetobacter* resistance is often driven by hospital-associated transmission and limited IPC capacity. Similarly, *Pseudomonas aeruginosa* shows substantial resistance, including 6.5% possible PDR, reflecting global challenges in managing this intrinsically resistant pathogen. These findings underscore the need for targeted interventions in hospital settings, including improved environmental hygiene, device-associated infection prevention, and antimicrobial stewardship.

Among gram positive organisms, the Maldives reports a high prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA), with rates approaching 40% in 2024. This aligns with global MRSA trends, where many countries report rates between 20% and 50%. The upward trend since 2022 is notable and warrants further investigation into community- and healthcare-associated transmission dynamics. In contrast, vancomycin-resistant enterococci (VRE) remain rare in the Maldives, consistent with lower VRE prevalence in many Asian countries compared to Europe and North America.

Overall, the Maldives' AMR patterns reflect a combination of global trends - particularly the rise of resistant Enterobacterales and MRSA - and regionally elevated resistance in non-fermenters. The data highlight the urgent need for sustained investment in stewardship, diagnostics, and IPC to prevent further escalation.

5.2 Implications for Clinical Care and the Healthcare System

The high levels of resistance observed in key pathogens have direct implications for clinical management. Increasing resistance to cephalosporins and fluoroquinolones reduces the effectiveness of commonly used empiric therapies for urinary tract infections, intra-abdominal infections, and sepsis. The growing reliance on carbapenems, combined with increasing resistance to carbapenems, raises concerns about the future availability of effective treatment options. The presence of possible PDR isolates - particularly among *Acinetobacter* spp. and *P. aeruginosa* - indicates that some infections may already be approaching therapeutic failure with available antibiotics.

From a public-health perspective, the findings underscore the importance of strengthening antimicrobial stewardship programs across all levels of care, improving diagnostic capacity, and enhancing infection prevention and control practices. The Maldives' participation in WHO GLASS provides a platform for benchmarking progress and aligning national strategies with global best practices.

5.3 Limitations of the Study

While this report provides the most comprehensive AMR dataset ever assembled in the Maldives, several limitations must be acknowledged when interpreting the findings:

- **Surveillance coverage and representativeness**: Although 196 healthcare facilities and 27 laboratories are part of the national network, only 19 out of 27 laboratories submitted data for 2024. This may introduce selection bias, as facilities with stronger laboratory capacity are more likely to contribute data. Some islands and atolls may be underrepresented.
- **Laboratory capacity and testing practices**: Not all laboratories use automated identification or susceptibility testing systems, and AST methods vary across sites. Differences in testing panels, manual interpretation, and quality assurance participation may affect data comparability. Carbapenemase confirmation is not routinely performed, limiting the ability to classify CRE accurately.
- **Data completeness and clinical metadata**: Clinical and demographic data were available for only 79% of laboratories. Limited information on patient comorbidities, prior antibiotic exposure, and healthcare-associated vs. community-associated infections limits epidemiological interpretation.
- **Modified definitions for XDR and PDR**: Due to limited antibiotic testing panels, the report uses modified definitions of possible XDR and PDR. These categories may over- or underestimate true resistance levels and should be interpreted cautiously.
- **Trend analysis constraints**: Longitudinal data were available from only three major hospitals (IGMH/DH, ADK, TTH). National trends may therefore not fully reflect changes across the entire health system.

5.4 Conclusion

Despite these limitations, the Maldives has successfully established a foundational AMR surveillance system that provides critical insights into national resistance patterns. The findings reveal high, and in some cases increasing levels of AMR, consistent with regional and global trends.

Strengthening laboratory capacity, expanding surveillance coverage, standardizing testing practices, and enhancing stewardship and IPC programs will be essential to mitigate the growing threat of AMR and safeguard the effectiveness of antimicrobial therapy in the Maldives.

6. POLICY RECOMMENDATIONS

6.1. Improve awareness and understanding of AMR

- Strengthen nationwide AMR awareness campaigns targeting the public, emphasizing the risks of inappropriate antibiotic use and the importance of completing prescribed treatments.
- Integrate AMR, antimicrobial stewardship (AMS), and infection prevention and control (IPC) topics into continuing professional development for clinicians, nurses, pharmacists, and laboratory staff.
- Promote community engagement through schools, local councils, and civil society to support responsible antibiotic use and hygiene practices.

