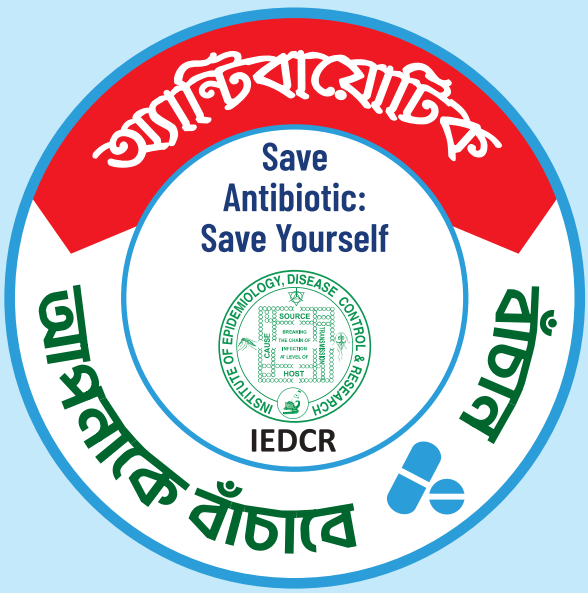
Report on

Antimicrobial Resistance Surveillance Bangladesh, 2025



Sectoral Co-ordination center (Human Health) and
National Reference Laboratory (NRL) for AMR Surveillance
Institute of Epidemiology, Disease Control & Research (IEDCR)
Ministry of Health and Family Welfare (MOH&FW)
Government of the People's Republic of Bangladesh

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Report on National Antimicrobial Resistance Surveillance, Bangladesh, 2025

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Abbreviations

AMC	Antimicrobial Consumption
AMR	Antimicrobial Resistance
AMRSurME	AMR Surveillance Monitoring and Evaluation
AMS	Antimicrobial Stewardship
AMU	Antimicrobial Use
AqH	Aquatic Health
ARC	Antimicrobial Resistance Containment
ARCH	Antibiotic Resistance in Communities and Hospitals
AST	Antimicrobial Susceptibility Testing
AWaRe	Access, Watch, Reserve
BCDS	Bangladesh Chemist & Druggist Samity
BITID	Bangladesh Institute of Tropical and Infectious Diseases
BLRI	Bangladesh Livestock Research Institute
BMMS	Bangladesh Medical Microbiology Society
BSL	Biosafety Level
CAMS	Comprehensive AMR Data Management System
CAPTURA	Capturing Data on AMR Patterns and Trends in Use in Regions of Asia
CCU	Coronary Care Unit
CDC	Communicable Disease Control
CDIL	Central Disease Investigation Laboratory
CLSI	Clinical and Laboratory Standards Institute
CMCH	Chittagong Medical College and Hospital
CoNS	Coagulase-negative Staphylococci
CoxMCH	Cox's Bazar Medical College and Sadar Hospital
CRE	Carbapenem-Resistant Enterobacterales
DDD	Defined Daily Doses
DGDA	Directorate General of Drug Administration
DGHS	Directorate General of Health Services
DLS	Department of Livestock Services
DMCH	Dhaka Medical College and Hospital
DoE	Department of Environment
DoF	Department of Fisheries
DRPM	Doripenem
EQA	External Quality Assurance
ESBL	Extended-Spectrum Beta-Lactamase
ETP	Effluent Treatment Plant
FAO	Food and Agriculture Organization of the United Nations
FDIL	Field Disease Investigation Laboratory
FETP	Field Epidemiology Training Program
FFCGB	Fleming Fund Country Grant to Bangladesh
FFCRG	Fleming Fund Centre for Regional Grants
FMCH	Faridpur Medical College and Hospital
GAP	Global Action Plan on AMR
GBD	Global Burden of Disease
GDP	Gross Domestic Product
GHSA	Global Health Security Agenda
GLASS	Global Antimicrobial Resistance and Use Surveillance System
GoB	Government of Bangladesh
HAI	Healthcare-Associated Infection
HICs	High-Income Countries
ICU	Intensive Care Unit
ID	Identification
IEDCR	Institute of Epidemiology, Disease Control and Research
IPC	Infection Prevention and Control
IPD	Inpatient Department
IPH	Institute of Public Health
IQA	Internal Quality Assurance
IQC	Internal Quality Control
JCI	Joint Commission International
JIMCH	Jahurul Islam Medical College and Hospital
KMCH	Khulna Medical College and Hospital

LBMs	Live Bird Markets
LMICs	Low- and Middle-Income Countries
LSHTM	London School of Hygiene & Tropical Medicine
MDR	Multidrug Resistance
MMCH	Mymensingh Medical College and Hospital
MoHFW	Ministry of Health and Family Welfare
MRSA	Methicillin-Resistant Staphylococcus aureus
NAP	National Action Plan
NAPS	National Antimicrobial Point Prevalence Survey
NCC	National Coordination Center
NEQAS	National External Quality Assurance Scheme
NIC	National Influenza Centre
NRL	National Reference Laboratory
NTC	National Technical Committee
OECD	Organisation for Economic Co-operation and Development
OPD	Outpatient Department
ORT	Oral Rehydration Therapy
PCR	Polymerase Chain Reaction
PDR	Pan-Drug Resistance
PEA	Political-Economic Analysis
PICU	Pediatric Intensive Care Unit
PPS	Point Prevalence Survey
PRTC	Poultry Research and Training Centre
PT	Proficiency Testing
QC	Quality Control
QoC	Quality of Care
RMCH	Rajshahi Medical College and Hospital
RP	Rohingya Population
RpMCH	Rangpur Medical College and Hospital
RT-PCR	Real-Time Polymerase Chain Reaction
SCC	Sectoral Coordination Center
SDG	Sustainable Development Goals
SOMCH	Sylhet Osmani Medical College and Hospital
SOPs	Standard Operating Procedures
STP	Sewage Treatment Plant
TrACSS	Tripartite AMR Country Self-Assessment Survey
UAMCH	Uttara Adhunik Medical College and Hospital
UHL	United Hospital Limited
UNEP	United Nations Environment Programme
UNGA	United Nations General Assembly
US-CDC	Centers for Disease Control and Prevention, Atlanta, USA
UTI	Urinary Tract Infection
VRE	Vancomycin-Resistant *Enterococci*
VRSA	Vancomycin-Resistant *Staphylococcus aureus*
WAAW	World Antimicrobial Awareness Week
WASH	Water, Sanitation, and Hygiene
WB	World Bank
WHO	World Health Organization
WOAH	World Organisation for Animal Health
XDR	Extensively Drug-Resistant

Glossary

Antibiogram: The report generated by analysis of antimicrobial susceptibility test results (usually from a single health care facility) from a defined period of time that reflects the percentage of first isolates (per patient) of a given species or organism group that is susceptible to each of the antimicrobial agents routinely tested. It helps guide the selection of appropriate antibiotics for treating infections.

CRE (Carbapenem-resistant *Enterobacteriaceae*): A family of Gram-negative bacteria that are resistant to carbapenem antibiotics, which are often considered the last line of defense against bacterial infections. The resistance mechanism in CRE is primarily due to the production of carbapenemase enzymes, which break down the antibiotic.

Isolate: Isolate refers to a pure culture of microorganisms obtained from clinical samples/specimens through laboratory culture, which can subsequently be used for downstream analyses.

MDR (Multidrug resistance): MDR is defined as non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories.

MRSA (Methicillin-resistant *Staphylococcus aureus*): Strains of *Staphylococcus aureus* that are resistant to penicillinase-resistant penicillin such as oxacillin, methicillin, cloxacillin, and nafcillin. These strains are resistant to all beta-lactam antibiotics, including cephalosporins and carbapenems.

PDR (Pan drug resistance): PDR is defined as non-susceptibility to all agents in all antimicrobial categories (i.e., no agents tested as susceptible for that organism)

Sample: A sample is a unit taken from a specimen. Samples include both isolates and specimens with no growth.

SDG indicator 3.d.2: Proportion of bloodstream infection due to MRSA) and *E.coli* resistant to third-generation cephalosporins (e.g., ESBL) among patients seeking care and whose blood sample is taken and tested. Presumptive MRSA isolates as defined by oxacillin minimum inhibitory concentration (MIC) and cefoxitin disc diffusion tests according to current internationally recognized clinical breakpoints (e.g., EUCAST or CLSI). *E.coli* resistant to third-generation cephalosporins: *E.coli* isolates that are resistant as defined by current internationally recognized clinical breakpoints for third-generation cephalosporins (e.g., EUCAST or CLSI), specifically ceftriaxone or cefotaxime or ceftazidime.

Specimen: A specimen is a discrete portion of a body fluid or tissue or other sample associated with the human body taken for laboratory diagnosis or analysis. In other words, it is a sample of biological origin intended for examination by a medical laboratory. Example: Blood, urine, stool, etc.

VRE (Vancomycin-resistant *Enterococci*): Strains of *Enterococcus* bacteria that have developed resistance to the antibiotic vancomycin, which is often used to treat serious infections. These bacteria are typically found in the gastrointestinal tract and can cause severe infections, especially in healthcare settings. The resistance to vancomycin is often due to genetic mutations that alter the target site of the antibiotic, rendering it ineffective.

XDR (Extensively drug resistance): XDR is defined as non-susceptibility to at least one agent in all but two or fewer antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two categories)

Preface

Antimicrobial resistance (AMR) poses a serious threat to global health and development, and Bangladesh is not an exception. Urgent action using a One Health Approach is needed. As we present the Annual Report of the National AMR Surveillance in Bangladesh for 2025, we find ourselves at a critical point in public health. The impact of AMR is strongly felt in Bangladesh, where the overuse and misuse of antibiotics have created a challenging environment for resistant pathogens.

This report is a collaborative effort of various stakeholders, including healthcare professionals, researchers, and governmental and non-governmental organizations. Thirteen medical colleges and institutes are included as sentinel sites for the AMR case-based surveillance, and twenty-two laboratories are included in laboratory-based AMR surveillance. All the sentinel sites send laboratory and epidemiological data weekly, and the central team at the Institute of Epidemiology, Disease Control and Research (IEDCR) regularly analyzes and updates the data. The data analyzed is uploaded yearly to the World Health Organization's (WHO) Global Antimicrobial Resistance System (GLASS) platform through the Communicable Disease Control Program of the Directorate General of Health Services (CDC, DGHS).

This report highlights our continued commitment to monitoring, analyzing, and disseminating information on the trends of AMR in Bangladesh. It consolidates data from diverse healthcare facilities, laboratories, and research institutions, emphasizing our collaborative initiatives and deepening our understanding of the complexities of AMR.

Alarming trends have been observed throughout the surveillance period. The rise in resistance rates for key pathogens underscores the urgency of implementing effective antimicrobial stewardship programs and enhancing infection prevention and control measures.

As we look to the future, we must work together with relevant stakeholders to tackle the complex challenges posed by AMR. The findings presented in this report not only reflect our current situation but also serve as a guide for strategic interventions in the coming years. By collaborating and fostering innovation, we can create meaningful solutions in the urgent fight against AMR.

We express our sincere gratitude to the surveillance physicians, nurses, laboratory personnel, project facilitators, and others who supported our activities with utmost sincerity at the sites. We would like to acknowledge the patients. We are thankful to the private laboratory personnel who have supported us with their valuable data. IEDCR is also thankful to the WHO for its continuous financial and technical support. IEDCR also acknowledges the Fleming Fund Country and Regional Grant and the Centers for Disease Control and Prevention (CDC), Atlanta, USA, for their support.

Your commitment and teamwork are crucial in combating antimicrobial resistance. Together, we can protect the effectiveness of our current antimicrobial agents and create a better environment for the citizens of Bangladesh.

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Editorial

Antimicrobial resistance (AMR) is no longer a distant forecast; it is a present reality reshaping clinical choices, agricultural practices, and public trust in medicine. AMR poses a serious threat to global health and development, and Bangladesh is no exception. This report highlights our continued commitment to monitoring, analyzing, and disseminating information on the trends of AMR in Bangladesh.

In 2025, our national AMR surveillance system stands at a critical juncture: no longer in its infancy, yet far from complacency. This year's AMR Surveillance Report of Bangladesh builds on nearly a decade of learning, refinement, and partnership, transforming data into direction and evidence into action.

Our first consolidated report, covering 2016–2023, documented the journey of building a nationwide surveillance platform, and the 2024 report sharpened the focus on site-specific antibiograms and robust analysis. The 2025 report takes the next step: using mature, higher-quality data to illuminate trends, identify emerging threats, and directly inform clinical practice, stewardship programmes, and policy decisions.

The strength of our system lies in its diversity. Case-based surveillance from our sentinel hospitals continues to provide rich, patient-level insights, while laboratory-based surveillance from both public and private facilities contributes to breadth and scale. Together, they offer a more nuanced picture of resistance patterns across population groups, geographies, and levels of care, an evolving example of effective public-private collaboration in public health.

This year, we have further strengthened data quality assurance, standardized laboratory methods, and expanded digital reporting. The 2025 report also places greater emphasis on translating surveillance outputs into tools that can be immediately used at the bedside and in programmatic planning. Updated national and site-specific antibiograms, together with the revised mini handbook for clinicians, aim to guide rational empirical therapy and safeguard the effectiveness of our remaining treatment options.

Preparing this report once again demanded a collective effort from clinicians, microbiologists, laboratory technologists, data managers, and field teams at all surveillance sites, as well as from the dedicated staff of the sectoral coordination center and the National Reference Laboratory (NRL) at IEDCR, supported by our development partners, particularly WHO. Their commitment turns isolated laboratory findings into a coherent national signal.

This report will be available on the IEDCR website. We invite constructive feedback, fresh ideas, and collaboration from all stakeholders. AMR will not be defeated by surveillance alone, but without strong surveillance, we cannot hope to win. Let this report be both a mirror of our current reality and a compass for the actions we must take next.

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Executive Summary

The 2025 AMR report presents data collected from 33 laboratories across eight divisions of Bangladesh from July 2024 to June 2025. The total sample (96,477) represents both case-based surveillance samples (17,620) from 11 medical colleges and institutes (mostly public) and pathogen isolates (78,857) from 24 laboratories of lab-based surveillance sites (mostly private). The culture positivity rate among case-based samples was 21% (n=3,653), and after cleaning bringing the total number of isolates to 82,497 from both surveillance types (Here, *E. coli* has been excluded from stool sample as it may represent normal flora of the gut and test for detection of pathogenic strains could not be done). So, the contribution of case-based surveillance includes 4.42% of total isolates.

Geographically, 57.9% of the total samples were from Dhaka Division, followed by 21.5% samples from Chattogram Division. More than half (60%) of the samples were from female patients , and the largest proportion of samples (16.9%) was collected from the 21 to 30 years age group.

Sample and isolate distribution

The combined dataset shows a continued predominance of urine specimens (55.9%) followed by blood (15.2%) and persistent differences in pathogen distribution and susceptibility by patient location (OPD, ward, ICU). The high proportions of urine and blood samples across all regions suggest that diagnostic testing for conditions requiring these specimen types (e.g., urinary tract infections, systemic infections, general health screenings) are the most prevalent or prioritized.

Key pathogen distribution and sample-level findings

E. coli followed by *K. pneumoniae* were the most commonly isolated pathogens collected from different specimens all over the country in eight divisions. *E. coli* remains the leading isolate in urine samples, whereas *S. Typhi, S. aureus, K. pneumoniae, Salmonella* spp. and *E. coli* are the most commonly isolated pathogens in blood, SSTI, LRTI, stool and genital samples, respectively.

Antibiogram of different sample

General Trend: Across all specimen types, Gram-negative organisms (especially *Acinetobacter* spp. and *Klebsiella pneumoniae*) demonstrate alarming multidrug resistance, often leaving Colistin or Carbapenems as the few remaining options. Gram-positive organisms generally retain high sensitivity to Linezolid and Vancomycin.

Urine: *E. coli* shows high resistance to Ampicillin (21%) but remains susceptible to Nitrofurantoin (78%) and Amikacin (88%). *Enterococcus* spp. shows excellent sensitivity to Vancomycin (91%) and Linezolid (88%).

Blood: *Salmonella* Typhi retains good sensitivity to Ceftriaxone (95%) and Meropenem (98%). *E. coli* shows varying resistance, retaining 80% sensitivity to Amikacin but dropping to 29% for Ceftriaxone.

SSTI (Skin and Soft Tissue): *S. aureus* retains excellent sensitivity to Vancomycin (96%) and Linezolid (89%) but Azithromycin performed poorly against it (23%). Among Gram-negatives, *Acinetobacter* spp. is highly resistant to carbapenems like Meropenem (34%), requiring Colistin (96%) for effective treatment. *E. coli* shows a disparity between Amikacin (79%) and Ampicillin (8%).

LRTI (Lower Respiratory Tract Infection): Gram-negative bacteria like *Acinetobacter* spp. display extreme resistance, with susceptibility often falling below 20% for most agents, while better sensitivity is observed against Colistin (96%). *Pseudomonas aeruginosa* also retains better sensitivity to Colistin (94%). Gram-positives like *S. aureus* show 100% sensitivity to Vancomycin in IPD settings.

Stool: *Vibrio cholerae* remains largely susceptible to Tetracycline (90%) and Azithromycin (84%).

Genital: *S. aureus* is highly sensitive to Linezolid (89%) and Gentamicin (73%). *N. gonorrhea* has shown high sensitivity to Ceftriaxone (88%), but extreme resistance to Azithromycin (21%).

Fungal Infections: Among the total specimens collected from laboratories across Bangladesh, fungal pathogen specimens constituted less than 1%. *Candida* spp. were predominant (99%) among the fungal pathogens, with *Candida tropicalis* is the most commonly identified (42%), followed by *Candida albicans* (33%). *Candida tropicalis* shows moderate susceptibility to Caspofungin (50%) and Fluconazole (50%), but high susceptibility to Micafungin (91%). *Candida albicans* are fully susceptible to Micafungin (100%), while showing significant resistance to Fluconazole (36%).

Overall AMR Burden and Critical Priority Pathogens

Overall Trends: AMR burden has increased relative to 2024. Historical trend analysis shows a concerning increase in Carbapenem-Resistant Enterobacterales (CRE); for instance, Imipenem resistance in *K. pneumoniae* rose from 23.1% in 2024 to 29.1% in 2025, and in *E. coli* from 8.4% to 9.8%.

***Acinetobacter* spp.:** Carbapenem-resistant *Acinetobacter* spp. remains a critical threat with resistance to Meropenem rising nationally from 68.5% (2024) to 71.0% (2025). Rates are alarmingly high in tertiary centers, with *Acinetobacter* spp. showing 96% carbapenem resistance at Dhaka Medical College Hospital (DMCH) and 93% at Mymensingh Medical College Hospital (MMCH).

P. aeruginosa: This pathogen shows increasing resistance trends; Imipenem resistance rose from 32.9% (2024) to 37.7% (2025), while Meropenem resistance increased from 34.8% to 37.0%. Nationally, 39% of *P. aeruginosa* isolates are classified as Multidrug-Resistant (MDR).

ESBL Production: The proportion of suspected ESBL-producing *E. coli* in bloodstreams showed a sharp increase to 84.3% in the first half of 2025, compared to 64.8% in 2024, reinforcing concerns about compromised empirical cephalosporin efficacy.

MRSA: While the overall national MRSA rate in bloodstream infections is 53.9%, prevalence remains substantial in specific sites; for example, Khulna Medical College and Hospital (KMCH) has reported 67% MDR *S. aureus* isolates with oxacillin resistance at 41%.

MDR and Suspected PDR pathogen: Overall 46% of MDR bacteria is found while in ICU it is 89%. *E. faecium* shows the highest MDR pattern (74%). While overall 6% pathogen is found to be suspected PDR, in the ICU, 41% of the pathogen are suspected PDR.

Location-Specific Susceptibility and Clinical Setting Differences

ICU Susceptibility: ICU isolates consistently show the lowest susceptibility. For example, at DMCH, 72% of all positive isolates originated from the ICU, corresponding with extremely high resistance rates (e.g., 100% MDR *E. coli* and *K. pneumoniae* in that setting).

OPD Susceptibility: OPD isolates retain higher susceptibility than the ward and ICU.

Antibiotic-Specific Patterns

Carbapenems: Overall, *Acinetobacter* spp. confers the lowest susceptibility towards carbapenem. While *E. coli* retains relatively high susceptibility overall (90%), this drops sharply in ICU isolates to nearly half, Imipenem 53%, Meropenem 51%, indicating strong selection pressure in critical care settings.

Aminoglycosides: Susceptibility in *E. coli* generally remains moderate to high, while activity against *K. pneumoniae* and *P. aeruginosa* is variable and substantially reduced in ICU isolates.

Oral Agents: Common oral agents show poor activity. *E. coli* in urine shows only 21% susceptibility to Ampicillin and 42% to Ciprofloxacin, while susceptibility frequently fall down in blood, ward, and ICU isolates.

Urinary Agents: Fosfomycin (93% susceptibility) and Nitrofurantoin (78% susceptibility) remain reliable for *E. coli* in urine.

Antibiotic Use

From the case-based surveillance, the antibiotic use data of the patients is collected. During the reporting period, 15,844 antibiotic use data have been collected. Among them, 48% data has been collected from the ICU of the different sentinel sites and 44% and 8% data from the indoor and outdoor patients, respectively. From 15,844 antibiotic prescriptions heavy reliance on broad-spectrum agents. Among the most used antibiotics at different sites. Ceftriaxone is at the top of the list. It is also the most used antibiotic in both Wards (41%) and the ICU (30%). In OPD, Azithromycin (24%) is the topmost used drug. Ceftriaxone is the overall topmost prescribed antibiotic.

ICU Prescribing: Although ceftriaxone is the most used drug It is immediately followed by Meropenem, accounting for 25% of all ICU prescriptions.

AWaRe (Access, Watch, Reserve) Categories: The use of Watch group antibiotics (like Ceftriaxone and Meropenem) is elevated. Reserve group antibiotics like Linezolid are detected in low numbers (e.g., n=5 documented cases in one analysis subset), primarily in ICU and wound swab samples, correlating with the high MRSA and VRE risks.

Site-Level Variability

This AMR report (July 2024-June 2025) analyzes data from 11 sites, revealing positive growth rates between 15% (RMCH) and 37% (RpMCH). DMCH, MMCH, and CMCH showed high ICU isolate percentages, while BITID had 74.3% from OPD. Urine was a prevalent sample type at RpMCH, RMCH, UAMCH, CoxMCH, and BITID.

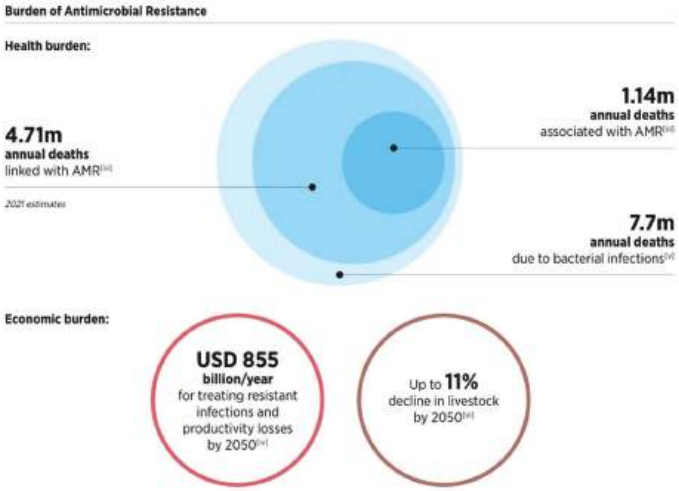
Aerobic Gram-negative bacteria predominated across all sites. Common pathogens varied: *Acinetobacter* spp. at DMCH (25.5%) and CMCH (41.9%); *K. pneumoniae* at MMCH (29.7%) and SBMCH (27.1%); and *E. coli* frequently dominated at RMCH (29.1%), RpMCH (32.2%), UAMCH (40.9%), CoxMCH (29.5%), and BITID (60.4%). *S. aureus* was highest at SOMCH (36.4%) and KMCH (23.3%).

Multidrug resistance (MDR) is alarming: *E. coli* showed 100% MDR at DMCH and SBMCH, with >90% at several other sites. *K. pneumoniae* was 100% MDR at DMCH, SBMCH, SOMCH, KMCH, and UAMCH. WHO critical priority pathogens, such as Carbapenem-resistant *Acinetobacter* spp., reached 96% at DMCH and 95% at RpMCH, while Ceftriaxone-resistant *E. coli* also reached 95% at DMCH. Ceftriaxone and Meropenem were the most common antibiotics.

Introduction

AMR has emerged as one of the most pressing global public health challenges of the 21st century. It occurs when microorganisms, including bacteria, viruses, fungi, and parasites, evolve mechanisms that render previously effective antimicrobial agents ineffective. As a result, common infections become increasingly difficult to treat, leading to higher morbidity and mortality, prolonged hospital stays, and escalating healthcare costs. Misuse and overuse of antimicrobials in human health, animal health, and agriculture, combined with inadequate infection prevention and control (IPC), poor sanitation, and insufficient hygiene practices, continue to accelerate this crisis. Recognizing its scale and urgency, the WHO has identified AMR as one of the top ten global public health threats.

In 2019, an estimated 4.95 million deaths were associated with bacterial AMR, including 1.27 million deaths directly attributable to drug-resistant infections, surpassing the combined annual global deaths from HIV/AIDS and malaria (1). Updated Global Burden of Disease (GBD) estimates indicate that in 2021, 4.71 million deaths were linked to AMR, of which 1.14 million were directly caused by resistant pathogens (2,3,4,5,6). Projections for 2050 are even more alarming, with forecasts suggesting 1.91 million deaths attributable to AMR and 8.22 million deaths associated with AMR globally (3, 4,5,6,7). South Asia, Latin America, and the Caribbean are expected to experience the highest all-age AMR mortality rates (3,4,5,6). (Figure 1)



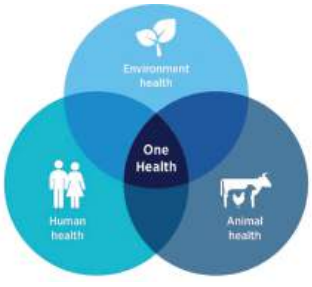
[Source: WHO Global Report on Antimicrobial Resistance 2024/2025]

Figure 1: The Health and Economic Burden of AMR

Beyond its health impact, AMR poses a profound economic threat. The World Bank (WB) estimates that by 2050, a high-AMR scenario could reduce global gross domestic product (GDP) by up to 3.8% annually and push an additional 28 million people into extreme poverty (4). Similarly, the Organization for Economic Co-operation and Development (OECD) projects that AMR could cost its member countries USD 3.5 billion annually in healthcare expenditures (5). Worldwide, treating drug-resistant infections may cost up to USD 412 billion each year, with an additional USD 443 billion lost due to reduced productivity (4,5,7).

Low- and middle-income countries (LMICs), including Bangladesh, bear a disproportionate burden of AMR. Resistance to key antibiotic classes, such as third-generation cephalosporins and fluoroquinolones, which are reported to be two to four times higher in LMICs compared to high-income countries (HICs). Limited diagnostic capacity, constrained access to effective antimicrobials, and weaker health systems further exacerbate the impact.

The One Health Perspective



[Source: WHO, WOAH, FAO, UNEP]

Figure 2: The One Health Triad

AMR is not confined to human health; it is a multisectoral challenge that spans humans, animals, plants, and the environment. Inappropriate use of antimicrobials in healthcare, livestock production, aquaculture, and crop cultivation accelerates the emergence and spread of resistance (8,9). Resistant organisms and genes disseminate through food chains, water systems, and soil, threatening ecosystems and undermining global health security.

The One Health approach provides a comprehensive framework (Figure 2) for addressing AMR through coordinated action across sectors. It emphasizes the interconnectedness of human, animal, and environmental health and calls for integrated strategies to promote responsible antimicrobial use, strengthen surveillance, and enhance IPC and biosecurity across all domains.

AMR and gender inequality

Women are disproportionately affected by AMR, contributing to gender inequality. For example, women's exposure to AMR and antimicrobial use is higher during pregnancy, childbirth, menstruation, and abortion. Additionally, women are more likely than men to serve as unpaid caregivers, and their greater presence on the front lines of caregiving roles in health and education further increases their vulnerability to AMR.

Global Antimicrobial Resistance and Use Surveillance System (GLASS)

Since its establishment in 2015, the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) has played a pivotal role in strengthening national AMR surveillance systems, harmonizing data collection, and generating evidence to guide policy and action (3,10). By the end of 2024, 127 countries and three territories had enrolled in GLASS, with more than 100 contributing AMR data for 2023 (3,10,11).

The Global AMR Report 2025 highlights widespread and increasing resistance to essential antibiotics, particularly among Gram-negative bacteria. First-line treatments for common bloodstream, urinary tract, and gastrointestinal infections are becoming less effective, with the highest burden observed in LMICs. GLASS data also indicate resistance among bloodstream infection pathogens is highest in the African Region, followed by the Eastern Mediterranean and South-East Asia Regions, with the lowest levels reported in the European and Western Pacific Regions (12). This distribution underscores the inequitable global burden of AMR. (Figure 3)

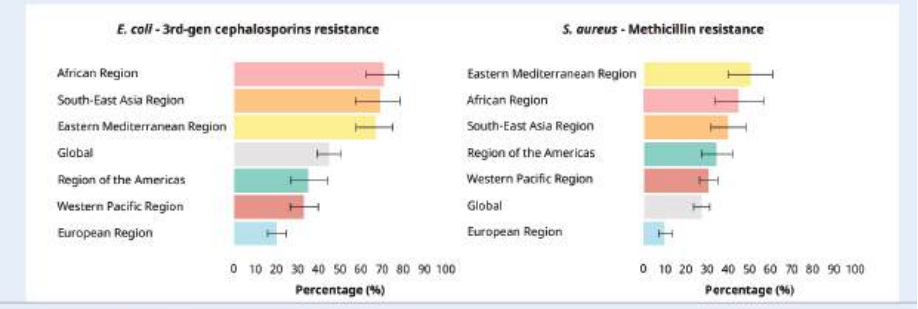


Figure 3: Percentage resistance to third-generation cephalosporins in *E. coli* and MRSA: global and regional estimates

Bangladesh formally joined GLASS in 2019. The national AMR surveillance system, coordinated by the IEDCR for the human health sector, has been operational since 2016. Surveillance data are routinely uploaded to the GLASS platform by CDC, DGHS. Antimicrobial consumption and use (AMC/AMU) data have been reported by the Directorate General of Drug Administration (DGDA) since 2023.

Global Response and Commitments

Since the adoption of the Global Action Plan on AMR (GAP) in 2015, countries have made significant progress in establishing the foundations of a coordinated global response. As of 2024, 178 countries had developed National Action Plans (NAPs) on AMR (13,19). Over 100 countries reported AMR data through the GLASS platform. The WHO AWaRe classification has strengthened antibiotic stewardship, with 58% of countries achieving the target of at least 60% "Access" antibiotic use (10,11,13,14,15,17).

In 2024, the United Nations General Assembly (UNGA) adopted a Political Declaration on AMR, setting ambitious global targets for 2030, including a 10% reduction in AMR-related deaths compared with the 2019 baseline (14). Fully funded NAPs in at least 60% of countries. At least 80% of countries are able to test resistance in all bacterial and fungal GLASS pathogens (20). At least 70% of antibiotics used belong to the Access category (11,14,15). Universal basic water, sanitation, and hygiene (WASH) services in all healthcare facilities. At least 90% of countries meet the WHO minimum infection IPC programme requirements at the national level (16).

AMR Containment Activities in Bangladesh

Communicable Disease Control (CDC), Disease Control Division, Directorate General of Health Services (DGHS)
Focal Point for AMR Containment and National Coordination Center (NCC) for AMR Surveillance

The CDC program under the DGHS continues to lead national efforts to contain AMR through governance, coordination, and a One Health approach. During 2024–2025, Bangladesh's CDC program led comprehensive AMR containment activities guided by the National Strategy and Action Plan for AMR Containment 2023–2028 and supported by various international partners (21).

Key Governance Activities include the approval of Antimicrobial Stewardship (AMS) Guidelines for Healthcare Facilities and the establishment of One Health AMR Divisional Hubs to enhance coordination across the human, animal, and environmental health sectors. Awareness campaigns during World Antimicrobial Awareness Week (WAAW) 2024 reached healthcare providers, students, and community members nationwide through seminars, rallies, and media engagement.

Critical data collection efforts included the third phase of the Point Prevalence Survey (PPS) on antimicrobial use in tertiary public hospitals and the National Antimicrobial Prescribing Survey (NAPS) in selected healthcare facilities (18). These surveys provided valuable insights into antimicrobial use patterns and prescribing practices.

AMS pilot programs were implemented at various levels of healthcare, providing valuable lessons for national scale-up. Workshops on AMS and clinical engagement were conducted across seven medical colleges, fostering multidisciplinary collaboration and practical strategies. Laboratory capacity was strengthened through equipment upgrades, refurbishments, and training programs on AMR testing and data management. The Institute of Public Health (IPH) initiated environmental AMR surveillance.

Several guidelines and protocols were developed or updated, including the AMR Surveillance Strategy 2025–2030, Environmental Surveillance Protocol, and AMU Surveillance Protocol for Human Health. Progress was also made on protocols for measuring AMR-attributable mortality and managing AMR outbreaks in healthcare facilities.

Knowledge dissemination efforts included publishing newsletters, participating in the Tripartite AMR Country Self-Assessment Survey (TrACSS), and submitting data to the GLASS platform, contributing to global AMR monitoring efforts. These comprehensive activities demonstrate Bangladesh's commitment to addressing AMR through improved governance, awareness, surveillance, and capacity building across multiple sectors.

Figure 4: Images from workshop on National AMR week and strategy meetings, Bangladesh

The Institute of Epidemiology, Disease Control and Research (IEDCR) Sectoral Coordination Center (SCC) and National Reference Laboratory (NRL) for AMR surveillance (Human Health)

The IEDCR has been conducting AMR surveillance for human health since 2017. IEDCR serves as the SCC for AMR surveillance in the human health sector, and the NRL for AMR is housed within the institute. Currently, two surveillance approaches are implemented: case-based surveillance and laboratory-based surveillance. These systems generate data on trends and patterns of antimicrobial-resistant microorganisms.

Each year, IEDCR disseminates AMR surveillance findings to relevant stakeholders through a central dissemination program. In addition, the interactive, real-time AMR dashboard hosted by IEDCR serves as a One Health platform, integrating data from human health, animal health, aquaculture, and environmental sectors. It is publicly accessible at https://dashboard.iedcr.gov.bd/amr/. Data management is conducted through the locally designed Comprehensive AMR Data Management System (CAMS), which serves as a centralized digital platform for AMR surveillance.

All AMR surveillance sentinel sites regularly prepare and disseminate their own antibiograms at the local level, with active technical support from the SCC at IEDCR. National AMR surveillance data are uploaded annually to the GLASS IT platform through the CDC, DGHS, which serves as the NCC for AMR surveillance.

Acknowledging the pivotal role of antibiograms in informing empirical therapy and mitigating AMR, IEDCR led nationwide capacity-building initiatives for surveillance staff and microbiologists, with support from WHO. In collaboration with the Bangladesh Medical Microbiology Society (BMMS), selected microbiologists underwent a three-day practical training program focused on standardized antibiogram development. Several additional training sessions on laboratory quality assurance and quality control were organized to enhance the precision, reliability, and uniformity of laboratory findings.

Figure 5a: Image from inception program of AMR surveillance in Faridpur Medical College and Hospital (FMCH), Bangladesh

Figure 5b: Image from training on Antibiogram preparation at IEDCR, Bangladesh

As part of broader AMR containment efforts, IEDCR, supported by WHO, also coordinated the observance of WAAW (18–24 November) at national and peripheral levels, including surveillance sites. The week featured dissemination meetings, publication of surveillance reports, preparation of antibiogram booklets, and dedicated awareness sessions for students to encourage responsible antimicrobial use and foster stronger community participation in AMR prevention.

In addition to surveillance activities, IEDCR has undertaken various awareness initiatives, and developed materials are accessible through the IEDCR website: https://dashboard.iedcr.gov.bd/amr_resource/.

Directorate General of Drug Administration (DGDA)
National Centre for AMU Surveillance

Antimicrobial Use (AMU) Surveillance (2019-2023), Bangladesh

As the National Centre for AMU Surveillance in Bangladesh, the DGDA began reporting to the WHO-GLASS platform in 2022. In 2024, the AMR Cell of DGDA continued this surveillance system and submitted data for the year 2023. The usage trend showed an increase in antimicrobial medicines during the COVID-19 pandemic period (2020–2022), followed by a decline in 2023. Antibiotics in the 'Watch' category were the most consumed from 2016 to 2023 (18,22).

Methods: AMU was analyzed according to the WHO Anatomical Therapeutic Chemical (ATC) classification and the defined daily dose (DDD) per 1,000 inhabitants per day methodology. Data on antimicrobial medicines dispatched from manufacturers' central warehouses were collected and categorized based on the WHO's AWaRe classification.

In Bangladesh, 98% of medicines are locally manufactured. Marketing authorization holders and manufacturers are the same; therefore, distribution (sales) data were collected directly from these companies, excluding export volumes. A data triangulation approach was applied to ensure that the distributed antimicrobials were neither expired nor returned nor misused.

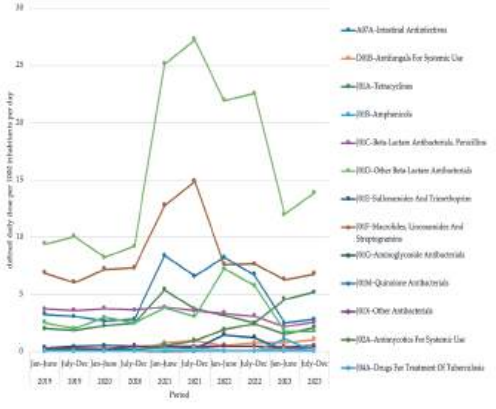


Figure 6: Antimicrobial use in Bangladesh from 2019 to 2023 at third level of Anatomical Therapeutic Chemical classification, based on defined daily dose per 1000 inhabitants per day [source: DGDA, WHO]

Antimicrobial Medicine Use (Defined Daily Dose Per 1000 Inhabitants Per Day)										
	Pre–COVID -19 Period		During COVID –19 Period							After COVID –19 Period
Dosage form	2019		2020		2021		2022		2023	2023
	Jan – June	July – Dec	Jan – June	July – Dec	Jan – June	July – Dec	Jan – June	July – Dec	Jan – June	July – Dec
Oral	28.02	26.97	27.45	28.74	60.91	61.30	54.67	52.13	33.01	36.49
Parenteral	0.55	0.58	0.46	0.46	1.38	1.06	1.48	1.16	0.73	0.88
Total	**28.57**	**27.55**	**27.91**	**29.20**	**62.28**	**62.36**	**56.14**	**53.29**	**33.73**	**37.37**

Figure 7: The overall national AMU (27.55 to 62.36 defined daily doses (DDDs) per 1000 inhabitants per day (DID)) from 2019 to 2023 [source: DGDA, WHO]

Antibiotic Use Trend According to WHO-AWaRe Classification of Antibiotics

Figure 8 shows the trend of oral antibiotic use in Bangladesh from 2019 to 2023 according to the WHO AWaRe classification. It is evident that the Watch-category antibiotics reached their peak of consumption in Bangladesh, estimated at 50 to 67%. Access antibiotic consumption showed a peak of 22 to 37%, and Reserve antibiotics had a peak of 0.14 to 0.24% for the oral route of administration.

Figure 9 highlights the trend of parenteral antibiotic use according to the WHO AWaRe classification in Bangladesh from 2019 to 2023. Watch-category antibiotics were found to be the most consumed antibiotics (70 to 91%) for the parenteral route of administration. Access-category antibiotics constituted 9 to 30%, and the Reserve-category range was from 0.22 to 0.63% for the parenteral route of administration.

The Drug and Cosmetics Act-2023 was approved by the country's National Parliament in September 2023, and 4th March 2024 marks the first day of its implementation. This Act prohibits the sale of antibiotics without a prescription. The implementation of this act in 2024 marks a milestone in efforts to curb antibiotic misuse.

Consumption as per AWaRe classification

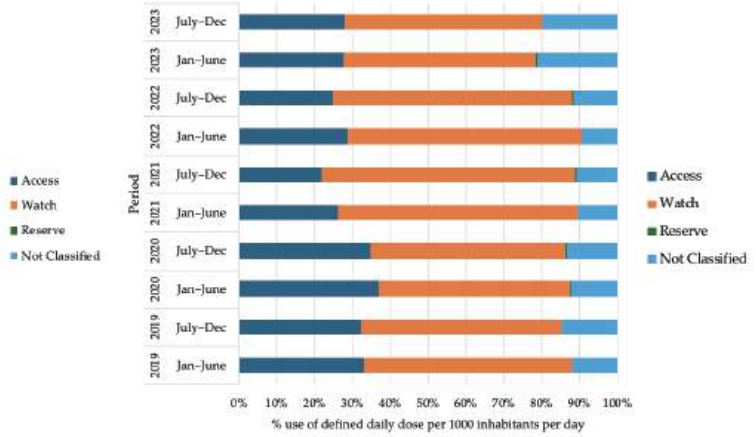


Figure 8. Oral antibiotic use by WHO AWaRe classification in Bangladesh (2019 to 2023) [Source: DGDA]

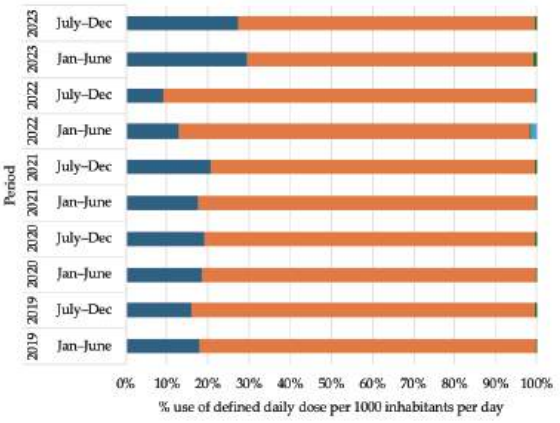


Figure 9. Parenteral antibiotic use by WHO AWaRe classification in Bangladesh (2019 to 2023) [Source: DGDA]

Implementation of the Drug and Cosmetics Act-2023 for OTC Selling of Antibiotics, Bangladesh

In 53 districts, mobile courts (law-enforcement agencies) filed 571 cases against pharmacies that sold antibiotics without prescriptions, resulting in fines totaling BDT 2,235,600 from March 2024 to March 2025. The combination of legislative measures, such as the Drug and Cosmetics Act-2023, and proactive enforcement actions, such as mobile courts, is an essential strategy for promoting responsible antibiotic use and safeguarding public health in Bangladesh.

DGDA Awareness initiatives

AMR awareness campaigns among drug sellers and Bangladesh Chemist & Druggist Samity (BCDS)

From January to July 2024, 119 awareness programs were conducted in 32 districts. During these campaigns, DGDA officials informed drug sellers about the new Drug and Cosmetics Act-2023. They recommended maintaining a register to keep records of the purchase and sale of antibiotics, as well as preserving prescriptions.

Figure 10: Informing the drug seller about the drug and cosmetics act-2023. [Source: DGDA, 2023]

Department of Livestock Services (DLS)
Sectoral Coordination Center (SCC) and
National Reference Laboratory (NRL) for AMR surveillance (Animal Health)

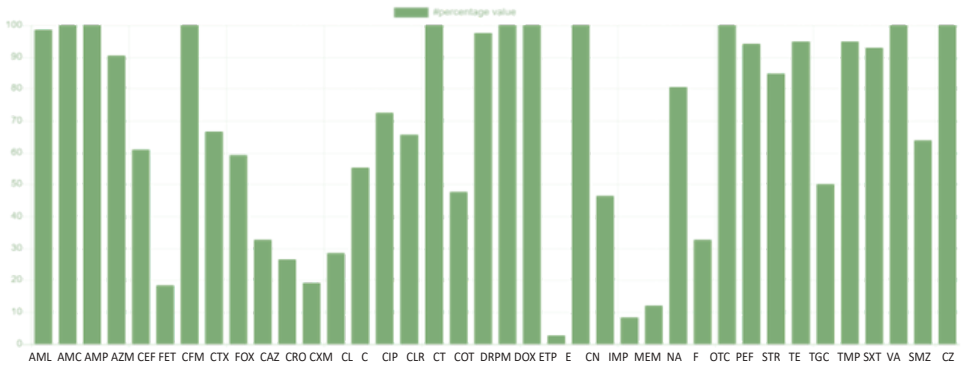
Findings for AMR surveillance

AMR Pattern in *E. coli* isolated from poultry (2023-25)

The organisms (*E. coli, Salmonella* spp., *Enterococcus* spp., and *Campylobacter* spp.) were isolated from fecal samples collected from farms and cecal samples from live bird markets in laboratories, including the Central Disease Investigation Laboratory (CDIL), Bangladesh Livestock Research Institute (BLRI), Poultry Research and Training Centre (PRTC), and Field Disease Investigation Laboratories (FDIL) of Feni and Joypurhat, Bangladesh.

These isolates were then tested for AMR using the disc diffusion method, assessing their sensitivity to various classes of antimicrobials. The antibiogram of *E. coli* (Figure 11) was used for detailed interpretation of resistance patterns.