6.2. Strengthen knowledge and evidence through surveillance and research

- Expand routine AMR data submission to ensure full participation of all enrolled laboratories and progressively include additional healthcare facilities.
- Standardize laboratory methods, AST panels, and interpretation guidelines (CLSI/EUCAST) across all sites to improve data comparability.
- Enhance the capacity of the National Reference Laboratory for AMR to perform confirmatory testing, carbapenemase detection, and molecular characterization of emerging resistance.
- Improve completeness of clinical metadata through better integration of LIS/HIS systems and standardized reporting templates.
- Continue contributing national data to WHO GLASS to support global benchmarking and trend analysis.

6.3. Reduce the incidence of infection through effective IPC

- Strengthen IPC programs in all healthcare facilities, with dedicated IPC focal points, regular audits, and compliance monitoring.
- Improve environmental hygiene, sterilization practices, and device- and procedure-associated infection prevention, particularly in high-risk units such as ICUs and surgical wards.
- Ensure consistent implementation of standard precautions, including hand hygiene, safe injection practices, and appropriate PPE use.
- Promote vaccination programs (e.g., pneumococcal, influenza) to reduce infection burden and antibiotic demand especially, for the vulnerable population.

6.4. Optimize the use of antimicrobial medicines in human health

- Develop and disseminate national antimicrobial treatment guidelines based on local cumulative antibiograms, updated annually.
- Establish AMS committees in all secondary and tertiary hospitals to monitor antibiotic use, review prescribing practices, and provide clinician feedback.
- Continue and strengthen antimicrobial consumption monitoring not only at the national level (sales data) but also at the facility level (consumption data, DDD), using the WHO AWaRe classification to guide stewardship interventions.

- Strengthen regulation of antibiotic dispensing, ensuring enforcement of prescription-only policies and oversight of private pharmacies.

6.5. Ensure sustainable investment in AMR activities

- Secure long-term financing for AMR surveillance, laboratory strengthening, AMS, and IPC programs through national budgets and partner support.
- Prioritize procurement of essential diagnostics, including automated AST systems, MALDI-ToF, and molecular platforms.
- Ensure reliable supply chains for quality-assured antibiotics, laboratory reagents, and IPC materials.
- Support workforce development through targeted training, mentorship programs, and incentives to retain skilled laboratory and clinical staff.
- Collaborate with academic research institutions to support AMR research and strengthen surveillance findings, informing and enhancing graduate-level curricula.

7. ANNEX

Annex 7.1 Abbreviations

%I	Percent intermediate
%MDR	Percent multidrug-resistant
%NS	Percent non-susceptible
%R	Percent resistant
%S	Percent susceptible
A. baumannii (ACI)	*Acinetobacter baumannii*
ACP-MLE	American College of Physicians-Medical Laboratory Evaluation
AMR	Antimicrobial resistance
AMS	Antimicrobial stewardship
API	Analytical Profile Index
AST	Antimicrobial susceptibility test
ATCC	American Type Culture Collection
BLI	Beta-lactamase inhibitor
C. albicans	*Candida albicans*
CA	Community-associated
CAESAR	Central Asian and Eastern European Surveillance of AMR
CAP	College of American Pathologists
CAP-Pt	CAP proficiency testing
CLSI	Clinical and Laboratory Standards Institute
CSF	Cerebrospinal fluid
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
EQAS	External quality assurance system
ESBL	Extended spectrum beta-lactamase
ESCR	Extended spectrum cephalosporin resistant
EUCAST	European Committee for Antimicrobial Susceptibility Testing
E. coli (ECOL)	*Escherichia coli*
E. faecalis (EFA)	*Enterococcus faecalis*
E. faecium (EFM)	*Enterococcus faecium*
FQR	Fluoroquinolone-resistant
GAS	Group A streptococci (*Streptococcus pyogenes*)
GBS	Group B streptococci (*Streptococcus agalactiae*)
GLASS	Global AMR Surveillance System (WHO)
HAI	Healthcare-associated infections
HIRMD	Health Information Management and Research Division
HIS	Hospital information system
HL	High level
HPA	Health Protection Agency
ICU	Intensive care unit
IPC	Infection prevention and control
IZD	Inhibition zone diameter (mm)
JCI	Joint Commission International
K. pneumoniae (KPN)	*Klebsiella pneumoniae*
LIS	Laboratory information system
MALDI-ToF	Matrix-assisted Laser-Desorption-Ionization Time of Flight
MDR	Multidrug resistance
MFDR	Maldives Food and Drug Authority
MIC	Minimal inhibitory concentration
MoH	Ministry of Health
MRGN	multi-resistant gram negative (rods)
MSSA	Methicillin- (oxacillin-) susceptible *S. aureus*
MRSA	Methicillin- (oxacillin-) resistant *S. aureus*
M. tuberculosis	*Mycobacterium tuberculosis*
NA	Not applicable
N. gonorrhoeae	*Neisseria gonorrhoeae*
N	Number
NM	non-meningitis
NRL-AMR	National Reference Laboratory for Antimicrobial Resistance
NS	non-susceptible
P. aeruginosa (PAE)	*Pseudomonas aeruginosa*
PHC	Primary Healthcare Center
PDR	Pandrug-resistant
QARD	Quality Assurance and Regulation Division
QC	Quality COntrol
R	Intrinsically resistant
RCPA	Royal College of Pathologists of Australia
REQAS	Regional External Quality Assurance Scheme
Resp.	Respiratory
SAL	Salmonella species
S. aureus (SAU)	*Staphylococcus aureus*
S. pneumoniae (SPN)	*Streptococcus pneumoniae*
SEARO	Southeast-Asia Regional Office
sp., spp.	Species
VRE	Vancomycin-resistant Enterococci
WHO	World Health Organization
XDR	Extensively drug resistant

Annex 7.2 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
ETP	Ertapenem
FCT	5-Fluorocytosine
FEP	Cefepime
FLC	Flucloxacillin
FLU	Fluconazole
FOS	Fosfomycin
FOX	Cefoxitin
FQ	Fluoroquinolones
GEH	Gentamicin (high level)
GEN	Gentamicin
IPM	Imipenem
LNZ	Linezolid
LVX	Levofloxacin
MEM	Meropenem
MET	Methicillin
MFX	Moxifloxacin
MIF	Micafungin
MNO	Minocycline
MUP	Mupirocin
NIT	Nitrofurantoin
NOR	Norfloxacin
OXA	Oxacillin
PEN	Penicillin G
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 7.3 List of Figures

Annex 7.4 List of Tables

Annex 7.5: Distribution of isolates/patients, by island

Table 4.1.2. Distribution of isolates/patients, Maldives, 2024, by island

Island	Isolates (N)	Isolates (%)	Patients (N)
Male	11’148	52.7	7’360
Hulhumale	6’793	32.1	5’390
Kulhudhuffushi	1’029	4.9	867
Hithadhoo	399	1.9	314
Thinadhoo	360	1.7	295
Ungoofaaru	314	1.5	196
Fuvamulah	258	1.2	212
Laamu Gan	190	0.9	161
Eydhafushi	141	0.7	141
Dhidhdhoo	120	0.6	92
Veymandoo Island	118	0.6	106
Nellaidhoo	75	0.4	68
Nilandhoo	58	0.3	58
Villingili	55	0.3	45
Muli	16	0.1	15
Makunudhoo	14	0.1	14
Nolhivaran	13	0.1	10
Hanimadhoo	12	0.1	12
Nolhivaranfaru	11	0.1	10
Kurinbi	8	0.0	7
Kumundhoo	4	0.0	4
Maamendhoo	4	0.0	4
Neykurendhoo	4	0.0	4
Konday	3	0.0	2
Naivaadhoo	3	0.0	2
Finey	2	0.0	2
Funadhoo	2	0.0	2
Gemanafushi	2	0.0	2
Hirimaradhoo	1	0.0	1
Kolamafushi	1	0.0	1
Total	**21’158**	**100**	**15’397**