All laboratories combined (n=741)



AML=Amoxycillin, AMC=Amoxycillin + Clavulanic acid, AMP=Ampicillin, AZM=Azithromycin, CEF=Cefepime, FET=Cefetamet, CFM= Cefixime, CTX=Cefotaxime, FOX=Cefoxitin, CAZ=Ceftazidime, CRO=Ceftriaxone, CXM=Cefuroxime, CL=Cephalexin, C=Chloramphenicol, CIP=Ciprofloxacin, CLR=Clarithromycin, CT=Colistin, COT=Cotrimoxazole, DRPM=Doripenem, DOX=Doxycycline, ETP=Ertapenem, E=Erythromycin, CN=Gentamicin, IMP=Imipenem, MEM=Meropenem, NA=Nalidixic acid, F=Nitrofurantoin, OTC=Oxytetracycline, PEF=Pefloxacin, STR=Streptomycin, TE=Tetracycline, TGC=Tigecycline, TMP=Trimethoprim, SXT=Sulfamethoxazole & Trimethoprim, VA=Vancomycin, SMZ=Sulfamethoxazole, CZ=Cefazolin.

Figure 11: Antibiogram of *E. coli* isolated at the designated laboratories under AMR surveillance (2023-25)

General Interpretation of AST Results

Resistance is notably widespread among commonly used antibiotics. β-lactams show extremely high resistance (90–100% to penicillin), with significant resistance to cephalosporins (up to 100%). This suggests the prevalence of ESBL-producing strains. Similarly, tetracyclines and sulfonamides display near-total resistance (95–100%), reflecting their historical overuse in animal production. Fluoroquinolones also show high resistance (up to 95%), indicating long-term selection pressure.

Crucially, the data reveals emerging threats to last-resort treatments. While most carbapenems remain effective, doripenem resistance reached 100%, indicating potential carbapenemase production. Furthermore, reserve-group agents such as colistin and tigecycline exhibit moderate resistance (~50%), which is concerning given that colistin is banned in Bangladesh, suggesting persistent environmental or historical exposure.

Interpretation by WHO AWaRe Classification

Access Group (First-line): Efficacy is severely compromised. Resistance is critically high (80–100%) for penicillin, cotrimoxazole, and tetracyclines, indicating these essential first-line agents have largely lost effectiveness due to heavy usage pressure. Only gentamicin and nitrofurantoin retained partial to moderate activity.

Watch Group (Second-line): This group shows alarming resistance levels. High resistance (80–100%) to cephalosporins and fluoroquinolones confirms the presence of ESBL-producing and quinolone-resistant E. coli. While most carbapenems remain effective, doripenem showed 100% resistance, raising serious concerns about potential carbapenemase production and public health risks via gene transfer.

Reserve Group (Last-resort): Both colistin and tigecycline display moderate resistance (~50%), indicating that even last-resort options are losing potency. The presence of colistin resistance, despite a national ban, suggests historical use or environmental persistence of resistance genes.

Overall Implication: The poultry isolates exhibit extensive MDR across all tiers, including emerging resistance to last-resort drugs. This underscores an urgent need for stricter enforcement of antibiotic bans, enhanced AMS, and sustained One Health surveillance to combat the spread of extensively drug-resistant (XDR) *E. coli*.

Bangladesh Livestock Research Institute (BLRI)
National Reference Laboratory (NRL) for AMR surveillance (Animal Health)

The surveillance study was conducted to determine the prevalence of major bacterial pathogens, including *E.coli, Salmonella* spp*., Campylobacter* spp. and AMR patterns in poultry samples collected from Live Bird Markets (LBMs) in the Savar region, Dhaka division, Bangladesh. Samples were examined in the AMR Reference Laboratory (Research), Animal Health Research Division and BLRI. A total of 288 poultry samples (144 layer cloacal swabs and 144 broiler cecal contents) were analyzed to assess bacterial prevalence and AMR.

E. coli was the most prevalent pathogen (63.89% in broilers, 43.75% in layers), followed by *Salmonella* spp. and *Campylobacter* spp. AMR analysis of *E. coli* isolates revealed alarming MDR. Layer isolates (n=20) showed peak resistance to tetracycline, with significant resistance to ampicillin, ciprofloxacin and ceftriaxone. Broiler isolates (n=25) exhibited even more critical patterns, with the highest resistance recorded against ceftazidime and meropenem (18 isolates each), followed closely by other cephalosporins.

The study highlights the emergence of resistance to critically important antibiotics, including carbapenems (meropenem) and fluoroquinolones, across both poultry types. These findings confirm the widespread circulation of MDR *E. coli* in poultry, posing a significant One Health risk by compromising the efficacy of essential human and veterinary medicines.

To ensure data reliability and laboratory performance, the National AMR Reference Laboratory (Research) at BLRI prepared a Proficiency Testing (PT) panel for the National External Quality Assurance Scheme (NEQAS). Under this quality assurance initiative, five test isolates were distributed among collaborating aquaculture laboratories for inter-laboratory validation. These included three *E. coli* isolates for both identification (ID) and antimicrobial susceptibility testing (AST), distributed to the Dhaka, Chattogram and Khulna laboratories, and two *Salmonella* spp. isolates for identification testing.

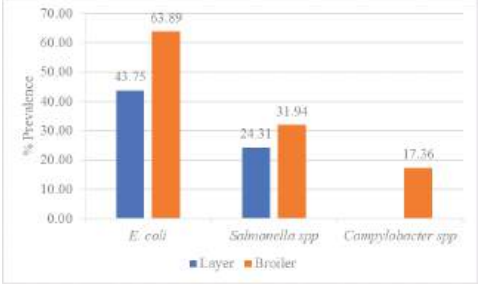


Figure 12: Prevalence of Bacterial Pathogens in Layer and Broiler Chickens from LBMs. [Source: BLRI]

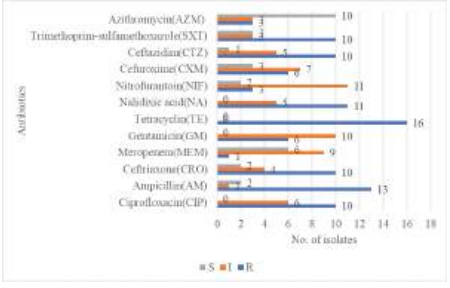


Figure 13: AMR patterns of *E. coli* in Layer from LBM. [Source: BLRI]

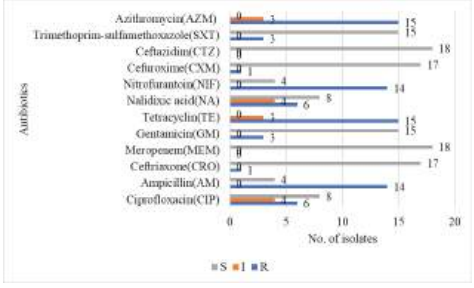


Figure 14: AMR patterns of *E. coli* in Broiler from LBM. [Source: BLRI]

Department of Fisheries (DoF)

AMR Surveillance in Aquaculture

Supported by the Fleming Fund Country Grant (FFCGB) (2023–2025), the DoF established a robust AMR surveillance program in Bangladesh's aquaculture sector. Initially launched at the Quality Control (QC) Laboratory in Dhaka, the initiative expanded in its second phase to include sentinel sites in Khulna and Chattogram.

Capacity building is a central pillar of this program. Laboratories received critical equipment (e.g., biosafety cabinets), reagents, and technical support. Human resource development included fellowships for four officials and extensive training on laboratory operations and epidemiology.

Surveillance activities have intensified annually. QC Lab, Dhaka, increased sampling from 135 fish and shrimp samples in 2023 to 316 in 2024, with 241 samples collected in early 2025. The Chattogram and Khulna laboratories are currently testing hundreds of samples. The program targets five key organisms, including *E. coli, Salmonella* spp. and *S. aureus*. Data reliability is ensured through participation in external Quality Assurance and Proficiency Testing programs (e.g., APHA Scientific VETQAS and EQAsia-11), yielding successful results.

Despite this progress, the report highlights the need for sustainability and improved data integration. Strategic recommendations include upgrading the QC Lab, Dhaka, to an NRL, implementing online data sharing, and launching AMU surveillance. Furthermore, legislative updates are recommended to empower DoF officials as prescribers, alongside encouragement of research into vaccines and alternative medicines.

Table-1: Summary of sampling and Isolation of target bacteria. [Source: DoF,]

Sl No	Sample type	Sample source	Number	*Salmonella* spp.	*V. Cholerae*	*E. coli*
1	Fish with pond water	Aquafarm(Gazipur)	32	4	2	17
2	Shrimp	Fish market (Savar)	60	9	25	25
3	Wild caught Fish	Fish market (Savar)	43	3	4	9
		Total	135	16	31	51

Table-2: Summary of sampling and Isolation of target bacteria (resistance vs antibiotic). [Source: DoF,]

Isolates	Resistance vs Antibiotic														
	AMP	AZM	C	CN	CTX	CIP	SXT	NA	TE	CRO	FEP	AML	F	FOX	CXM
E.coli	72.55	52.95	1.96	1.96	7.84	5.88	19.6	5.88	5.88	0	1.96	68.62	0	13.72	0
Salmonella spp.	65	ND	0	0	0	6.25	6.25	0	6.25	0	0	81.25	0	18.75	0
Vibrio cholerae	96.77	ND	0	0	0	0	0	0	0	0	0	93.54	0	0	0

Table-3: Summary of sample collection in 2024. [Source: DoF,]

Sl No.	Sample Category	Selected District	Number of samples to be collected	Samples Already Collected
1	Cultured fin fish	Manikgonj	124	100
2	Cultured shellfish	Dhaka (fish market)	96	84
3	Wild Caught	Dhaka (fish market)	96	88
	Total		316	272

Table-4: Summary of sample isolates in 2024 (identified pathogen). [Source: DoF,]

Sample type	Sample source	Total sample	Test completed	*Salmonella*	*V. Cholerae*	*E. coli*	*S. aureus*	*L. monocytogenes*
Fish	Manikgonj District & Wet markets of Dhaka	272	272	35	72	188	79	54

Antimicrobial Resistance Surveillance in Bangladesh

According to the WHO Global Action Plan (GAP), surveillance is one of the main strategies for AMR containment. National AMR Surveillance in Bangladesh has been implemented by the IEDCR under the Ministry of Health and Family Welfare (MoHFW) since 2016. The main objective of the surveillance is to establish a system to monitor the status of AMR among selected microbial pathogens of public health importance in Bangladesh and to strengthen the capacity of sentinel site laboratories so that they can function as regional reference laboratories.

The surveillance activities are carried out in accordance with the GLASS protocol. Here, the CDC, DGHS serves as the NCC, while IEDCR functions as the SCC for human health and as the NRL for AMR surveillance. The national surveillance data are submitted annually to the WHO GLASS IT platform by CDC, DGHS.

The surveillance system comprises two components:

1. Case-based surveillance: At present, thirteen sentinel sites are functioning, where clinically diagnosed cases are identified. Comprehensive clinical, epidemiological, and microbiological data are collected from patients with suspected infections. The quality of participating laboratories is strictly maintained through internal and external QC measures, complemented by regular monitoring and supervision.

Table 5: National AMR surveillance sites in Bangladesh

National AMR surveillance sites in Bangladesh	
Case-based Surveillance	**Laboratory-based Surveillance**
Dhaka	
1. Dhaka Medical College and Hospital 2. Uttara Adhunik Medical College and Hospital 3. Faridpur Medical College & Hospital 4. Jahurul Islam Medical college Hospital	1. National Institute of Neurosciences and Hospital 2. Popular Diagnostic Centre Ltd. (Badda, Dhanmondi, English Road, Mirpur, Shantinagar) 3. Popular Diagnostic Centre Ltd. (Gazipur) 4. Popular Diagnostic Centre Ltd. (Narayanganj) 5. Popular Diagnostic Centre Ltd. (Savar) 6. Square Hospitals Ltd (Banani, Mirpur, Panthapath, Uttara) 7. The Ibn Sina Trust (Dhanmondi) 8. United Hospital Limited
Chattogram	
1. Chittagong Medical College and Hospital 2. Bangladesh Institute of Tropical and Infectious Diseases (BITID) 3. Cox's Bazar Medical College and Hospital	1. Popular Diagnostic Centre Ltd. (Chattogram) 2. Popular Diagnostic Centre Ltd. (Noakhali) 3. Epic Health Care Ltd
Khulna	
1. Khulna Medical College and Hospital, Khulna	1. Popular Diagnostic Centre Ltd. (Khulna) 2. Popular Diagnostic Centre Ltd. (Kushtia)
Barishal	
1. Sher-e-bangla Medical College and Hospital	1. Popular Diagnostic Centre Ltd. (Barishal)
Mymensingh	
1. Mymensingh Medical College and Hospital	1. Popular Diagnostic Centre Ltd. (Mymensingh)
Rajshahi	
1. Rajshahi Medical College and Hospital	1. Popular Diagnostic Centre Ltd. (Rajshahi)
Sylhet	
1. Sylhet MAG Osmani Medical college and Hospital	1. Square Hospitals Ltd (Shylet)
Rangpur	
1. Rangpur Medical College and Hospital	

2. Laboratory-based surveillance: Following a comprehensive evaluation process, twenty-two private and two public microbiology laboratories have been included in the AMR surveillance network. Only laboratory data are collected in this passive surveillance system.

Data Management

Data management is conducted through the locally designed CAMS software, implemented by IEDCR, which serves as a centralized digital platform for AMR surveillance. The system enables real-time entry, integration, and analysis of clinical and laboratory data from sentinel sites across Bangladesh.

A key feature of the software is its monitoring dashboard, which provides instant visualization of priority pathogens, resistance patterns, and data submission status to support timely decision-making. The platform also includes an automated antibiogram preparation module that enables participating facilities to generate standardized, site-specific antibiograms directly from surveillance data.

To expand the impact of this innovation, work is ongoing to align with the standardized guidelines for antibiogram generation through the CAMS platform. This initiative aims to enable private and other laboratories to utilize their own data to prepare quality-assured, standardized antibiograms, thereby strengthening nationwide AMR monitoring and promoting evidence-based antimicrobial use.

Data Visualization and Dissemination

A designated online dashboard is available on the IEDCR website for visualizing AMR-related data analyzed through CAMS. The dashboard can be accessed at (dashboard link - https://dashboard.iedcr.gov.bd/amr/).

Surveillance findings are disseminated annually, both centrally at IEDCR and individually at each sentinel site, to clinicians and other stakeholders. Detailed surveillance results are compiled in the “Annual AMR Report”, with soft copies available on the IEDCR website.

To learn more about AMR surveillance in Bangladesh, see the following links:

- **National AMR Surveillance in Bangladesh: 2016-2023** *(https://dashboard.iedcr.gov.bd/amr/report2016-23.php)*
- **National AMR Surveillance in Bangladesh: 2024** *(https://iedcr.gov.bd/pages/static-pages/6922dcde933eb65569e1277d)*

AMR Surveillance in Rohingya Population (RP)

A total of 958,614 Rohingya individuals (excluding Bhasan Char) are officially registered and residing in 33 highly congested camps in the Ukhiya and Teknaf upazilas of Cox's Bazar. An additional 35,510 individuals are reported to reside on Bhasan Char Island in Noakhali District. The convergence of overcrowding, suboptimal hygiene conditions, and comparatively low immunization coverage renders this displaced population highly vulnerable to a broad spectrum of infectious diseases. The etiological agents, AMR patterns, and clinical outcomes of infections in this population may differ from those observed in the host community, underscoring the need for dedicated AMR surveillance to guide appropriate clinical management.

Although Bangladesh has an established National AMR Surveillance system that substantially contributes to understanding the national resistance scenario, the unique environmental conditions of the camps and the distinct ethnic background of the RP necessitate a more targeted surveillance approach. National surveillance alone may not fully capture the evolving patterns of resistance and epidemiological dynamics in this humanitarian setting.

In this context, AMR surveillance among the RP and adjacent host communities in Cox’s Bazar has been implemented since September 2024. The initiative is conducted under the national AMR surveillance

programme, led by the IEDCR, in collaboration with the WHO and CoxMCH, to address specific public health challenges in densely populated RP settings.

The surveillance implemented a case-based design, with systematic data collection from ten sentinel health facilities across Ukhiya and Teknaf upazilas. Clinical specimens, including urine, blood, stool, and wound samples, are collected and tested at the IEDCR field laboratory at CoxMCH for laboratory confirmation and antimicrobial susceptibility testing.

V. cholerae was identified as the most frequently isolated pathogen, predominantly associated with diarrhoeal illnesses, highlighting the persistent vulnerability of the camp population to cholera outbreaks. A significant decline in stool sample positivity was observed following the oral cholera vaccination campaigns conducted in early 2025, indicating the vaccination's positive impact on disease transmission dynamics. Camp-wise analysis provides critical insights into identifying site-specific risk factors. Such evidence supports targeted interventions and informs the prioritization and strengthening of WASH systems within the respective camps to reduce disease transmission and improve public health outcomes.

Another key finding is that resistance levels among several pathogens were lower than those reported in the national AMR surveillance, although variability was observed across organisms and specimen types. This comparatively favorable resistance profile may be partially attributable to restricted access to over-the-counter antimicrobials within the camps. The findings further indicated that azithromycin was the most frequently prescribed antibiotic, particularly for diarrhoeal illnesses, which may explain the relatively reduced susceptibility observed for this agent compared to others. Data management is conducted through the CAMS software, with quality assurance ensured by the NRL and coordinated dissemination of findings to health sector partners.

Therefore, it is evident that diarrhoeal diseases caused by *V. cholerae* remain a major public health concern in the RP. At the same time, the overall resistance profile appears relatively favorable compared to national data. However, the observed mismatch between antibiotic utilization and susceptibility patterns, along with the ongoing risk of outbreaks, underscores the critical importance of sustained AMR surveillance and continued vaccination efforts. Strengthening awareness among clinicians and communities is also essential to promote rational antibiotic use and prevent the emergence and spread of resistance in this vulnerable population.

Figure 15: Monitoring visit to Rohingya camp & dissemination program of AMR surveillance in RP

Recently included AMR Surveillance Sites

Faridpur Medical College and Hospital (FMCH), Bangladesh

Faridpur Medical College and Hospital (FMCH) was established in 1992, also runs five-year MBBS courses under the affiliation of the University of Dhaka. It has a 1,000-bedded hospital with the following wards: medicine (5 units), surgery (3 units), gynecology (3 units), pediatrics (2 units), and an isolation ward (80 beds). It also has a 10-bedded ICU and a 16-bedded burn unit, along with other specialized units such as the Pediatric Intensive Care Unit (PICU), High Dependency Unit (HDU), and orthopedic units. The average bed occupancy is 96/day (as per last year's hospital data), with 2,000 patients being treated in the different OPDs annually.

The Microbiology Department has 1 associate professor, 1 assistant professor, and 4 lecturers. The laboratory has 2 medical technologists. The microbiology laboratory currently performs culture and sensitivity tests for urine, stool, blood, pus, wound swabs clinical samples. Culture sensitivity testing is conducted using conventional methods except for blood, which is automated using BacT/ALERT 3D system.

The laboratory is also established as a BSL-II facility. The laboratory conducted COVID-19 tests from 2020 to 2024. The microbiology laboratory has been included in the National AMR Surveillance System since November 2025 as a sentinel site for case-based AMR Surveillance.

Figure 16: Images of Faridpur Medical College and Hospital, Bangladesh

Jahurul Islam Medical College and Hospital (JIMCH), Bangladesh

Jahurul Islam Medical College and Hospital (JIMCH) was established in 1992, runs five-year MBBS courses under the affiliation of the University of Dhaka. It has a 513 bedded hospital with the following wards: medicine (1 unit, 119 beds), surgery (2 units, 80 beds), gynecology (1 unit, 59 beds), pediatrics (1 unit, 88 beds), and an isolation ward (5 beds). It also has a 3-bedded ICU and a 2-bedded burn unit. The average bed occupancy is 394/day (as per last year's hospital data), with 596,446 patients treated in the different OPDs annually.

The Microbiology Department of JIMCH currently has 2 professors, 1 associate professor, 1 assistant professor, and 4 lecturers. The laboratory has 2 medical technologists. The department of microbiology provides 2-year training for FCPS in Microbiology.

The microbiology laboratory performs culture and sensitivity tests for urine, stool, blood, sputum, pus, wound swabs, throat swabs, nipple discharge, various body fluids, pleural fluid, and ascitic fluid. It processes approximately 330 different pathological samples per week, of which 9% are blood cultures, 75% are urine

cultures, and 16% are other samples. Culture sensitivity testing is conducted using conventional methods except for blood, which is automated using BacT/ALERT 3D system. The laboratory is established as a biosafety level 2 (BSL-II) facility and has molecular testing capacity. It conducted 63,044 COVID-19 tests during 2020–2022. The microbiology laboratory has been included in the National AMR Surveillance System since 14 May 2025 as a sentinel site for case-based AMR Surveillance.

JIMCH has an active IPC committee and performs routine internal QC. The hospital has also established a combined Effluent Treatment Plant (ETP) and Sewage Treatment Plant (STP) for waste management. Standard Operating Procedures (SOPs) provided by IEDCR for antibiotic use are strictly followed.

Figure 17: Images of Jahurul Islam Medical College and Hospital, Bangladesh

United Hospital Limited (UHL), Bangladesh

United Hospital Limited (UHL) is a Joint Commission International (JCI)-accredited private hospital with a 500-bed capacity. The hospital has an ISO-accredited pathology laboratory, including a fully equipped microbiology lab with automated blood culture and identification systems, such as VITEK-2. This ensures accurate and timely detection of organisms and AST. The lab performs a wide range of microbiological investigations, including bacteriology, mycology, parasitology, and serology.

In accordance with international quality assurance standards, the lab participates in external quality assurance (EQA) programs and maintains strict biosafety practices. The Microbiology team collaborates closely with the infection control and antimicrobial stewardship teams to support rational antibiotic use, outbreak investigations, and hospital-wide infection prevention initiatives.

Figure 18: Image of United Hospital Limited, Bangladesh

Healthcare-Associated Infection (HAI) Surveillance

HAI prevention is a core component of any IPC programme. Implementation of the HAI surveillance system is significantly important in secondary and tertiary care hospitals, where infection risk is elevated due to complex medical interventions and the presence of highly vulnerable patient populations.

In Bangladesh, there is little to no routine HAI surveillance, particularly in public sector facilities. Existing protocols primarily focus on device-associated infections and rely heavily on advanced laboratory capacity, which is often unavailable. In response, a context-appropriate surveillance system designed to integrate with the existing healthcare infrastructure and operate using available resources was developed and implemented. With support from the WHO, the HAI surveillance program was initiated in September 2024. Three workshops were conducted between September 2024 and January 2025 to develop the HAI surveillance protocol. These workshops brought together a multidisciplinary group of experts, including laboratory professionals, epidemiologists, clinicians, ICU consultants, statisticians, IT specialists, and representatives from national health authorities such as CDC, DGHS, and Hospital Services.

This HAI surveillance system uses an active, targeted, prospective design and was implemented in two AMR surveillance tertiary care hospitals: RMCH and KMCH. Surveillance focused on selected high-risk wards, including ICUs, general surgery, and obstetrics wards. A structured governance mechanism was established to support effective implementation and long-term sustainability. Each site formed an HAI Surveillance Committee, chaired by the Hospital Director, with the Medical College Principal or Vice Principal as co-chair, and the IPC committee member serving as the secretary responsible for coordination. Members include departmental heads, ward masters, and nursing supervisors. The committee structure aligns with existing IPC committees, in accordance with DGHS guidelines and recommendations.

Figure 19: HAI surveillance inception program at RMCH & HAI protocol development workshop at IEDCR.

Operationally, the surveillance team comprises an IPC focal person, a local surveillance coordinator (where available), surveillance physicians assigned to each ward, surveillance nurses, and IPC nurses. This structure was intentionally designed to ensure continuity beyond the project period by relying primarily on existing hospital staff. To facilitate efficient data management, an Android-based HAI software application was developed, and data collectors were equipped with tablets to support standardized data entry, compilation, and analysis.

Multiple capacity-building activities were undertaken to ensure consistent implementation. Orientation sessions were conducted at both surveillance sites in January 2025, followed by centralized training at IEDCR

for surveillance physicians, nurses, and facilitators to strengthen their understanding of the protocol and standardize data collection and reporting. Recognizing the important role of intern doctors in tertiary hospitals, dedicated training sessions were held for them in March 2025, focusing on surveillance procedures and their specific responsibilities within the system. Regular weekly web-based meetings with site teams supported coordination, problem-solving, and close monitoring during the initial implementation phase. Pilot report review meetings were also conducted at the site level to identify operational bottlenecks and develop feasible, context-specific solutions to ensure long-term sustainability.

Surveillance findings were disseminated within the respective hospitals among key stakeholders at RMCH and KMCH. While substantial progress has been achieved, several challenges were identified during implementation. Addressing these challenges and securing sustained institutional commitment will be essential for scaling up the surveillance model nationally and improving patient safety and overall quality of care (QoC).

Role of development partners in AMR containment of Bangladesh

World Health Organization (WHO)

As part of broader AMR containment efforts, WHO has extended support to the DGHS, the DGDA, the IEDCR, and the CDC to implement initiatives addressing AMR. WHO Bangladesh continues to support the Government of Bangladesh (GoB) in implementing a comprehensive strategy to prevent, detect, and respond to AMR. Key outputs include strengthening the AMR surveillance system, updating technical and clinical guidance documents, enhancing national AMR policies and governance mechanisms, and improving systems for monitoring antimicrobial consumption. Governance strengthening efforts were supported through facilitating National AMR Technical Group meetings and developing national guidelines.

Since 2018, the WHO has provided sustained support to the country's National AMR Surveillance System to enhance and standardize surveillance practices nationwide. This support encompasses the continuation of routine surveillance activities; capacity development of surveillance personnel through updated SOPs and protocols; periodic analysis and dissemination of AMR surveillance data at national and subnational levels; development of local and national antibiograms; and the establishment of sentinel surveillance sites as models for comprehensive AMR containment. During the year, two new surveillance sites were established at FMCH and JIMCH.

FMCH, a public tertiary-level teaching hospital and major government referral institution serving the southwestern region of the country, previously lacked microbiological culture facilities. Through the establishment of an AMR surveillance site, microbiological culture capacity was developed, including the installation of a laboratory equipped with modern diagnostic machinery. JIMCH, established in 1992 and recognized as the second-oldest private medical college in Bangladesh, is in a rural setting and serves as a key healthcare provider for the population of Kishoreganj district. This intervention significantly strengthened institutional capacity for AMR detection and reporting.

Recognizing the critical importance of antibiograms in guiding empirical treatment and reducing the burden of AMR, WHO supported capacity-building initiatives for both surveillance personnel and microbiologists nationwide. In collaboration with the BMMS, selected microbiologists participated in a three-day hands-on training program on standardized antibiogram preparation. In addition, multiple training sessions on laboratory quality assurance and quality control were conducted to ensure the accuracy, reliability, and consistency of laboratory data.

Figure 20: WAAW celebration 2024 & training on antibiogram preparation at IEDCR

Public awareness was further promoted as an essential component of AMR containment efforts. WHO also supported the observance of WAAW (18–24 November) at both central and peripheral levels, including surveillance sites. Activities conducted during the week included dissemination meetings, preparation and

publication of surveillance reports, development of antibiogram booklets, rallies, poster exhibitions, hospital-based wall campaigns, production of awareness-raising animation videos, and educational competitions. Targeted awareness sessions were also organized for students at medical colleges, secondary schools, and universities to promote responsible antimicrobial use and strengthen community engagement in AMR prevention efforts. CDC, DGHS successfully organized seminars across all 64 districts through their strategic partnership with WHO. These seminars convened a broad range of stakeholders, including healthcare providers, pharmacists, GoB officials from the livestock, fisheries, and education sectors, and community representatives, to foster coordinated, multisectoral engagement.

In November 2024, the National Technical Committee (NTC) convened with WHO facilitation, during which the AMS Guidelines for Healthcare Facilities were formally reviewed and approved. Subsequently, in March 2025, a national stakeholder workshop was organized to establish sustainable One Health AMR Divisional Hubs. The workshop engaged over 100 participants from key government agencies, including DGHS, DoF, DLS, Department of Environment (DoE), IEDCR, IPH, and DGDA, as well as WHO and other relevant stakeholders. The establishment of these divisional hubs is expected to enhance multisectoral coordination and strengthen the implementation of AMR containment strategies nationwide.

AMS pilot programs were also implemented across primary, secondary, and tertiary healthcare facilities with facilitation from the WHO, CDC, and DGHS. These pilots assessed the feasibility and operationalization of AMS interventions at different levels of care, engaging clinicians, pharmacists, and healthcare administrators. The findings, disseminated on 3 September 2025, provided critical insights and practical recommendations to inform the national scale-up. Furthermore, with WHO facilitation, Bangladesh has reached the final stage of developing a national protocol for measuring AMR-attributable mortality. It has developed guidelines for AMR outbreak management in healthcare facilities.

WHO also supported activities to enhance national capacity for monitoring antimicrobial consumption, contributing to evidence-based policy development and programmatic decision-making. The AMR bulletin of DGDA is developed and shared on the DGDA website, accessible to all with WHO support.

Figure 21: AMR awareness program with students of FMCH

Fleming Fund Country Grant to Bangladesh (FFCGB)

The FFCGB, operating under a One Health approach, significantly advanced national AMR surveillance capacity across human, animal, aquaculture, and environmental sectors in 2025. This effort involved close collaboration with key government agencies, including DGHS, DLS, DoF, and DoE.

Key Achievements in AMR and AMU Surveillance include finalizing a National AMR Surveillance Strategic Framework and an AMR Surveillance Protocol for the Environment, with environmental sampling already underway. The AMU Protocol for Human Health was finalized, and comprehensive AMU studies for poultry, cattle, and aquaculture were submitted for publication after completion. Phase 3 of the PPS, informing a national policy brief for AMS, was conducted. FFCGB consistently provides logistical and reagent support, ensuring high-quality AMR surveillance across all sentinel sites and NRLs.

Laboratory Capacity Building and Quality Assurance were strengthened through on-site training in microbiology and data management for laboratory personnel across all sectors. Regular quarterly supportive supervision maintained data quality and biosafety standards. Site assessments using tools from The London School of Hygiene & Tropical Medicine (LSHTM) strengthened the foundation for sustainable quality assurance systems.

In Research, Policy, and Advocacy, a Political-Economic Analysis (PEA) Policy Brief and a Gender and Equity in AMR study were completed and disseminated to policymakers. Protocols for data sharing and quality assurance were developed to harmonize reporting. Seven Clinical Engagement Programs were organized to promote AMS, IPC, and Diagnostic Stewardship in medical colleges. Coordination, communication, and knowledge sharing were maintained through regular intersectoral working group meetings and quarterly newsletters, fostering collaboration and disseminating lessons learned.

As the FFCGB approaches completion in March 2026, the primary focus is on ensuring the sustainability and institutionalization of these activities within the national framework, with the GoB committed to integrating AMR and AMU surveillance into national programs and budgets.

Figure 22: Clinical engagement workshops in different medical colleges, Bangladesh

The Centers for Disease Control and Prevention, Atlanta, USA (US-CDC)

The US-CDC is a global leader in AMR, which threatens to make common infections fatal. Committed to protecting human, veterinary, and agricultural health, the US-CDC has partnered with Bangladesh for over 50 years to address this challenge. In collaboration with national institutions like IEDCR, icddr,b, DLS, and BLRI, the US-CDC supports projects to understand AMR transmission patterns and slow its spread. Notable initiatives include the Antibiotic Resistance in Communities and Hospitals (ARCH) study with icddr,b, and efforts to strengthen IPC and AMS in tertiary hospitals. Additionally, US-CDC works with the DGHS to map stakeholders, document policies, and support IEDCR-led national AMR surveillance, thereby strengthening Bangladesh's health system and protecting its citizens from AMR.

For more details: https://www.cdc.gov/antimicrobial-resistance/index.html

CAPTURA 2 and TACE Projects in Bangladesh

Bangladesh is actively strengthening its national AMR efforts through the CAPTURA project, focusing on evidence-based tools for antimicrobial stewardship. Two primary components are the National Antimicrobial Point Prevalence Survey (NAPS) and the AMR Surveillance Monitoring and Evaluation (AMRSurME) Framework.

The NAPS aims to assess the prevalence, patterns, and quality of antimicrobial prescribing in healthcare facilities, identify adherence to standard treatment guidelines, and pinpoint areas for AMS intervention. Activities included national-level training for healthcare professionals and data collection using standardized methodology from four diverse hospitals. Preliminary findings revealed high use of broad-spectrum antibiotics (cephalosporins and fluoroquinolones), a prevalence of empirical prescribing, and low adherence to guidelines, highlighting significant opportunities for stewardship. NAPS achieved the first nationally coordinated PPS on antimicrobial use, establishing crucial baseline evidence and enhancing local teams' capacity in AMU data collection and analysis.

The AMRSurME framework was developed to standardize the assessment of the national AMR surveillance system's functionality, performance, and sustainability. This involved drafting the framework with expert support, conducting multiple stakeholder consultations, and refining indicators through pilot testing. AMRSurME successfully built consensus on national indicators for surveillance monitoring and fostered enhanced coordination among health stakeholders, making the framework ready for national adoption.

Moving forward, CAPTURA plans to expand NAPS to more hospitals, institutionalize regular PPS, and implement the AMRSurME framework nationally to track surveillance performance. The evidence generated will guide policy, stewardship interventions, and resource allocation. Through these initiatives, CAPTURA significantly contributes to Bangladesh's NAP on AMR by generating essential data, building capacity, and strengthening surveillance systems for a sustainable national response.

Figure 23: Images from hands on training of various hospital staffs National antimicrobial prescription survey tool, Bangladesh

Safetynet Bangladesh

SAFETYNET Bangladesh, established in November 2020, is a leading public health organization dedicated to strengthening national health systems, Field Epidemiology Training Program (FETP) capacity, infectious disease surveillance, and public health workforce development. Collaborating with the Ministry of Health, DGHS, US-CDC, and various partners, SAFETYNET has significantly contributed to COVID-19 risk communication, urban health, CRVS, and supporting IEDCR's capabilities. A major focus has been on IPC and AMS.

Since 2021, SAFETYNET has provided technical and logistical support, notably participating in a national initiative to strengthen IPC and AMS in 12 tertiary care hospitals, generating valuable scientific publications, and contributing to global AMR knowledge. The organization also supports complementary public health initiatives, including infectious disease surveillance among urban pregnant women and piloting a dengue patient management form. SAFETYNET has also developed a national digital repository for public health policies on the DGHS website.

Most importantly, SAFETYNET Bangladesh is leading the development of the National Guideline for Managing Outbreaks of AMR Pathogens in Healthcare Facilities, in collaboration with DGHS and WHO. This landmark initiative aims to evaluate hospital and laboratory capacities, identify system gaps, and establish standardized protocols for AMR outbreak detection, containment, and reporting, marking a significant milestone in Bangladesh's AMR containment efforts.

Figure 24: SafetyNet collaborative meetings, Bangladesh

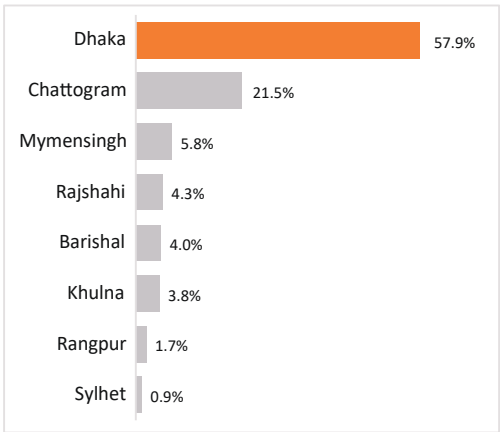
RESULTS

Overview

96,477
Total samples (N)

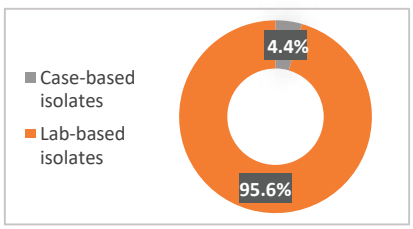
The 2025 AMR data were collected from 33 laboratories across eight divisions of Bangladesh. The total sample represents both case-based surveillance samples and pathogen isolates from lab-based surveillance, totaling 17,620 case-based and 78,857 isolates from lab-based surveillance (Figure 25.2). The culture positivity rate among case-based samples was 20.7% (n=3,653) (Figure 25.5), bringing the total number of pathogens after cleaning for analysis to 82,497 from both surveillance types.

25.1. Geographical distribution of samples (N=96,477)



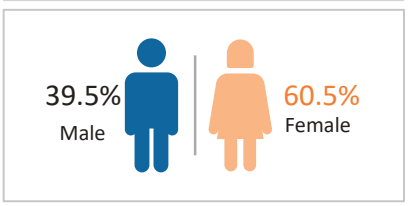
Geographically, approximately 57.9% of the total samples were from Dhaka Division, followed by 21.5% from Chattogram Division (Figure 25.1). The predominance of samples from Dhaka is due to a higher number of laboratories participating in and contributing to the surveillance system within this division. More than half (60%) of the samples were from female patients (Figure 25.3), and the largest proportion of samples (16.9%) was collected from the 21 to 30 years age group (Figure 25.4). Urine was the most common specimen type, accounting for 55.9% of all samples (Figure 25.5).

25.2. Distribution of isolates by source (n=82,497)

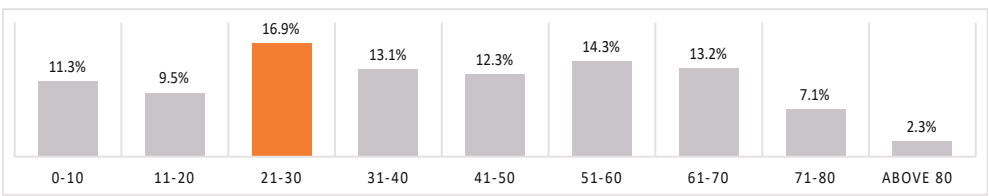


Within the case-based surveillance data, positively yielding isolates (n=3,653) were further analyzed to determine the origin of infection (community- or hospital-originated) based on the GLASS definition (Figure 25.6). While analyzing the distribution of samples by hospital department, approximately 68.7% were found to be undocumented, as they were derived from lab-based surveillance, where the scope of getting on hospital departments was limited (Figure 25.8).

25.3. Distribution of samples by sex (N=96,477)



25.4. Age-wise distribution of samples (N=96,477)



25.5. Culture yield of case-based samples (n=17,620)

20.7%
Growth (n= 3,653)

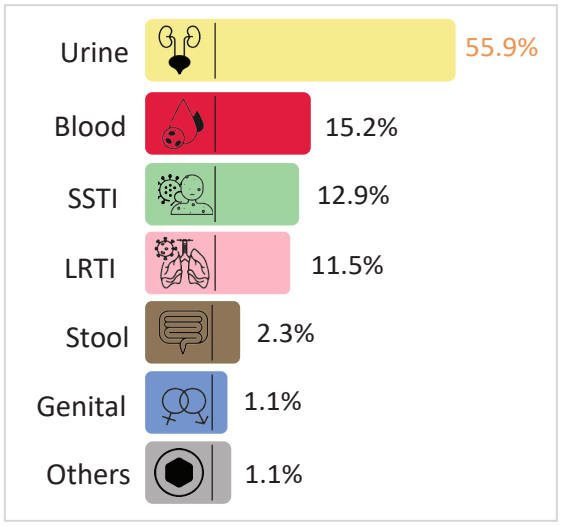
79.3%
No Growth (n= 13,967)

25.6. Infection origin of case-based isolates (n= 3,653)

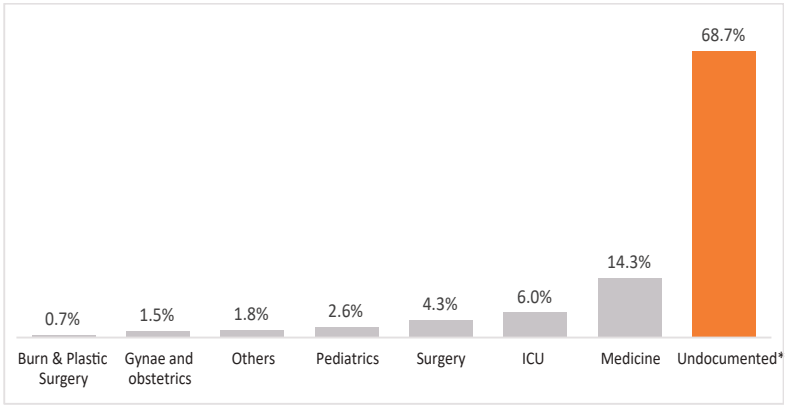
43.2%
Community Origin

56.8%
Hospital Origin

25.7. Sample distribution by specimen type (N=96,477)



25.8. Sample distribution by hospital department (N=96,477)



* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

Figure 25. Geographical distribution of sample, specimen category, hospital, and patient characteristics of the AMR samples, 2025 (N=96,477)

Most Frequent Isolates

E. coli, followed by *K. pneumoniae* and *S. aureus*, were the most commonly identified organisms across all analyzed samples. Isolate distribution varies from specimen to specimen. The distribution of the most frequently detected bacteria by specimen category is presented in Figure 26.

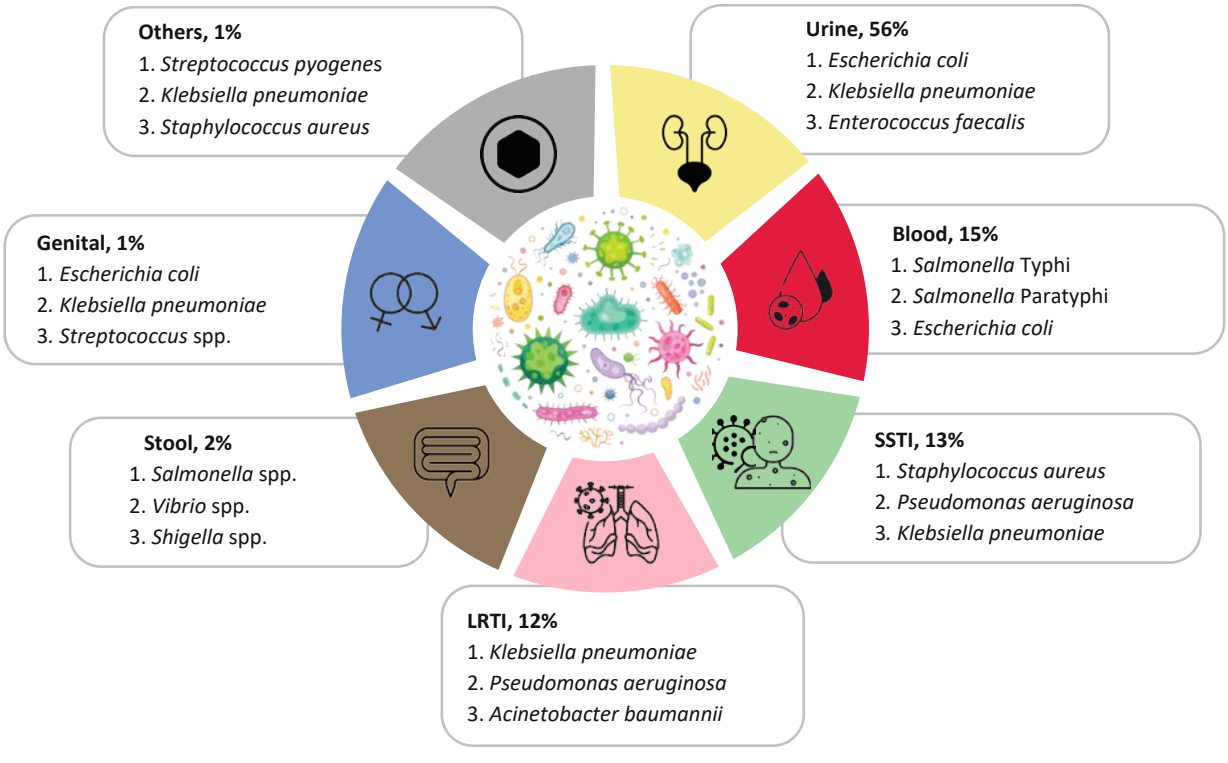


Figure 26. Most common AMR isolates by specimen type in Bangladesh, 2025 (N=82,497)

Distribution of samples according to division - Bangladesh

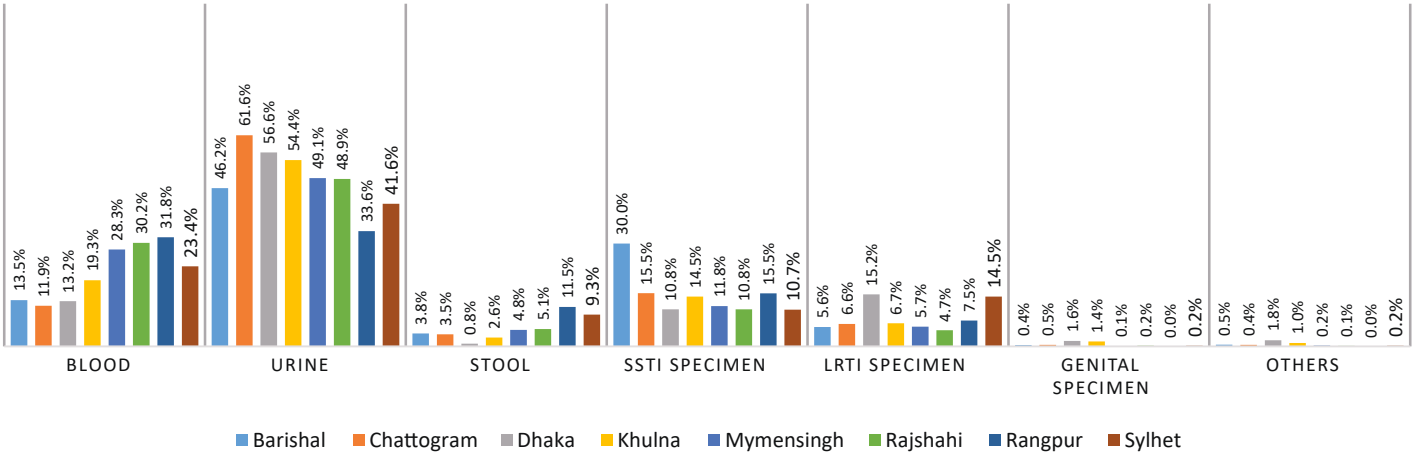


Figure 27. Distribution of samples by specimen type and division, Bangladesh (N=96,477)

Geographical distribution of the five most frequent isolates (n=82,497) – Bangladesh

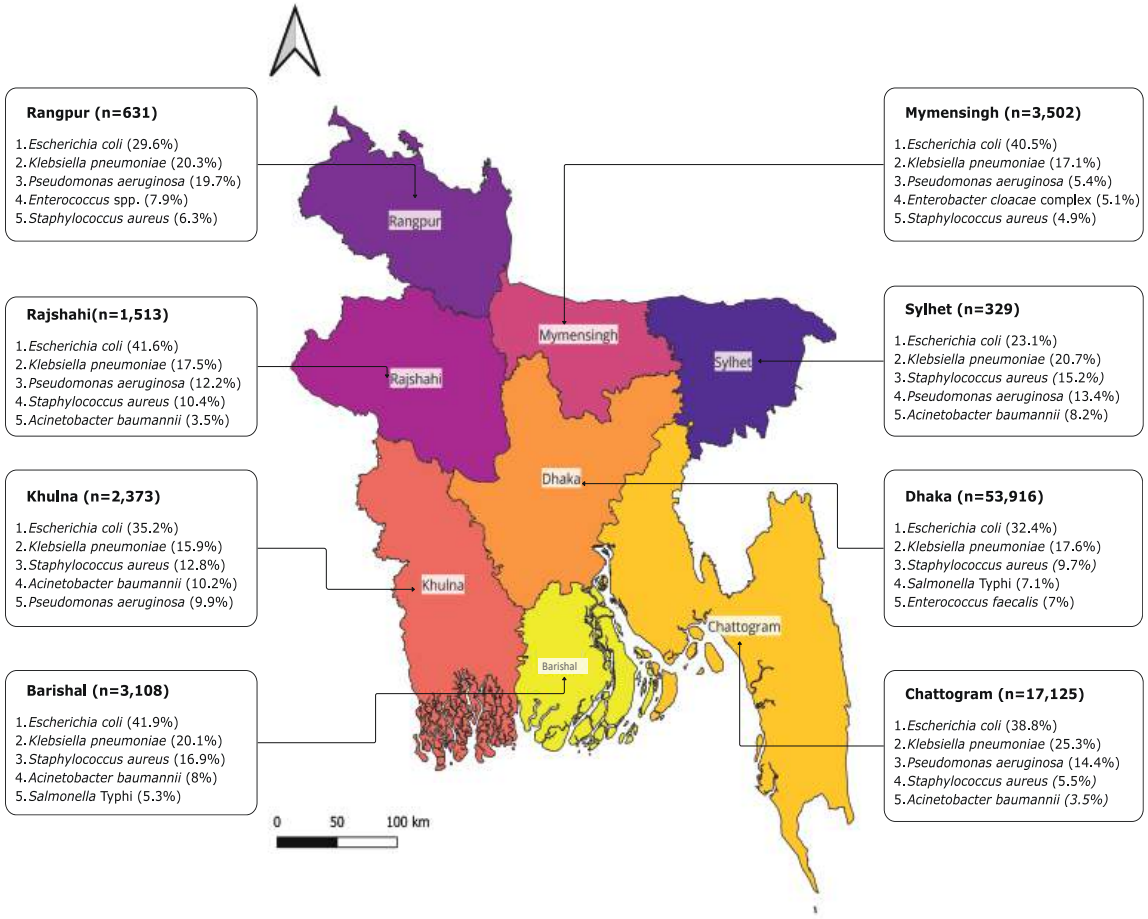


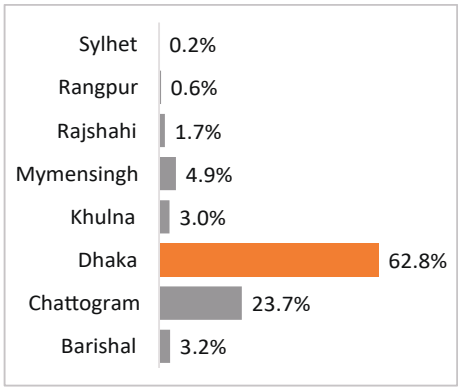
Figure 28. Geographical distribution of the five most frequent isolates, Bangladesh (N=82,497)

Specimen: Urine

53,929
Total urine samples (N)

Of the total samples received from laboratories across Bangladesh, more than half (56%; N=53,929) were urine samples, making it the most predominant sample type. The total number of urine samples comprised 5,613 from case-based surveillance and 48,316 isolates from lab-based surveillance.

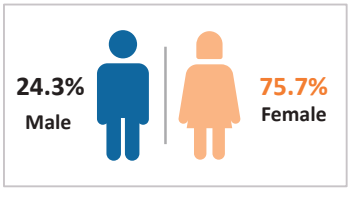
29.1. Geographical Distribution of urine isolates (n= 49,460)



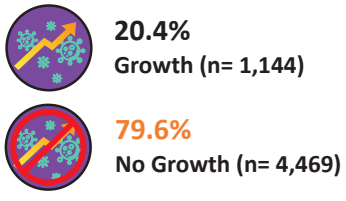
The culture positivity rate for urine samples from case-based surveillance was 1,144 (21%) (Figure 29.3), bringing the total number of bacterial isolates analyzed to 49,460 from both surveillance types. Samples came predominantly from females (75.7%) (Figure 29.2).

Geographically, the majority of the urine isolates (62.8%) were reported by the Dhaka Division, followed by 23.7% from Chattogram, with the remaining 13.5% combined from other divisions (Figure 29.1). Analyzing the case-based urine isolates (n=309), 88% were from community origin, and 12% were from hospital origin (Figure 29.4). *E. coli, K. pneumoniae* and *E. faecalis* were identified as the most common organisms isolated from urine samples (Figure 29.8).

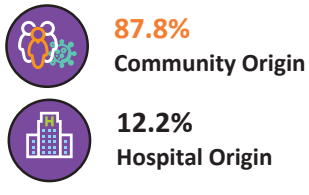
29.2. Sex-wise distribution of urine isolates (n= 49,460)



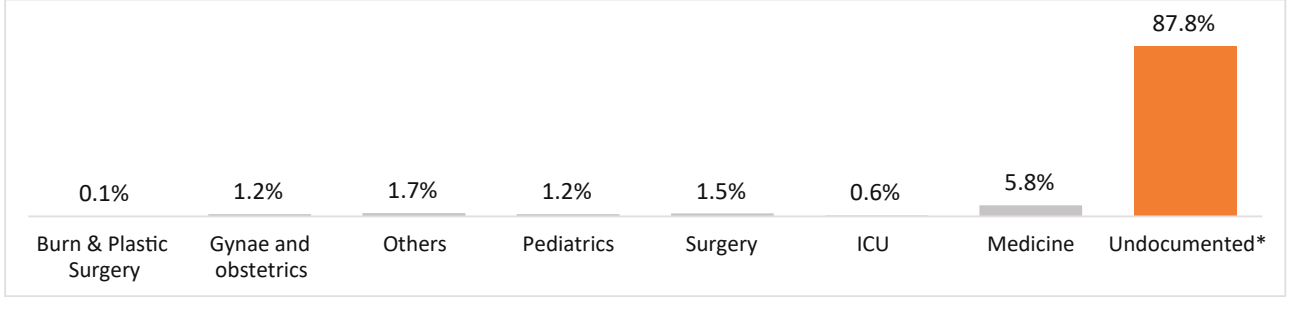
29.3. Culture yield of case-based samples (n= 5,613)



29.4. Infection origin of urine isolates (case-based samples, n=1,144)

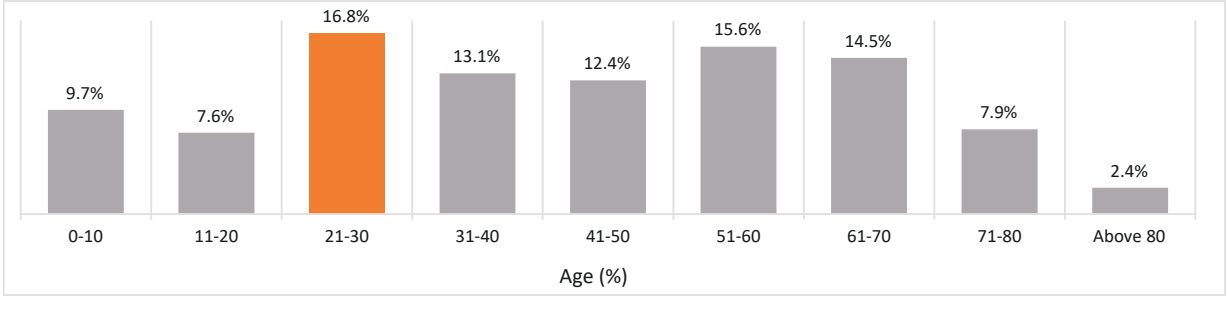


29.5. Distribution of urine isolates by hospital department (n= 49,460)

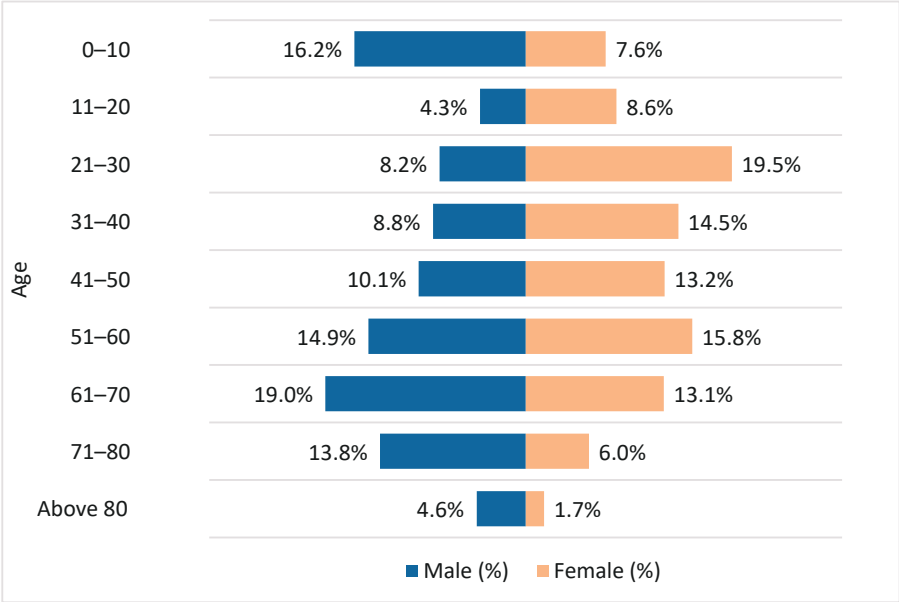


* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

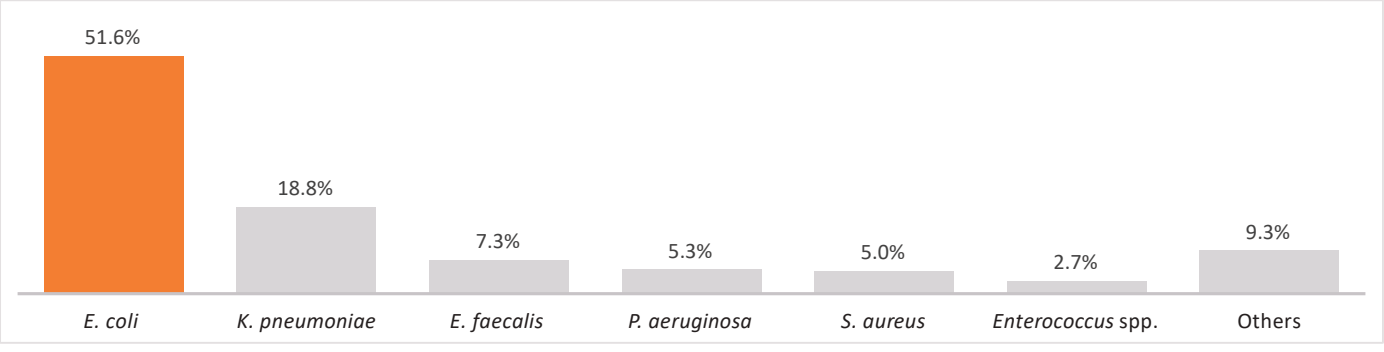
29.6. Age-wise distribution of urine isolates (n= 49,460)



29.7. Distribution of urine isolates by age and sex (n= 49,460)



29.8. Most frequent organisms in urine (n=49,460)



Gender-wise distribution of the most frequent urine pathogens

29.9. Most frequent organisms found in Urine - Male (n= 12,003)

29.10. Most frequent organisms found in Urine - Female (n=37,457)

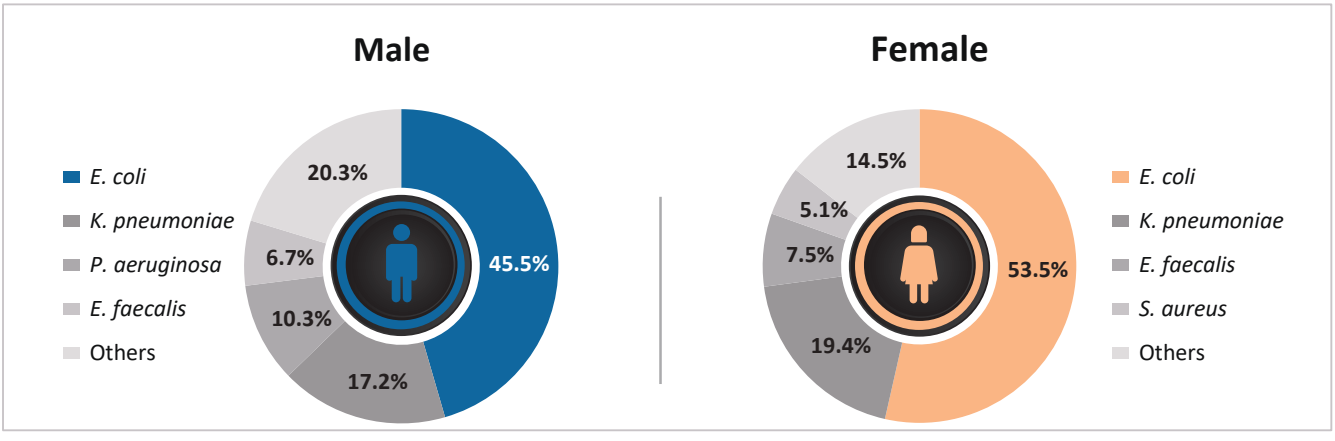


Figure 29: Distribution of urine isolates by specimen category, hospital, and patient characteristics, Bangladesh

Table 6: Antibiogram of Gram-Negative and Gram-Positive Bacteria from Urine Specimens: Isolates from Case-based and Lab-based Surveillance

Organisms	Location	Susceptible %																											
		Amoxicillin-Clavulanate	Amikacin	Ampicillin	Azithromycin	Aztreonam	Oxacillin	Cefexime	Ceftazidime	Ciprofloxacin	Cefepime	Ceftriaxone	Cefuroxime	Clindamycin	Colistin*	Doxycycline	Gentamicin	Imipenem	Meropenem	Linezolid	Penicillin	Piperacillin-tazobactam	Sulfamethoxazole-Trimethoprim	Tetracycline	Fosfomycin	Nitrofurantoin	Cefazolin	Vancomycin	Netilmycin
Gram-negative																													
E. coli	Overall	58↑	88↑	21↑	-	53≈	-	42↑	56↑	42↓	57≈	44↑	28↓	-	-	-	76↓	92↓	92↓	-	-	74↓	44↓	75↑	93↓	78≈	18↑	-	-
	ICU	19	51	-	-	-	-	-	-	5	13	16	6	-	-	-	44	52	49	-	-	32	26	-	93	-	-	-	-
	IPD	29	71	9	-	29	-	17	27	24	32	28	14	-	-	-	70	77	76	-	-	57	38	48	88	67	24	-	-
	OPD	58	89	21	-	54	-	43	58	42	59	44	30	-	-	-	76	93	93	-	-	75	45	75	94	79	20	-	-
K. pneumoniae	Overall	59↑	83↓	-	-	61↓	-	52↑	64↑	52↓	66↓	56↓	38↓	-	-	-	73↓	83↓	83↓	-	-	68↓	49↓	76↑	-	45↑	32	-	-
	IPD	37	47	-	-	27	-	18	27	21	26	26	16	-	-	-	59	50	46	-	-	42	43	58	-	16	33	-	-
	OPD	59	86	-	-	65	-	55	63	-	70	58	40	-	-	-	73	86	86	-	-	69	51	76	-	47	33	-	-
Proteus spp.	Overall	57	90	-	-	78	-	80	81	54	80	72	50	-	-	-	71	85	93	-	-	-	-	52	-	-	-	-	-
	OPD	60	91	-	-	82	-	74	84	56	85	75	52	-	-	-	72	88	95	-	-	-	-	-	-	-	-	-	-
P. aeruginosa	Overall	-	73↓	-	-	48↑	-	-	54↑	51↓	58↑	-	-	-	88	-	-	68↓	67↓	-	-	77≈	-	-	-	-	-	-	63↓
	IPD	-	25	-	-	22	-	-	14	15	14	-	-	-	84	-	-	16	21	-	-	-	-	-	-	-	-	-	-
	OPD	-	81	-	-	52	-	-	59	57	67	-	-	-	89	-	-	79	78	-	-	81	-	-	-	-	-	-	70
Gram positive																													
S. aureus	Overall	-	-	-	-	-	60↑	-	-	39↑	-	-	-	-	-	50↓	74↓	-	-	79↓	47↑	-	22↓	-	-	77↓	-	93↓	-
	IPD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	89	-	-	-	-	-	81	-	-	-
	OPD	-	-	-	-	-	66	-	-	44	-	-	-	-	-	52	74	-	-	88	21	-	22	-	-	88	-	92	-
Enterococcus spp.	Overall	-	-	74	-	-	-	-	-	29	-	-	-	-	-	-	-	-	-	88	-	-	-	53	-	84	-	91	-
	IPD	-	-	46	-	-	-	-	-	17	-	-	-	-	-	-	-	-	-	87	-	-	-	22	-	71	-	81	-
	OPD	-	-	76	-	-	-	-	-	31	-	-	-	-	-	-	-	-	-	88	-	-	-	54	-	86	-	92	-

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

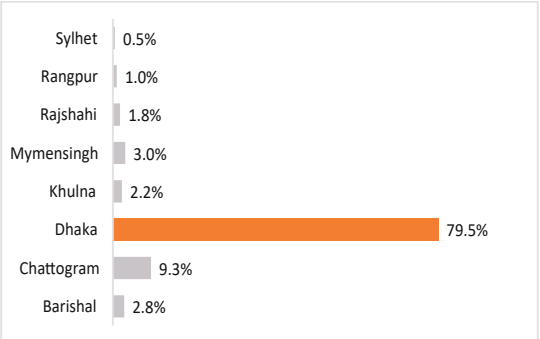
Reference: CLSI M100, 35th Edition

Specimen: Blood

14,629
Total blood samples

Of the total samples received from laboratories across Bangladesh, 15% (14,629) were blood samples. Total 7,096 blood samples were from case-based surveillance, and 7,533 isolates were from lab-based surveillance. The culture positivity rate of blood samples from case-based surveillance was 10.9% (773) (Figure 30.3). In total, 8,306 isolates were analyzed, and more than half (55.6%) of the isolates were from males (Figure 30.2).

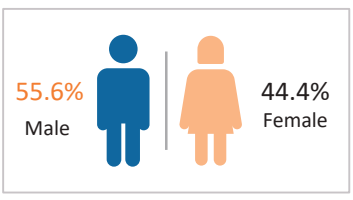
30.1. Geographical distribution of blood isolates (n= 8,306)



Geographically, most blood isolates (79.5%) were reported from the Dhaka Division, followed by 9.3% from Chattogram, with the remaining 11.2% from other divisions (Figure 30.1). Analyzing the positively yielded case-based blood isolates (n=748), 58.6% were from community origin, and 41.4% were from hospital origin (Figure 30.4).

S. Typhi, *S.* Paratyphi A and *E. coli* were identified as the most frequent pathogens isolated from blood samples (Figure 30.8).

30.2: Sex-wise distribution of blood isolates (n= 8,306)



30.3: Culture yield of case-based samples (n= 7,096)

10.9%
Growth (n= 773)

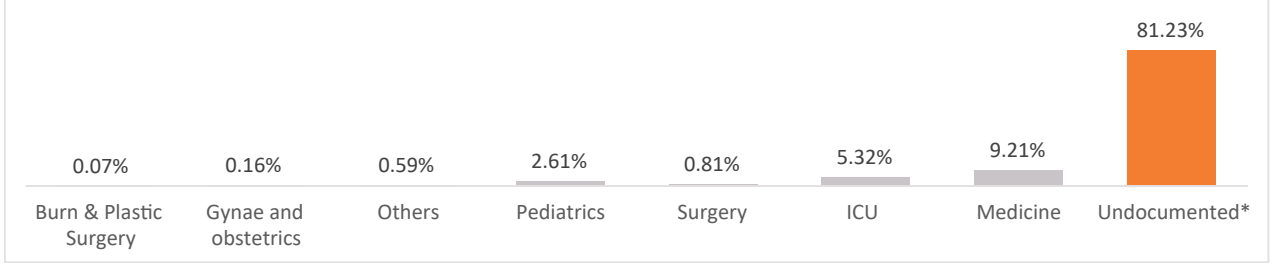
89.1%
No Growth (n= 6,323)

30.4: Infection origin of blood isolates (n=773)

58.6%
Community Origin

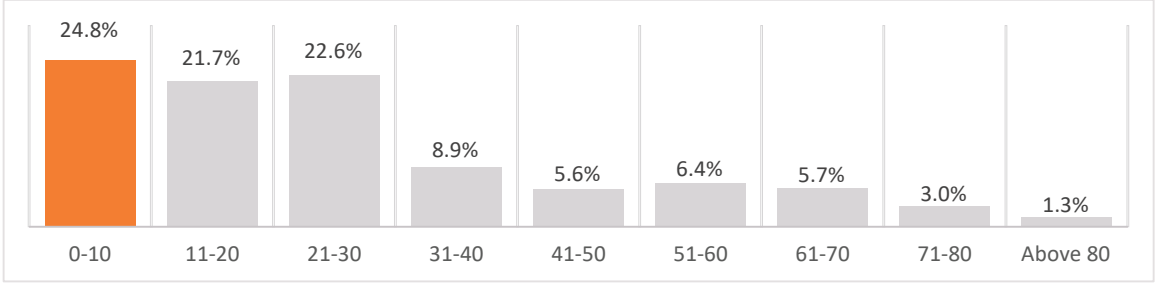
41.4%
Hospital Origin

30.5: Distribution of blood isolates by hospital department (n=8,306)

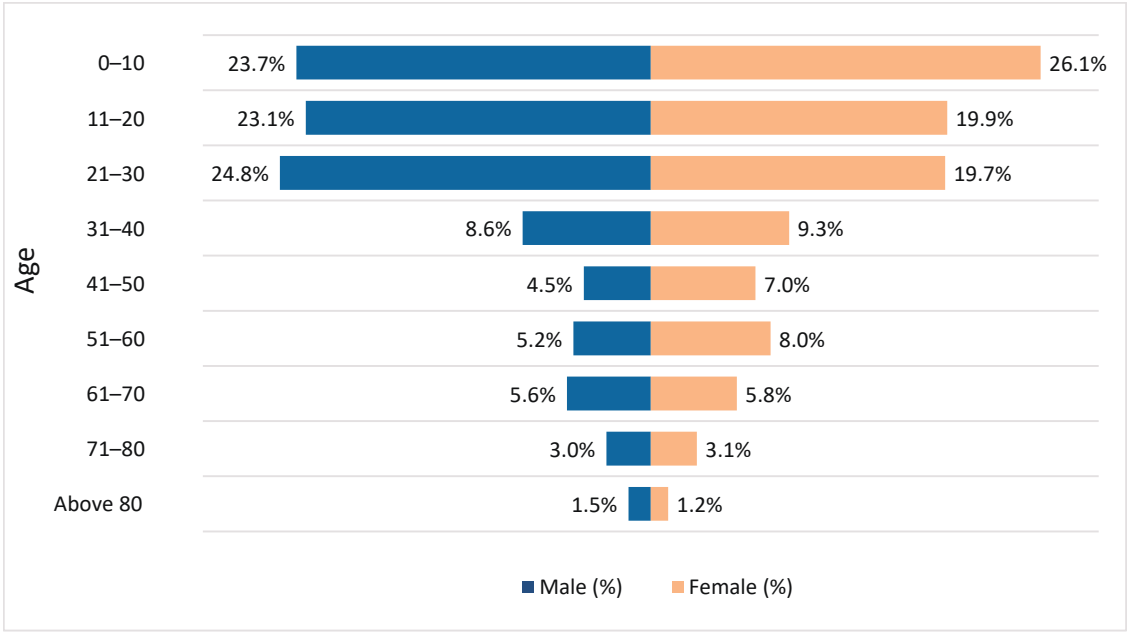


* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

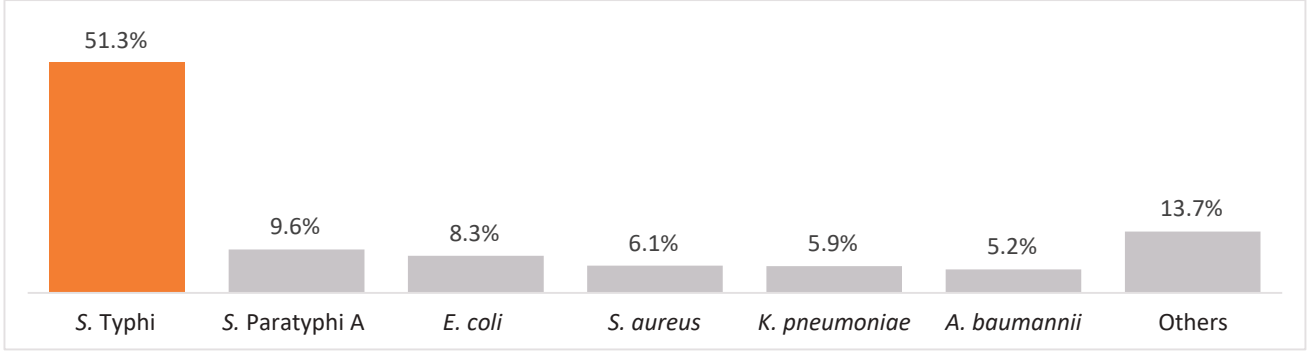
30.6: Age-wise distribution of blood isolates (n=8,306)



30.7: Distribution of blood isolates by age and sex (n=8,306)



30.8: Most frequent organisms in blood (n=8,306)



Gender-wise distribution of the most frequent blood pathogens

30.9. Most frequent organism found in Blood - Male (n=4,614)

30.10. Most frequent organism found in Blood - Female (n=3,692)

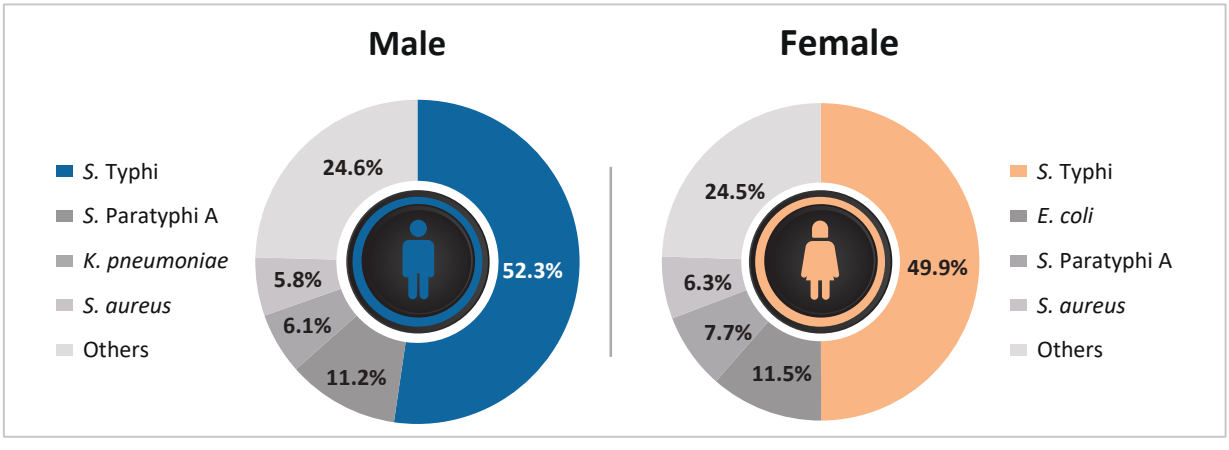


Figure 30: Distribution of blood isolates by specimen category, hospital, and patient characteristics, Bangladesh, 2025

Table 7: Antibiogram of Gram-Negative and Gram-Positive Bacteria from Blood Specimens: Isolates from Case-based and Lab-based Surveillance

Organisms	Location	Susceptible %																										
		Amoxicillin-Clavulanate	Amikacin	Ampicillin	Azithromycin	Aztreonam	Oxacillin	Cefixime	Ceftazidime	Ciprofloxacin	Cefepime	Ceftriaxone	Cefuroxime	Clindamycin	Colistin*	Doxycycline	Gentamicin	Imipenem	Meropenem	Linezolid	Levofloxacin	Penicillin	Piperacillin-tazobactam	Sulfamethoxazole-Trimethoprim	Tetracycline	Vancomycin	Netilmycin	Tobramycin
Gram-negative																												
E. coli	Overall	42≈	80↓	10↑	-	34↓	-	33↑	40↑	25↓	35↓	29↓	13↓	-	-	-	69↓	78↓	77↓	-	-	-	60↓	33↓	66↑	-	-	-
	ICU	-	-	-	-	-	-	-	-	12	-	6	0	-	-	-	-	54	51	-	-	-	-	23	-	-	-	-
	Ward	28	67	2	-	24	-	10	24	19	22	21	9	-	-	-	62	77	72	-	-	-	52	34	65	-	-	-
	OPD	56	88	25	-	48	-	48	56	29	47	31	19	-	-	-	76	84	86	-	-	-	87	-	72	-	-	-
K. pneumoniae	Overall	15↓	39↑	-	-	20≈	-	40↑	17↓	21↓	56↓	14↓	8↓	-	-	-	46↑	32↓	31↓	-	-	-	29↑	28↓	36↓	-	-	-
	ICU	7↑	15↓	-	-	5	-	-	3≈	6↑	6↑	5↑	5↑	-	-	-	13↑	15↓	15↓	-	-	-	9↓	19↑	31	-	-	-
	Ward	17	38	-	-	20	-	-	15	26	22	16	8	-	-	-	60	45	32	-	-	-	26	40	52	-	-	-
	OPD	-	48	-	-	38	-	29	37	26	24	23	12	-	-	-	57	36	42	-	-	-	62	-	31	-	-	-
P. aeruginosa	Overall	-	-	-	-	32↓	-	-	57↑	51↓	50↑	-	-	-	59	-	-	53↓	56↓	-	-	-	51↓	-	-	-	45↓	12
	ICU	-	-	-	-	-	-	-	28	42	24	-	-	-	-	-	-	37	34	-	-	-	46	-	-	-	-	-
	Ward	-	-	-	-	30**	-	-	61	53	61	-	-	-	46	-	-	58	63	-	-	-	57	-	-	-	53	-
	OPD	-	-	-	-	51	-	-	74	54	52	-	-	-	76	-	-	56	57	-	-	-	62	-	-	-	64	-
S.Typhi	Overall	-	-	80↓	40↓	-	-	-	-	23↓	-	88↓	-	-	-	-	-	96↓	97↓	-	80↓	-	-	62	-	-	-	-
	Ward	-	-	81	71	-	-	-	-	7	-	95	-	-	-	-	-	97	98	-	89	-	-	81	-	-	-	-
	OPD	-	-	80	37	-	-	-	-	24	-	88	-	-	-	-	-	96	97	-	79	-	-	55	-	-	-	-
Acinetobacter spp.	Overall	-	36↓	-	-	-	-	-	18↓	28↓	23↓	15↓	-	-	89↓	-	29↓	23↓	25↓	-	-	-	30↓	40↓	-	-	-	35
	ICU	-	29↑	-	-	-	-	-	11↓	21↑	21↑	11↑	-	-	-	-	15↓	15≈	14↑	-	-	-	18↑	36↑	-	-	-	31
	Ward	-	32	-	-	-	-	-	21	34	25	-	-	-	-	-	34	35	33	-	-	-	50	52	-	-	-	44
	OPD	-	47	-	-	-	-	-	35	35	25	21	-	-	85	-	46	29	40	-	-	-	-	-	-	-	-	-
Gram positive																												
S. aureus	Overall	-	-	-	34↑	-	41≈	-	-	43↓	-	-	-	47↓	-	48↓	48↓	-	-	80↓	-	12↑	-	34↓	-	94↓	-	-
	ICU	-	-	-	-	-	19↑	-	-	26↓	-	-	-	35↑	-	-	52↑	-	-	79↑	-	7↑	-	35↓	-	-	-	-
	Ward	-	-	-	18	-	40	-	-	42	-	-	-	64	-	86	79	-	-	97	-	8	-	40	-	100	-	-
	OPD	-	-	-	8	-	52	-	-	46	-	-	-	38	-	64	76	-	-	87	-	15	-	27	-	88	-	-

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

Reference: CLSI M100, 35th Edition

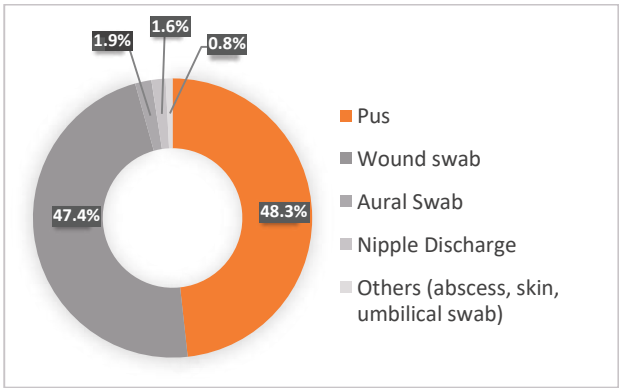
Specimen: Skin and Soft Tissue Infection (SSTI)

12,421
Total SSTI samples

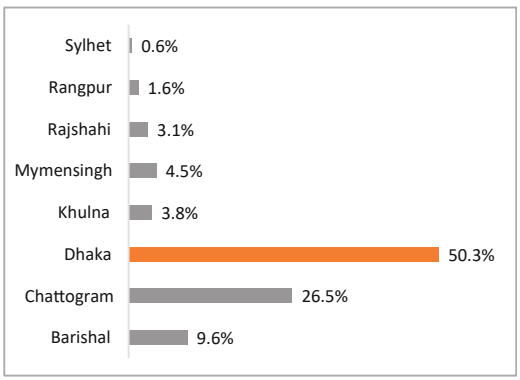
Of the total samples received from the laboratories across Bangladesh, 13% (n=12,421) were SSTI samples. These total SSTI samples comprised of 1,816 samples from case-based surveillance and 10,605 isolates from lab-based surveillance.

The culture positivity rate for SSTI samples from case-based surveillance was 55% (Figure 31.4). Thus, a total of 11,604 SSTI bacterial isolates were analyzed. Among the isolates, 48% were obtained from pus and 47% from wound swabs, with the remaining isolates collected from aural swabs, nipple discharge, abscesses, skin and umbilical swabs (Figure 31.1).

31.1: Distribution of SSTI specimen types



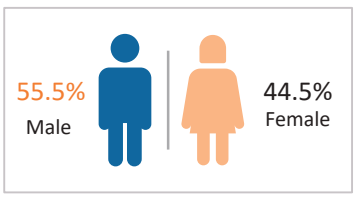
31.2: Geographical distribution of SSTI isolates (n= 11,604)



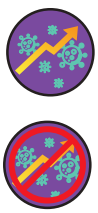
Geographically, almost half of the SSTI isolates (50.3%) were from Dhaka Division, followed by 26.5% from Chattogram, with the remaining 23.2% from other divisions (Figure 31.2). Analyzing case-based SSTI isolates (n=944), 34.9% were community-origin, and 65.1% were hospital-origin (Figure 31.5).

S. aureus, *P. aeruginosa* and *K. pneumoniae* were identified as the most common organisms isolated from SSTI samples (Figure 31.8).

31.3: Sex-wise distribution of SSTI isolates (n=11,604)

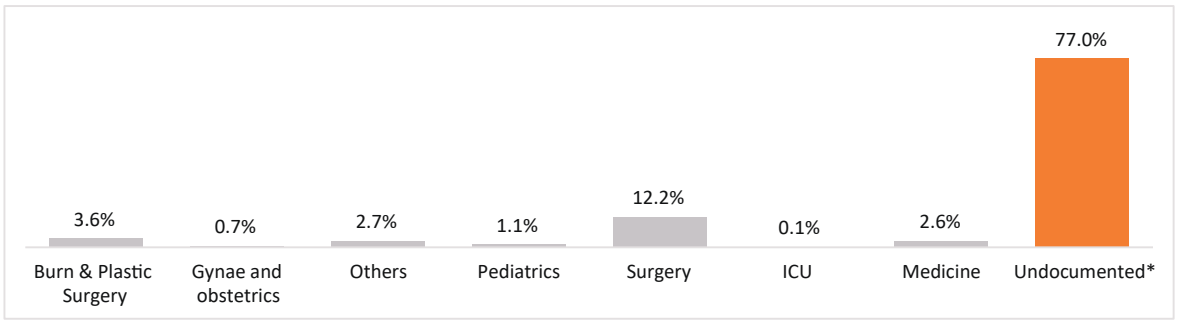


31.4: Culture yield of case-based samples (n= 1,816)



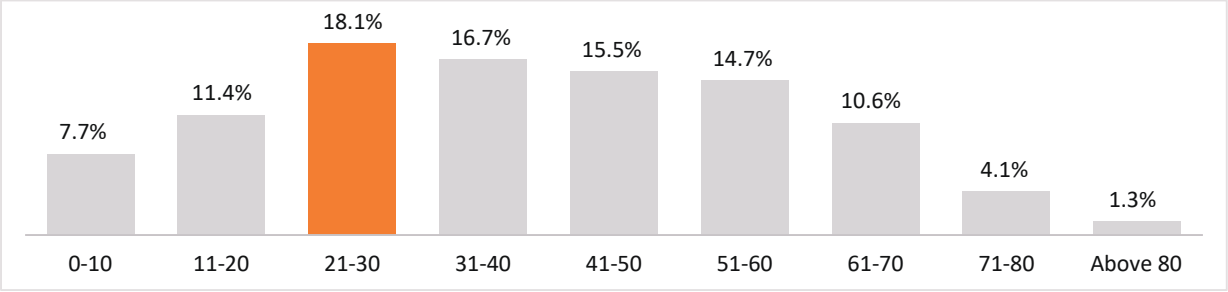
31.5: Infection origin of SSTI isolates (n=999)

31.6: Distribution of SSTI isolates by hospital department (n= 11,604)

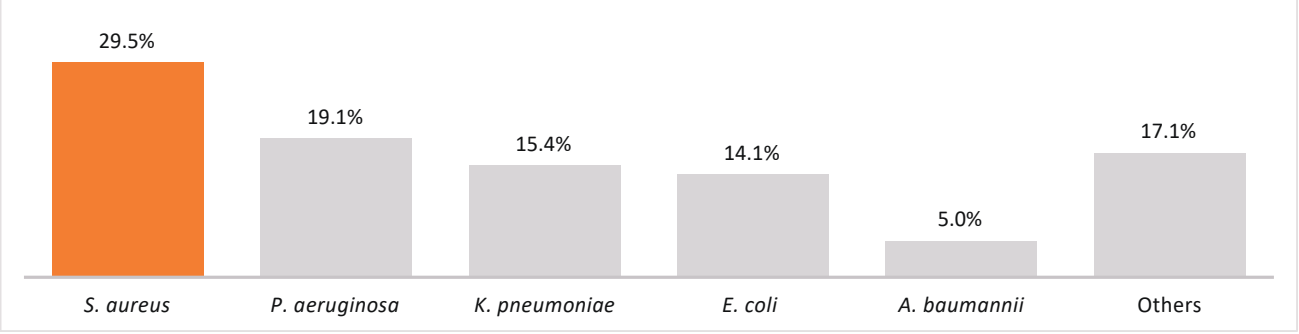


* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

31.7: Age-wise distribution of SSTI isolates (n= 11,604)



31.8: Most frequent organisms in SSTI (n= 11,604)



Gender-wise Distribution of the Most Frequent SSTI Pathogens

31.9: Most frequent organism found in SSTI – Male (n=6,443)

31.10: Most frequent organism found in SSTI – Female (n=5,161)

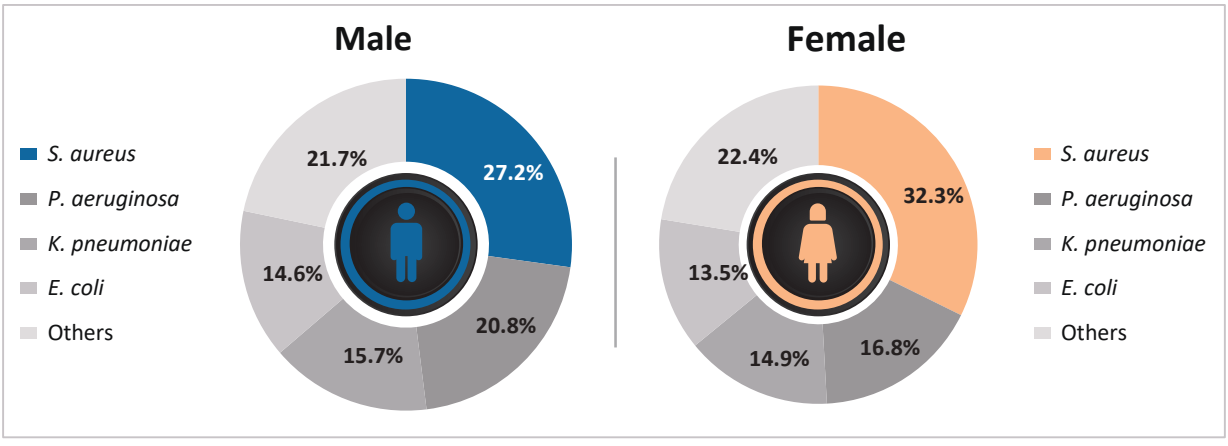


Figure 31: Distribution of SSTI isolates by specimen category, hospital, and patient characteristics, Bangladesh, 2025

Table 8: Antibiogram of Gram-Negative and Gram-Positive Bacteria from SSTI: Isolates from Case-based and Lab-based Surveillance

Organism	Location	Susceptible %																									
		Amikacin	Ampicillin	Amoclillin-clavulanate	Azithromycin	Aztreonam	Cefixime	Ceftazidime	Ciprofloxacin	Cefepime	Ceftriaxone	Cefuroxime	Clindamycin	Colistin*	Doxycycline	Gentamicin	Imipenem	Linezolid	Meropenem	Oxacillin	Penicillin	Piperacillin-tazobactam	Sulfamethoxazole-Trimethoprim	Tetracycline	Tobramycin	Netilmycin	Vancomycin
Gram-negative																											
E. coli	Overall	79	8	30	-	33	40	38	27	43	29	15	-	-	-	65	77	-	79	-	-	58	31	54	-	-	-
	IPD	73	2	11	-	20	18	18	27	27	16	6	-	-	-	59	72	-	74	-	-	35	32	39	-	-	-
Acinetobacter spp.	Overall	41	-	-	-	-	-	27	30	28	26	-	-	96	-	41	35	-	34	-	-	52	37	-	36	-	-
	IPD	20	-	-	-	-	-	20	14	20	16	-	-	-	-	42	30	-	26	-	-	36	33	-	31	-	-
P. aeruginosa	Overall	-	-	-	-	42	-	39	30	41	-	-	-	90	-	-	57	-	55	-	-	55	-	-	35	52	-
	IPD	-	-	-	-	37	-	27	36	30	-	-	-	78	-	-	50	-	44	-	-	47	-	-	33	42	-
K. pneumoniae	Overall	58	-	28	-	34	36	36	27	37	30	18	-	-	-	54	59	-	57	-	-	49	21	49	-	-	-
	IPD	36	-	13	-	17	17	17	19	21	17	9	-	-	-	45	49	-	39	-	-	26	19	38	-	-	-
Gram positive																											
S.aureus	Overall	-	-	-	23	-	-	-	34	-	-	-	52	-	59	79	-	89	-	58	14	-	-	-	-	-	96
	IPD	-	-	-	21	-	-	-	28	-	-	-	63	-	80	77	-	86	-	-	-	-	-	-	-	-	100

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

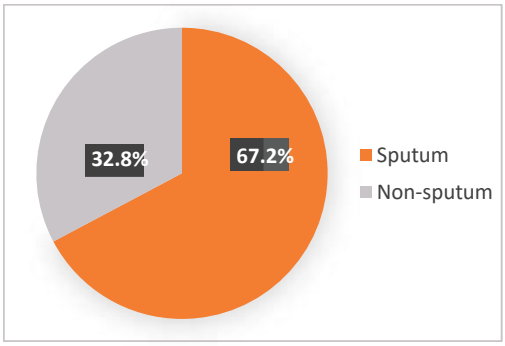
Reference: CLSI M100, 35th Edition

Specimen: Lower Respiratory Tract Infection (LRTI)

11,080
Total LRTI samples

Of the total samples received from laboratories across Bangladesh, 12% (n=11,080) were LRTI samples. These total LRTI samples comprised 1,110 samples from case-based surveillance and 9,970 isolates from lab-based surveillance. The culture positivity rate of LRTI samples from case-based surveillance was 59.4% (n=659) (Figure 32.4). Therefore, in total, 10,629 LRTI bacterial isolates were analyzed. Male LRTI isolates were predominant (62.5%) (Figure 32.3).