Annex 7.6: Distribution of isolates/patients, by nationality

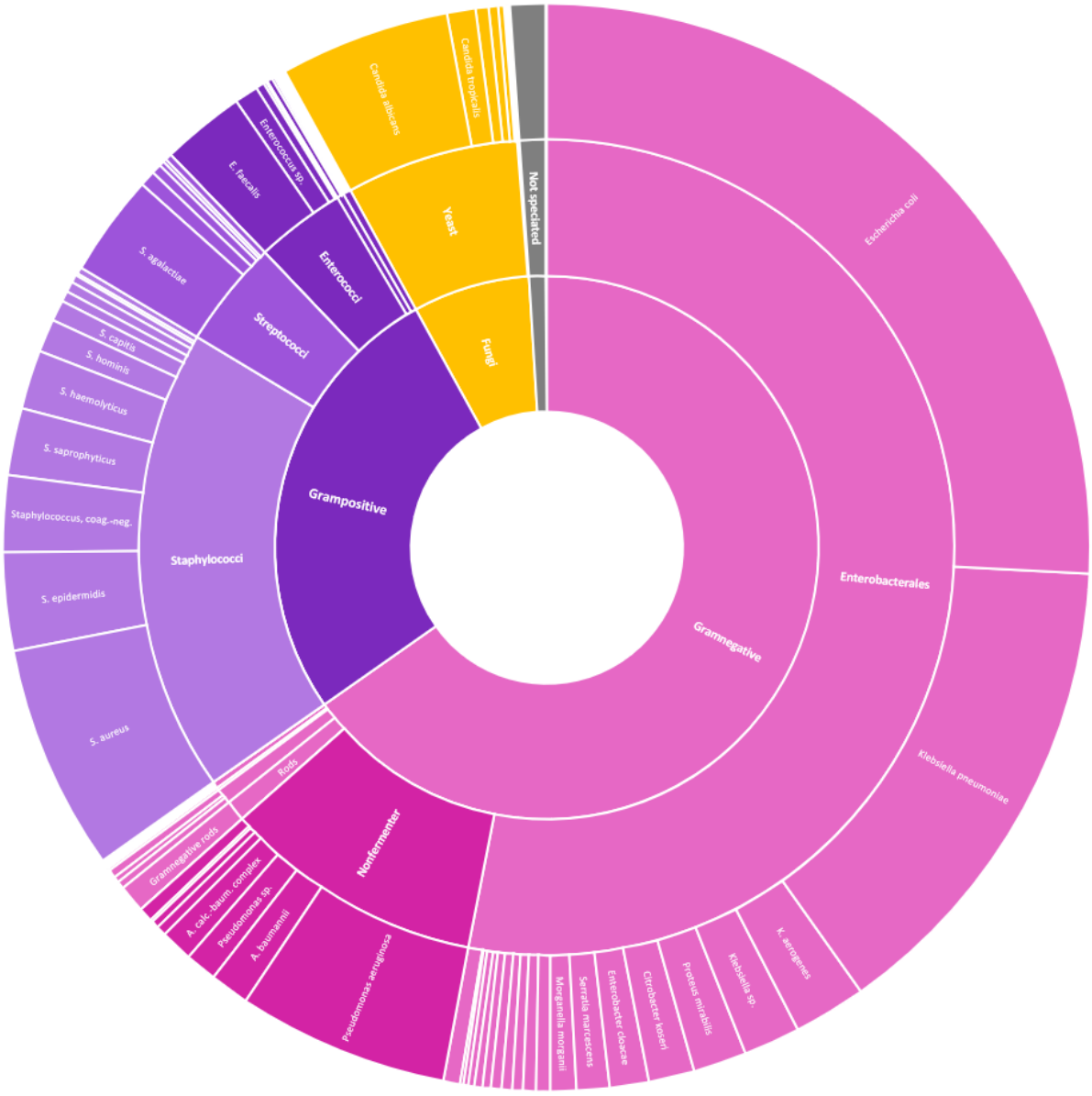
Table 4.1.4. Distribution of patients, Maldives, 2024, by nationality

Nationality	Isolates (N)	Isolates (%)	Patients (N)
Maldivian	3’945	18.6	3’294
Indian	22	0.1	20
Bangladeshi	12	0.1	11
Sri Lankan	6	0.0	6
Nepalese	5	0.0	5
Egyptian	3	0.0	3
Kazakhstani	3	0.0	2
British	2	0.0	1
Italian	2	0.0	2
Swiss	2	0.0	1
Expatriate	1	0.0	1
German	1	0.0	1
Malaysian	1	0.0	1
Sudanese	1	0.0	1
Tunisian	1	0.0	1
Unknown	17’151	81.1	12’030
Total	**21’158**	**100.0**	**15,380**

Note: Nationality was known for n=4’007 (18.9 %) isolates only.

Annex 7.7: Distribution of isolates: organisms, by genus and species

Figure 4.1.7. Distribution of isolates, Maldives, 2024, organisms by genus and species



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