32.1: Distribution of LRTI specimen types (n=10,629)

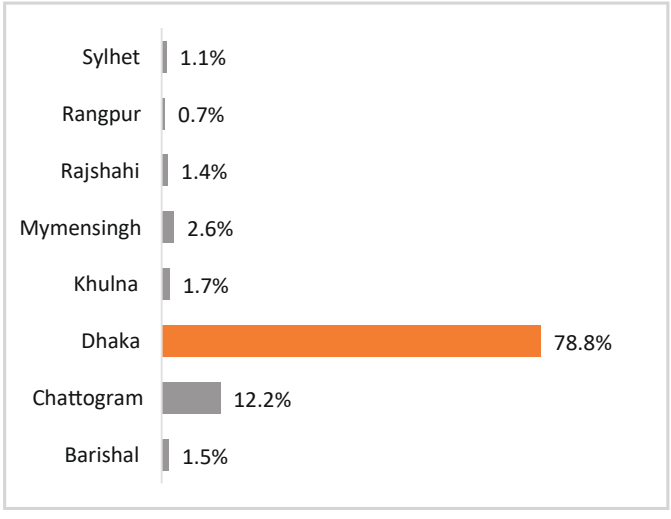


Among the analyzed LRTI bacterial isolates, more than half (67.2%, n=7,147) were obtained from sputum (Figure 32.1). Other sources included endotracheal aspirate, tracheal aspirate, broncho-alveolar lavage, etc.

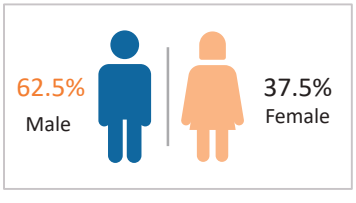
Geographically, more than half of the LRTI isolates (78.8%) were from the Dhaka Division, followed by 12.1% from Chattogram, with the remaining 9.1% from other divisions (Figure 32.2). Analyzing the positively yielded case-based LRTI isolates (n=659), 29.1% were from community origin and 71.9% were from hospital origin (Figure 32.5).

K. pneumoniae, P. aeruginosa and *A. baumannii* were identified as the most common organisms isolated from LRTI samples (Figure 32.8).

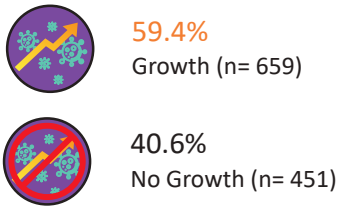
32.2: Geographical distribution of LRTI isolates (n=10,629)



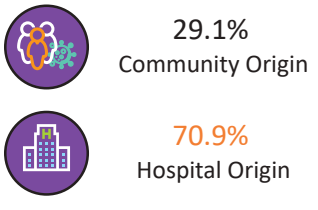
32.3: Sex-wise distribution of LRTI isolates (n=10,629)



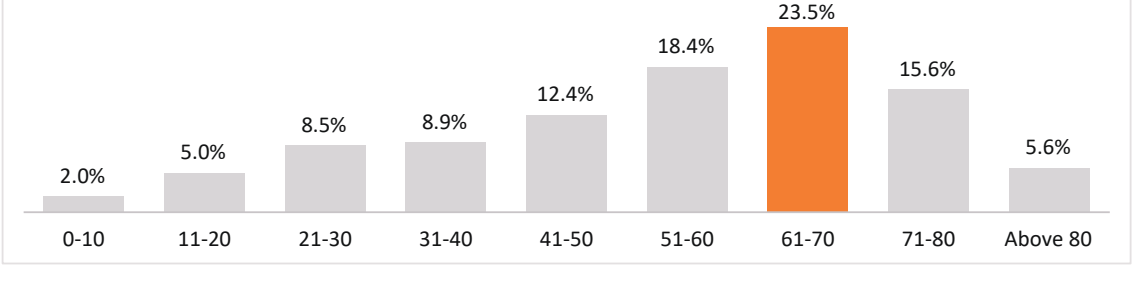
32.4: Culture yield of case-based samples (n= 1,110)



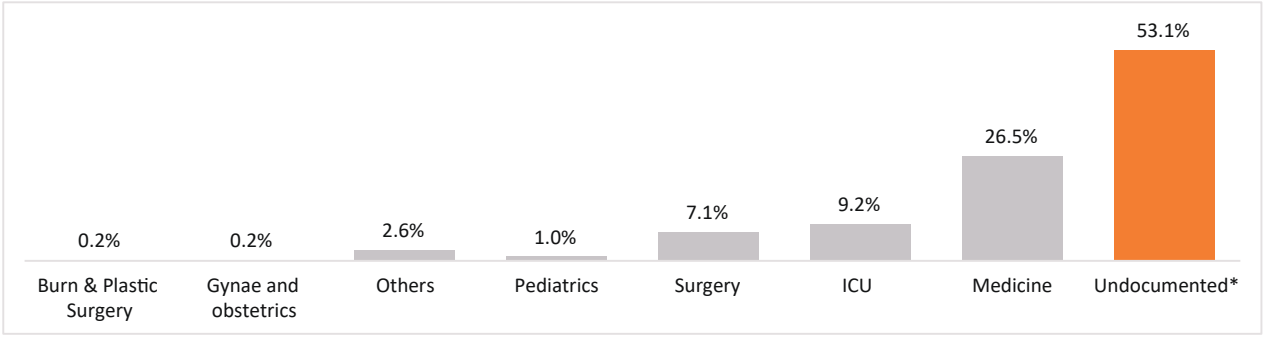
32.5: Infection origin of LRTI isolates (n=659)



32.6: Age-wise distribution of LRTI isolates (n=10,629)

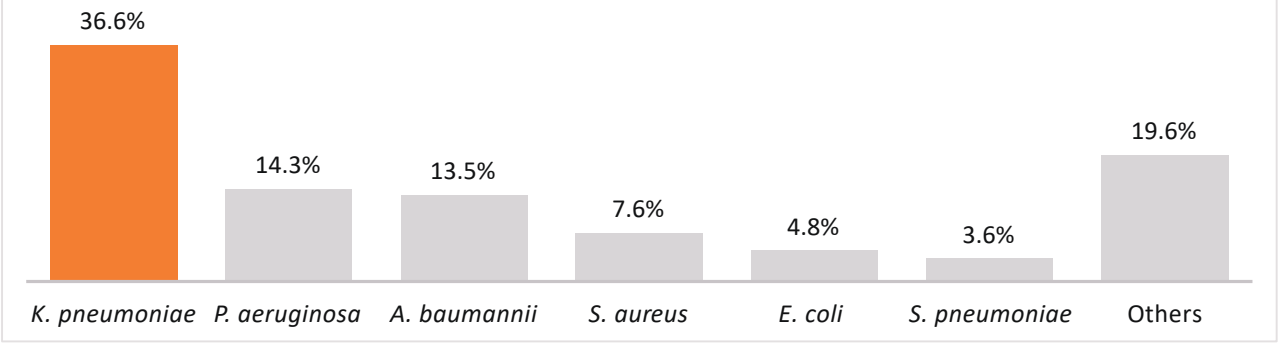


32.7: Distribution of LRTI isolates by hospital department (n=10,629)



* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

32.8: Most frequent organisms in LRTI (n=10,629)



Gender-wise Distribution of the Most Frequent LRTI Pathogens

32.9: Most frequent organism found in LRTI – Male (n= 6,640)

32.10: Most frequent organism found in LRTI – Female (n=3,989)

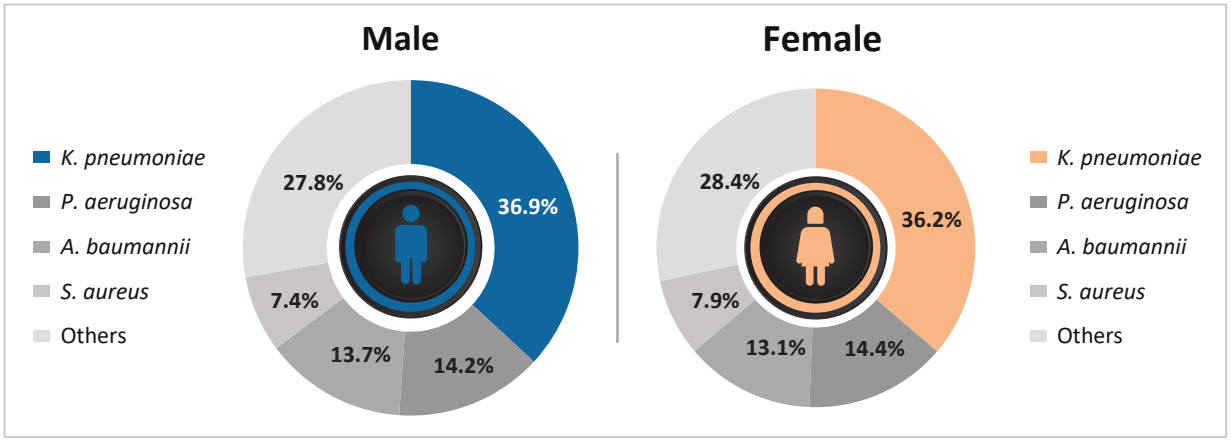


Figure 32: Distribution of LRTI isolates by specimen category, hospital, and patient characteristics, Bangladesh, 2025

Table 9: Antibiogram of Gram-Negative and Gram-Positive Bacteria from LRTI: Isolates from Case-based and Lab-based Surveillance

Organism	Location	Susceptible %																										
		Amikacin	Amocillin-clavulanate	Azithromycin	Aztreonam	Cefixime	Ceftazidime	Ciprofloxacin	Cefepime	Ceftriaxone	Cefuroxime	Clindamycin	Colistin*	Doxycycline	Linezolid	Levofloxacin	Gentamicin	Imipenem	Meropenem	Netilmycin	Oxacillin	Penicillin	Piperacillin-tazobactam	Sulfamethoxazole-Trimethoprim	Tetracycline	Vancomycin	Tobramycin
Gram-negative																												
E. coli	Overall	79	41	-	46	46	59	27	51	40	30	-	-	-	-	-	70	71	79	-	-	-	60	-	49	-	-
	IPD	76	-	-	13	8	24	17	30	18	11	-	-	-	-	-	-	51	78	-	-	-	-	-	41	-	-
K. pneumoniae	Overall	62	42	-	40	53	56	39	54	48	33	-	-	-	-	-	69	58	58	-	-	-	53	23	62	-	-
	ICU	24	5	-	6	-	7	6	-	5	2	-	-	-	-	-	22	16	14	-	-	-	9	20	39	-	-
	IPD	42	-	-	9	-	22	10	23	21	15	-	-	-	-	-	51	24	38	-	-	-	-	-	55	-	-
P. aeruginosa	Overall	-	-	-	48	-	56	49	55	-	-	-	94	-	-	-	-	57	62	61	-	-	48	-	-	-	-
	ICU	-	-	-	26	-	17	25	23	-	-	-	-	-	-	-	-	32	25	35	-	-	31	-	-	-	-
	IPD	-	-	-	47	-	46	29	32	-	-	-	87	-	-	-	-	34	54	58	-	-	-	-	-	-	-
Acinetobacter spp.	Overall	19	-	-	-	-	12	12	9	7	-	-	96	-	-	-	19	11	12	-	-	-	7	30	-	-	13
	ICU	12					4	5	4	0			93	-	-	-	8	4	5	-	-	-	6	29	-	-	20
	IPD	11					4	4	3	3			99	-	-	-	8	4	8	-	-	-	-	-	-	-	-
															-	-											
Gram positive																												
S.aureus	Overall	-	-	25	-	-	-	31	-	-	-	39	-	38	87	-	65	-	-	-	40	8	-	-	-	80	-
	IPD	-	-	-	-	-	-	21	-	-	-	43	-	-	98	-	-	-	-	-	-	-	-	-	-	100	-
CoNS	Overall	-	-	-	-	-	-	-	-	-	-	15	-	-	89	-	-	-	-	-	-	-	-	-	-	98	-
	IPD	-	-	-	-	-	-	-	-	-	-	16	-	-	92	-	-	-	-	-	-	-	-	-	-	100	-
S. pneumoniae	Overall	-	-	-	-	-	-	68	98	93	98	53	-	-	99	71	-	98	98	-	-	-	-	41	-	96	-

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

Reference: CLSI M100, 35th Edition

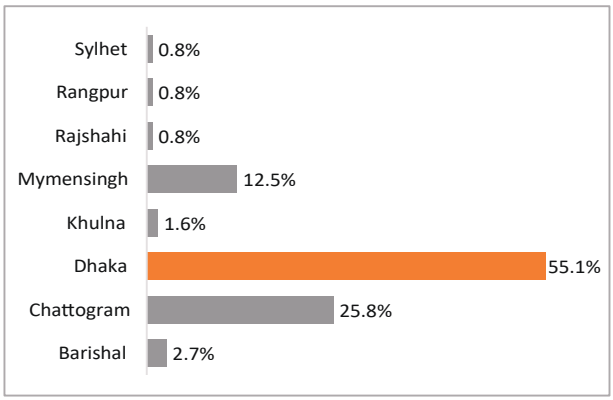
Specimen: Stool

2,176
Total stool samples

Of the total samples received from laboratories across Bangladesh, 2% (n=2,176) were stool samples. These total stool samples comprised 1,985 samples from case-based surveillance and 191 isolates from lab-based surveillance. The culture positivity rate of stool samples from case-based surveillance was approximately 4% (n=78) (Figure 33.3). A total of 256 stool isolates were analyzed.

E. coli from stool was not considered in this analysis, as the pathogenicity of the strains was not determined.

33.1: Geographical distribution of stool isolates (n=256)

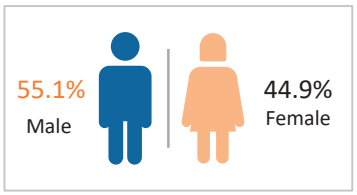


Geographically, most stool isolates (55.1%) were reported from the Dhaka Division, followed by 25.8% from Chattogram, with the remaining 19.1% from other divisions (Figure 33.1). Analyzing the positively yielded case-based stool isolates (n=78) (Figure 33.3), 97% were from community origin and 3% were from hospital origin (Figure 33.4).

Salmonella spp., *V. cholerae* and *Shigella* spp. were identified as the most common organisms isolated from stool samples (Figure 33.7).

Klebsiella spp. are part of the normal intestinal flora and their isolation often represents commensal colonization rather than true pathogenic infection.

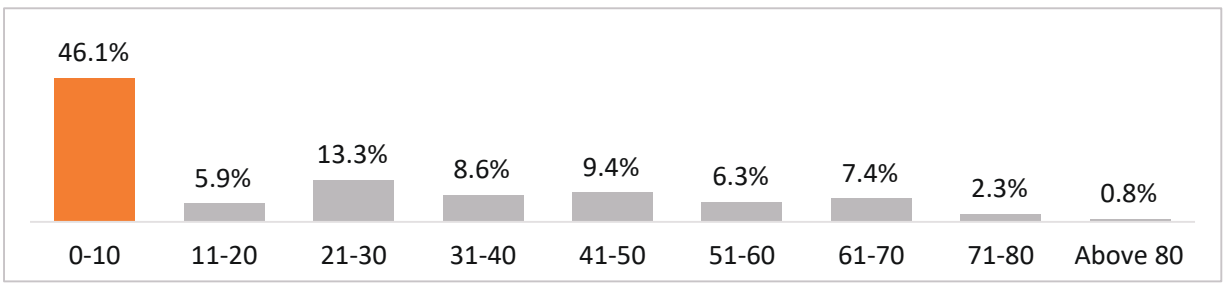
33.2: Sex-wise distribution of stool isolates (n=256)



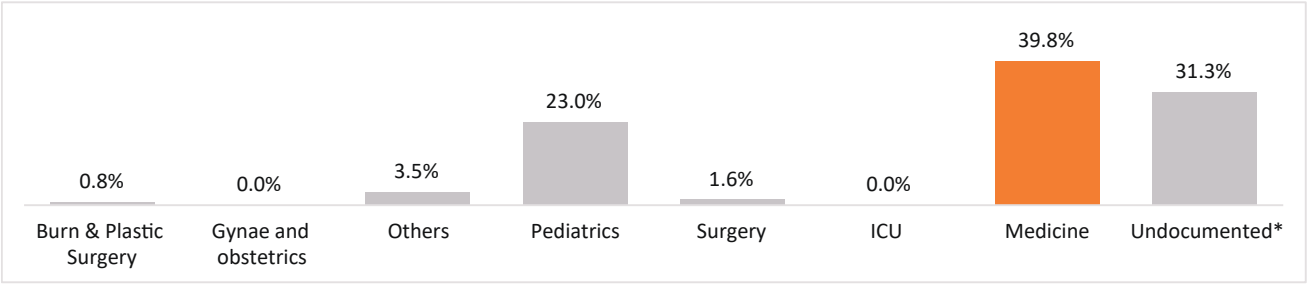
33.3: Culture yield of case-based samples (n= 1,985)

33.4: Infection origin of stool isolates (n=78)

33.5: Age-wise distribution of stool isolates (n=256)

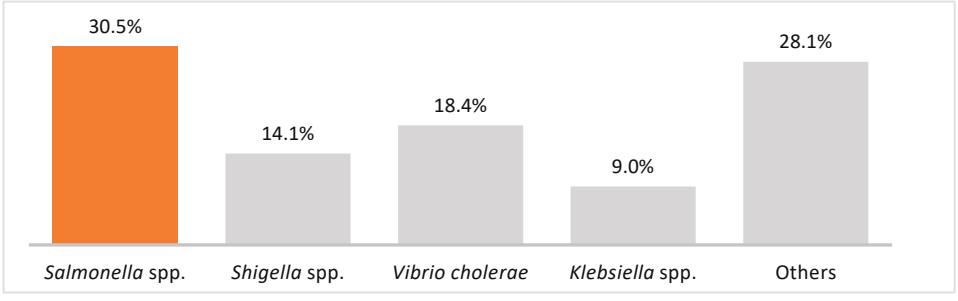


33.6: Distribution of stool isolates by hospital department (n= 256)



* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

33.7: Most frequent organisms in stool (n=256)



Gender-wise Distribution of the Most Frequent Pathogens in Stool

33.8: Most frequent organism found in Stool Male (n= 141)

33.9: Most frequent organism found in Stool Female (n=115)

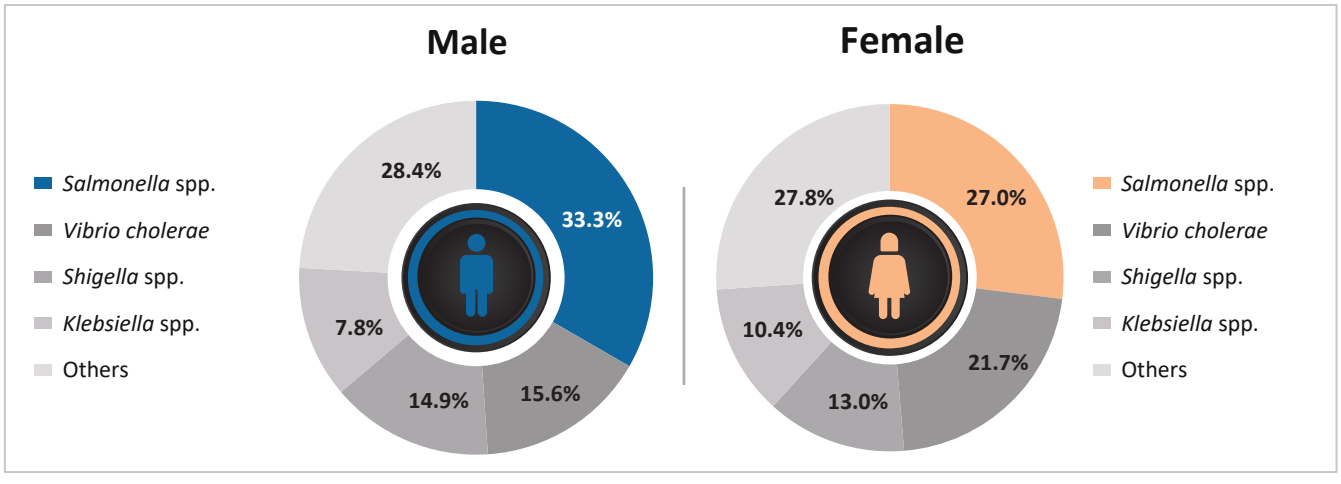


Figure 33: Distribution of stool isolates by specimen category, hospital, and patient characteristics, Bangladesh, 2025

Table-10: Antibiogram of bacteria from stool specimen: Isolates from Case-based and Lab-based Surveillance

Organism	Location	Susceptible %					
		Azithromycin	Ampicillin	Ciprofloxacin	Cholramphenicol	Sulfamethoxazole-Trimethoprim	Tetracycline
Gram-negative							
V. cholerae	Overall	84	12	70	57	12	90
	IPD	84	12	71	57	12	90
Shigella spp.*	Overall	-	20	4	-	27	-

*Identified from July, 2023 to June, 2025

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

Reference: CLSI M100, 35th Edition

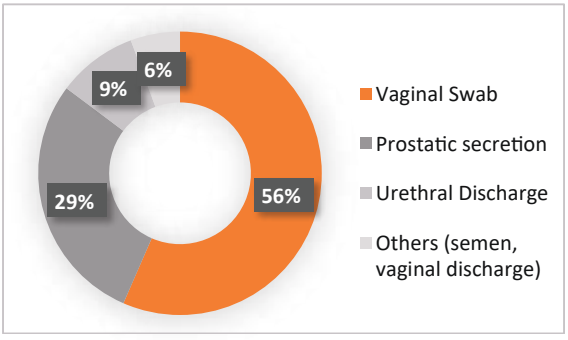
Specimen: Genital

1,063
Total genital samples

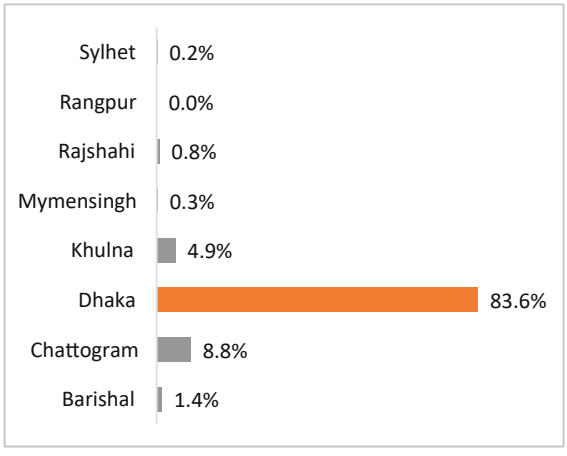
Among the total samples received from laboratories across Bangladesh, approximately 1% (n=1,063) were genital isolates from lab-based surveillance. Among these genital isolates, more than half were obtained from vaginal swabs (56.5%, n=601), followed by prostatic secretion (28.7%, n=305), urethral discharge (9.1%, n=97) and others (5.6%, n=60) (Figure 34.1).

Significant proportion of genital isolates were from the surgery department (n=285) (Figure 34.4) and among these, almost 99% (n=282) were from the urology department. Typically, a substantial proportion of genital isolates originate from skin venereal disease and gynecology/obstetrics departments. However, in this surveillance a large number of hospital department data were undocumented, so some cases may also belong to these departments.

34.1: Distribution of genital isolates into specimen types (n=1,063)

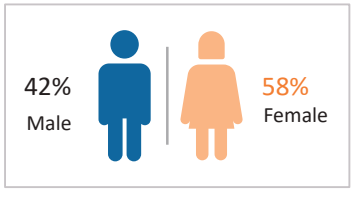


34.2: Geographical distribution of genital isolates (n=1,063)

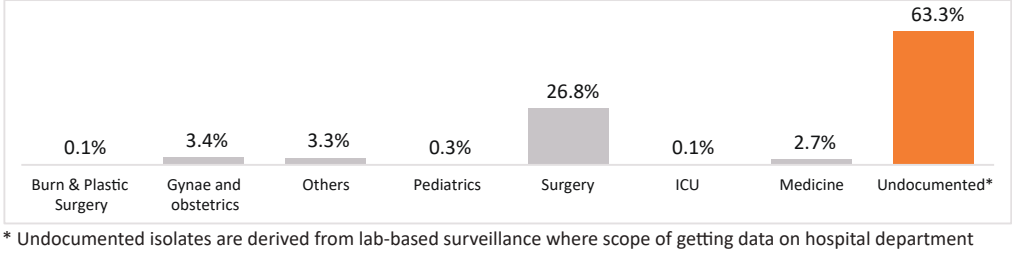


Geographically, more than half (83.6%) of the genital isolates were from the Dhaka Division, followed by 8.8% from Chattogram, with the remaining 7.5% from other divisions (Figure 34.2). Among the urology isolates, 96% (n=272) were from males and 4% (n=10) from females (Figure 34.3), predominantly aged 21 to 40 years (Figure 34.6). Among patients aged 0 -10 years, a total of 14 isolates were identified. The majority were obtained from vaginal swabs and urethral discharge (n=6, 42.9% each), while a smaller proportion was identified from high vaginal swabs (n=2, 14.3%). *E. coli* and *K. pneumoniae* were identified as one of the most common organisms isolated from genital samples (Figure 34.7).

34.3: Sex-wise distribution of genital isolates (n=1,063)

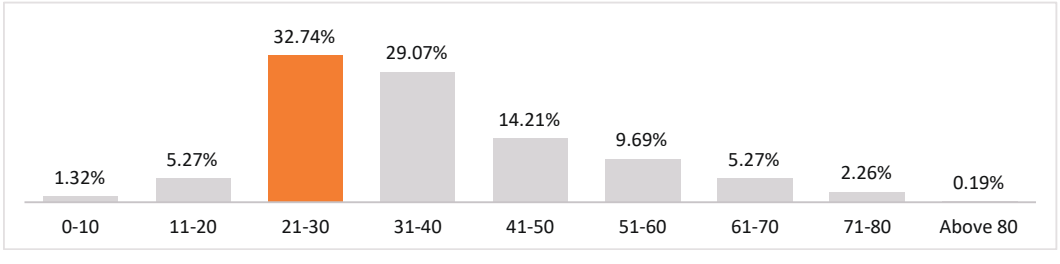


34.4: Distribution of genital isolates by hospital department (n=1,063)

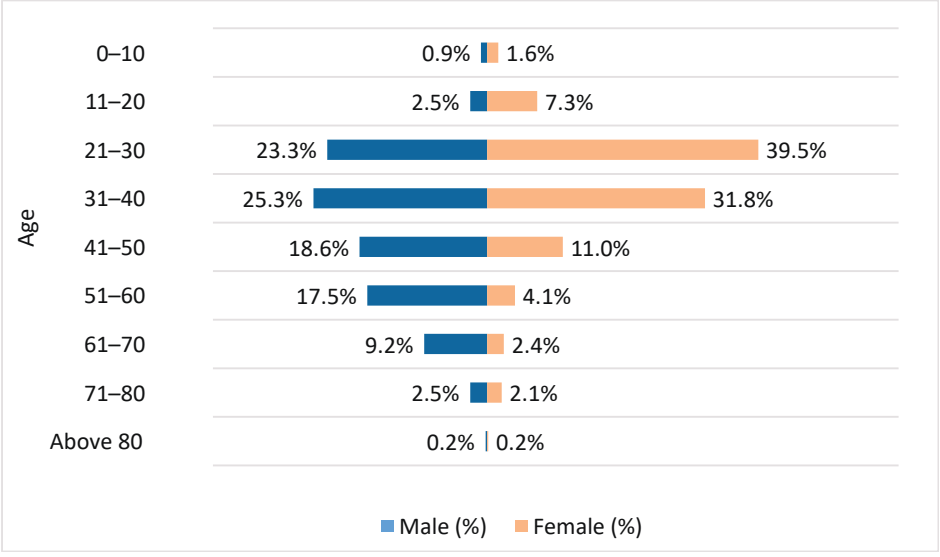


* Undocumented isolates are derived from lab-based surveillance where scope of getting data on hospital department was limited.

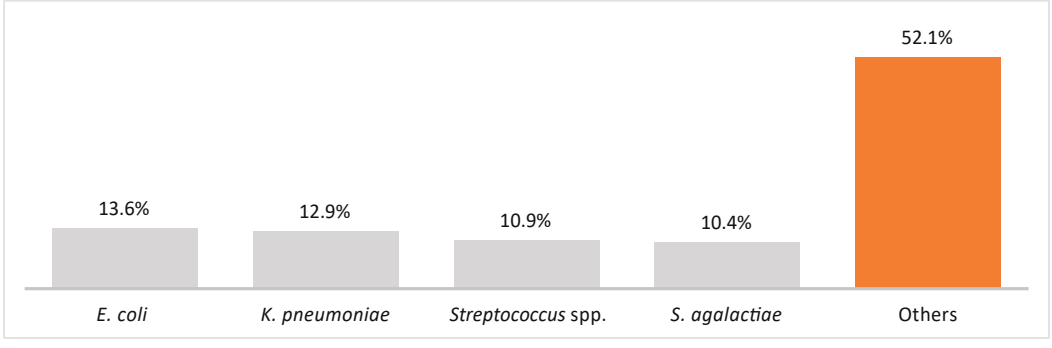
34.5: Age-wise distribution of genital isolates (n=1,063)



34.6: Distribution of genital isolates by age and sex (n= 1,063)



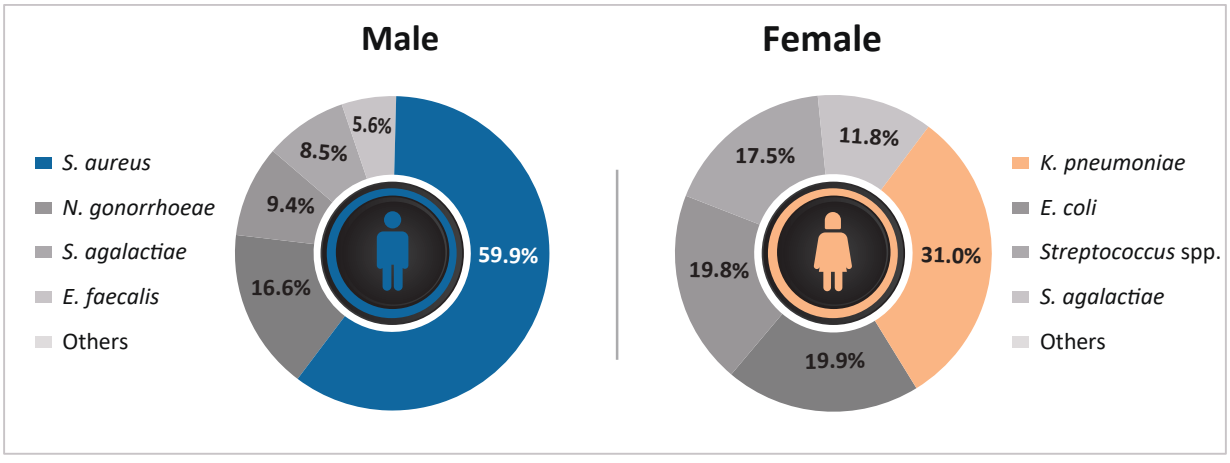
34.7: Distribution of Most frequent organism found in Genital specimen (n=1,063)



Gender-wise Distribution of the Most Frequent Genital Pathogens

34.8: Most frequent organism found in Genital isolates Male (n= 446)

34.9: Most frequent organism found in genital isolates-Female (n=617)



Pathogen highlight: *Neisseria gonorrhoeae (N. gonorrhoeae)*

N. gonorrhoeae is a looming threat due to its high transmissibility and frequent asymptomatic nature. This asymptomatic nature of *N. gonorrhoeae* is often associated with underdiagnosis, continued undetected transmission, and delayed treatment. Gonococcal infection has serious reproductive health consequences, particularly among females, and significant association with HIV transmission. Untreated gonococcal infection could potentially lead to serious complications for females, such as pelvic inflammatory diseases, ectopic pregnancy, and infertility. In males, gonococcal infection commonly presents as acute urethritis with presentable symptoms, which facilitates earlier health-seeking behavior. This makes men an important sentinel population for monitoring AMR, as male-to-female transmission of *N. gonorrhoeae* is generally more efficient than female-to-male transmission.

In this analysis, among the genital isolates analyzed (n=1,063), *N. gonorrhoeae* accounted for 5.2% (n=55). *N. gonorrhoeae* was found more frequently in males (n=42) than in females (n=13) and was predominant in the age group 21 to 30 years old for both sexes. (Figure 34.10). *N. gonorrhoeae* was more frequent in the reproductive age group for both males and females.

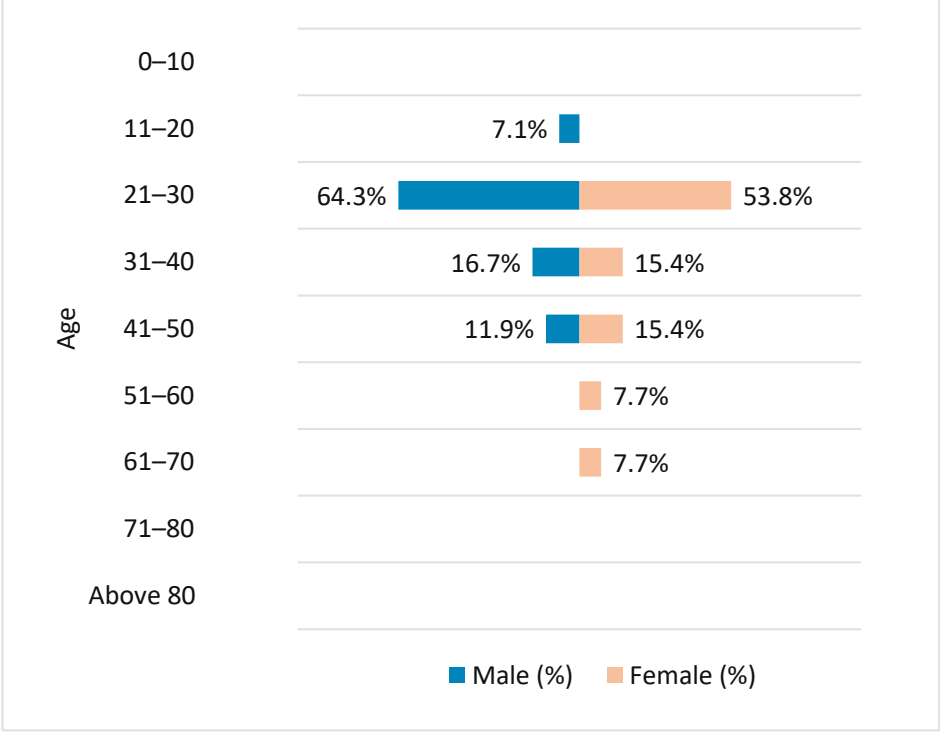


Figure 34.10: Age Distribution of *N. gonorrhoeae* according to sex (n=55)

Figure 34: Distribution of genital isolates by specimen category, hospital, and patient characteristics, Bangladesh, 2025

Table 11: Antibiogram of Gram-Negative and Gram-Positive Bacteria from genital specimen: Isolates from Case-based and Lab-based Surveillance

Organism	Location	Susceptible %											
		Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamicin	Linezolid	Azithromycin	Vancomycin	Ceftriaxone	Cefixime	Tetracyline	Penicillin
Gram-negative													
N. gonorrhoeae	Overall	-	63	-	-	-	-	21	-	88	60	54*	17**
Gram-positive													
S.aureus	Overall	59	48	57	54	73	89	8	-	-	-	-	-

*n=13

**n= 12

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

Reference: CLSI M100, 35th Edition

Specimen: Others (body fluid, and throat)

1,179

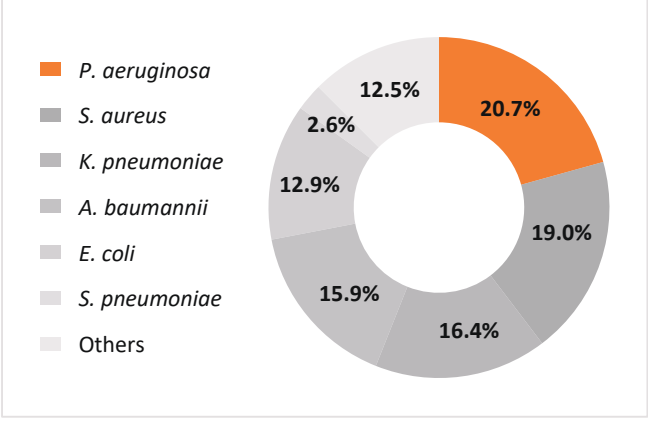
Total other samples

Among the total specimens, "Others" accounted for approximately 1% (n=1,179) of samples collected from laboratories across Bangladesh. Within this category, throat swabs were the most common (78%, n=881), followed by body fluids (20%, n=232) and other specimen types (5%, n=66). Mostly, the "others isolate" were from lab-based surveillance.

Geographically, nearly 90% (n=800) of throat swab isolates were reported from the Dhaka Division, followed by 4.7% (n=42) from Chattogram. For body fluids, the majority of isolates originated from Dhaka Division (69.4%, n=161), followed by Chattogram (16.8%, n=39).

The most frequently identified organisms in body fluid isolates were *P. aeruginosa, S. aureus* and *K. pneumoniae* (Figure 35.1). In throat swabs, the most common organisms were *S. pyogenes, K. pneumoniae* and *Streptococcus* spp. (Figure 35.2).

35.1: Distribution of Most frequent organism in Body fluids (n=232)



35.2: Distribution of most frequent organism found in Throat swabs (n=881)

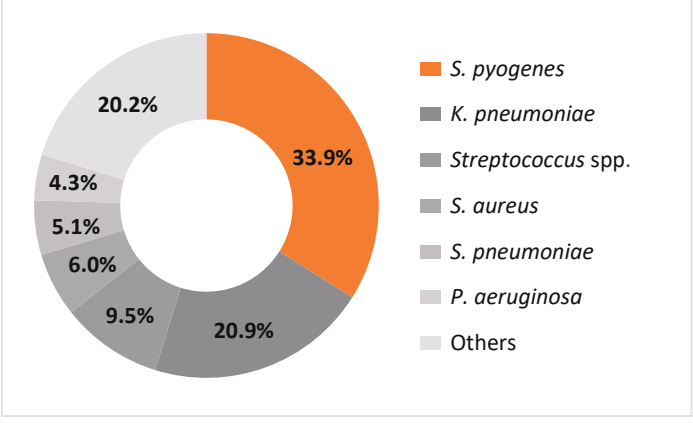


Figure 35: Distribution, specimen category, hospital and patient characteristics of the isolates from other samples

Fungal Pathogens

AMR has been globally recognized as one of the major global health threats. While the focus of AMR has predominantly been on drug-resistant bacterial pathogens (23,24), fungal infections and antifungal resistance represent an equally significant threat to human health. However, fungal infections and antifungal resistance received comparatively less global attention and investment (1,2). Moreover, the increasing presence and detection of fungal pathogens in hospital environments, especially in ICUs and operating theaters, has compounded the situation, making it more complex and deadly

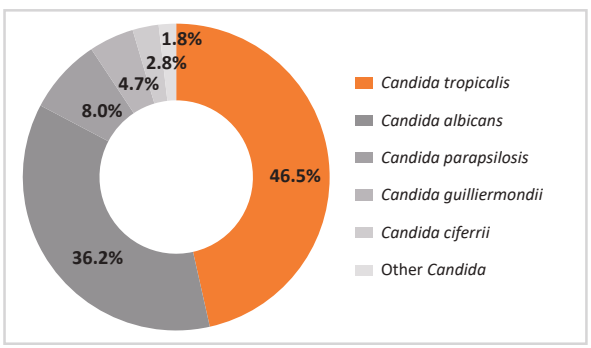
Recognizing the growing concerns about fungal infections, WHO published the first Fungal Priority Pathogens List in 2022, following the Bacterial Priority Pathogens List of 2017 (23,24). In that priority report, WHO classified fungal pathogens into three categories (critical, high, and medium), with the critical group including *Cryptococcus neoformans (C. neoformans),Candida auris (C. auris), Aspergillus fumigatus (A. fumigatus),* and *Candida albicans (C. albicans)* (23,24). Given this global context, this report placed special emphasis on fungal pathogens to better understand their status and situation in Bangladesh, as captured through the National Antimicrobial Surveillance System.

Among the total specimens collected in this surveillance (2024-25) from laboratories across Bangladesh, fungal pathogen specimens constituted less than 1% (n = 742). *Candida* spp. was predominant (≈99%, n =723) among the fungal pathogens. However, species-level identification was available for 654 isolates, and only these were included in the final analysis.

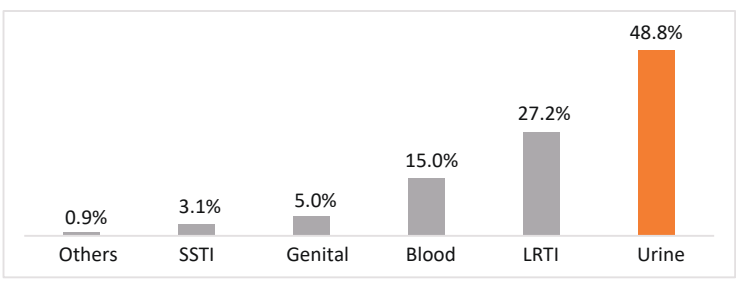
C. tropicalis was the most commonly identified (46.5%, n = 304), followed by *C. albicans* (6%, n = 237) (Figure 36.1). By specimen type, the majority of *Candida* spp. were from urine (48.8%, n = 319), followed by LRTI (27.2%, n = 178), blood (15%, n = 98), genital (5%, n = 33), SSTI (3.1%, n = 20), and others (0.9%, n = 6) (Figure 36.2). The most identified *Candida* spp. across blood, urine, LRTI, SSTI and genital samples were *C. tropicalis*, *C. albicans* and *C. parapsilosis* (Figure 36.3).

In terms of hospital department distribution, 8% of *Candida* spp. (n = 55) were from the ICU, while 92% were undocumented. Geographically, almost 80% of *Candida* spp. were from laboratories in the Dhaka division, 17.1% from Chattogram, and 2.9% combined from Mymensingh, Khulna, and Rajshahi. No isolates were reported from Rangpur, Sylhet and Barishal divisions. *C. tropicalis* was the dominant species in Dhaka, whereas *C. albicans* predominated in Chattogram.

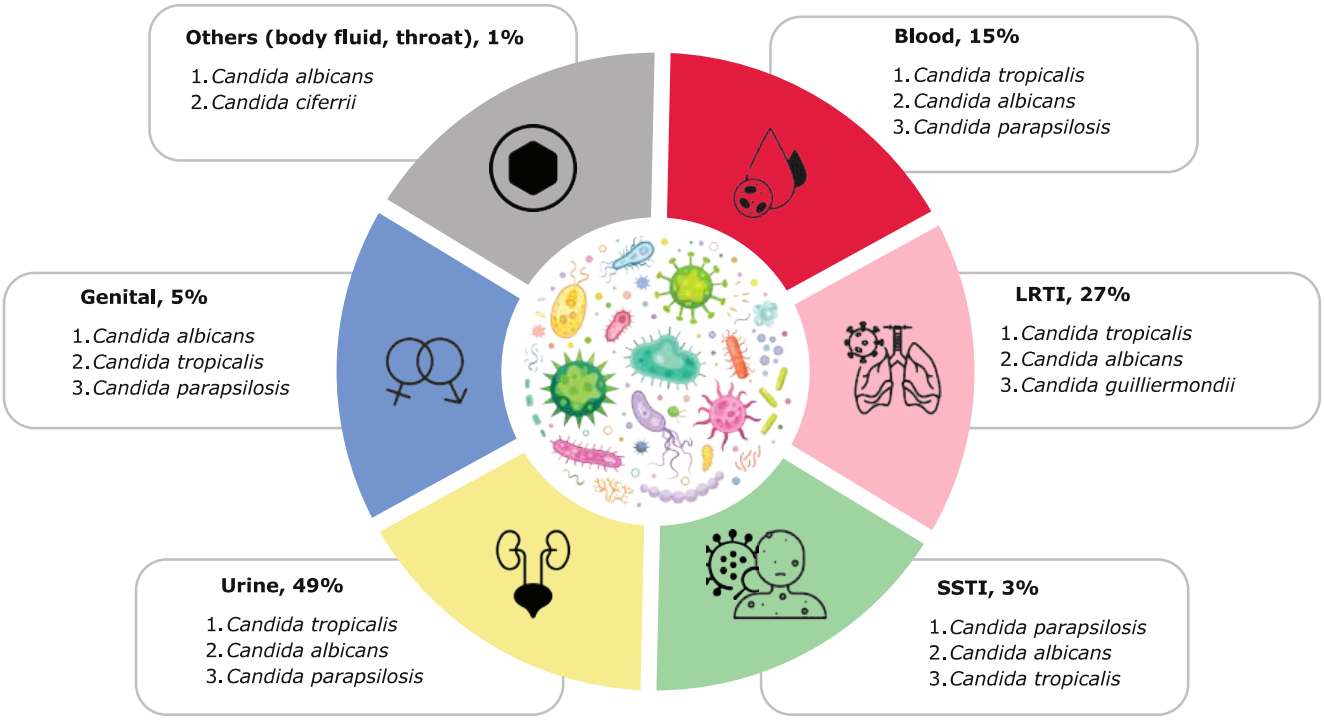
36.1: : Distribution of *Candida* species (n=654)



36.2: Distribution of *Candida* species by specimen type (n=654)

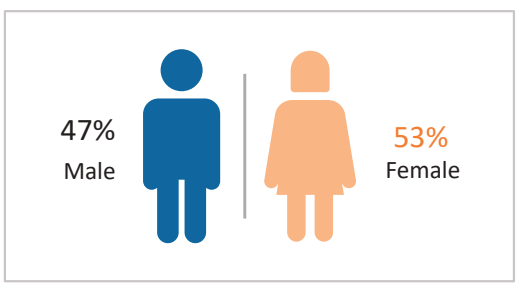


36.3: Distribution of most commonly found *Candida* spp. by specimen (n=654)

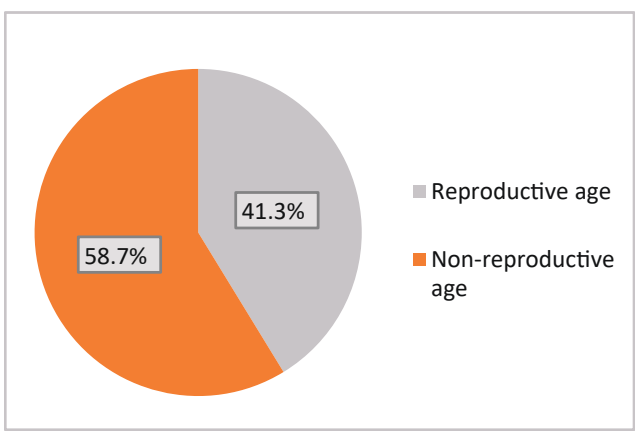


53.4 % of *Candida* spp. were from females, and 46.6 % were from males (Figure 36.4). The highest number of isolates in both sexes was observed in the 61 -70-year age group (females: 18.9%, n = 66; males: 22.3%, n = 68) (Figure 36.6). Among females, 41% (n = 144) were in reproductive age (15 -49 years) and 59% (n = 205) in non-reproductive age groups (Figure 36.5). *C. tropicalis, C. albicans* and *C. parapsilosis* were more prevalent among males, while *C. tropicalis* and *C. albicans* predominated among females (Figure 36.7).

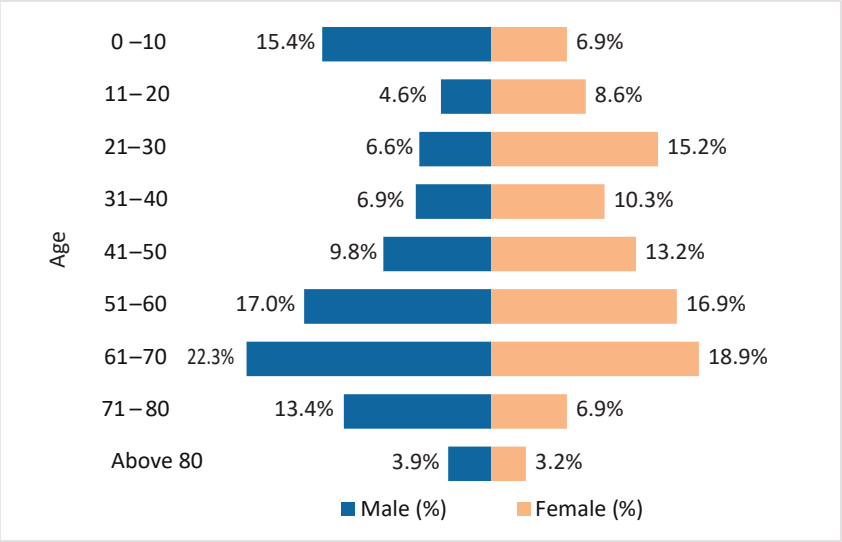
36.4: Distribution of *Candida* spp. by sex (n=654)



36.5: Distribution of *Candida* spp. by reproductive age of women (n=349)



36.6: Distribution of *Candida* spp. by age and sex(n=654)



36.7: Prevalence of *Candida* spp. by among male and female (n=349)

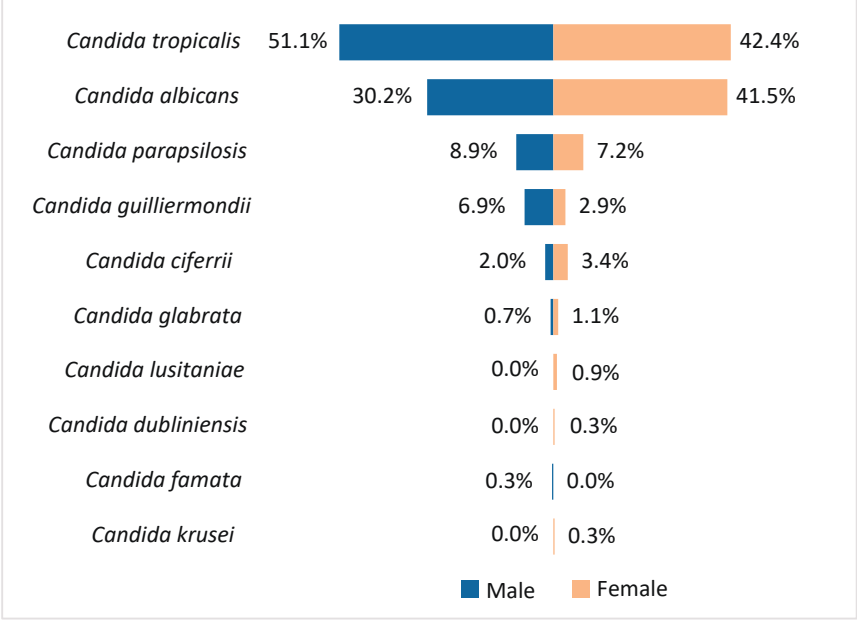
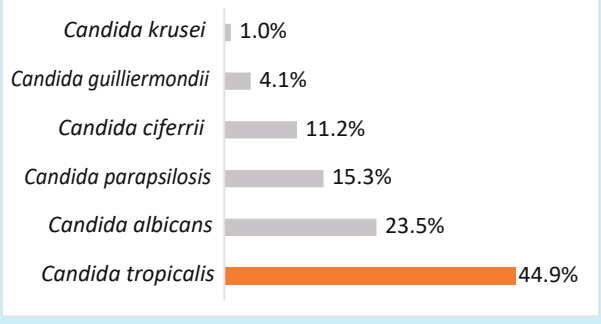


Figure 36.8: Distribution of *Candida* spp. in blood



Fungal Bloodstream Infections: Clinical importance

The presence of fungal pathogens (15%) in the blood (sterile body fluid) is clinically significant as it indicates invasive infection with potential systemic dissemination. Bloodstream infections, particularly caused by *Candida* spp., are associated with high morbidity and mortality, often occur in immunocompromised or hospitalized patients, and are life-threatening. *C. tropicalis* and *C. albicans* were among the most identified *candida* spp. in blood (Figure 36.8)

Figure 36: Distribution of fungal pathogen (*Candida*) isolates by specimen type, geographical, and patient characteristics, Bangladesh, 2025

Table 12: Antibiogram of *Candida* spp. from blood: Isolates from Case-based and Lab-based Surveillance

Organisms	Susceptible %				
	Caspofungin	Fluconazole	Micafungin	Voriconazole	Amphotericin B
Fungi					
C. tropicalis	50	50	91	58	-
C. albicans	45	36	100	-	58

Color coding

Color	Susceptible (S)% value
Green	≥80%
Yellow	60%-80%
Red	<60%
Reference	Chapter 4,CLSI M39, 5th Edition

Increased than 2024 AMR Report	↑
Decreased than 2024 AMR Report	↓
No change with 2024 AMR Report	≈
Not tested /Not indicated	_

*	Intermediate
^	Urine only

Note: Cells without any signs was not reported previous year

Reference: CLSI M100, 35th Edition

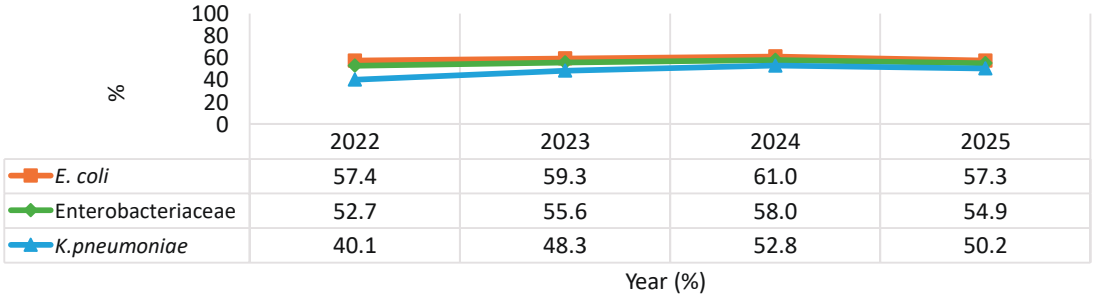


Figure 37: Yearly Trends of WHO Critical Priority Pathogen (Ceftriaxone resistant Enterobacterales)

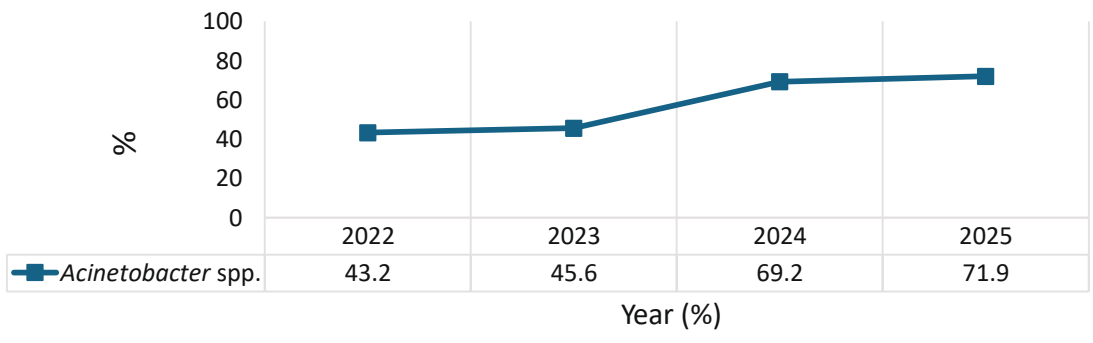


Figure 38: Yearly Trends of WHO Critical Priority Pathogen (Imipenem resistant *Acinetobacter* spp.)

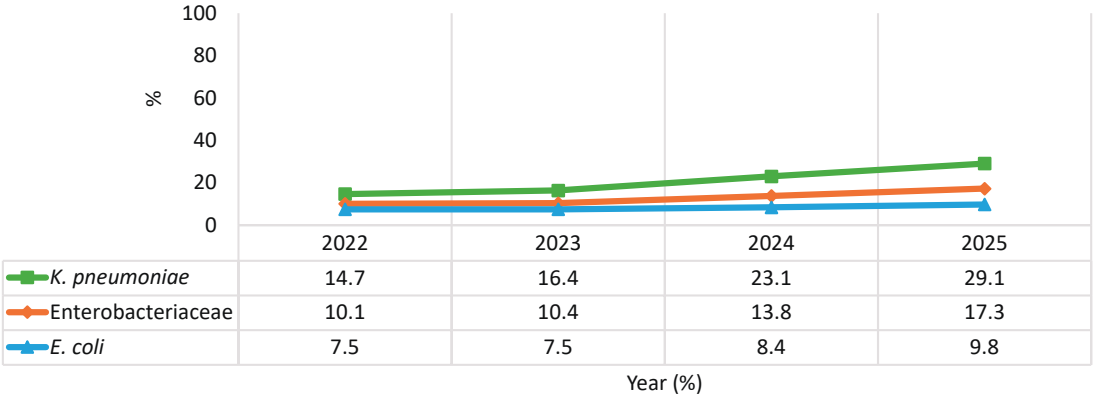


Figure 39: Yearly Trends of WHO Critical Priority Pathogen (Imipenem resistant Enterobacterales)

Meropenem resistant:

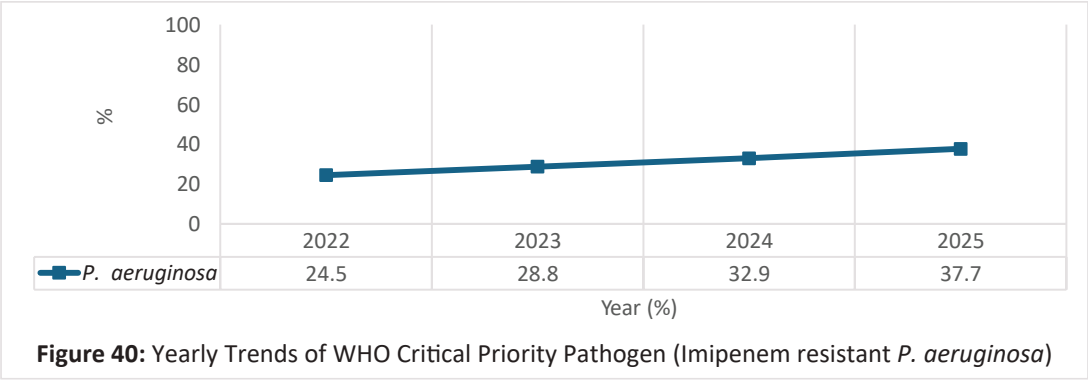


Figure 40: Yearly Trends of WHO Critical Priority Pathogen (Imipenem resistant *P. aeruginosa*)

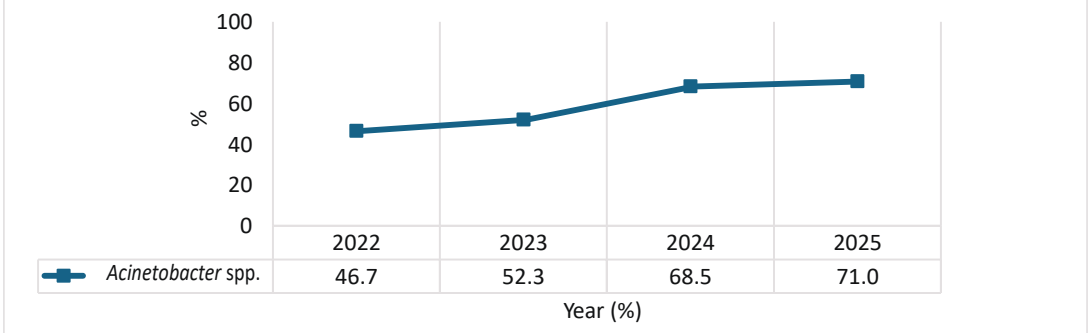


Figure 41: Yearly Trends of WHO Critical Priority Pathogen (Meropenem resistant *Acinetobacter* spp.)

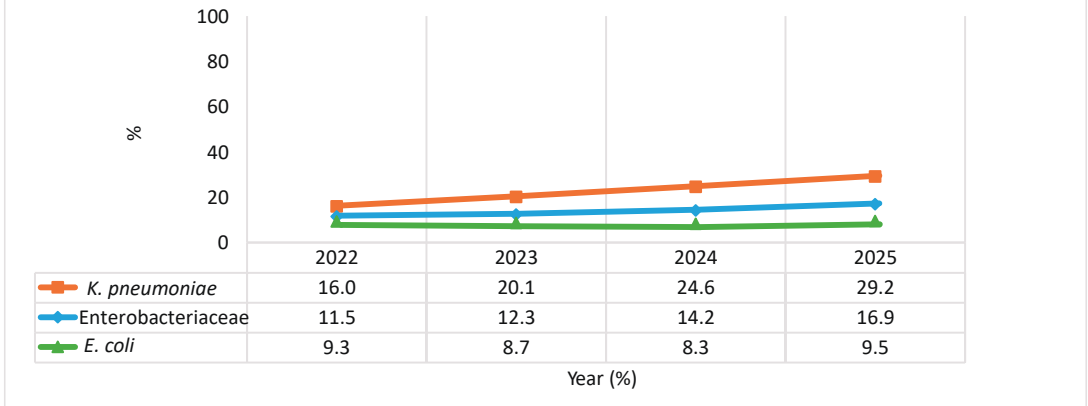


Figure 42: Yearly Trends of WHO Critical Priority Pathogen (Meropenem resistant Enterobacterales)

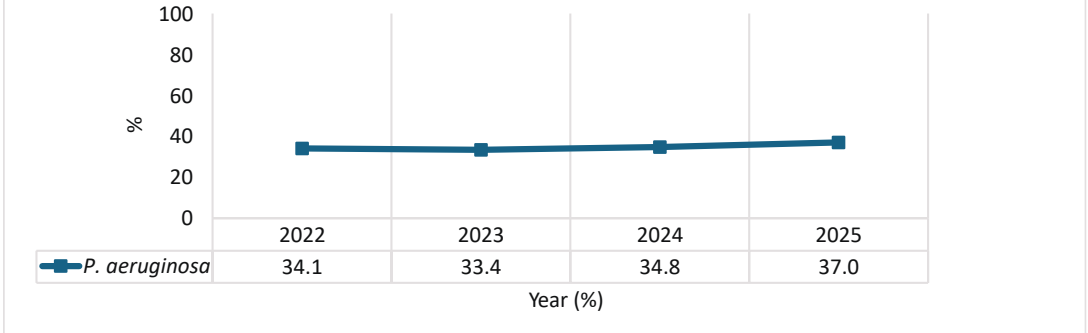


Figure 43: Yearly Trends of WHO Critical Priority Pathogen (Meropenem resistant *P. aeruginosa*)

SDG Target 3.d.2 | Bloodstream infections due to selected antimicrobial-resistant organisms

Indicator name:

Indicator 3.d.2: Proportion of bloodstream infections due to selected antimicrobial-resistant organisms (%)

Table 13: Bloodstream infections from selected antimicrobial-resistant organisms (MRSA and ESBL *E. coli*)

Year	MRSA (%)	ESBL *E. coli* (%)
2022	60.6	72.8
2023	56.4	73.3
2024	68.7	64.8

Prevalence of suspected Pandrug Resistant (PDR) Pathogen

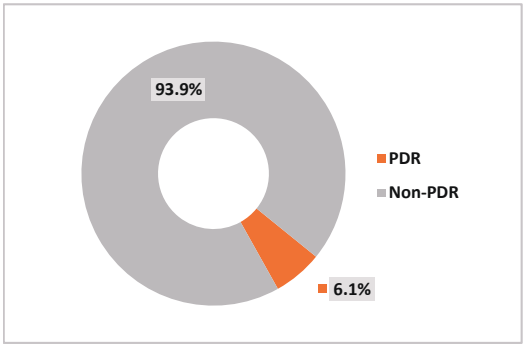


Figure 44: Overall distribution of suspected PDR* pathogen, Bangladesh.

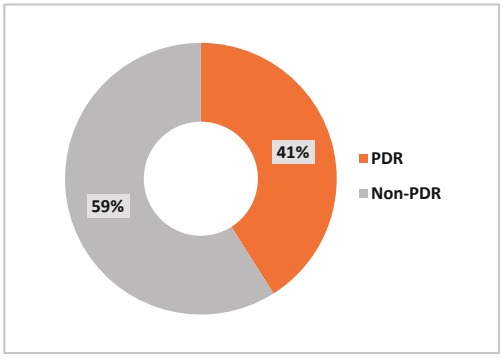


Figure 45: Distribution of suspected PDR pathogen in ICU, Bangladesh.

Table 14: Organism wise suspected PDR

Organism	Total Number of isolates	Suspected PDR (n)	Suspected PDR (%)
Acinetobacter spp.	2,758	752	27%
P. aeruginosa	5,617	867	15%
E. faecium	293	35	12%
K. pneumoniae	14,860	1,582	11%
S. aureus	5,950	196	3%
E. faecalis	2,577	61	2%
E. coli	27,094	412	2%

*Pan Drug Resistance (PDR) is defined as non-susceptibility to all agents in every antimicrobial category for a bacterium. We have used a working definition: isolates that seem resistant to all agents tested in the laboratory.

Prevalence of Multidrug Resistant (MDR) Pathogen

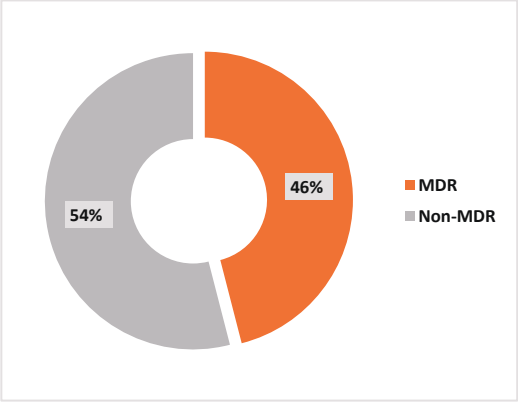


Figure 46: Overall distribution of MDR pathogen, Bangladesh.

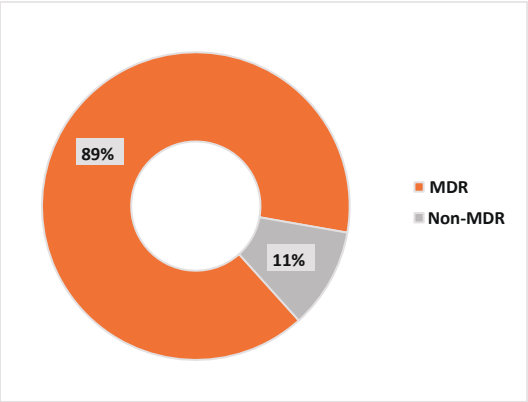


Figure 47: Distribution of MDR pathogen in ICU, Bangladesh.

Table 15: Organism wise suspected MDR

Organism	Total Number of isolates	MDR (n)	MDR (%)
E. faecium	293	217	74%
Acinetobacter spp.	2,758	1,790	65%
K. pneumoniae	14,860	7,949	53%
E. coli	27,094	14,102	52%
P. aeruginosa	5,617	2,214	39%
S. aureus	5,950	2,008	34%
E. faecalis	2,577	730	28%

Antibiotic Use

From the case-based surveillance, the antibiotic use data of patients were collected. During the reporting period, 15,844 antibiotic-use records were gathered. Among these, 48% of the data came from ICUs of different sentinel sites, 44% from IPDs, and 8% from OPDs.

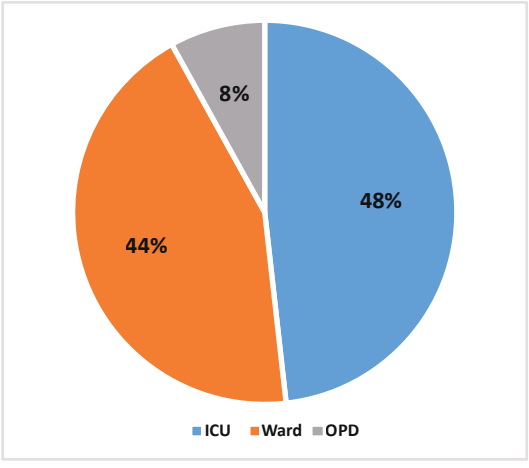


Figure 48: Distribution of antibiotic used in different locations (n=15,844)

Table 16. Ten most commonly prescribed antibiotics by location (N=15,844)

Ten most commonly prescribed antibiotics in different locations (n=15844)		
ICU (n=7640)	**Ward (n=6930)**	**OPD (n=1274)**
Ceftriaxone (30%)	Ceftriaxone (41%)	Azithromycin (24%)
Meropenem (25%)	Ciprofloxacin (9%)	Cefixime (24%)
Cefixime (8%)	Azithromycin (9%)	Ciprofloxacin (16%)
Amikacin (5%)	Meropenem (9%)	Ceftriaxone (9%)
Ciprofloxacin (5%)	Cefixime (8%)	Cefuroxime+ clavulanic acid (6%)
Vancomycin (5%)	Cefuroxime (6%)	Amikacin (5%)
Cefuroxime (4%)	Cefuroxime+ clavulanic acid (4%)	Levofloxacin (4%)
Moxifloxacin Hydrochloride (3%)	Metronidazole (3%)	Cefuroxime (3%)
Metronidazole (3%)	Levofloxacin (2%)	Metronidazole (2%)
Cefuroxime+ clavulanic acid (2%)	Amikacin (2%)	Moxifloxacin Hydrochloride (2%)

Table 17: Antibiotic usage by case type and location (N=15,828)

Ten most commonly used antibiotics in different locations (n=15828)											
Blood (n=7614)	ICU (n=4266)	Ceftriaxone (28%)	Meropenem (25%)	Amikacin (9%)	Cefixime (8%)	Vancomycin (5%)	Ciprofloxacin (4%)	Cefuroxime (4%)	Moxifloxacin Hydrochloride (3%)	Levofloxacin (3%)	Metronidazole (3%)
	Ward (n=3188)	Ceftriaxone (55%)	Meropenem (11%)	Cefixime (6%)	Azithromycin (5%)	Cefuroxime+ clavulanic acid (4%)	Doxycycline (3%)	Vancomycin (3%)	Amikacin (2%)	Ciprofloxacin (2%)	Cefuroxime (2%)
	OPD (n=160)	Azithromycin (27%)	Ceftriaxone (20%)	Cefixime (18%)	Amikacin (11%)	Ciprofloxacin (6%)	Cefuroxime+ clavulanic acid (4%)	Cefuroxime (3%)	Doxycycline (2%)	Levofloxacin (2%)	Meropenem (2%)
Endotracheal aspirate (n=1626)	ICU (n=1 626)	Meropenem (34%)	Ceftriaxone (19%)	Cefixime (11%)	Vancomycin (5%)	Metronidazole (5%)	Moxifloxacin Hydrochloride (5%)	Ciprofloxacin (4%)	Cefuroxime+ clavulanic acid (3%)	Levofloxacin (2%)	Cefuroxime (2%)
Diarrhea (n=1393)	ICU (n=51)	Ciprofloxacin (51%)	Azithromycin (29%)	Ceftriaxone (16%)	Doxycycline (2%)	Metronidazole (2%)	-	-	-	-	-
	Ward (n=1102)	Ciprofloxacin (43%)	Azithromycin (38%)	Ceftriaxone (12%)	Metronidazole (3%)	Cefixime (1%)	Doxycycline (0.5%)	Meropenem (0.5%)	Ceftazidime (0.4%)	Piperacillin+ Tazobactam (0.4%)	Amikacin (0.2%)
	OPD (n=240)	Amikacin (92%)	Ampicillin (3%)	Azithromycin (2%)	Ceftriaxone (1%)	Ciprofloxacin (1%)	Doxycycline (1%)	Gentamycin (1%)	Metronidazole (0.4%)	-	-
Urine (n=3139)	ICU (n=1796)	Ceftriaxone (46%)	Meropenem (18%)	Cefixime (7%)	Ciprofloxacin (6%)	Cefuroxime (6%)	Vancomycin (4%)	Cefuroxime+ clavulanic acid (2%)	Piperacillin+ Tazobactam (2%)	Metronidazole (2%)	Moxifloxacin Hydrochloride (2%)
	Ward (n=618)	Ceftriaxone (49%)	Meropenem (13%)	Cefixime (8%)	Cefuroxime (6%)	Azithromycin (5%)	Ciprofloxacin (3%)	Vancomycin (3%)	Levofloxacin (2%)	Amikacin (2%)	Metronidazole (2%)
	OPD (n=725)	Cefixime (31%)	Ciprofloxacin (24%)	Ceftriaxone (10%)	Cefuroxime+ clavulanic acid (7%)	Azithromycin (6%)	Amikacin (5%)	Levofloxacin (4%)	Cefuroxime (3%)	Moxifloxacin Hydrochloride (2%)	Metronidazole (2%)
Wound swab (n=2056)	ICU (n=11)	Ceftriaxone (36%)	Cefixime (18%)	Meropenem (18%)	Cefuroxime+ clavulanic acid (9%)	Ciprofloxacin (9%)	Metronidazole (9%)	-	-	-	-
	Ward (n=1901)	Ceftriaxone (34%)	Cefuroxime (16%)	Cefixime (13%)	Meropenem (8%)	Cefuroxime+ clavulanic acid (7%)	Metronidazole (6%)	Levofloxacin (5%)	Ciprofloxacin (3%)	Amikacin (3%)	Clindamycin (1%)
	OPD (n=144)	Cefixime (38%)	Levofloxacin (13%)	Cefuroxime+ clavulanic acid (10%)	Ciprofloxacin (9%)	Cefuroxime (8%)	Ceftriaxone (6%)	Doxycycline (3%)	Amikacin (2%)	Flucloxacillin (2%)	Metronidazole (2%)

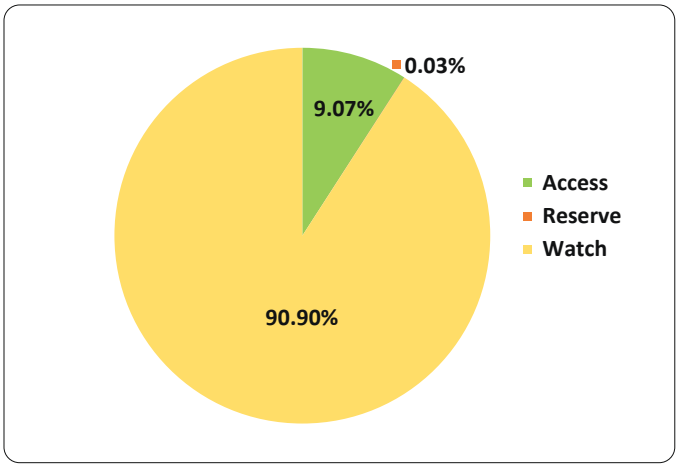


Figure 49: Distribution of Antibiotic used in different locations by AWaRe classification (n=15,844)

Site-wise AMR Report

(July 2024- June 2025)

Dhaka Medical College and Hospital (DMCH)

Sample size and Culture test

Out of 1,362 samples, a total of 361 (27%) samples yielded growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 77.6%, Female- 22.4%
- Highest growth was observed in 51-60 age group

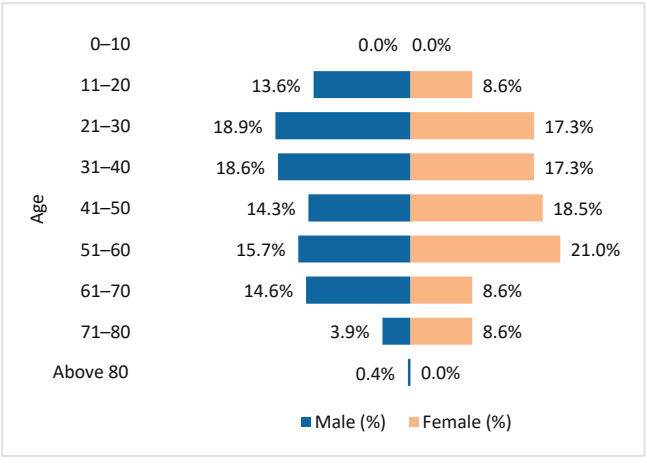


Figure 50 : Distribution of isolates by sex and age group (n=361)

Sample Collection Locations

Table 18: Distribution of isolates by location

Location	Number of isolates	(%)
OPD	13	3.6
IPD	88	24.4
ICU	260	72

Specimen Types

Table 19: Distribution of specimen types

Specimen type	Number of isolates	(%)
Endotracheal aspirate	184	51
Wound swab	76	21.1
Blood	52	14.4
Urine	49	13.6

Organism statistics

Organism frequencies

Table 20: Distribution of isolates by organism type

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	5	1.4
Aerobic Gram -negative bacteria	356	98.6

Table 21: Distribution of the five most common organisms

Organism	Number of isolates	(%)
Acinetobacter spp.	92	25.5
P. aeruginosa	90	24.9
K. pneumoniae	63	17.5
E. coli	61	16.9
Enterobacter spp.	31	8.6

Most Common Organisms

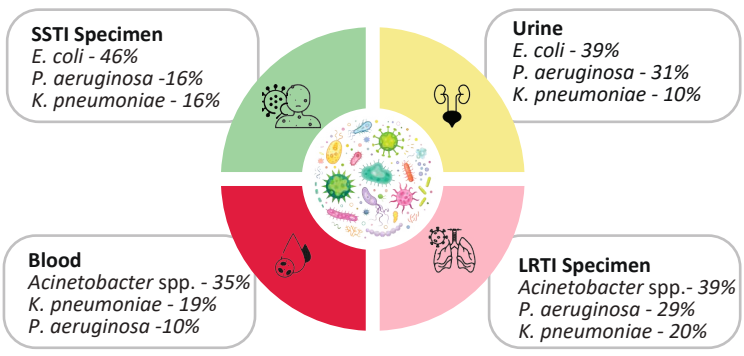


Figure 51: Most common organisms by specimen category

Frequncy of Multidrug resistance Pathogen:

Table 22: Frequency of multidrug-resistant (MDR) pathogens

Organism	MDR (%)
S. aureus (N=5)	60
E. coli (N=61)	100
K. pneumoniae (N=36)	100
P. aeruginosa (N=90)	90

Distribution of WHO Critical Priority Pathogen

Table 23: Frequency of WHO critical priority pathogens

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter* spp. (N=92)	96%
Carbapenem resistance *P. aeruginosa* (N=89)	79%
Ceftriaxone-resistant *E .coli* (N=61)	97%
Meropenem-resistant *E. coli* (N=61)	52%

Antibiogram

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Table 24: Antibiogram

Organism	Amikacin	Amoxicillin-Clavulanate	Ampicillin	Aztreonam	Cefepime	Ceftazidime	Ceftazidime/Avibactam	Ceftriaxone	Cefuroxime	Ciprofloxacin	Gentamycin	Imipenem	Meropenem	Netilmicin	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole
Acinetobacter spp.	5	-	-	-	3	1	-	0	-	0	5	3	4	-	5	-	21
P. aeruginosa	-	-	-	18	16	12	-	-	-	17	-	24	21	30	24	-	-
K. pneumoniae	18	-	-	8	6	6	-	2	0	2	11	10	8	-	10	40	13
E. coli	49	8	5	8	7	2	62	3	0	3	44	49	48	-	31	48	21
Enterobacter spp.	19	-	0	0	0	3	-	0	0	0	10	29	29	-	13	20	13

Antibiotic Use:

A total of 1,620 antibiotic administrations were recorded among patients

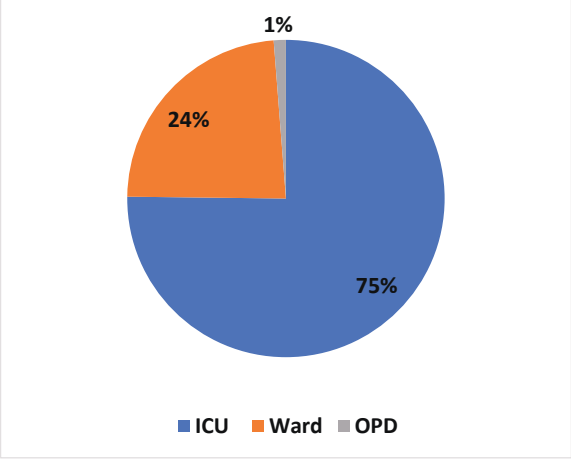


Figure 52: Distribution of antibiotic usage by location (IPD, OPD, ward) (n=1,620)

Table 25: Antibiotic usage by case type and location (IPD, OPD, ward) (n=1,620)

Table 25.1: Ten most commonly used antibiotics by location (n=1,620)

Ten most commonly used antibiotics (n=1,620)										
ICU (n=1,257)	Meropenem (31%)	Cefixime (16%)	Vancomycin (11%)	Ceftriaxone (9%)	Moxifloxacin (7%)	Levofloxacin (6%)	Metronidazole (5%)	Cefuroxime (4%)	Cefuroxime+ clavulanic acid (3%)	Ceftazidime (2%)
WARD (n=382)	Ceftriaxone (27%)	Meropenem (24%)	Metronidazole (20%)	Cefuroxime (8%)	Cefixime (5%)	Cefuroxime+ clavulanic acid (4%)	Amikacin (4%)	Levofloxacin (2%)	Clarithromycin (1%)	Azithromycin (1%)
OPD (n=20)	Cefixime (35%)	Ceftriaxone (20%)	Azithromycin (10%)	Cefuroxime+ clavulanic acid (10%)	Cefuroxime (10%)	Levofloxacin (5%)	Meropenem (5%)	Metronidazole (5%)	-	-

Table 25.2: Antibiotics used according to cases (n=1,620)

Ten most commonly used antibiotics for cases (n=1620)											
Blood (n=657)	**ICU (n=516)**	Meropenem (32%)	Cefixime (16%)	Vancomycin (11%)	Ceftriaxone (9%)	Moxifloxacin (7%)	Levofloxacin (6%)	Metronidazole (5%)	Cefuroxime (4%)	Cefuroxime+ clavulanic acid (3%)	Ceftazidime (2%)
	Ward (n=136)	Ceftriaxone (38%)	Meropenem (24%)	Cefuroxime+ clavulanic acid (8%)	Metronidazole (6%)	Cefixime (5%)	Cefuroxime (5%)	Amikacin (3%)	Clarithromycin (2%)	Moxifloxacin (2%)	Azithromycin (1%)
	OPD (n=5)	Ceftriaxone (40%)	Cefixime (20%)	Cefuroxime (20%)	Levofloxacin (20%)	-	-	-	-	-	-
Endotracheal aspirate (n=470)	**ICU (n=470)**	Meropenem (31%)	Cefixime (17%)	Vancomycin (11%)	Ceftriaxone (8%)	Moxifloxacin (7%)	Levofloxacin (6%)	Metronidazole (4%)	Cefuroxime (4%)	Cefuroxime+ clavulanic acid (3%)	Ceftazidime (3%)
Urine (n=295)	**ICU (n=237)**	Meropenem (31%)	Cefixime (16%)	Ceftriaxone (12%)	Vancomycin (9%)	Moxifloxacin (7%)	Metronidazole (5%)	Levofloxacin (5%)	Ceftazidime (3%)	Cefuroxime (3%)	Clindamycin (3%)
	Ward (n=50)	Ceftriaxone (44%)	Meropenem (20%)	Cefuroxime+ clavulanic acid (8%)	Metronidazole (8%)	Azithromycin (4%)	Cefixime (4%)	Clarithromycin (4%)	Levofloxacin (4%)	Ceftazidime (2%)	Cefuroxime (2%)
	OPD (n=8)	Cefixime (43%)	Azithromycin (14%)	Ceftriaxone (14%)	Cefuroxime+ clavulanic acid (14%)	Cefuroxime (14%)	-	-	-	-	-
Wound swab (n=198)	**ICU (n=1)**	Ceftriaxone (100%)	-	-	-	-	-	-	-	-	-
	Ward (n=192)	Metronidazole (34%)	Meropenem (27%)	Ceftriaxone (15%)	Cefuroxime (11%)	Amikacin (5%)	Cefixime (4%)	Levofloxacin (1%)	Ceftazidime (1%)	Cefuroxime+ clavulanic acid (1%)	Ciprofloxacin (1%)
	OPD (n=5)	Cefixime (60%)	Cefixime (20%)	Cefixime (20%)	-	-	-	-	-	-	-

Mymensingh Medical College and Hospital (MMCH)

Sample size and Culture test

Out of 2,652 samples, a total of 455 (17%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 48.4%, Female- 51.6%
- Highest growth was observed in 31-40 age group

Sample Collection Locations

Table 26: Distribution of isolates by location at MMCH, 2025

Location	Number of isolates	(%)
OPD	57	12.5
IPD	194	42.6
ICU	204	44.8

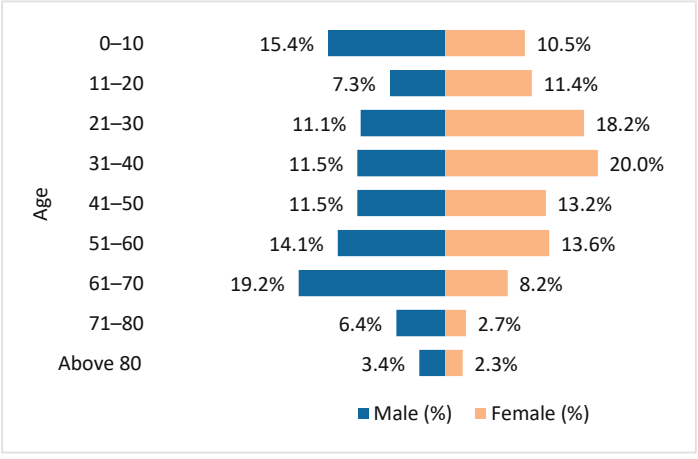


Figure 53: Distribution of isolates by sex and age group at MMCH, 2025

Specimen Types

Table 27: Distribution of specimen types at MMCH, 2025

Specimen type	Number of isolates	(%)
Endotracheal aspirate	159	34.9
Blood	114	25.1
Urine	83	18.2
Wound swab	68	14.9
Stool	31	6.8

Organism statistics
Organism frequencies

Table 28: Distribution of isolates by organism type at MMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram-positive bacteria	19	4.2
Aerobic Gram-negative bacteria	436	95.8

Table 29: Distribution of the five most common organisms at MMCH, 2025

Organism	Number of isolates	(%)
K. pneumoniae	135	29.7
E. coli	74	16.3
Acinetobacter spp.	95	20.8
P. aeruginosa	72	15.8
Salmonella spp.	30	6.6

Most Common Organisms

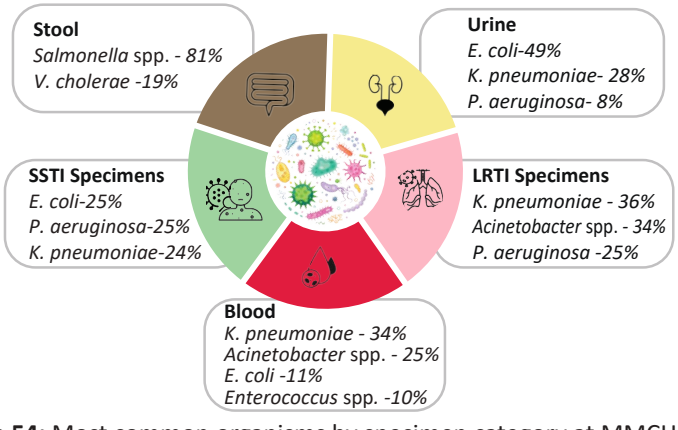


Figure 54: Most common organisms by specimen category at MMCH, 2025

Frequency of Multidrug Resistant Pathogen

Table 30: Frequency of multidrug-resistant (MDR) pathogens at MMCH, 2025

Organism	MDR (%)
S. aureus (N=7)	71
E. coli (N=74)	71
K. pneumoniae (N=135)	96
P. aeruginosa (N=72)	79

Distribution of WHO Critical Priority Pathogen

Table 31: Frequency of WHO critical priority pathogens at MMCH, 2025

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter* spp. (N=94)	93%
Carbapenem resistance *P. aeruginosa* (N=71)	80%
Ceftriaxone-resistant *E. coli* (N=73)	80%
Meropenem-resistant *E. coli* (N=73)	37%

Antibiogram

Table 32: Antibiogram at MMCH, 2025

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Organism	Amikacin	Ampicilin	Amoxicillin/clavulanate	Azithromycin	Aztreonam	Cefepime	Cefixime	Ceftazidime/avibactam	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin	Gentamicin	Imipenem	Meropenem	Netilmicin	Nitrofurantoin	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Levofloxacin	Cefazolin	Tobramycin
K. pneumoniae	14	-	8	-	15	12	3	-	12	12	6	11	-	25	30	22	-	-	13	47	21	-	-	-
Acinetobacter spp.	4		-	-	-	3	-	-	3	4	-	1	-	13	7	3	-	-	6	-	13	-	-	17
P. aeruginosa	-	-	-	-	18	16	-	-	21	-	-	20	-	-	17	20	20	-	22	-	-	-	-	-
E. coli	30	4	25	-	25	19	-	64	19	19	9	12	100	54	75	62	-	54	42	41	28	-	24	-

Antibiotic Use

A total of 2,351 antibiotic administrations were recorded among patients

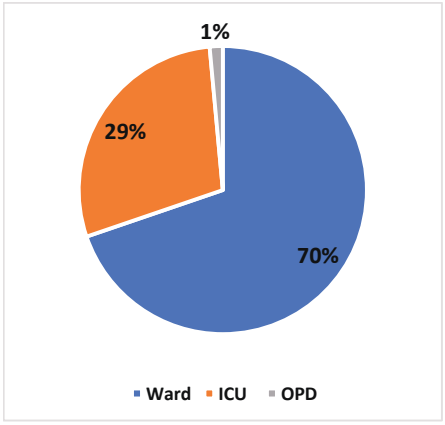


Figure 55: Distribution of antibiotic usage by location (IPD, OPD, ward) at MMCH, 2025 (n=2,351)

Table 33: Antibiotic usage by case type and location (IPD, OPD, ward) at MMCH, 2025 (n=2,391)

Ten most commonly prescribed antibiotics in different locations (n=2,391)										
ICU (n=688)	Meropenem (36%)	Amikacin (20%)	Ceftriaxone (15%)	Metronidazole (8%)	Cefixime (8%)	Vancomycin (3%)	Cefuroxime+ clavulanic acid (3%)	Ciprofloxacin (3%)	Piperacillin+ Tazobactam (1%)	Cefuroxime (1%)
Ward n=1668)	Ceftriaxone (64%)	Ciprofloxacin (9%)	Meropenem (6%)	Cefuroxime (4%)	Cefuroxime+ clavulanic acid (3%)	Doxycycline (3%)	Cefixime (3%)	Metronidazole (3%)	Amikacin (2%)	Azithromycin (1%)
OPD (n=35)	Ceftriaxone (46%)	Ciprofloxacin (14%)	Cefuroxime+ clavulanic acid (11%)	Amikacin (9%)	Meropenem (9%)	Metronidazole (9%)	Amoxicillin + Clavulanic acid (3%)	-	-	-

Table 33.1: Antibiotics used according to cases (n=2,378)

Ten most commonly used antibiotics in different locations (n=2,378)											
Blood (n=1501)	**ICU (n=395)**	Amikacin (33%)	Meropenem (24%)	Ceftriaxone (22%)	Cefixime (6%)	Metronidazole (6%)	Vancomycin (3%)	Cefuroxime+ clavulanic acid (2%)	Cefuroxime (1%)	Piperacillin+ Tazobactam (1%)	Ciprofloxacin (1%)
	Ward (n=1100)	Ceftriaxone (74%)	Meropenem (7%)	Doxycycline (4%)	Cefuroxime+ clavulanic acid (4%)	Cefixime (2%)	Metronidazole (2%)	Amikacin (2%)	Cefuroxime (1%)	Ciprofloxacin (1%)	Moxifloxacin (1%)
	OPD (n=6)	Ceftriaxone (50%)	Amikacin (17%)	Meropenem (17%)	Metronidazol e (17%)	-	-	-	-	-	-
Endotracheal aspirate (n=296)	**ICU (n=296)**	Meropenem (56%)	Metronidazole (13%)	Cefixime (10%)	Cefuroxime+ clavulanic acid (4%)	Vancomycin (4%)	Ceftriaxone (4%)	Amikacin (3%)	Piperacillin+ Tazobactam (2%)	Azithromycin (1%)	Clindamycin (1%)
Diarrhea (n=185)	**ICU (n=15)**	Ciprofloxacin (100%)	-	-	-	-	-	-	-	-	-
	Ward (n=170)	Ciprofloxacin (74%)	Ceftriaxone (16%)	Azithromycin (8%)	Doxycycline (1%)	Cefixime (1%)	-	-	-	-	-
Urine (n=116)	**ICU (n=3)**	Ceftriaxone (100%)	-	-	-	-	-	-	-	-	-
	Ward (n=85)	Ceftriaxone (73%)	Ciprofloxacin (7%)	Cefuroxime (6%)	Meropenem (4%)	Metronidazole (4%)	Amikacin (2%)	Cefixime (2%)	Doxycycline (1%)	Vancomycin (1%)	-
	OPD (n=28)	Ceftriaxone (46%)	Ciprofloxacin (18%)	Cefuroxime+ clavulanic acid (14%)	Amikacin (7%)	Metronidazole (7%)	Amoxicillin + Clavulanic acid (4%)	Meropenem (4%)	-	-	-
Wound swab (n=280)	**ICU (n=2)**	Ceftriaxone (50%)	Meropenem (50%)	-	-	-	-	-	-	-	-
	Ward (n=278)	Ceftriaxone (58%)	Cefuroxime (21%)	Cefuroxime+ clavulanic acid (6%)	Metronidazole (4%)	Cefixime (3%)	Amikacin (2%)	Ciprofloxacin (1%)	Clindamycin (1%)	Meropenem (1%)	Azithromycin (0.4%)

Rajshahi Medical College and Hospital (RMCH)

Sample size and Culture test

Out of 3,441 samples, a total of 530 (15%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 56.8%, Female- 43.2%
- Highest growth was observed in 31-40 and 41-50 age group

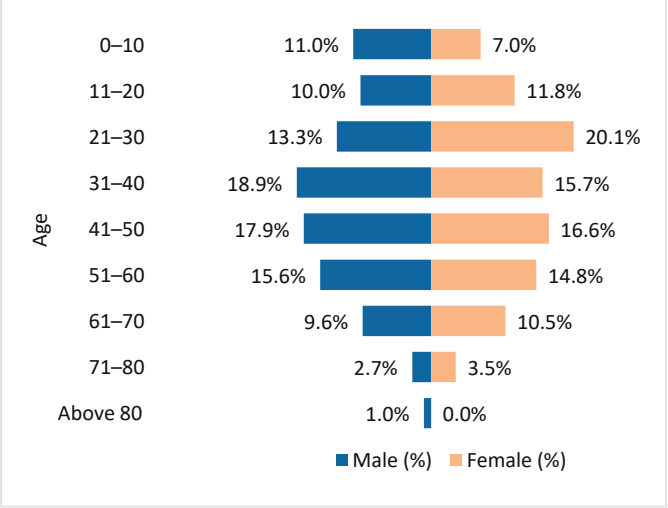


Figure 56: Distribution of isolates by sex and age group at RMCH, 2025

Sample Collection Locations

Table 34: Distribution of isolates by location at RMCH, 2025

Location	Number of isolates	(%)
OPD	141	26.6
IPD	185	34.9
ICU	204	38.5

Specimen Types

Table 35: Distribution of specimen types at RMCH, 2025

Specimen type	Number of isolates	(%)
Urine	223	42.1
Wound swab	154	29.1
Blood	119	22.5
Endotracheal aspirate	34	6.4

Organism statistics

Organism frequencies

Table 36: Distribution of isolates by organism type at RMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram-positive bacteria	93	17.5
Aerobic Gram-negative bacteria	424	80.0

Table 37: Distribution of the five most common organisms at RMCH, 2025

Organism	Number of isolates	(%)
E. coli	154	29.1
P. aeruginosa	97	18.3
K. pneumoniae	80	15.1
S. aureus	78	14.7
Acinetobacter spp.	38	7.2

Most Common Organisms

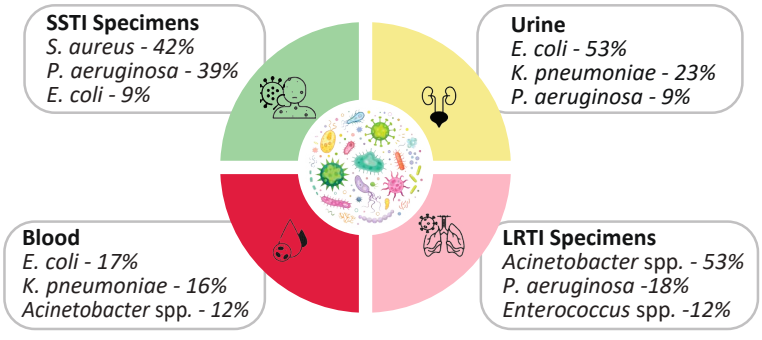


Figure 57: Most common organisms by specimen category at RMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 38: Frequency of multidrug-resistant (MDR) pathogens at RMCH, 2025

Organism	MDR (%)
S. aureus (N=78)	67
E. coli (N=154)	95
K. pneumoniae (N=80)	90
P. aeruginosa (N=97)	78

WHO Critical Priority Pathogens

Table 39: Frequency of WHO critical priority pathogens at RMCH, 2025

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter* spp. (N=38)	89%
Carbapenem resistance *P. aeruginosa* (N=97)	57%
Ceftriaxone-resistant *E. coli* (N=140)	82%
Meropenem-resistant *E. coli* (N=153)	33%

Antibiogram

Table 40: Antibiogram at RMCH, 2025

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% -80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamicin	Linezolid	Penicillin	Trimethoprim/Sulfamethoxazole	Vancomycin
S. aureus	20	50	10	68	80	84	70	4	75	100

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Ceftazidime	Ceftazidime/Avibactam	Ceftriaxone	Cefuroxime	Ciprofloxacin	Colistin*	Fosfomycin(Urine only)	Gentamicin	Imipenem	Meropenem	Netilmicin	Nitrofurantoin(Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Cefazolin(Urine only)
E. coli	62	10	27	16	19	67	18	5	17	-	94	67	67	67	-	78	37	47	40	18
P. aeruginosa	43	-	30	11	17	75	-	-	33	6	-	-	44	43	54	-	35	-	-	-
K. pneumoniae	41	-	52	28	38	75	37	11	22	-	-	59	58	58	-	28	12	67	49	-
Acinetobacter spp.	16	-	-	8	-	-	0	-	8	0	-	21	10	10	-	-	10	-	47	-

Antibiotic Usage : A total of 3,562 antibiotic administrations were recorded among patients

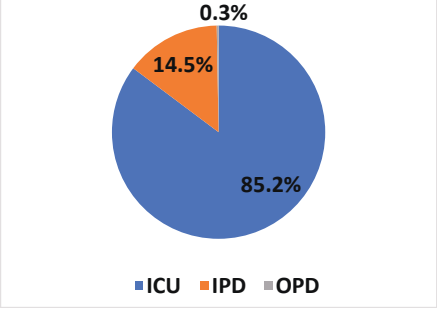


Figure 58: Distribution of antibiotic usage by location at RMCH, 2025 (n=3,562)

Table 41: Antibiotic usage by case type and location at RMCH, 2025 (n=3,562)

Ten most commonly used antibiotics in different locations (n=3,562)										
ICU (n=3038)	Ceftriaxone (51%)	Meropenem (15%)	Ciprofloxacin (6%)	Cefixime (6%)	Cefuroxime (6%)	Vancomycin (5%)	Cefuroxime+ clavulanic acid (3%)	Piperacillin+ Tazobactam (2%)	Metronidazole (2%)	Moxifloxacin (1%)
Ward (n=514)	Ceftriaxone (36%)	Azithromycin (22%)	Cefuroxime (15%)	Meropenem (10%)	Cefixime (5%)	Doxycycline (3%)	Vancomycin (3%)	Piperacillin+ Tazobactam (1%)	Ciprofloxacin (1%)	Moxifloxacin (1%)
OPD (n=10)	Cefixime (30%)	Ciprofloxacin (30%)	Levofloxacin (20%)	Azithromycin (10%)	Ceftriaxone (10%)	-	-	-	-	-

Table 41.1: Antibiotics used according to cases (n=3,562)

Ten most commonly used antibiotics in different locations (n=3,562)											
Blood (n=1707)	**ICU (n=1478)**	Ceftriaxone (52%)	Meropenem (15%)	Cefixime (6%)	Cefuroxime (6%)	Vancomycin (6%)	Ciprofloxacin (6%)	Cefuroxime+ clavulanic acid (2%)	Piperacillin+ Tazobactam (2%)	Metronidazole (2%)	Moxifloxacin (1%)
	Ward (n=228)	Azithromycin (49%)	Ceftriaxone (23%)	Meropenem (11%)	Doxycycline (7%)	Cefixime (4%)	Piperacillin+ Tazobactam (2%)	Vancomycin (2%)	Cefuroxime (1%)	Moxifloxacin (1%)	Amikacin (1%)
	OPD (n=1)	Cefixime (100%)	-	-	-	-	-	-	-	-	-
Endotracheal aspirate (n=145)	**ICU (n=145)**	Ceftriaxone (29%)	Meropenem (18%)	Ciprofloxacin (12%)	Cefuroxime (6%)	Vancomycin (6%)	Cefixime (5%)	Cefuroxime+ clavulanic acid (4%)	Piperacillin+ Tazobactam (4%)	Clindamycin (3%)	Doxycycline (3%)
Diarrhea (n=4)	**Ward (n=4)**	Ceftriaxone (50%)	Ceftazidime (25%)	Ciprofloxacin (25%)	-	-	-	-	-	-	-
Urine (n=1485)	**ICU (n=1415)**	Ceftriaxone (53%)	Meropenem (14%)	Ciprofloxacin (7%)	Cefuroxime (6%)	Cefixime (6%)	Vancomycin (3%)	Piperacillin+ Tazobactam (3%)	Cefuroxime+ clavulanic acid (3%)	Metronidazole (2%)	Moxifloxacin (1%)
	Ward (n=61)	Ceftriaxone (36%)	Meropenem (26%)	Vancomycin (15%)	Azithromycin (7%)	Cefixime (5%)	Piperacillin+ Tazobactam (5%)	Moxifloxacin Hydrochloride (3%)	Cefuroxime+ clavulanic acid (2%)	Ciprofloxacin (2%)	-
	OPD (n=9)	Ciprofloxacin (33%)	Cefixime (22%)	Levofloxacin (22%)	Azithromycin (11%)	Ceftriaxone (11%)	-	-	-	-	-
Wound swab (n=221)	**Ward (n=221)**	Ceftriaxone (48%)	Cefuroxime (34%)	Cefixime (7%)	Meropenem (6%)	Ciprofloxacin (1%)	Levofloxacin (1%)	Ceftazidime (1%)	Amoxicillin + Clavulanic acid (1%)	-	-

Rangpur Medical College and Hospital (RpMCH)

Sample size and Culture test

Out of 1,506 samples, a total of 552 (37%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 45.3%, Female- 54.7%
- Highest growth was observed in 0-10 age group

Sample Collection Locations

Table 42: Distribution of isolates by location at RpMCH, 2025

Location	Number of isolates	(%)
OPD	251	45.5
IPD	301	54.5

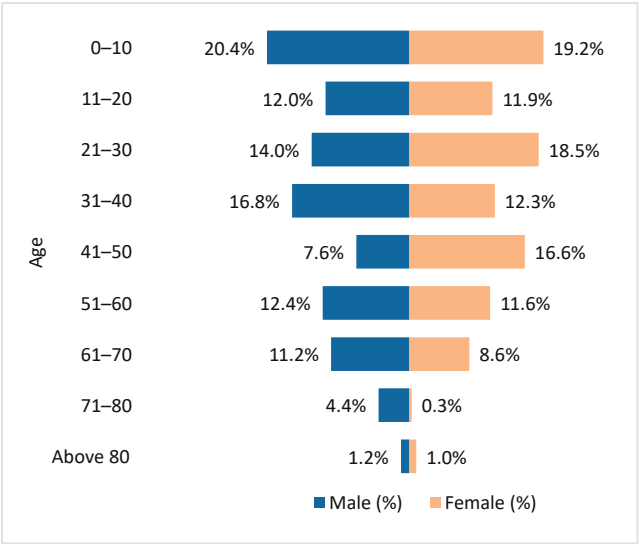


Figure 59: Distribution of isolates by sex and age group at RpMCH, 2025

Specimen Types

Table 43: Distribution of specimen types at RpMCH, 2025

Specimen type	Number of isolates	(%)
Urine	262	47.5
Wound swab	178	32.2
Blood	69	12.5
Endotracheal aspirate	41	7.4
Stool	2	0.4

Organism statistics

Organism frequencies

Table 44: Distribution of isolates by organism type at RpMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	86	15.6
Aerobic Gram -negative bacteria	442	80.1
Fungi	24	4.3

Table 45: Distribution of the five most common organisms at RpMCH, 2025

Organism	Number of isolates	(%)
E. coli	178	32.2
P. aeruginosa	115	20.8
K. pneumoniae	106	19.2
Enterococcus spp.	50	9.1
S. aureus	36	6.5

Most Common Organisms

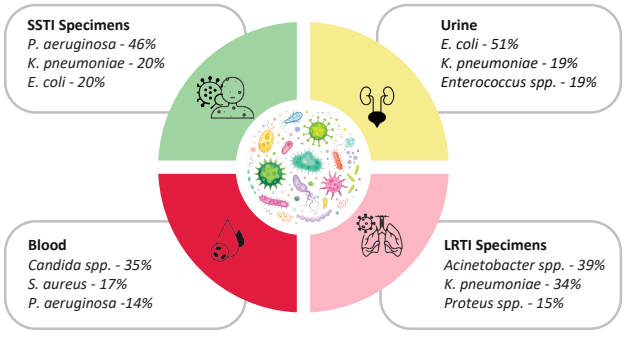


Figure 60: Most common organisms by specimen category at RpMCH, 2025

Multidrug-Resistant (MDR) Path

Table 46: Frequency of multidrug-resistant (MDR) pathogens at RpMCH, 2025

Organism	MDR (%)
S. aureus(N=36)	81
E. coli (N=178)	97
K. pneumoniae (N=106)	91
P. aeruginosa (N=115)	78

WHO Critical Priority Pathogens

Table 47: Frequency of WHO critical priority pathogens at RpMCH, 2025

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter* spp. (N=21)	95%
Carbapenem resistance *P. aeruginosa* (N=115)	70%
Ceftriaxone-resistant *E. coli* (N=178)	80%
Meropenem-resistant *E. coli* (N=178)	37%

Antibiogram

Table 48: Antibiogram at RpMCH, 2025

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Ampicillin	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Fosfomycin	Gentamicin	Linezolid	Nitrofurantoin	Penicillin	Tetracycline	Trimethoprim/Sulfamethoxazole	Vancomycin
Enterococcus spp.	14	-	-	14	-	-	40	-	78	39	4	22	-	-
S. aureus	-	18	36	31	64	78	-	75	78	-	6	-	47	64

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Ceftazidime/Avibactam	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine only)	Gentamicin	Imipenem	Meropenem	Netilmicin	Nitrofurantoin (Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Cefazolin (Urine only)
E.coli	62	2	26	33	32	16	20	11	34	72	56	68	64	-	64	47	36	35	12
P. aeruginosa	-	-	36	25	-	10	-	-	26	-	-	41	30	24	-	43	-	-	-
K.pneumoniae	40	-	26	29	-	18	26	13	33	-	49	49	43	-	33	37	32	29	4
Acinetobacter spp.	14	-	-	14	-	10	5	-	14	-	14	5	5	-	-	14	-	38	-

Antibiotic Use

A total of 830 antibiotic administrations were recorded among the patients.

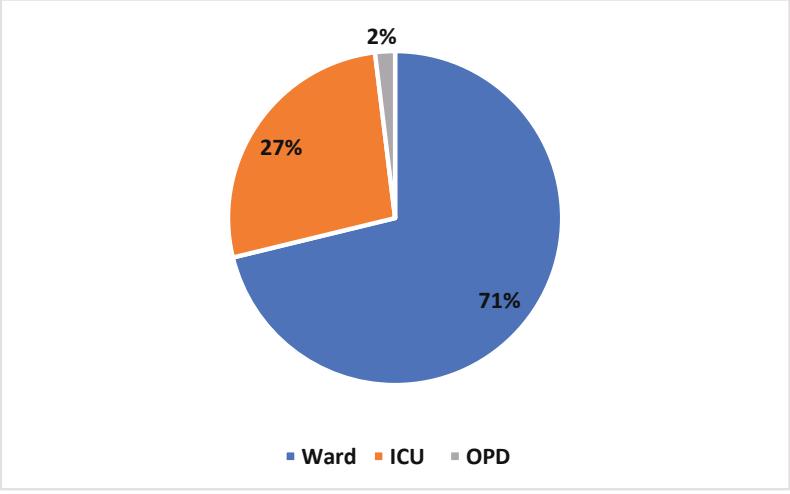


Figure 61: Distribution of antibiotic usage by location at RpMCH, 2025 (n=830)

Table 49: Antibiotic usage by case type and location at RpMCH, 2025 (n=830)

Ten most commonly used antibiotics in different locations (n=830)										
ICU (n=223)	Meropenem (46%)	Ceftriaxone (39%)	Levofloxacin (3%)	Moxifloxacin (3%)	Piperacillin+ Tazobactam (3%)	Amoxicillin + Clavulanic acid (1%)	Piperacillin (1%)	Cefuroxime+ clavulanic acid (1%)	Clindamycin (1%)	Cefixime (1%)
Ward (n=591)	Ceftriaxone (40%)	Cefixime (19%)	Azithromycin (16%)	Levofloxacin (10%)	Ciprofloxacin (9%)	Meropenem (3%)	Cefuroxime (1%)	Clindamycin (1%)	Doxycycline (1%)	Metronidazole (1%)
OPD (n=16)	Ciprofloxacin (38%)	Cefixime (31%)	Levofloxacin (19%)	Azithromycin (6%)	Ceftriaxone (6%)	-	-	-	-	-

Table 49.1: Antibiotics used according to cases (n=830)

Ten most commonly used antibiotics in different locations (n=830)											
Blood (n=267)	**ICU (n=48)**	Meropenem (48%)	Ceftriaxone (44%)	Levofloxacin (4%)	Moxifloxacin (2%)	Piperacillin+ Tazobactam (2%)	-	-	-	-	-
	Ward (n=212)	Ceftriaxone (66%)	Cefixime (11%)	Ciprofloxacin (11%)	Levofloxacin (6%)	Azithromycin (3%)	Meropenem (2%)	Metronidazole (1%)	-	-	-
	OPD (n=7)	Cefixime (43%)	Ciprofloxacin (43%)	Ceftriaxone (14%)	-	-	-	-	-	-	-
Endotracheal aspirate (n=114)	**ICU (n=114)**	Meropenem (44%)	Ceftriaxone (41%)	Moxifloxacin (4%)	Amoxicillin + Clavulanic acid (3%)	Piperacillin (2%)	Piperacillin+ Tazobactam (2%)	Cefixime (1%)	Cefuroxime+ clavulanic acid (1%)	Clindamycin (1%)	Imipenem (1%)
Diarrhea (n=127)	**Ward (n=127)**	Azithromycin (65%)	Ceftriaxone (22%)	Ciprofloxacin (10%)	Cefixime (2%)	Metronidazole (1%)	-	-	-	-	-
Urine (n=78)	**ICU (n=61)**	Meropenem (49%)	Ceftriaxone (33%)	Levofloxacin (7%)	Cefuroxime+ clavulanic acid (2%)	Ciprofloxacin (2%)	Clindamycin (2%)	Metronidazole (2%)	Moxifloxacin (2%)	Piperacillin (2%)	Piperacillin+ Tazobactam (2%)
	Ward (n=9)	Ceftriaxone (89%)	Cefixime (11%)	-	-	-	-	-	-	-	-
	OPD (n=8)	Ciprofloxacin (38%)	Cefixime (25%)	Levofloxacin (25%)	Azithromycin (13%)	-	-	-	-	-	-
Wound swab (n=244)	**Ward (n=243)**	Cefixime (35%)	Ceftriaxone (25%)	Levofloxacin (19%)	Ciprofloxacin (7%)	Meropenem (5%)	Azithromycin (2%)	Cefuroxime (2%)	Clindamycin (2%)	Doxycycline (2%)	Amikacin (1%)
	OPD (n=1)	Levofloxacin (100%)	-	-	-	-	-	-	-	-	-

Chittagong Medical College and Hospital (CMCH)

Sample size and Culture test

Out of 2,305 samples, a total of 503 (22%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 63%, Female- 37%
- Highest growth was observed in 0-10 age group

Sample Collection Locations

Table 50: Distribution of isolates by location at CMCH, 2025

Location	Number of isolates	(%)
OPD	27	5.4
IPD	181	36
ICU	295	58.6

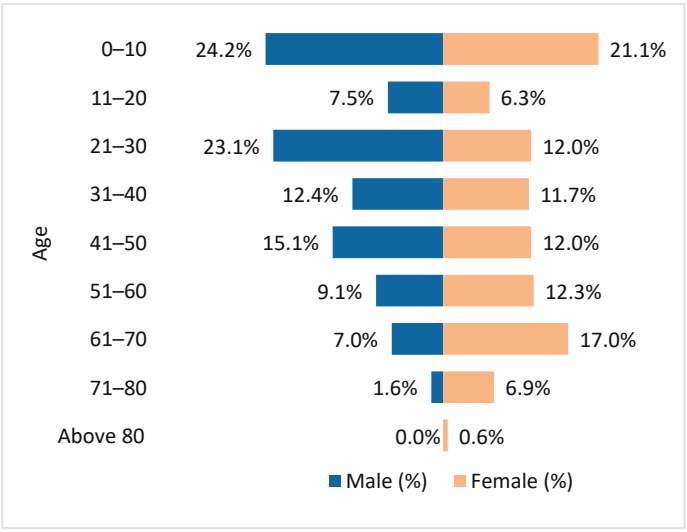


Figure 62: Distribution of isolates by sex and age group at CMCH, 2025

Specimen Types

Table 51: Distribution of specimen types at CMCH, 2025

Specimen type	Number of isolates	(%)
Blood	182	36.2
Endotracheal aspirate	160	31.8
Wound swab	124	24.7
Urine	33	6.5
Stool	4	0.8

Organism statistics

Organism frequencies

Table 52: Distribution of isolates by organism type at CMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	19	3.8
Aerobic Gram -negative bacteria	484	96.2

Table 53: Distribution of the five most common organisms at CMCH, 2025

Organism	Number of isolates	(%)
Acinetobacter spp.	221	41.9
P. aeruginosa	135	25.6
K. pneumoniae	89	16.9
E. coli	35	6.9
S. aureus	19	3.6

Most Common Organisms

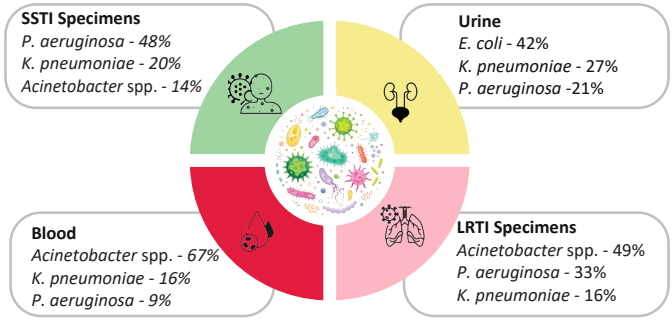


Figure 63: Most common organisms by specimen category at CMCH, 2025

Frequency of Multidrug resistant pathogen

Table 54: Frequency of multidrug-resistant (MDR) pathogens at CMCH, 2025

Organism	MDR (%)
S. aureus (N=19)	37
E. coli (N=35)	85
K. pneumoniae (N=26)	92
P. aeruginosa (N=135)	53

Distribution of WHO Critical Priority Pathogen

Table 55: Frequency of WHO critical priority pathogens at CMCH, 2025

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter spp. (N=221)*	76%
Carbapenem resistance *P. aeruginosa (N=133)*	47%
Ceftriaxone resistant *E. coli (N=35)*	83%
Meropenem resistant *E. coli (N=35)*	37%

Antibiogram

Table 56: Antibiogram at CMCH, 2025

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Cefixime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Gentamycin	Imipenem	Meropenem	Netilmicin	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole
Acinetobacter spp.	41	-	-	23	-	16	12	-	27	18	23	24	-	27	-	43
P. aeruginosa	-	-	46	43	-	37	-	-	46	-	63	53	54	54	-	-
E. coli	54	12	31	32	-	34	17	18	21	37	67	63	-	45	44	51
K. pneumoniae	26	-	20	16	4	14	8	5	13	34	38	29	-	21	38	24

Antibiotic Use

A total of 2,523 antibiotic administrations were recorded among patients

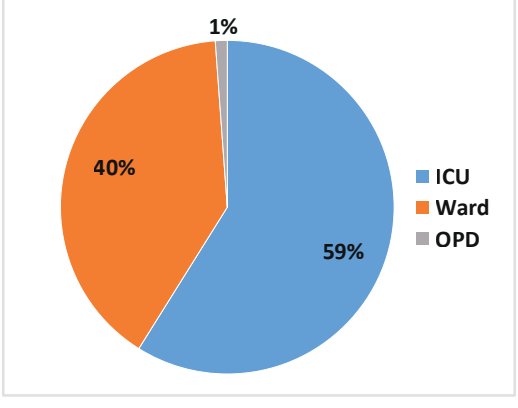


Figure 64: Distribution of antibiotic usage by location (IPD, OPD, ward) at CMCH, 2025 (n=2,523)

Table 57: Antibiotic usage by case type and location (IPD, OPD, ward) at CMCH, 2025 (n=2,523)

Ten most commonly used antibiotics in different locations (n=2,523)										
ICU (n=1486)	Meropenem (28%)	Amikacin (15%)	Ceftriaxone (13%)	Cefixime (9%)	Ceftazidime (6%)	Ciprofloxacin (6%)	Levofloxacin (6%)	Piperacillin+ Tazobactam (4%)	Cefuroxime (3%)	Vancomycin (3%)
Ward (n=1008)	Ceftriaxone (25%)	Ciprofloxacin (19%)	Meropenem (12%)	Cefixime (11%)	Cefuroxime+ clavulanic acid (10%)	Amikacin (6%)	Cefuroxime (6%)	Vancomycin (5%)	Piperacillin+ Tazobactam (2%)	Levofloxacin (1%)
OPD (n=29)	Cefixime (28%)	Ciprofloxacin (28%)	Ceftriaxone (21%)	Cefuroxime+ clavulanic acid (14%)	Azithromycin (3%)	Cefuroxime (3%)	Meropenem (3%)	-	-	-

Table 57.1: Antibiotics used according to cases (n=2,520)

Ten most commonly used antibiotics in different locations (n=2,520)											
Blood (n=1807)	**ICU (n=1232)**	Meropenem (30%)	Amikacin (18%)	Ceftriaxone (11%)	Cefixime (8%)	Ceftazidime (7%)	Levofloxacin (7%)	Ciprofloxacin (4%)	Piperacillin+ Tazobactam (3%)	Vancomycin (3%)	Cefuroxime (3%)
	Ward (n=573)	Ceftriaxone (33%)	Meropenem (17%)	Cefixime (13%)	Vancomycin (9%)	Amikacin (8%)	Cefuroxime (5%)	Cefuroxime+ clavulanic acid (3%)	Piperacillin+ Tazobactam (2%)	Levofloxacin (2%)	Ciprofloxacin (2%)
	OPD (n=2)	Cefuroxime+ clavulanic acid (50%)	Ciprofloxacin (50%)	-	-	-	-	-	-	-	-
Endotracheal aspirate (n=235)	**ICU (n=235)**	Ceftriaxon (26%)	Meropenem (24%)	Cefixime (18%)	Ciprofloxacin (13%)	Piperacillin+ Tazobactam (8%)	Cefuroxime+ clavulanic acid (4%)	Cefuroxime (2%)	Amikacin (1%)	Ceftazidime (1%)	Clarithromycin (0.4%)
Diarrhea (n=194)	**ICU (n=3)**	Ciprofloxacin (100%)	-	-	-	-	-	-	-	-	-
	Ward (n=191)	Ciprofloxacin (92%)	Ceftriaxone (3%)	Piperacillin+ Tazobactam (2%)	Cefixime (1%)	Cefuroxime+ clavulanic acid (1%)	Cefuroxime (1%)	Meropenem (1%)	Metronidazole (1%)		-
Urine (n=129)	**ICU (n=20)**	Meropenem (25%)	Cefuroxime (20%)	Ceftriaxone (15%)	Cefixime (10%)	Ceftazidime (10%)	Ciprofloxacin (10%)	Piperacillin+ Tazobactam (10%)	-	-	-
	Ward (n=82)	Ceftriaxone (49%)	Cefixime (11%)	Meropenem (11%)	Cefuroxime (10%)	Amikacin (9%)	Piperacillin+ Tazobactam (4%)	Ciprofloxacin (2%)	Azithromycin (1%)	Cefuroxime+ clavulanic acid (1%)	Clindamycin (1%)
	OPD (n=27)	Cefixime (30%)	Ciprofloxacin (26%)	Ceftriaxone (22%)	Cefuroxime+ clavulanic acid (11%)	Azithromycin (4%)	Cefuroxime (4%)	Meropenem (4%)	-	-	-
Wound swab (n=155)	**Ward (n=155)**	Cefuroxime+ clavulanic acid (52%)	Cefixime (14%)	Cefuroxime (11%)	Ceftriaxone (6%)	Meropenem (5%)	Amikacin (3%)	Ciprofloxacin (3%)	Metronidazole (3%)	Levofloxacin (1%)	Moxifloxacin (1%)

Sher-E- Bangla Medical College and Hospital

Sample size and Culture test

Out of 820 samples, a total of 155 (19%) samples yielded positive growth. Among them, 95 were detected in 2024, and 60 in 2025.

Patient Demographics and Sample Characteristics

- Sex: Male- 34.8%, Female- 65.2%
- Highest growth was observed in 41-50 age group

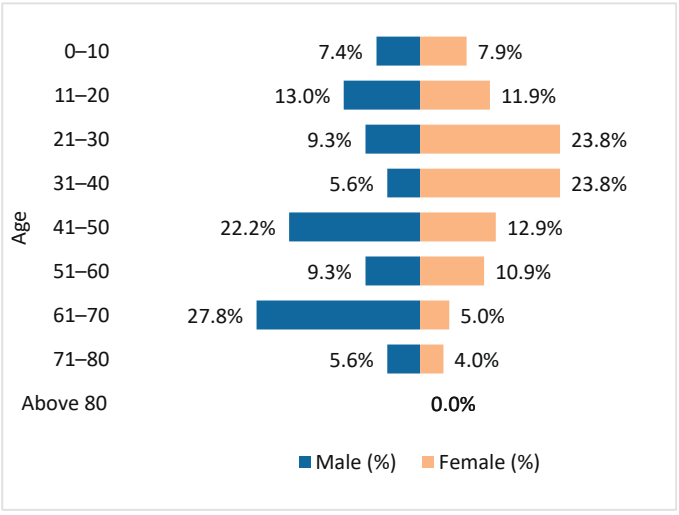


Figure 65: Distribution of isolates by sex and age group at SBMCH, 2025

Sample Collection Locations

Table 58: Distribution of isolates by location at SBMCH, 2025

Location	Number of isolates	(%)
OPD	30	19.4
IPD	90	58.1
ICU	35	22.5

Specimen Types

Table 59: Distribution of specimen types at SBMCH, 2025

Specimen type	Number of isolates	(%)
Wound swab	59	38.1
Urine	39	25.2
Endotracheal aspirate	34	21.9
Blood	16	10.3
Stool	7	4.5

Organism statistics

Organism frequencies

Table 60: Distribution of isolates by organism type at SBMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	13	8.4
Aerobic Gram -negative bacteria	140	90.3
Fungi	2	1.3

Table 61: Distribution of the five most common organisms at SBMCH, 2025

Organism	Number of isolates	(%)
K. pneumoniae	42	27.1
P. aeruginosa	42	27.1
E. coli	28	18.1
Acinetobacter spp.	17	11
S. aureus	13	8.4

Most Common Organisms

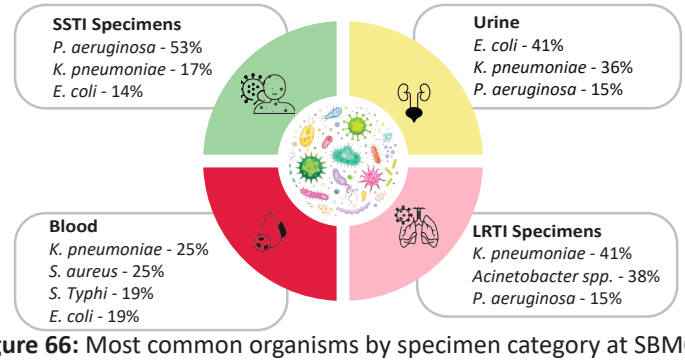


Figure 66: Most common organisms by specimen category at SBMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 62: Frequency of multidrug-resistant (MDR) pathogens at SBMCH, 2025

Organism	MDR (%)
S. aureus(N=13)	92
E. coli (N=28)	100
K. pneumoniae (N=14)	100
P. aeruginosa (N=42)	62

WHO Critical Priority Pathogens

Table 63: Frequency of WHO critical priority pathogens at SBMCH, 2025

Critical Priority Organism	Number (%)
Carbapenem-resistance *Acinetobacter* spp. (N=17)	77%
Carbapenem resistance *P. aeruginosa* (N=42)	48%
Ceftriaxone resistant *E. coli* (N=28)	86%
Meropenem resistant *E.coli* (N=25)	20%

Antibiogram

Table 64: Antibiogram at SBMCH, 2025

Color coding	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamycin	Linezolid	Penicillin	Trimethoprim/Sulfamethoxazole
S. aureus	9	100	58	60	85	92	100	0	46

Gram-negative

Organism	Amikacin	Ampicillin	Amoxicillin -clavulanate	Aztreonam	Cefepime	Ceftazidime	Ceftazidime -avibactam	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine only)	Gentamycin	Imipenem	Meropenem	Nitrofurantoin(Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole
E. coli	57	4	7	27	15	8	56	14	8	29	80	63	71	80	57	38	62	25

Antibiotic Use

A total of 669 antibiotic administrations were recorded among the patients.

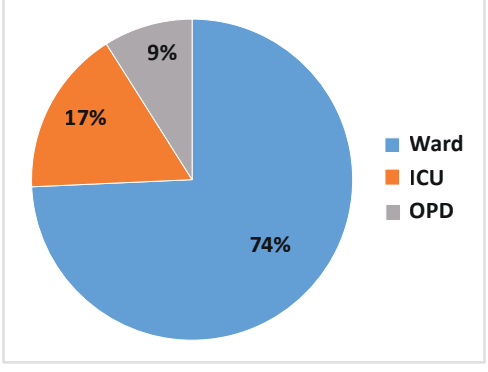


Figure 67: Distribution of antibiotic usage by location at SBMCH, 2025 (n=669)

Table 65: Antibiotic usage by case type and location at SBMCH, 2025 (n=669)

Ten most commonly used antibiotics in different locations (n=669)										
ICU (n=112)	Ceftriaxone (46%)	Meropenem (23%)	Cefuroxime+ clavulanic acid (7%)	Cotrimoxazole (7%)	Metronidazole (6%)	Moxifloxacin (4%)	Amikacin (2%)	Cefuroxime (2%)	Levofloxacin (2%)	Cefixime (1%)
Ward (n=497)	Ceftriaxone (36%)	Azithromycin (20%)	Cefuroxime (11%)	Meropenem (41%)	Cefixime (8%)	Cefuroxime+ clavulanic acid (5%)	Ciprofloxacin (3%)	Metronidazole (2%)	Amikacin (2%)	Vancomycin (1%)
OPD (n=60)	Azithromycin (18%)	Cefixime (18%)	Levofloxacin (15%)	Ceftriaxone (13%)	Cefuroxime (12%)	Cefuroxime+ clavulanic acid (8%)	Ciprofloxacin (8%)	Clarithromycin (2%)	Meropenem (2%)	Metronidazole (2%)

Table 65.1: Antibiotics used according to cases (n=669)

Ten most commonly used antibiotics in different locations (n=669)											
Blood (n=212)	**ICU (n=8)**	Ceftriaxone (38%)	Meropenem (38%)	Amikacin (13%)	Cefuroxime+ clavulanic acid (13%)	-	-	-	-	-	-
	Ward (n=194)	Ceftriaxone (60%)	Meropenem (12%)	Cefuroxime+ clavulanic acid (8%)	Cefixime (5%)	Vancomycin (3%)	Ciprofloxacin (2%)	Azithromycin (2%)	Doxycycline (2%)	Levofloxacin (2%)	Amikacin (1%)
	OPD (n=10)	Ceftriaxone (40%)	Azithromycin (30%)	Cefixime (20%)	Cefuroxime (10%)	-	-	-	-	-	-
Endotracheal aspirate (n=104)	**ICU (n=104)**	Ceftriaxone (47%)	Meropenem (21%)	Cotrimoxazole (8%)	Metronidazole (8%)	Cefuroxime+ clavulanic acid (7%)	Moxifloxacin (3%)	Cefuroxime (2%)	Levofloxacin (2%)	Amikacin (1%)	Cefixime (1%)
Diarrhea (n=105)	**Ward (n=105)**	Azithromycin (90%)	Metronidazole (6%)	Ciprofloxacin (5%)							
Urine (n=77)	**ICU (n=6)**	Ceftriaxone (33%)	Meropenem (33%)	Cefuroxime+ clavulanic acid (17%)	Moxifloxacin (17%)	-	-	-	-	-	-
	Ward (n=28)	Ceftriaxone (46%)	Cefixime (18%)	Meropenem (14%)	Cefuroxime (7%)	Metronidazole (7%)	Ciprofloxacin (4%)	Vancomycin (4%)	-	-	-
	OPD (n=43)	Levofloxacin (19%)	Azithromycin (16%)	Cefixime (16%)	Cefuroxime (12%)	Ciprofloxacin (12%)	Ceftriaxone (9%)	Cefuroxime+ clavulanic acid (9%)	Clarithromycin (2%)	Meropenem (2%)	Metronidazole (2%)
Wound swab (n=171)	**Ward (n=165)**	Cefuroxime (31%)	Ceftriaxone (29%)	Cefixime (14%)	Meropenem (7%)	Cefuroxime+ clavulanic acid (6%)	Amikacin (4%)	Ciprofloxacin (4%)	Moxifloxacin (2%)	Levofloxacin (1%)	Metronidazole (1%)
	OPD (n=6)	Cefixime (33%)	Azithromycin (17%)	Cefuroxime (17%)	Levofloxacin (17%)	Moxifloxacin (17%)	-	-	-	-	-

Sylhet MAG Osmani Medical College and Hospital (SOMCH)

Sample size and Culture test

Out of 693 samples, a total of 129 (19%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 42.6%, Female- 57.4%
- Highest growth was observed in 41-50 age group

Sample Collection Locations

Table 66: Distribution of isolates by location at SOMCH, 2025

Location	Number of isolates	(%)
OPD	43	33.3
IPD	56	43.4
ICU	30	23.3

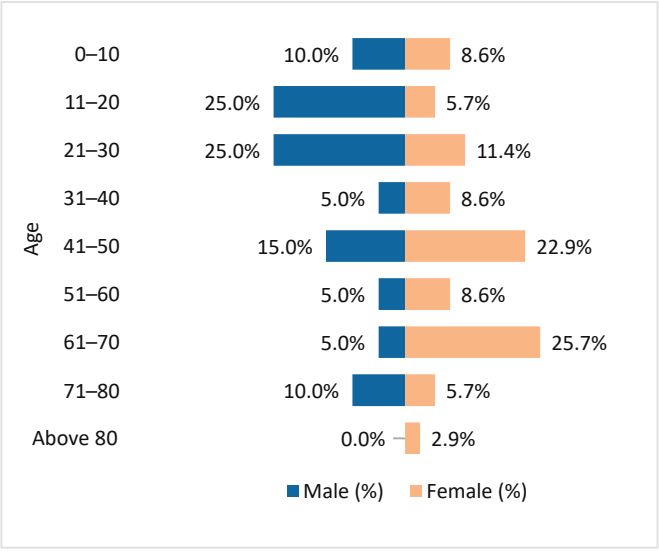


Figure 68: Distribution of isolates by sex and age group at SOMCH, 2025

Specimen Types

Table 67: Distribution of specimen types at SOMCH, 2025

Specimen type	Number of isolates	(%)
Wound swab	46	35.7
Urine	33	25.6
Blood	29	22.5
Endotracheal aspirate	20	15.5
Stool	1	0.7

Organism statistics

Organism frequencies

Table 68: Distribution of isolates by organism type at SOMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	48	37.2
Aerobic Gram -negative bacteria	81	62.8

Table 69: Distribution of the five most common organisms at SOMCH, 2025

Organism	Number of isolates	(%)
S. aureus	47	36.4
E. coli	33	25.6
K. pneumoniae	18	14.0
P. aeruginosa	14	10.9
Acinetobacter spp.	8	6.2

Most Common Organisms

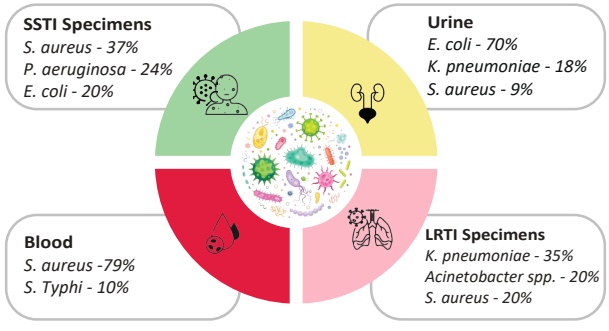


Figure 69: Most common organisms by specimen category at SOMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 70: Frequency of multidrug-resistant (MDR) pathogens at SOMCH, 2025

Organism	MDR (%)
S. aureus (N=47)	81
E. coli (N=33)	91
K. pneumoniae (N=8)	100
P. aeruginosa (N=14)	71

WHO Critical Priority Pathogens

Table 71: Frequency of WHO critical priority pathogens at SOMCH, 2025

Organism	Number (%)
Carbapenem-resistance *Acinetobacter* spp. (N=6)	50%
Carbapenem resistance *Pseudomonas aeruginosa* (N=11)	36%
Ceftriaxone resistant *Escherichia coli* (N=30)	73%
Meropenem resistant *Escherichia coli* (N=33)	12%

Antibiogram

Table 72: Antibiogram at SOMCH, 2025

Color coding

Color	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamycin	Linezolid	Penicillin	Trimethoprim/ Sulfamethoxazole
S. aureus	7	27	13	48	83	62	83	2	31

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine only)	Imipenem	Meropenem	Nitrofurantoin Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Cefazolin Urine only)
E. coli	73	0	34	29	54	27	24	61	92	94	88	30	27	62	36	10

Antibiotic Use

A total of 360 antibiotic administrations were recorded among the patients.

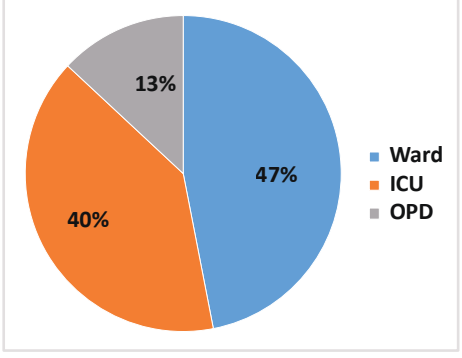


Figure 70: Distribution of antibiotic usage by location at SOMCH, 2025 (n=360)

Table 73: Antibiotic usage by case type and location at SOMCH, 2025 (n=360)

Ten most commonly used antibiotics in different locations (n=360)										
ICU (n=144)	Ceftriaxone (35%)	Meropenem (30%)	Metronidazole (13%)	Moxifloxacin (10%)	Clindamycin (3%)	Cefuroxime (2%)	Vancomycin (2%)	Flucloxacillin (1%)	Gentamycin (1%)	Cefuroxime+ clavulanic acid (1%)
Ward (n=169)	Ceftriaxone (62%)	Ciprofloxacin (9%)	Meropenem (9%)	Cefuroxime (5%)	Azithromycin (3%)	Vancomycin (3%)	Cefixime (2%)	Cefuroxime+ clavulanic acid (2%)	Clindamycin (1%)	Metronidazole (1%)
OPD (n=47)	Azithromycin (21%)	Cefixime (17%)	Ciprofloxacin (15%)	Ceftriaxone (13%)	Cefuroxime (9%)	Cefuroxime+ clavulanic acid (6%)	Levofloxacin (4%)	Moxifloxacin (4%)	Amikacin (2%)	Ceftibuten (2%)

Table 73.1: Antibiotics used according to cases (n=360)

Ten most commonly used antibiotics in different locations (n=360)											
Blood (n=125)	**ICU (n=56)**	Ceftriaxone (32%)	Meropenem (30%)	Metronidazole (16%)	Moxifloxacin (11%)	Vancomycin (4%)	Cefuroxime (2%)	Clindamycin (2%)	Flucloxacillin (2%)	Gentamycin (2%)	-
	Ward (n=61)	Ceftriaxone (74%)	Meropenem (10%)	Vancomycin (5%)	Azithromycin (3%)	Cefuroxime+ clavulanic acid (2%)	Clindamycin (2%)	Flucloxacillin (2%)	Levofloxacin (2%)	Moxifloxacin Hydrochloride (2%)	-
	OPD (n=8)	Azithromycin (50%)	Amikacin (13%)	Cefixime (13%)	Levofloxacin (13%)	Moxifloxacin (13%)	-	-	-	-	-
Endotracheal aspirate (n=64)	**ICU (n=64)**	Ceftriaxone (34%)	Meropenem (31%)	Moxifloxacin (9%)	Metronidazole (8%)	Clindamycin (6%)	Cefuroxime+ clavulanic acid (2%)	Cefuroxime (2%)	Flucloxacillin (2%)	Gentamycin (2%)	Imipenem (2%)
Diarrhea (n=16)	**Ward (n=16)**	Ciprofloxacin (81%)	Azithromycin (6%)	Ceftriaxone (6%)	Metronidazole (6%)	-	-	-	-	-	-
Urine (n=73)	**ICU (n=20)**	Ceftriaxone (40%)	Meropenem (25%)	Metronidazole (15%)	Moxifloxacin (15%)	Cefuroxime (5%)	-	-	-	-	-
	Ward (n=21)	Ceftriaxone (67%)	Meropenem (14%)	Azithromycin (10%)	Vancomycin (10%)	-	-	-	-	-	-
	OPD (n=32)	Azithromycin (19%)	Cefixime (19%)	Ciprofloxacin (19%)	Ceftriaxone (16%)	Cefuroxime+ clavulanic acid (6%)	Ceftibuten (3%)	Cefuroxime (3%)	Chloramphenicol (3%)	Flucloxacillin (3%)	Levofloxacin (3%)
Wound swab (n=82)	**ICU (n=4)**	Ceftriaxone (50%)	Meropenem (25%)	Metronidazole (25%)	-	-	-	-	-	-	-
	Ward (n=71)	Ceftriaxone (63%)	Cefuroxime (11%)	Meropenem (8%)	Cefixime (4%)	Ciprofloxacin (4%)	Cefuroxime+ clavulanic acid (3%)	Clindamycin (1%)	Doxycycline (1%)	Linezolid (1%)	Metronidazole (1%)
	OPD (n=7)	Cefuroxime (43%)	Cefixime (14%)	Ceftriaxone (14%)	Cefuroxime+ clavulanic acid (14%)	Ciprofloxacin (14%)	-	-	-	-	-

Khulna Medical College and Hospital (KMCH)

Sample size and Culture test

Out of 1,280 samples, a total of 296 (23%) samples yielded positive growth. Among them, 117 were detected in 2024, and 179 in 2025.

Patient Demographics and Sample Characteristics

- Sex: Male- 45.6%, Female- 54.4%
- Highest growth was observed in 51-60 age group

Sample Collection Locations

Table 74: Distribution of isolates by location at KMCH, 2025

Location	Number of isolates	(%)
OPD	58	19.6
IPD	192	64.8
ICU	46	15.5

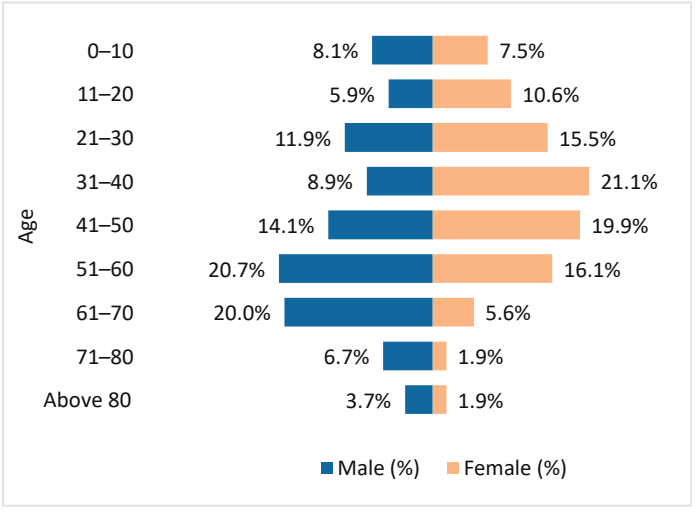


Figure 71: Distribution of isolates by sex and age group at KMCH, 2025

Specimen Types

Table 75: Distribution of specimen types at KMCH, 2025

Specimen type	Number of isolates	(%)
Wound swab	148	50
Urine	74	25
Blood	54	18.2
Endotracheal as	18	6.1
Stool	2	0.7

Organism statistics

Organism frequencies

Table 76: Distribution of isolates by organism type at KMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	72	24.3
Aerobic Gram -negative bacteria	224	75.7

Table 77: Distribution of the five most common organisms at KMCH, 2025

Organism	Number of isolates	(%)
S. aureus	69	23.3
P. aeruginosa	62	20.9
Acinetobacter spp.	54	18.2
E. coli	48	16.2
K. pneumoniae	32	10.8

Most Common Organisms

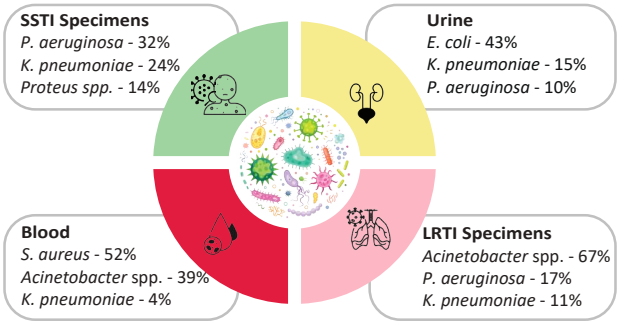


Figure 72: Most common organisms by specimen category at KMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 78: Frequency of multidrug-resistant (MDR) pathogens at KMCH, 2025

Organism	MDR (%)
S. aureus (N=69)	67
E. coli (N=48)	92
K. pneumoniae (N=36)	100
P. aeruginosa (N=61)	54

WHO Critical Priority Pathogens

Table 79: Frequency of WHO critical priority pathogens at KMCH, 2025

Critical Priority Organism	%
Carbapenem resistance *Acinetobacter* spp. (N=46)	72%
Carbapenem resistance *P. aeruginosa* (N=60)	32%
Ceftriaxone resistant *E. coli* (N=30)	63%
Meropenem resistant *E. coli* (N=44)	23%

Antibiogram

Table 80: Antibiogram at KMCH, 2025

Color coding	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamicin	Linezolid	Penicillin	Trimethoprim/Sulfamethoxazole
S. aureus	19	41	44	45	81	81	93	12	76

Gram-negative

Organism	Amikacin	Ampicillin	Amoxicillin/clavulanate	Aztreonam	Cefepime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin(Urine only)	Gentamicin	Imipenem	Meropenem	Netilmicin	Nitrofurantoin(Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Cefazolin (Urine only)
P. aeruginosa	-	-	-	53	41	28	-	-	46	-	-	66	50	61	-	67	-	-	-
Acinetobacter spp.	36	-	-	-	25	11	13	-	26	-	37	30	17	-	-	24	-	49	-
E. coli	73	9	25	37	33	17	37	6	21	96	69	79	77	-	45	66	47	51	10
K. pneumoniae	56	-	22	33	31	28	24	6	28	-	59	62	43	-	-	47	38	26	-

Antibiotic Use

A total of 946 antibiotic administrations were recorded among patients

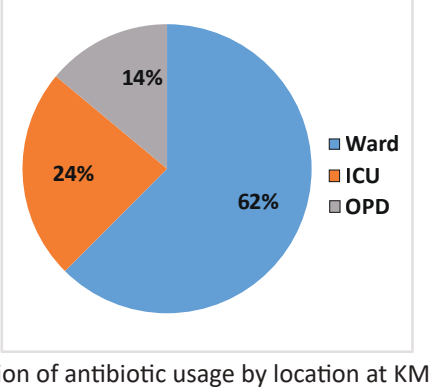


Figure 73: Distribution of antibiotic usage by location at KMCH, 2025 (n=946)

Table 81: Antibiotic usage by case type and location at KMCH, 2025

Ten most commonly used antibiotics in different locations (n=946)										
ICU (n=223)	Meropenem (60%)	Cefixime (16%)	Ceftriaxone (10%)	Cefuroxime+ clavulanic acid (3%)	Vancomycin (3%)	Cefuroxime (2%)	Amoxicillin + Clavulanic acid (1%)	Ceftazidime (1%)	Ciprofloxacin (1%)	Erythromycin (1%)
Ward (n=591)	Ceftriaxone (34%)	Cefuroxime (16%)	Cefixime (14%)	Meropenem (9%)	Levofloxacin (8%)	Cefuroxime+ clavulanic acid (6%)	Azithromycin (3%)	Vancomycin (2%)	Ciprofloxacin (2%)	Amikacin (1%)
OPD (n=132)	Cefixime (18%)	Cefuroxime+ clavulanic acid (17%)	Ciprofloxacin (17%)	Ceftriaxone (12%)	Levofloxacin (8%)	Cefuroxime (7%)	Azithromycin (6%)	Ceftazidime (4%)	Doxycycline (4%)	Meropenem (3%)

Table 81.1: Antibiotics used according to cases (n=946)

Ten most commonly used antibiotics in different locations (n=946)											
Blood (n=409)	**ICU (n=147)**	Meropenem (57%)	Cefixime (16%)	Ceftriaxone (13%)	Cefuroxime+ clavulanic acid (3%)	Vancomycin (3%)	Cefuroxime (2%)	Amoxicillin + Clavulanic acid (1%)	Ceftazidime (1%)	Erythromycin (1%)	Levofloxacin (1%)
	Ward (n=228)	Ceftriaxone (47%)	Meropenem (14%)	Cefixime (7%)	Cefuroxime+ clavulanic acid (7%)	Cefuroxime (7%)	Vancomycin (5%)	Azithromycin (4%)	Amikacin (2%)	Levofloxacin (2%)	Amoxicillin + Clavulanic acid (1%)
	OPD (n=34)	Azithromycin (18%)	Cefixime (18%)	Ceftriaxone (18%)	Cefuroxime+ clavulanic acid (15%)	Ciprofloxacin (12%)	Doxycycline (6%)	Amikacin (3%)	Ceftazidime (3%)	Cefuroxime (3%)	Levofloxacin (3%)
Endotracheal aspirate (n=77)	**ICU (n=77)**	Meropenem (66%)	Cefixime (16%)	Ceftriaxone (5%)	Ceftazidime (3%)	Ciprofloxacin (3%)	Cefuroxime+ clavulanic acid (1%)	Cefuroxime (1%)	Erythromycin (1%)	Moxifloxacin (1%)	Amoxicillin + Clavulanic acid (1%)
Diarrhea (n=28)	**Ward (n=28)**	Azithromycin (36%)	Ceftriaxone (36%)	Ciprofloxacin (11%)	Cefixime (7%)	Ceftazidime (4%)	Erythromycin (4%)	Vancomycin (4%)	-	-	-
Urine (n=190)	**ICU (n=1)**	Cefuroxime (100%)	-	-	-	-	-	-	-	-	-
	Ward (n=100)	Ceftriaxone (35%)	Cefuroxime (18%)	Cefixime (17%)	Meropenem (15%)	Levofloxacin (9%)	Vancomycin (2%)	Amikacin (1%)	Doxycycline (1%)	Ciprofloxacin (1%)	Piperacillin (1%)
	OPD (n=89)	Cefixime (19%)	Ciprofloxacin (19%)	Cefuroxime+ clavulanic acid (18%)	Ceftriaxone (9%)	Levofloxacin (9%)	Cefuroxime (7%)	Ceftazidime (4%)	Doxycycline (3%)	Meropenem (3%)	Moxifloxacin (3%)
Wound swab (n=242)	**Ward (n=233)**	Cefuroxime (27%)	Ceftriaxone (21%)	Cefixime (19%)	Levofloxacin (14%)	Cefuroxime+ clavulanic acid (7%)	Meropenem (3%)	Ciprofloxacin (2%)	Amikacin (1%)	Amoxicillin + Clavulanic acid (1%)	Clindamycin (1%)
	OPD (n=9)	Ceftriaxone (22%)	Cefuroxime (22%)	Cefixime (11%)	Cefuroxime+ clavulanic acid (11%)	Ciprofloxacin (11%)	Levofloxacin (11%)	Metronidazole (11%)	-	-	-

Uttara Adhunik Medical College and Hospital (UAMCH)

Sample size and Culture test

Out of 1,611 samples, a total of 352 (22%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male - 44.3%, Female - 55.7%
- Highest growth was observed in 51-60 age group

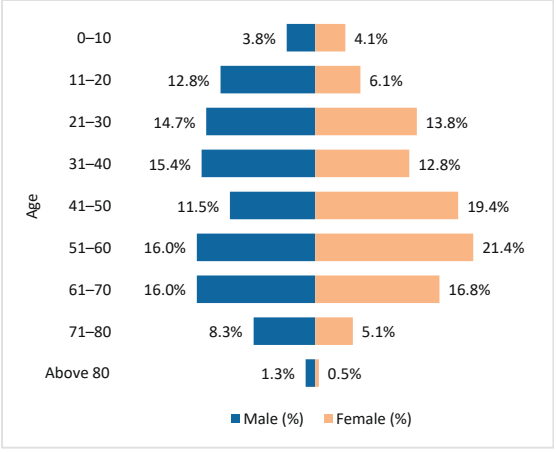


Figure 74: Distribution of isolates by sex and age group at UAMCH, 2025

Sample Collection Locations

Table 82: Distribution of isolates by location at UAMCH, 2025

Location	Number of isolates	(%)
OPD	120	34.1
IPD	215	61.1
ICU	17	4.8

Specimen Types

Table 83: Distribution of specimen types at UAMCH, 2025

Specimen type	Number of isolates	(%)
Urine	153	43.5
Blood	114	32.4
Wound	76	21.6
Endotracheal aspirate	9	2.5

Organism statistics
Organism frequencies

Table 84: Distribution of isolates by organism type at UAMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	32	9.1
Aerobic Gram -negative bacteria	320	90.9

Table 85: Distribution of the five most common organisms at UAMCH, 2025

Organism	Number of isolates	(%)
E. coli	144	40.9
Salmonella spp.	81	23.0
K. pneumoniae	58	16.5
S. aureus	26	7.4
P. aeruginosa	18	5.1

Most Common Organisms

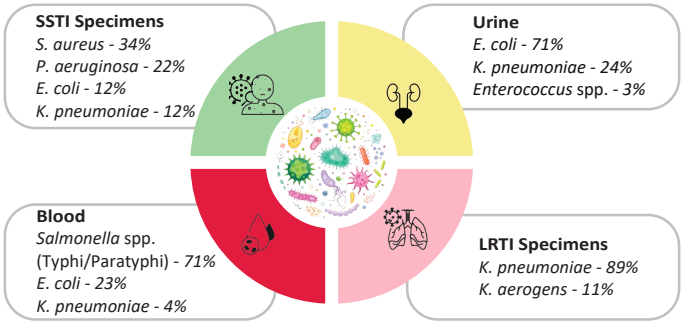


Figure 75: Most common organisms by specimen category at UAMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 86: Frequency of multidrug-resistant (MDR) pathogens at UAMCH, 2025

Organism	MDR (%)
S. aureus (N=26)	35
E. coli (N=144)	90
K. pneumoniae (N=58)	100
P. aeruginosa (N=18)	22

WHO Critical Priority Pathogens

Table 87: Frequency of WHO critical priority pathogens at UAMCH, 2025

Critical Priority Organism	Number (%)
Carbapenem resistance *P.aeruginosa* (N=18)	22%
Ceftriaxone resistant *E.coli* (N=144)	56%
Meropenem resistant *E.coli* (N=144)	6%

Antibiogram

Table 88: Antibiogram at UAMCH, 2025

Color coding	Color	Green	Yellow	Red
	% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamycin	Linezolid	Penicillin	Trimethoprim/ Sulfamethoxazole
S. aureus	27	77	46	65	88	100	88	12	69

Gram-negative

Organism	Amikacin	Ampicillin	Azithromycin	Aztreonam	Cefepime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine only)	Gentamicin	Imipenem	Meropenem	Nitrofurantoin (Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Levofloxacin	Cefazolin (Urine only)
E. coli	50	15	-	45	44	40	44	11	32	97	55	94	94	85	67	62	49	-	41
S. Typhi	-	92	84	-	-	-	96	-	4	-	-	100	100	-	-	-	88	92	-
K. pneumoniae	58	-	-	61	61	59	61	26	47	-	58	90	88	35	42	68	65	-	60

Antibiotic Use

A total of 1,536 antibiotic administrations were recorded among the patients

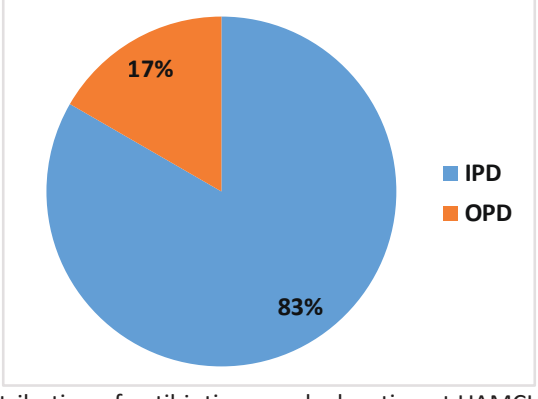


Figure 76: Distribution of antibiotic usage by location at UAMCH, 2025 (n=1,536)

Table 89: Antibiotic usage by case type and location at UAMCH, 2025 (n=1,536)

Ten most commonly prescribed antibiotics in different locations (n=1,536)										
ICU (n=432)	Ceftriaxone (25%)	Meropenem (21%)	Moxifloxacin (20%)	Ciprofloxacin (9%)	Metronidazole (5%)	Flucloxacillin (4%)	Cefuroxime+ clavulanic acid (3%)	Clindamycin (2%)	Doxycycline (2%)	Imipenem (2%)
Ward (n=851)	Ceftriaxone (36%)	Cefixime (9%)	Ciprofloxacin (8%)	Meropenem (7%)	Metronidazole (6%)	Doxycycline (6%)	Moxifloxacin (6%)	Azithromycin (4%)	Cefuroxime+ clavulanic acid (3%)	Cefuroxime+ clavulanic acid (3%)
OPD (n=253)	Cefixime (38%)	Cefuroxime+ clavulanic acid (13%)	Levofloxacin (9%)	Ciprofloxacin (8%)	Ceftriaxone (7%)	Moxifloxacin (6%)	Doxycycline (4%)	Cefuroxime (4%)	Azithromycin (3%)	Amikacin (2%)

Table 89.1: Antibiotics used according to cases (n=1536)

Ten most commonly used antibiotics in different locations (n=1,536)											
Blood (n=675)	**ICU (n=362)**	Ceftriaxone (25%)	Meropenem (22%)	Moxifloxacin (21%)	Ciprofloxacin (8%)	Metronidazole (6%)	Flucloxacillin (4%)	Cefuroxime+ clavulanic acid (3%)	Doxycycline (2%)	Clindamycin (2%)	Imipenem (2%)
	Ward (n=313)	Ceftriaxone (46%)	Cefixime (8%)	Meropenem (7%)	Ciprofloxacin (7%)	Doxycycline (7%)	Moxifloxacin (5%)	Metronidazole (4%)	Cefuroxime+ clavulanic acid (4%)	Levofloxacin (4%)	Azithromycin (4%)
Endotracheal aspirate (n=121)	**ICU (n=121)**	Ceftriaxone (26%)	MoxifloxacinHydrochloride (24%)	Meropenem (11%)	Ciprofloxacin (9%)	Doxycycline (6%)	Cefixime (4%)	Flucloxacillin (4%)	Levofloxacin (3%)	Metronidazole (3%)	Cefuroxime+ clavulanic acid (2%)
Diarrhea (n=138)	**ICU (n=5)**	Ceftriaxone (60%)	Doxycycline (20%)	Metronidazole (20%)	-	-	-	-	-	-	-
	Ward (n=126)	Ceftriaxone (36%)	Ciprofloxacin (23%)	Azithromycin (15%)	Metronidazole (13%)	Meropenem (3%)	Doxycycline (2%)	Cefixime (2%)	Ceftazidime (2%)	Moxifloxacin (2%)	Amikacin (1%)
	OPD (n=7)	Ciprofloxacin (29%)	Ciprofloxacin (29%)	Azithromycin (14%)	Ceftriaxone (14%)	Doxycycline (14%)	-	-	-	-	-
Urine (n=238)	**ICU (n=9)**	Ceftriaxone (33%)	Meropenem (33%)	Metronidazole (11%)	Moxifloxacin (11%)	Ciprofloxacin (11%)	-	-	-	-	-
	Ward (n=99)	Ceftriaxone (52%)	Meropenem (11%)	Moxifloxacin Hydrochloride (9%)	Doxycycline (7%)	Cefixime (4%)	Cefuroxime+ clavulanic acid (3%)	Metronidazole (3%)	Azithromycin (2%)	Flucloxacillin (2%)	Levofloxacin (2%)
	OPD (n=130)	Cefixime (38%)	Cefuroxime+ clavulanic acid (16%)	Ceftriaxone (9%)	Moxifloxacin (9%)	Levofloxacin (6%)	Azithromycin (5%)	Ciprofloxacin (5%)	Doxycycline (3%)	Cefuroxime (2%)	Amikacin (2%)
Wound swab (n=364)	**ICU (n=4)**	Cefixime (50%)	Cefuroxime+ clavulanic acid (25%)	Ciprofloxacin (25%)	-	-	-	-	-	-	-
	Ward (n=244)	Ceftriaxone (20%)	Cefixime (18%)	Meropenem (8%)	Metronidazole (8%)	Amikacin (7%)	Levofloxacin (6%)	Doxycycline (5%)	Cefuroxime+ clavulanic acid (5%)	Flucloxacillin (5%)	Cefuroxime (4%)
	OPD (n=116)	Cefixime (41%)	Levofloxacin (14%)	Cefuroxime+ clavulanic acid (9%)	Ciprofloxacin (9%)	Cefuroxime (5%)	Ceftriaxone (4%)	Doxycycline (4%)	Amikacin (3%)	Flucloxacillin (3%)	Amoxicillin + Clavulanic acid (2%)

Cox's Bazar Medical College and Sadar Hospital (CoxMCH)

Sample size and Culture test

Out of 1,097 samples, a total of 176 (16%) samples yielded positive growth.

Patient Demographics and Sample Characteristics

- Sex: Male- 60%, Female- 40%
- Highest growth was observed in 21-30 age group

Sample Collection Locations

Table 90: Distribution of isolates by location at CoxMCH, 2025

Location	Number of isolates	(%)
OPD	68	38.6
IPD	95	54.0
ICU	13	7.4

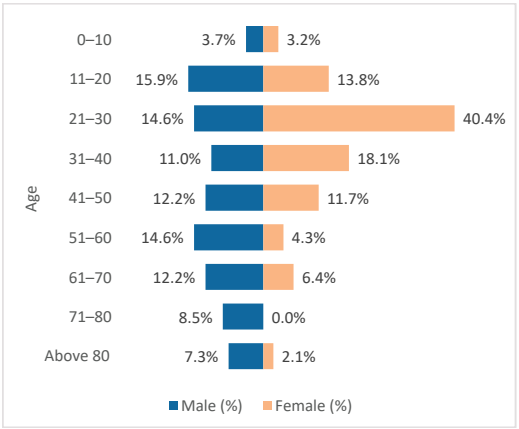


Figure 77: Distribution of isolates by sex and age group at CoxMCH, 2025

Specimen Types

Table 91: Distribution of specimen types at CoxMCH, 2025

Specimen type	Number of isolates	(%)
Urine	81	46.0
Wound swab	70	39.8
Blood	19	10.8
Stool	6	3.4

Organism statistics
Organism frequencies

Table 92: Distribution of isolates by organism type at CoxMCH, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	38	21.6
Aerobic Gram -negative bacteria	138	78.4

Table 93: Distribution of the five most common organisms at CoxMCH, 2025

Organism	Number of isolates	(%)
E. coli	52	29.5
P. aeruginosa	52	29.5
S. aureus	38	21.6
Enterobacter spp.	21	11.9
Proteus spp.	4	2.3

Most Common Organisms

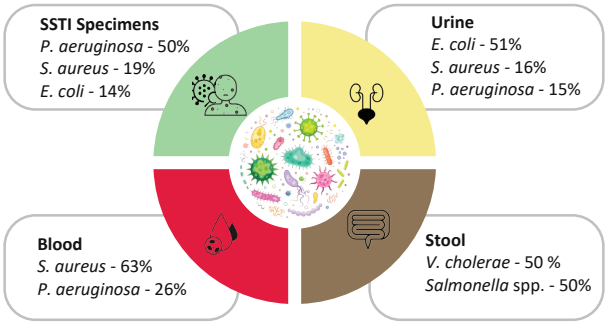


Figure 78: Most common organisms by specimen category at CoxMCH, 2025

Multidrug-Resistant (MDR) Pathogens

Table 94: Frequency of multidrug-resistant (MDR) pathogens at CoxMCH, 2025

Organism	MDR (%)
S. aureus (N=35)	51
E. coli (N=52)	73
K. pneumoniae (N=25)	92
P. aeruginosa (N=46)	52

WHO Critical Priority Pathogens

Table 95: Frequency of WHO critical priority pathogens at CoxMCH, 2025

Critical Priority Organism	%
Ceftriaxone resistant *E. coli* (N=52)	58%
Meropenem resistant *E. coli* (N=52)	6%

Antibiogram

Table 96: Antibiogram at CoxMCH, 2025

Color coding	Green	Yellow	Red
% (S)	>80%	60% - 80%	≤60%

Gram-positive

Organism	Azithromycin	Oxacillin	Ciprofloxacin	Clindamycin	Doxycycline	Gentamycin	Linezolid	Penicillin	Trimethoprim/ Sulfamethoxazole
S. aureus	12	51	57	77	77	83	94	8	74

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine Only)	Gentamycin	Imipenem	Meropenem	Netilmicin	Nitrofurantoin (Urine Only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Tobramycin
P. aeruginosa	-	-	46	69	41	-	-	76	-	-	67	65	65	-	72	-	-	70
E. coli	94	14	60	69	44	42	31	76	97	92	94	94	-	49	92	70	67	-

Antibiotic Use

A total of 479 antibiotic administrations were recorded among patients

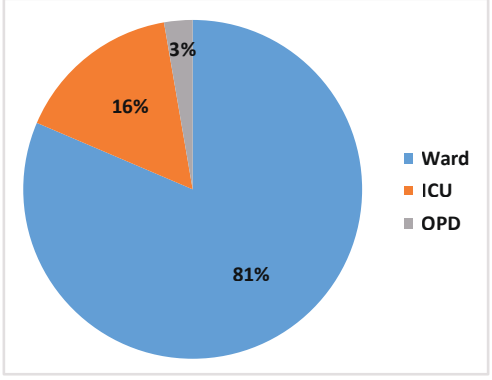


Figure 79: Distribution of antibiotic usage by location at CoxMCH, 2025 (n=479)

Table 97: Antibiotic usage by case type and location at CoxMCH, 2025 (n=479)

Most commonly used antibiotics in different locations (n=479)								
ICU (n=76)	Meropenem (36%)	Ceftriaxone (26%)	Azithromycin (20%)	Ciprofloxacin (11%)	Levofloxacin (5%)	Vancomycin (3%)		
Ward (n=390)	Ceftriaxone (48%)	Ciprofloxacin (28%)	Meropenem (13%)	Azithromycin (9%)	Cefuroxime (1%)	Levofloxacin (1%)	Clindamycin (1%)	Vancomycin (1%)
OPD (n=13)	Ceftriaxone (46%)	Ciprofloxacin (38%)	Azithromycin (8%)	Cefixime (8%)				

Table 97.1: Antibiotics used according to cases (n=479)

Most commonly used antibiotics in different locations (n=479)							
Blood (n=132)	**ICU (n=24)**	Meropenem (58%)	Ceftriaxone (29%)	Levofloxacin (8%)	Vancomycin (4%)	-	-
	Ward (n=108)	Ceftriaxone (71%)	Meropenem (21%)	Cefuroxime (4%)	Levofloxacin (2%)	Clindamycin (1%)	Vancomycin (1%)
Diarrhea (n=180)	**ICU (n=28)**	Azithromycin (54%)	Ciprofloxacin (29%)	Ceftriaxone (18%)	-	-	-
	Ward (n=152)	Ciprofloxacin (70%)	Azithromycin (22%)	Ceftriaxone (8%)	-	-	-
Urine (n=68)	**ICU (n=24)**	Meropenem (54%)	Ceftriaxone (33%)	Levofloxacin (8%)	Vancomycin (4%)	-	-
	Ward (n=31)	Ceftriaxone (58%)	Meropenem (35%)	Levofloxacin (3%)	Vancomycin (3%)	-	-
	OPD (n=13)	Ceftriaxone (46%)	Ciprofloxacin (38%)	Azithromycin (8%)	Cefixime (8%)	-	-
Wound swab (n=99)	**Ward (n=99)**	Ceftriaxone (82%)	Meropenem (15%)	Ciprofloxacin (2%)	Clindamycin (1%)	-	-

Bangladesh Institute of Tropical and Infectious Diseases (BITID)

Sample size and Culture test:

Out of 853 samples, a total of 144 (17%) samples yielded positive growth

Patient Demographics and Sample Characteristics

- Sex: Male- 25.7%, Female- 74.3%
- Highest growth was observed in 21-30 age group

Sample Collection Locations

Table 98: Distribution of isolates by location at BITID, 2025

Location	Number of isolates	(%)
OPD	107	74.3
IPD	37	25.7

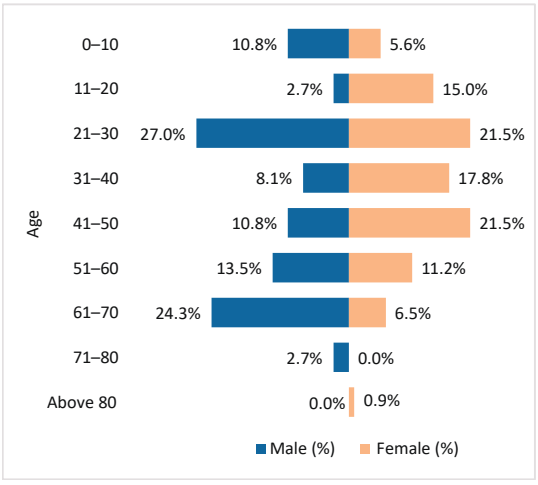


Figure 80: Distribution of isolates by sex and age group at BITID, 2025

Specimen Types

Table 99: Distribution of specimen types at BITID, 2025

Specimen type	Number of isolates	(%)
Blood	5	3.5
Stool	25	17.4
Urine	114	79.2

Organism statistics
Organism frequencies

Table 100: Distribution of isolates by organism type at BITID, 2025

Organism type	Number of isolates	(%)
Aerobic Gram -positive bacteria	12	8.3
Aerobic Gram -negative bacteria	132	91.7

Table 101: Distribution of the five most common organisms at BITID, 2025

Organism	Number of isolates	(%)
E. coli	87	60.4
V. cholerae	24	16.7
K. pneumoniae	13	9
Coagulase Negative Staphylococcus spp.	9	6.3
Salmonella spp.	5	3.5

Most Common Organisms

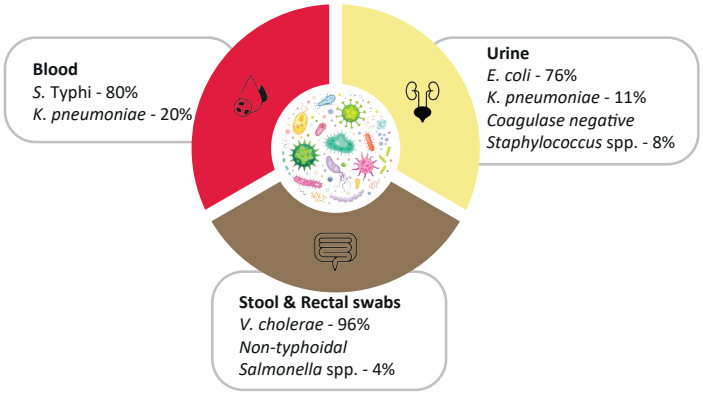


Figure 81: Most common organisms by specimen category at BITID, 2025

Multidrug-Resistant (MDR) Pathogens

Table 102: Frequency of multidrug-resistant (MDR) pathogens at BITID, 2025

Organism	MDR (%)
S. aureus (N=3)	100
E. coli (N=87)	95
K. pneumoniae (N=13)	46
P. aeruginosa (N=2)	50

WHO Critical Priority Pathogens

Table 103: Frequency of WHO critical priority pathogens at BITID, 2025

Critical Priority Organism	%
Carbapenem resistance *P. aeruginosa* (N=2)	50%
Ceftriaxone resistant *E. coli* (N=85)	72%
Meropenem resistant *E. coli* (N=85)	11%

Antibiogram

Table 104: Antibiogram at BITID, 2025

Color coding	Color	Green	Yellow	Red
	% (S)	>80%	60% -80%	≤60%

Gram-negative

Organism	Amikacin	Ampicillin	Aztreonam	Cefepime	Ceftazidime	Ceftriaxone	Cefuroxime	Ciprofloxacin	Fosfomycin (Urine only)	Gentamycin	Imipenem	Meropenem	Nitrofurantoin (Urine only)	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole	Cefazolin (Urine only)
E. coli	36	6	39	36	22	28	4	16	98	52	92	89	59	49	64	51	8
V. cholerae	-	4	-	-	-	-	-	62	-	-	-	-	-	-	100	4	-

Antibiotic Use

A total of 82 antibiotic administrations were recorded among patients

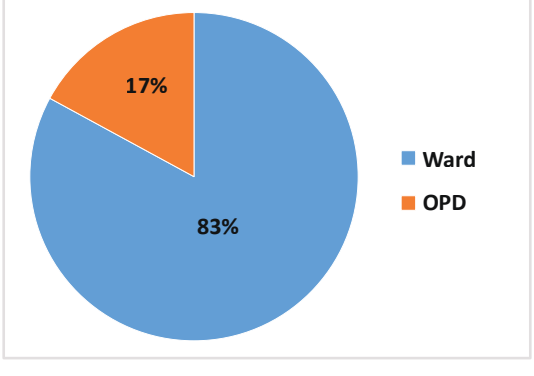


Figure 82: Distribution of antibiotic usage by location at BITID, 2025 (n=82)

Table 105: Antibiotic usage by case type and location at BITID, 2025 (n=82)

Most commonly used antibiotics in different locations (n=82)							
Ward (n=68)	Azithromycin (38%)	Ceftriaxone (26%)	Metronidazole (13%)	Ciprofloxacin (12%)	Cefixime (9%)	Cefuroxime (1%)	-
OPD (n=14)	Azithromycin (64%)	Ciprofloxacin (29%)	Cefuroxime+ clavulanic acid (7%)	-	-	-	-

Table 105.1: Antibiotics used according to cases (n=82)

Most commonly used antibiotics in different locations (n=82)							
Blood (n=25)	**Ward (n=20)**	Azithromycin (40%)	Ceftriaxone (35%)	Cefixime (15%)	Ciprofloxacin (10%)	-	-
	OPD (n=5)	Azithromycin (80%)	Cefuroxime+ clavulanic acid (20%)	-	-	-	-
Diarrhea (n=16)	**Ward (n=15)**	Metronidazole (60%)	Ceftriaxone (20%)	Ciprofloxacin (20%)	-	-	-
	OPD (n=1)	Ciprofloxacin (100%)	-	-	-	-	-
Urine (n=41)	**Ward (n=33)**	Azithromycin (55%)	Ceftriaxone (24%)	Cefixime (9%)	Ciprofloxacin (9%)	Cefuroxime (3%)	-
	OPD (n=8)	Azithromycin (63%)	Ciprofloxacin (38%)	-	-	-	-

Summary of results from the sentinel sites

Table 106: Summary of results from the sentinel sites

Site	Top organisms (major %)	MDR / critical highlights	ICU share of isolates	Top ICU antibiotic (by use)
DMCH	*Acinetobacter* spp.; *P. aeruginosa*; *K. pneumoniae*; *E. coli*	Very high carbapenem resistance in *Acinetobacter* spp. (96%); *E. coli* ceftriaxone resistance 97%; *E. coli* MDR 100%.	72% of isolates from ICU.	Meropenem (31% ICU use).
MMCH	*K. pneumoniae; Acinetobacter* spp.; *E. coli*; *P. aeruginosa*	*K. pneumoniae* MDR 96%; carbapenem-resistant *Acinetobacter* spp. 93%; ceftriaxone-resistant *E. coli* 80%.	44.8% ICU isolates.	Meropenem (36% ICU use).
RMCH	*E. coli*; *P. aeruginosa*; *K. pneumoniae*; *S. aureus; Acinetobacter* spp	*E. coli* MDR 95%; carbapenem-resistant *Acinetobacter* spp. 89%; meropenem-resistant *E. coli* 33%.	38.5% of ICU isolates.	Ceftriaxone (51% ICU use) then meropenem.
RpMCH	*E. coli*; *P. aeruginosa*; *K. pneumoniae*; *Enterococcus* spp.; *S. aureus*	*E. coli* MDR 97%; *K. pneumoniae* MDR 91%; carbapenem-resistant *Acinetobacter* spp. 95%.	54.5% IPD; ICU share not dominant but significant.	Meropenem (46% ICU use).
CMCH	*Acinetobacter* spp.; *P. aeruginosa*; *K. pneumoniae*; *E. coli*	Very large *Acinetobacter* spp. burden (41.9%); carbapenem resistance in *Acinetobacter* spp. 76%; *K. pneumoniae* MDR 92%.	58.6% isolates from ICU.	Meropenem (28% ICU use) then amikacin.
SBMCH, SOMCH, KMCH, UAMCH, CoxMCH, BITID	Mixed patterns: some sites with Gram positive predominance (SOMCH, KMCH wound/SSTI) and others dominated by Gram negatives	Many sites show >80% MDR in *E. coli* and high carbapenem resistance in *Acinetobacter* spp. across sites; site-specific MDR rates vary 62–100%.	ICU proportions vary widely; several tertiary sites show ICU >40% of isolates.	Meropenem and Ceftriaxone dominate ICU/ward prescribing across sites.

Organism Variation, Origin

- **Predominant Organisms:** Gram-negative bacteria dominate the landscape across all sites. *E. coli, K. pneumoniae, Acinetobacter* spp. and *P. aeruginosa* are the most frequent isolates.
- **Site-Specific Variations:**

  o DMCH and CMCH: Strikingly high prevalence of *Acinetobacter* spp. (25.5% and 41.9% respectively), heavily correlating with their high proportion of ICU samples.

  o MMCH, SBMCH and UAMCH: Higher rates of *K. pneumoniae* and *E. coli*.

  o SOMCH and KMCH: A notably higher prevalence of *S. aureus* (36.4% and 23.3%) compared to other sites.

  o BITID: BITID, an infectious disease hospital without ICU facilities, had a high proportion of OPD samples (74.3%). The predominant organisms included *V. cholerae* (16.7%) and *Salmonella* spp., along with *E. coli*. The majority of specimens were stool and urine.

- **Relation to Sample Origin:**

  o Endotracheal aspirates are heavily represented by *Acinetobacter* spp. and *P. aeruginosa*. These specimen organism links are consistent across sites and explain why ICU respiratory samples drive carbapenem resistance statistics.

  o Urine isolates are predominantly *E. coli*

  o IPD (Indoor) and OPD (Outdoor) samples are more frequently associated with *E. coli* (especially from urine) and *S. aureus* (wound swabs).

Resistance Patterns, MDR, and Critical Priority Pathogens

- **MDR (Multidrug Resistance):** MDR rates are alarmingly high across the sites. For *E. coli* and *K. pneumoniae*, MDR rates frequently ranged from 90% to 100% at almost all sites (e.g., DMCH, SBMCH, SOMCH, UAMCH).
- **WHO Critical Priority Pathogens:**
  - o Carbapenem-resistant *Acinetobacter* spp. is critically high, particularly in ICUs: DMCH (96%), RpMCH (95%), MMCH (93%) and RMCH (89%).
  - o Carbapenem-resistant *P. aeruginosa* is also highly prevalent, ranging from 32% (KMCH) to 80% (MMCH).
  - o Ceftriaxone-resistant *E. coli* is ubiquitous, generally exceeding 70-80% at all sites, peaking at 97% in DMCH.

Antibiotic Usage and Resistance Patterns

- **Ward/IPD and OPD Usage:** Ceftriaxone is consistently the top prescribed antibiotic in Wards across nearly all hospitals (e.g., MMCH 64%, RMCH 36%, SBMCH 36%).
- Widespread third generation cephalosporin resistance in Enterobacterales; ceftriaxone resistance in *E. coli* is very high at many sites (e.g., DMCH 97%, MMCH 80%, RpMCH 80%), indicating extended spectrum beta lactamase (ESBL) prevalence and limiting empirical use of ceftriaxone for severe infections.
- High ICU burden correlates with high resistance; Sites with a large proportion of isolates from ICU (DMCH 72%, CMCH 58.6%, MMCH 44.8%) show the highest rates of carbapenem resistance and MDR among *Acinetobacter* spp., *P. aeruginosa, K. pneumoniae* and *E. coli*. This suggests selection pressure from heavy broad spectrum antibiotic use and frequent invasive procedures in ICU settings.
- Meropenem use is high in ICUs and often mirrors resistance. Meropenem is the most used ICU antibiotic at many sites (DMCH 31%, MMCH 36%, RpMCH, CMCH). High meropenem use coexists with substantial meropenem resistance in *E. coli* and *P. aeruginosa* at several sites, suggesting both empirical overuse and therapeutic escalation in response to resistance.
- Use of amikacin/amikacin containing regimens at some ICUs where aminoglycosin susceptibilities remain relatively higher for certain organisms, suggesting targeted combination therapy in some centers.

Concordance (or mismatch) between antibiotic use and resistance

- High ceftriaxone use despite high ceftriaxone resistance. Many wards and ICUs list ceftriaxone among top antibiotics while ceftriaxone resistant *E. coli* and *K. pneumoniae* are common. Ceftriaxone-resistant *E. coli* and *K. pneumoniae* are endemic (often >80-90% resistant). This indicates empirical prescribing that is unlikely to cover prevalent pathogens and may drive further resistance.
- Heavy meropenem use where carbapenem resistance is already high. At DMCH and CMCH, meropenem is heavily used in the ICU, while carbapenem resistance in *Acinetobacter* spp. and *P. aeruginosa* is high, reducing meropenem effectiveness.

XDR / PDR risk and stewardship implications

- XDR risk is high in ICU pathogens. Very high carbapenem resistance in *Acinetobacter* spp. and substantial resistance in *P. aeruginosa.* Enterobacterales indicate a real risk of extensively drug resistant (XDR) isolates emerging, especially in ICUs with heavy carbapenem use. Surveillance data show MDR rates for *E. coli* and *K. pneumoniae* often ≥90% at multiple sites, which is an early warning for XDR emergence.
- PDR not explicitly reported but plausible locally. The combination of high MDR and high carbapenem resistance, together with frequent use of last line agents, raises the possibility of isolates with very limited therapeutic options at some centers. Active monitoring for colistin and novel agent susceptibility is needed.

Final inference

Across the surveillance sites there is a consistent pattern. ICUs concentrate the most resistant pathogens (notably *Acinetobacter* spp. and *P. aeruginosa*). Massive presence of Carbapenem-resistant *Acinetobacter* spp. at ICU suggests severe issues with hospital-acquired infections (HAIs) and environmental contamination. Empirical antibiotic use (ceftriaxone and meropenem) often does not align with local susceptibility. Very high third generation cephalosporin resistance is observed in Enterobacterales. The standard reliance on ceftriaxone for general admissions and meropenem for ICU patients is likely resulting in high clinical failure rates, driving further resistance. Immediate stewardship interventions focused on ICU prescribing, diagnostic stewardship and infection prevention will likely yield the fastest reduction in selection pressure and transmission.

Overall Analysis

Overall analysis of the National AMR Surveillance results

1. Background and Scope

This report synthesizes the updated national antibiogram, integrating case-based and laboratory-based surveillance across OPD, ward, and ICU settings, and across major clinical specimens (urine, blood, LRTI, SSTI, stool, genital, and fungal isolates). Susceptibility interpretations follow CLSI M100 (35th Edition) standards.

The objective is to translate susceptibility patterns into microbiological insight, clinical relevance, and AMR containment priorities.

2. Overall Resistance Landscape

2.1 Dominant Microbiological Patterns

Two resistance ecosystems dominate the national picture:

- Community-driven ESBLs, such as Enterobacterales, particularly *E. coli* and *K. pneumoniae*, reflected by:
  - o Low susceptibility to third generation cephalosporins (*E. coli* isolates from shows 34% susceptibility to ceftriaxone)
  - o Poor fluoroquinolone activity (43% susceptibility to ceftriaxone in *E. coli* isolates from OPD)
- Hospital-driven carbapenem-resistant non-fermenters, especially *Acinetobacter* spp. and Pseudomonas aeruginosa, concentrated in ICU and LRTI specimens.

Carbapenems remain broadly active in national averages but mask severe ICU-level failure, particularly for *K. pneumoniae* and *Acinetobacter* spp.

3. Location Specific Analysis

3.1 Intensive Care Units (ICU)

ICU antibiograms reveal the highest AMR pressure:

- ***K. pneumoniae:*** imipenem 18%, meropenem 16%
- ***Acinetobacter* spp.:** imipenem 8%, meropenem 8%
- ***P. aeruginosa:*** poor susceptibility to aminoglycoside (6% susceptibility to tobramycin); higher susceptibility to colistin 100%

Interpretation:

ICUs are functioning as reservoirs for CRKP and CRAB, with therapeutic reliance shifting toward last line agents. Carbapenem escalation alone is no longer a dependable strategy.

3.2 Inpatient Wards (IPD)

- Enterobacterales show moderate susceptibility to carbapenems *K. pneumoniae* (40% susceptible to imipenem, 39% susceptibility to meropenem)
- Third-generation cephalosporins remain unreliable
- *S. aureus* shows oxacillin susceptibility 45–50%, indicating a substantial MRSA burden

Interpretation:

Ward-level resistance bridges community and ICU patterns, emphasizing the need for early risk stratification before ICU transfer.

3.3 Outpatient Departments (OPD)

- *E. coli* retains carbapenem susceptibility >80%
- Fluoroquinolones and oral cephalosporins remain weak
- Aminoglycosides show moderate activity

Interpretation:

OPD data reflect community ESBL pressure but still offer stewardship opportunities through appropriate oral agent selection, especially for UTIs.

4. Specimen Specific Analysis

4.1 Urine

- *E. coli:*
  - o Fosfomycin 93%
  - o Nitrofurantoin 78%
  - o Ceftriaxone 44%, ciprofloxacin 42%
- *K. pneumoniae:*
  - o Nitrofurantoin 45%

Clinical implication:

Uncomplicated cystitis due to *E. coli* remains treatable with urinary-specific agents, but UTIs by *K. pneumoniae* lack reliable oral options.

4.2 Bloodstream Infections

- *E. coli:* amikacin 80%, carbapenems 77-78%
- *K. pneumoniae:* carbapenems 31-32%
- *Acinetobacter* spp.: carbapenems <30%

Clinical implication:

Bloodstream *Klebsiella* behaves as a high-risk MDR pathogen, demanding early recognition and escalation pathways distinct from urinary isolates.

4.3 Lower Respiratory Tract Infections (LRTI)

- Dominated by *K. pneumoniae, P. aeruginosa*, and *Acinetobacter* spp.
- ICU LRTI isolates show single - digit susceptibility to most β-lactams

Clinical implication:

Ventilator-associated and hospital-acquired pneumonia represent the epicenter of AMR containment needs.

4.4 Skin and Soft Tissue Infections (SSTI)

- Mixed Gram-positive and Gram-negative ecology
- MRSA prevalence significant
- Gram-negative coverage increasingly relevant in hospital-origin SSTI

4.5 Enteric Pathogens (Stool)

- *V. cholerae:*
  - o Azithromycin 84%
  - o Tetracycline 90%
  - o Ampicillin and SXT 12%

Public health implications:

Current cholera treatment options remain effective, but legacy agents should be avoided.

4.6 Genital Specimens

- *Neisseria gonorrhoeae:*
  - o Ceftriaxone 88%
  - o Cefixime 60%
  - o Azithromycin 21%

Interpretation:

Ceftriaxone remains the cornerstone; azithromycin resistance undermines dual therapy assumptions.

4.7 Fungal Bloodstream Infections

- *C. albicans / C. tropicalis*:
  - o Fluconazole susceptibility 36-50%
  - o Micafungin 91-100%

Clinical implication:

Empirical fluconazole is increasingly unreliable for candidemia; echinocandins are more dependable.

5. Overall Interpretation

5.1 Microbiological Perspective

- ESBL-like resistance is entrenched in community Enterobacterales
- Carbapenem resistance is concentrated but severe in ICU non-fermenters
- Colistin dependence signals late-stage resistance ecology

5.2 Clinical Perspective

- Empirical therapy must be syndrome and setting - specific
- National averages may be misleading for ICU and bloodstream infections because resistant bacteria are more common in these settings
- Oral treatment options are narrowing outside uncomplicated UTIs

5.3 Epidemiological Perspective

- Surveillance stratification by location meaningfully reveals hidden risk

5.4 AMR Containment Perspective

Three leverage points emerge clearly:

1. ICU focused containment: Using strict infection-prevention practices for medical devices, keeping infected patients together to avoid spread and rapid detection of Carbapenem-Resistant *K. pneumoniae* and Carbapenem-Resistant *A. baumannii*
2. UTI stewardship at scale: Preserve carbapenems by prioritizing fosfomycin /nitrofurantoin for *E. coli*
3. Sepsis pathway redesign: Early MDR risk screening, especially for suspected bacteremia by *K. pneumoniae*

The AMR data show that AMR in Bangladesh is no longer driven by isolated misuse or single pathogens, it is driven by care pathways. AMR containment must focus on ICUs, UTIs, and sepsis pathways because these three domains sit at the intersection of highest resistance pressure, highest antibiotic consumption, and highest clinical risk, and the report shows that interventions here will yield the largest and fastest system level impact.

Gender based analysis

More than half (60%) of the samples were from female patients, and the largest proportion of samples (16.9%) was collected from the 21 to 30 years age group (Figure 1D).

Samples came predominantly from females (75.7%).

Table 107. Summary table of gender patterns by specimen

Specimen	Male (%)	Female (%)	Key gender finding
All samples (overall)	40%	60%	Females contribute the majority of submitted samples.
Urine	24.3%	75.7%	Strong female predominance: urine data drive overall female bias.
Blood	55.6%	44.4%	Male predominance among bloodstream isolates.
LRTI	62.5%	37.5%	Marked male predominance in respiratory isolates.
SSTI	55.5%	44.5%	More isolates from males than females (male majority).
Stool	55.1%	44.9%	More male stool isolates: children skew noted elsewhere.
Genital	42%	58%	Female predominance overall, but *N. gonorrhoeae* more frequent in males (9% vs 2%).

Interpretation and implications

- Sampling bias toward females is driven largely by urine specimens. Because urine makes up 56% of all samples and is 76% female, the overall dataset shows a female majority; this can distort national pathogen prevalence if not adjusted for specimen type.
- Different clinical syndromes show opposite gender patterns. Respiratory and bloodstream infections are male skewed, while genitourinary isolates are female skewed. This suggests distinct epidemiologic drivers (e.g., care seeking patterns, exposure risks, or sampling practices) across syndromes.
- STI signal concentrated in males for gonorrhoea. Although genital isolates are more often from females overall, *N. gonorrhoeae* was detected predominantly in males (9% male vs 2% female), indicating men may be important sentinels for gonococcal AMR surveillance.

Justification for AMR Containment strategy to prioritize ICUs, UTIs, and Sepsis Pathways

1. Intensive Care Units: The primary amplifier of advanced resistance

ICUs emerge from the report as the core amplification zone for carbapenem resistant organisms, particularly *K. pneumoniae* and *Acinetobacter* spp. Carbapenem susceptibility in ICU isolates has fallen to critically low levels, while colistin remains the only consistently active agent for many non fermenters. This pattern reflects sustained selection pressure from broad spectrum antibiotics, high device utilization, and prolonged patient stays, creating ideal conditions for transmission and persistence of MDR organisms.

From a policy perspective, antibiotic stewardship alone cannot reverse ICU resistance once established. The greatest gains will come from strengthening infection prevention and control, ventilator and central line bundles, environmental decontamination, cohorting, and rapid detection of carbapenem resistant organisms. Targeting ICUs therefore interrupts resistance at its most potent source, preventing spillover into wards and the community.

2. Urinary Tract Infections: The largest and most preventable driver of antibiotic pressure

UTIs account for the largest volume of isolates and antibiotic exposure nationally, and most are community origin. Despite widespread ESBL/AmpC pressure, the report shows that *E. coli*, the dominant uropathogen, remains highly susceptible to fosfomycin and nitrofurantoin. This creates a rare and powerful stewardship opportunity: effective oral alternatives exist that can safely replace cephalosporins and carbapenems for uncomplicated infections.

Policy focus on UTI specific stewardship has disproportionate impact because it reduces unnecessary broad spectrum antibiotic use at scale, lowers selection pressure in the community reservoir, and ultimately decreases the influx of resistant organisms into hospitals. In contrast, failure to act here accelerates carbapenem dependence downstream, particularly in ICUs.

3. Sepsis and bloodstream pathways: Where resistance determines survival

The report highlights a critical divergence between urinary and bloodstream isolates, especially for Klebsiella pneumoniae. Bloodstream isolates show markedly lower carbapenem susceptibility than urinary isolates, indicating enrichment of MDR phenotypes in severe infections. National averages obscure this risk, creating false reassurance and increasing the likelihood of inappropriate empirical therapy.

Early MDR risk stratification in sepsis pathways, based on recent hospitalization, ICU exposure, prior antibiotics, and device use, allows clinicians to escalate therapy when necessary while avoiding blanket overuse of last line agents. This approach protects patient outcomes while preserving antibiotic effectiveness, making it a cornerstone of rational AMR containment policy.

These three priorities form a coherent containment strategy:

- ICU IPC strengthening reduces generation and transmission of untreatable organisms.
- UTI focused stewardship reduces upstream antibiotic pressure and community reservoirs.
- Sepsis pathway stratification ensures timely, appropriate therapy without accelerating resistance.

Together, they address AMR at its source (community use), amplifier (ICU transmission), and clinical decision point (empirical treatment of severe infection). The surveillance data clearly indicate that concentrating resources and policy action in these domains will yield the greatest national impact on AMR control.

Take away message

Key Messages from the 2024–25 AMR Surveillance and National Antibiogram

1. AMR in Bangladesh is stratified by care pathway. Resistance patterns differ markedly between OPD, ward, and ICU, with ICU and LRTI settings carrying the highest MDR burden.
2. Community ESBL like Enterobacterales are now established. Low susceptibility of *E. coli* and *K. pneumoniae* to third generation cephalosporins and fluoroquinolones reflects widespread ESBL/AmpC pressure beyond hospitals.
3. Carbapenems remain effective in national averages but fail critically in ICUs. ICU level susceptibility for *K. pneumoniae* and *Acinetobacter* spp. has dropped to alarming levels, masking risk when only aggregate data are used.
4. ICUs are the epicenter of carbapenem resistance. CRKP and CRAB dominate ICU and LRTI isolates, driving dependence on last line agents.
5. Colistin dependence signals late stage resistance ecology. Near universal colistin susceptibility in ICU non fermenters reflects shrinking therapeutic options and urgent containment needs.
6. Uncomplicated E. coli UTI still has reliable oral options. Fosfomycin and nitrofurantoin remain effective and represent major stewardship opportunities to spare carbapenems.
7. *K. pneumoniae* behaves differently by syndrome. Urinary isolates retain moderate susceptibility, while bloodstream and ICU isolates show high MDR phenotypes.
8. Fluoroquinolones are no longer reliable for enteric fever. Very low ciprofloxacin susceptibility in *S.* Typhi confirms the end of fluoroquinolone based typhoid therapy.
9. MRSA is structurally present across care settings. Oxacillin susceptibility around 50% necessitates explicit MRSA risk assessment, while vancomycin and linezolid remain dependable.
10. Greatest containment gains will come from ICUs, UTIs, and sepsis pathways. Targeted IPC in ICUs, UTI focused stewardship, and early MDR risk stratification in bloodstream infections offer the highest impact.

Conclusion and recommendation

Conclusion:

The 2025 surveillance cycle reaffirms and amplifies the 2024 report's core messages: AMR remains a growing national threat in Bangladesh, with worrying increases in resistance among Enterobacterales and persistent very high levels of carbapenem-resistant *Acinetobacter* in tertiary and ICU settings. Expansion of passive lab reporting has improved detection capacity but also highlights the urgent need for strengthened stewardship, IPC, laboratory standardization, and targeted national interventions to contain transmission, optimize antibiotic use, and preserve the utility of last-line agents. Immediate, coordinated action across clinical, laboratory, and public health domains is essential to reverse the upward trajectory of critical AMR phenotypes.

Priority recommendations :

1. **Implement Strict Antimicrobial Stewardship Programs (ASP):** Strengthen antimicrobial stewardship across hospital levels: Implement or scale up stewardship teams, formulary restrictions for Reserve agents, targeted audit-and-feedback, and point-of-prescribing decision support aligned with updated antibiograms. There needs to be a hard restriction on the use of Meropenem and Ceftriaxone. Prescriptions for these drugs should require justification or a culture report.
2. **Revise Empirical Guidelines:** Update empirical treatment guidelines using sentinel and lab-based antibiogram data, with ICU-specific recommendations reflecting high resistance levels. Promote narrow-spectrum, Access-group agents where susceptibility supports them. Ceftriaxone should be removed as a first-line empirical treatment for indoor/ward patients given the near-universal resistance. Local antibiograms must dictate initial therapy.
3. Expand and standardize infection prevention and control (IPC) interventions, with priority support for ICUs and high-prevalence tertiary centers to reduce transmission of CRE and carbapenem-resistant *Acinetobacter* spp. Aggressive IPC measures must be instituted in ICUs to curb the spread of MDR *Acinetobacter* spp. and *P. aeruginosa*.
4. **Mandatory Culture Sensitivity:** Emphasize sending samples for culture before initiating antibiotic therapy, especially in ICUs.
5. **Enhance laboratory capacity and data quality:** Continue expansion of passive lab reporting, standardize susceptibility testing (including carbapenemase detection), and increase routine ESBL and CRE confirmation to refine burden estimates.
6. **Optimize antibiotic use surveillance:** Integrate AWaRe monitoring with clinical data to identify high-impact stewardship targets and measure intervention outcomes.
7. Support targeted public health interventions for typhoidal *Salmonella* and community-preserved pathogens where susceptibility permits effective oral therapy, while monitoring trends in fluoroquinolone and cephalosporin resistance.
8. Prioritize sentinel-site and district-level training on IPC, AMS, and microbiology diagnostics to reduce site-level variability and disseminate best practices.
9. Strengthen One Health linkages and broader surveillance for antimicrobial use and resistance in animal, food and environmental sectors to support national AMR action planning

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Current Publications of AMR surveillance sites

microbiology research

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Article

Bacterial Profile and Antimicrobial Resistance Pattern from Different Clinical Specimens at Uttara Adhunik Medical College Hospital, Dhaka

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Abstract: Introduction: Antimicrobial resistance (AMR) is a critical global public health issue, leading to prolonged illness, increased morbidity and mortality, and rising healthcare costs. The effectiveness of antibiotics is diminishing due to the emergence of resistant bacterial strains. This study aimed to determine the bacterial profile and AMR patterns of clinical isolates at Uttara Adhunik Medical College Hospital (UAMCH), Dhaka. Methods: A retrospective study was conducted at UAMCH from January 2017 to December 2019. A total of 32,187 clinical specimens (urine, blood, stool, wound swabs/pus, and sputum) were processed, of which 4232 yielded positive cultures. Bacterial identification followed standard bacteriological methods, and antibiotic susceptibility was assessed using the Kirby–Bauer disc diffusion method per CLSI guidelines. Data analysis was conducted using WHONET and QAAPT. Results: The highest proportion of positive cultures was from urine (47.5%), followed by blood (35.0%) and wound swabs/pus (10.1%). The most common isolates were Escherichia coli (37.2%), Salmonella typhi (25.7%), and Klebsiella sp. (11.5%). Gram-negative bacteria showed high resistance to commonly used antibiotics such as amoxicillin/clavulanic acid, cefixime, and ceftriaxone, while the resistance rates were lower for gentamicin, amikacin, and meropenem. However, Acinetobactersp. exhibited alarming resistance to all tested antibiotics. Conclusions: This study highlights concerning resistance patterns among bacterial isolates, emphasizing the need for ongoing AMR surveillance to inform treatment strategies and improve patient care in Bangladesh.

Mapping antimicrobial susceptibility of community-acquired uropathogenic Escherichia coli across low, middle and high-income countries highlights significant differences: insights for empiric treatment

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Mapping antimicrobial susceptibility of community-acquired uropathogenic Escherichia coli across low, middle and high-income countries highlights significant differences: insights for empiric treatment

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ABSTRACT

Objectives: Rising antimicrobial resistance (AMR) in Escherichia coli urinary tract infections (UTI) poses a global challenge. Evidence-based treatment of cystitis requires local resistance data. The DASH to Protect Antibiotics (https://dashuti.com/), a multi-regional group, supports centers in generating and sharing focused antibiograms to guide stewardship in community UTIs. This multi-country study aimed to describe antimicrobial susceptibility patterns of community-acquired E. coli isolates in low, middle, and high-income countries (LMICs and HICs).

Methods: The study was conducted in 37 representative centers across 13 countries in Asia (Middle East and Indian Subcontinent), Africa, Europe, and North America. A rigorous comparative analysis of the antimicrobial susceptibility of E. coli isolated from cases of simple cystitis presenting in outpatient or emergency departments was carried out. The impact of gross domestic product, climate, and population density per km^2 on E. coli susceptibility profile was analyzed using the Kruskal-Wallis test and two-way analysis of variance.

Results: Antimicrobial susceptibility varied significantly between LMICs and HICs, with nitrofurantoin (89%) and fosfomycin (96%) emerging as empiric choices globally. Across most centers, susceptibility to other oral antimicrobials was low: co-trimoxazole <60%, amoxicillin-clavulanic acid <70%, first-generation cephalosporins <50%, fluoroquinolones <60%. Injectable antibiotics fared better: piperacillin-tazobactam >70%, amikacin and meropenem >80%. Higher susceptibilities were noted in countries with high gross domestic product ($P < 0.001$) and humidity ($P = 0.002$).

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Original Research Article

Bacteriological Profile of UTI and their Antimicrobial Resistance Pattern Among Adult Patients Attending at RMCH

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Abstract: Background : Urinary tract infection (UTI) is one of the most important causes of bacterial infections across the globe. Increasing antibiotic resistance among urinary pathogens to commonly prescribed drugs has become a therapeutic challenge. Gram negative bacilli pred ominating the infections. Periodic evaluation of antimicrobial activity of different antibiotics is essential as the pattern of antibiotic sensitivity may vary over periods. Objectives: The present study was designed to find out the bacteriological profile of urinary tract infection and their antibiotic resistance pattern among adult patients. Material and Methods: A cross - sectional study was done in the department of Microbiology, Rajshahi Medical College from July to December 2024. Midstream urine samples were collected from clinically suspected cases of UTI among adult patients from various indoor and outdoor department attending at Rajshahi Medical College hospital. Results: Out of 1710 cases, 243 (14.2%) were culture positive, where female were 139(57.2 %) and male were 104(42.8%). Most common isolates identified was Escherisia coli 140(57.6%), followed by Klebsiella spp.41(16.9%), Pseudomonas aeruginosa 20(8.2%) and Enterococci spp. 27(11.1%). Gram negative organisms showed highest resistance to cefixime, ceftriaxone, cefuroxime, azithromycin and amoxiclav and highest sensitivity to colistin, nitrofurantoin and imipenem. Gram positive bacteria were highly resistant against cefixime, Cotrimoxazole, ceftriaxone, cefuroxime, azithromycin, amoxiclav and ciprofl oxacin and highest sensitivity to vancomycin, linezolid, nitrofurantoin and imipenem. Conclusion: This study indicated that mainly gram -negative bacilli were found to be responsible for UTI and most frequent isolated bacteria was E - coli. and all isolates showed resistance to commonly used antimicrobial agents. As the drug -resistant pattern of the uropathogens varies according to the geographical area and time, the selection of appropriate drug for UTIs should be assured after sensitivity pattern analysis of th e urinary cultures .

Keywords: Urinary Tract Infection, Uropathogens, Gram -Negative Bacteria, Antimicrobial Resistance .

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Research Article

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Bacteriological Profile and Antibiotic Susceptibility Pattern of Clinical Isolates from A Tertiary Care Hospital in Dhaka, Bangladesh

Dr. Noshin Nawal [1], Dr. Mosammat Fahmida Begum [2], Dr. Mahfuza Nasrin [3], Dr. Farha Rahman [*,4], Dr. Rezina Karim [5], Dr. Md. Shah Alam [6], Dr. Mohammad Moniruzzaman Bhuiyan [7], Mohammad Julhas Sujan [8]

Abstract

Antimicrobial resistance (AMR) has emerged as one of the most significant public health challenges worldwide, posing a serious threat to the effective treatment of infectious diseases. This study aimed to identify bacterial isolates among various clinical samples and to determine their antimicrobial susceptibility profile. This observational study was carried out from January to December, 2022 in the Department of Microbiology at Uttara Adhunik Medical College Hospital (UAMCH). Clinical samples such as urine, sputum, blood and wound swabs were collected from different body site infections that occurred among patients who visited the hospital within the study period. These samples were sent to the microbiology laboratory for processing, identification and antimicrobial susceptibility testing (AST). Standard microbiological protocols were followed. Among 12,337 clinical samples only 1,679 (13.60%) yielded bacterial growth. Rate of bacterial growth was highest in wound swab (46.36%). Out of culture-positive cases, Escherichia coli was the most predominant one which accounted for 565 (37.16%) of all the bacterial isolates, followed by Salmonella Typhi 408 (24.30%) and Klebsiella species 208 (12.40%). In case of Escherichia coli increased level of susceptibility were observed in case of meropenem (99.75%), amikacin (90.78%), nitrofurantoin (85.79%), gentamicin (83.99%) and piperacillin/tazobactam (71.13%). Increased susceptibility of Klebsiella species were observed for meropenem (93.50%), amikacin (89.17%) and gentamicin (88.64%). All the 2nd, 3rd and 4th generation of cephalosporins showed reduce level of susceptibility towardsEscherichia coli and Klebsiella species. All the isolates of Salmonella Typhi and Paratyphi A were susceptible to ceftriaxone and meropenem and almost all the strains of Salmonella Typhi and Paratyphi A were resistant to ciprofloxacin. All the isolates of Gram positive organisms were susceptible towards linezolid and vancomycin. In conclusion, the study highlights the concerning trends in antimicrobial susceptibility among bacterial isolates, emphasizing the need for continuous surveillance, antibiogram, rational antibiotic use and the implementation of effective infection control measures to combat this growing public health threat.

Keywords: Antibiogram, Antimicrobial susceptibility pattern, Antimicrobial resistance

Introduction

Antimicrobial resistance (AMR) occurs when pathogenic microorganisms develop resistance to the drugs used to control these microorganisms, made treatments less effective or ineffective [1]. The global spread of antimicrobial

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Research Article

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Antibiogram and Antimicrobial Susceptibility Pattern of Bacterial Isolates from A Tertiary Care Hospital in Dhaka

Mahfuza Nasrin [1], Most. Fahmida Begum [2], Farha Rahman [*, 3], Rezina Karim [4], Mohammad Moniruzzaman Bhuiyan [5], Noshin Nawal [6], Md. Shah Alam [7], Mohammad Julhas Sujan [8]

Abstract

Antimicrobial resistance (AM R) has emerged as one of the most significant public health challenges worldwide, posing a serious threat to the effective treatment of infectious diseases. This study aimed to identify bacterial isolates among various clinical samples and to determine their antimicrobial susceptibility profile. This observational study was carried out from January to December, 2023 in the Department of Microbiology at a tertiary care hospital in Dhaka, Bangladesh. Clinical samples were collected from both outpatients and inpatients who visited the hospital within the study period. The specimens included urine, stool, sputum and blood samples, as well as swabs from wounds, ears and the vaginal area. These samples were sent to the microbiology laboratory for processing, identification and antimicrobial susceptibility testing (AST). Standard microbiological protocols were followed. Among 8554 clinical samples only 941 (11%) yielded bacterial growth. Out of culture-positive cases, Escherichia coli was the most predominant one which accounted for 397 (42.19%) of all the bacterial isolates, followed by Salmonella Typhi 174 (18.49%) and Klebsiella species 142 (15.10%). In case of Escherichia coli increased level of susceptibility were observed in case of meropenem 97%, nitrofurantoin 83%, amikacin 82%, gentamicin 80% and piperacillin-tazobactam 75% respectively. In case of Klebsiella species elevated level of sensitivity were seen in case of meropenem 85%, amikacin 78% and gentamicin 70% respectively. All the 2nd, 3rd and 4th generation of cephalosporins showed reduce level of sensitivity in case of Escherichia coli and Klebsiella species. All the isolates of Salmonella Typhi and Paratyphi were susceptible to ceftriaxone and meropenem. Almost all the strains of Salmonella Typhi and Paratyphi were resistant to ciprofloxacin. Gram-positive organisms observed increased level of sensitivity towards linezolid, vancomycin and nitrofurantoin. In conclusion, the study highlights the concerning trends in antimicrobial resistance among bacterial isolates, emphasizing the need for continuous surveillance, antibiogram, rational antibiotic use and the implementation of effective infection control measures to combat this growing public health threat.

Keywords: Antibiogram, Antimicrobial susceptibility pattern, antimicrobial resistance, Bacterial pathogens

Introduction

Antimicrobial resistance (AMR) has emerged as one of the most significant public health challenges worldwide, posing a serious threat to

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Original Article

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Determination of Rate of Catheter Associated Urinary Tract Infection in a Tertiary Care Hospital: An Emergence to Establish IPC Department

Ayesha Ahmed Khan[1] Abul Kalam[2] Md. Akram Hossain[3] Mahfuza Nasrin[4] Farhan Fuad Bin Hossen[5] Pompy Dey[6] Afreen Sultana[7] Milupa Nasrin[8] Shamima Akther[9] Imranul Mawa[10] Md. Shakeel Ahmed[11]*

ABSTRACT

Background: Hospital Acquired Infections (HAIs) are posing an imminent threat to patient safety as well as the general well-being of healthcare personnel on a worldwide scale. The World Health Organization (WHO) estimates that at any given time, around 1.4 million people suffer from infectious complications because of HAI. One of the most common healthcare associated infections is Catheter Associated Urinary Tract Infection (CAUTI). This current study was aimed to identify base line CAUTI rate and risk factors responsible for it.

Materials and methods: A longitudinal study was conducted from July 2022 to June 2023 in the Department of Microbiology, Chittagong Medical College. The current study brought attention to highlight the rate of CAUTI in the Chittagong Medical College Hospital. The data were analyzed by using SPSS version 27 and the results were summarized by using tables and graphs. The protocol was approved by the Committee of the research cell and ethical clearance was taken from the Ethical Review Committee (ERC) of Chittagong Medical College.

Results: 330 catheterized urine sample were collected for research purpose from clinically suspected CAUTI. 52.42% were confirmed CAUTI. Current study showed most of the CAUTI patients were female (69.09%) and from Obstetrics and Gynaecology ward (45.66%) with a CAUTI rate 8.12 per thousand catheter days. Whereas overall CAUTI rate was 7.39 per thousand catheter days. Current study shows type 2 diabetes mellitus was the most common comorbidities associated with CAUTI cases (39.88%).

Conclusions: The study's findings provide valuable insights into the rate and risk factors associated with CAUTIs.

Key words: Catheter Associated Urinary Tract Infection (CAUTI); Hospital Acquired Infection (HAIs). Infection Prevention and Control (IPC).

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Introduction

A HAI is defined by the WHO as "An infection that a patient acquires while undergoing treatment in a hospital or other healthcare facility, provided that the illness is not active or incubating at the time of admission". This includes illnesses contracted while a patient is being treated as well as illnesses picked up while a patient was receiving treatment but developing after discharge. These infections typically develop after being hospitalized and show up 48 hours after being admitted. WHO found HAI prevalence ranged from 5.7% to 19.1% in low-income and middle-income countries.[1]

Approximately 10% of infected people die as a consequence of HAIs affects, 7% of patients in industrialized and 10% in poor nations on average at any moment. To assess the burden of endemic HAIs,

Articles

Rethinking cholera diagnostic test performance, interpretation, and evaluation: afield-based latent-class analysis in Bangladesh

Javier Perez-Saez*, Tajur Rahman Bhuiyan*, Sonia T Hegde*, Ishtiakul Islam Khan, Md Taslim, Zahid Hasan Khan, Mohammad Ashraful Amin, Juan Dent Hulse, Shakeel Ahmed, Mamunur Rashid, Rumana Rashid, Md Zakir Hossain, Ashraful Islam Khan, Firdausi Qadri, Andrew S Azman†

Summary

Background Accurate and reliable diagnostics, including rapid diagnostic tests (RDTs), are crucial components of cholera control programmes, although their estimated performance has varied greatly across studies. The aim of this study was to assess cholera diagnostics performance accounting for possible sources of variability, including reference assay choice and patient-level and sampling characteristics, and the implications on result interpretation and test performance evaluation.

Methods We enrolled all individuals aged 1 year and older presenting with suspected cholera seeking care at two health-care facilities in Sitakunda, Bangladesh. All participants (or, if younger than 18 years, their legal guardians) provided written informed consent and were given a short structured questionnaire on patient history and demographics, alongside a rectal swab or stool sample. All stool samples were tested with the CholKit Rapid Diagnostic Test (CholKit RDT; Incepta, Dhaka, Bangladesh), and a subset of samples (all positive RDTs and a random subset of approximately half of negative RDTs) were tested by PCR and culture. Test performance was estimated using a latent-class Bayesian framework accounting for imperfect test performance, incomplete PCR and culture testing, and time-varying changes in cholera incidence. Patient-level factor effects (including age [age 1–4 years vs ≥5 years] and previous antibiotic use) and sampling factor effects (season and testing delays) were estimated, and simulations were used to assess the bias in RDT performance estimates for sensitivity and specificity with 95% credible intervals (CrIs) when using traditional reference assays.

Findings Between Jan 24, 2021, and Aug 31, 2022, we enrolled 3744 individuals with suspected cholera. Of the 3744 overall participants, 1918 (51·2%) were male and 1826 (48·8%) were female; 1095 (29·2%) were aged 1–4 years and 2649 (70·8%) were 5 years and older. Among the suspected cases of cholera, 692 (18·5%) participants tested positive by the CholKit RDT. Among the RDT-positive samples, 573 (82·8%) also tested positive by PCR, and 450 (65·0%) tested positive by culture. For RDT, PCR, and culture, we estimated a sensitivity of 93·5% (95% CrI 91·3–95·4), 90·3% (88·4–92·1), and 73·7% (70·8–76·5), respectively; and a specificity of 97·3% (96·7–97·8) and 97·2% (96·6–97·8) for RDT and PCR, respectively. Culture specificity was assumed perfect at 100%. We found that younger age (1–4 years), antibiotic use, and testing delays decreased culture sensitivity, but RDT performance remained relatively constant. The RDT positive predictive value ranged from <15% in children aged 1–4 years to >80% in participants 5 years and older, varying greatly across seasons. Simulations of field trials demonstrated underestimation of RDT sensitivity in low prevalence settings when evaluated against PCR, and underestimation of specificity in high prevalence settings regardless of the reference assay.

Interpretation Our results provide potential mechanisms leading to the heterogeneous cholera RDT performance esti-

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Dinkum Journal of Medical Innovations

Original Article

Detection of Causative Agents of Acute Upper Respiratory Tract Infection by Film Array Respiratory Panel at Point of Care in a Tertiary Care Hospital

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Abstract: Acute respiratory tract infections are the most prevalent illnesses in individuals of all age groups and are a significant contributor to hospitalization, morbidity, and mortality. In cases of severe infections, it is vital to quickly diagnose these infections for effective management. This study rapidly detected the causative organism of acute upper respiratory tract infection using the Film Array Respiratory Panel 2.1 plus (FARP). It was a cross-sectional study, where N=471 nasopharyngeal swab specimens were collected from suspected patients with acute upper respiratory tract infections attending the outpatient department (OPD) of the Bangladesh Institute of Tropical and Infectious Diseases (BITID). The specimens were tested with the FARP 2.1 plus, an automated multiplex PCR assay that detects 23 targets, including 19 viruses and 4 bacteria respectively.A total of 471 samples were tested by FARP 2.1 plus, and we found a notable 71% (333/471) were positive for either single (60%) or multiple (11%) pathogens. Influenza B virus (22.9%) was the most prevalent,followed by influenza A (20.2%), Human Rhino/Entero (11.3%), respiratory syncytial virus (8.1%), and SARS-COV-2 (5.2%). Influenza virus (Flu) and SARS-CoV-2 had a significant impact in single infection (P values <0.0001 and 0.0397), where Adeno virus and Bordetella pertussis had a significant impact in coinfection (P values <0.0001 and 0.001). Among the co-infections, SARS-CoV-2 and Influenza B virus (12%) were the most common, where 42% of the time was Human Rhino/Entero.The prevalence of organisms differed by age, and influenza viruses (A or B)were most common in all age groups, as in Bangladesh, the influenza virus is mostly involved in respiratory tract infections.Film Array Respiratory Panel 2.1 Plus allows the rapid simultaneous detection of a wide number of respiratory organisms, with limited hands-on time in patients with acute upper respiratory tract infection.

Keywords: acute respiratory tract infections, film array respiratory panel, real-time rt-PCR

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Original Research Article

Detection and Antimicrobial Susceptibility Pattern of Bacteria Isolated from Ventilator Associated Pneumonia in Intensive Care Unit Patients in Rajshahi Medical College Hospital

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Abstract: ***Background*** : Ventilator associated pneumonia is a major cause of higher morbidity and mortality among hospitalized patients especially in intensive care unit despite of recent advances in diagnosis and treatment. It occurs mainly among Gram negative pathogens. Most of the bacteria are multidrug resistant bacteria including penicillin's, 3rd generation of cephalosporins and carbapenems. Objective: To isolate and identify bacteria from ventilator associated pneumonia in intensive care unit patients with their antibiogram in rajshahi medical college hospital. Materials Method: A Cross -sectional type of descriptive study was done during the period of July 2017 to June 2018. Endotracheal aspirates were collected from VAP patients in intensive care units of Rajshahi Medical Co llege Hospital. The specimens were inoculated in blood agar, nutrient agar and MacConkey's agar media and incubated aerobically at 370 C for 24 hours. The isolated bacteria were identified by their colony morphology, pigment production, hemolysis on blood agar plate, motility test, Gram staining and relevant biochemical tests. Susceptibility tests of the bacterial isolates were done by using the modified Kirby Bauer disk diffusion method on Mueller Hinton agar media. Results: Out of a total 80 samples, Cult ure yielded growth were 71(88.75%) and 09(11.25%) had yielded no growth. Among the culture positive isolates, Gram negative organisms were higher 57(80.30%) than gram positive 14(19.70%). P. aeruginosa 24(33.8%) was the predominant organism followed by S. aureus 14(19.7%), Klebsiella spp. 11(15.5%), Acinetobacter spp. 10(14.1%) and E. coli 8(11.3%). Among 71 isolates, 41(57.8%) were MDR pathogens. Conclusion: It may be concluded that, most of the isolated bacteria isolated from VAP are multidrug resistant and causes complicated life-threatening infections. Due to the increasing incidence of multidrug resistant bacteria in ICU, early and correct diagnosis of VA P is an urgent challenge for an optimal antibiotic treatment .

Keywords: Ventilator Associated Pneumonia, Endotracheal Aspirates, Intensive Care Unit, Antimicrobial Susceptibility Pattern, Multidrug Resistant Bacteria .

Cite this as : Ahsanul Haque et al. Impact of Early Goal -Directed Therapy on Mortality and Organ Dysfunction in ARDS Patients in Emergency Settings . BMCJ. 202 5;11(1): 88-92

Species Identification and Antifungal Susceptibility Pattern of Candida Isolates in Patients with Vulvovaginitis from Mymensingh, Bangladesh

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Affiliations + expand
PMID: 37391952

Abstract

Vulvovaginal Candidiasis (VVC), a frequent and cumbersome reproductive tract infection affects women's physical and mental health. Although Candida albicans was reported as the most common agent of VVC yet, recently there are significant changes in the pattern of Candida species causing VVC with varying antifungal susceptibility pattern. Therefore this cross-sectional, descriptive type of observational study conducted to identify the spectrum of Candida species associated with VVC and assesses their antifungal susceptibility pattern from March 2021 to February 2022. High vaginal swabs from 175 patients clinically suspected of VVC were collected and cultured on Sabouraud dextrose agar with Chloramphenicol. Species were identified by phenotypic methods like- germ tube test, sub-culture in chromogenic agar media and genotypic methods like- Polymerase chain reaction (PCR), Restriction fragment length polymorphism (RFLP). Antifungal susceptibility was done by disk diffusion method. Out of 175 patients, 52(29.7%) were positive for Candida species. Of the isolates- C. albicans 34(65.0%), Non albicans Candida (NAC) 18(35.0%). Among NAC, C. glabrata 5(9.6%), C. tropicalis 5(9.6%), C. parapsilosis 4(7.7%) and each of C. krusei, C. kefyr, C. ciferrii, C. dubliniensis were 1(1.9%). On susceptibility testing highest resistance was to Clotrimazole 31.0% followed by Nystatin 13.0%, Itraconazole 12.0% and Fluconazole 10.0%. Resistance to azole was higher in NAC than in albicans. Of these patients, 16(31.0%) had history of recurrent VVC (RVVC) of which 12(75.0%) were by NAC, predominantly C. glabrata 5(32.0%). The results showed the increasing incidence of NAC associated vaginitis with higher resistance and recurrence that should be considered in gynecology clinics.

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Original Research Article

MDR Pseudomonas aeruginosa isolate from wound infection in Rajshahi Medical College Hospital

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Abstract: ***Background*** : Emergence of resistant bacteria causing nosocomial infections increases the morbidity and mortality. Antibiotic resistance is a major problem in treating infections in hospitals. During the past decade, infecting bacteria that are resistant to several avai lable antibiotics have emerged. The worldwide spread of multi drug resistant bacteria specially Pseudomonas aeruginosa is a predominant isolate which is usually multi drug resistant. Objective: To identify Antibiotic resistance pattern of Pseudomonas aeruginosa isolat ed from wound infection. Methods: A descriptive type of cross -sectional study on wound infection was carried out in the Department of Microbiology of Rajshahi Medical College, Rajshahi during the period from July 2014 to June 2015. A total of 150 wound swabs were collected from patients admitted in surgery and its allied branches and cultured on appropriate bacteriological culture media. Results: Culture had yielded growth in 131(87.33%) cases and Pseudomonas aeruginosa was 27(18%), Staphylococcus aureus wa s 22(14.66%), Escherichia coli was 56(37.33%), Proteus spp was 19(12.67%), Klebsiella spp. was 7(4.67%) respectively. Antibiogram was tested on Pseudomonas aeruginosa with 7 different groups of antibiotics and found 4(14.81%) were resistant to 3 groups of drugs, 2(7.41%) were resistant to 4 groups, 5(18.52%) were resistant to 5 groups, 10(37.04%) were resistant to 6 groups and 6(22.22%) were resistant to 7 groups. A total of 27(18%) isolates were resistant to 3 -7 groups of antibiotics. Conclusion: Pseudomon as aeruginosa is still a predominant isolate next to E. coli for wound infections. 27(18%) isolates were resistant to 3 -7 groups of commonly used antibiotics. Recommendation: All wound infections should be treated only after performing antibiogram with ade quate dose and duration of antibiotics .

Keywords: Wound Infection, Pseudomonas Aeruginosa, Multidrug Resistance, Hospital Patients .

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Phenotypic Detection of MRSA And ESBL Producing Bacteria with their Antimicrobial Resistance Pattern Isolated from Infected Wound Patients in Rajshahi Region

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Abstract: ***Background:*** Methicillin -resistant Staphylococcus aureus (MRSA) and Extended Spectrum Beta -Lactamase (ESBL) producing bacteria are significant public health threats, both globally and locally, due to their multidrug resistance, including resistance to third -generation cephalosporins and carbapenems. ***Objective:*** This study aimed to detect MRSA and ESBL -producing bacteria and analyze their antimicrobial resistance patterns in infected wound patients from the Rajshahi region. ***Materials and Methods:*** A cross -sectional descrip tive study was conducted from July 2017 to June 2018, collecting wound swabs from surgical units at Rajshahi Medical College Hospital. Specimens were cultured on blood agar, nutrient agar, and MacConkey's agar, and incubated at 37°C for 24 hours. Bacterial susceptibility was tested using the modified Kirby Bauer disk diffusion method on Mueller Hinton agar. MRSA was identified by Cefoxitin disk diffusion, and ESBL -producing bacteria were detected via the disk diffusion test. ***Results:*** Out of 250 samples, 213 (85.2%) yielded bacterial growth, identifying a total of 231 bacterial isolates. Among these, 136 (58.8%) were gram -negative, and 95 (41.2%) were gram -positive. Females were more predominant (146, 58.4%) compared to males (104, 41.6%), with a male -to-fema le ratio of 1:1.4. The most common isolate was *S. aureus* (71, 30.8%), followed by *Pseudomonas aeruginosa* (47, 20.3%). Of the *S. aureus* isolates, 53.5% were MRSA. Additionally, 41.3% of gram -negative isolates were ESBL producers, with high resistance to thi rd-generation cephalosporins (65%) and carbapenems (40%). Conclusions: MRSA and ESBL -producing bacteria pose significant resistance challenges in wound infections in Rajshahi .

Keywords: Wound infection, antimicrobial susceptibility, MRSA, ESBL, Multidrug resistant bacteria .

Original Research Article

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Bacteriological Profile of UTI and their Antimicrobial Resistance Pattern in Pediatric Age group patients at RMCH

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ABSTRACT: ***Background:*** Urinary tract infections (UTIs) are common pediatric infections and contribute to high morbidity. Gram negative bacilli predominating the infec tions. At present, the antimicrobial resistance has quadrupled worldwide and poses a serious threat to the treatment of patients. Objectives: The present study was designed to find out the bacteriological profile of urinary tract infection and their antibi otic resistance pattern in children. Material and Methods: A cross -sectional study was done in the department of Microbiology, Rajshahi Medical College from July to December 2024. Midstream urine samples were collected from clinically suspected cases of UT I in the age group of 0 to 18 years from various indoor and outdoor patients attending at Rajshahi Medical College hospital. Results: Out of 984 cases, 195 (19.8%) were culture positives, where females were 110(56.4%) and male were 85(43.6%). Most common i solate identified was Escherichia coli 113(57.9%), followed by Klebsiella spp.31(15.9%), Pseudomonas aeruginosa 18(9.2%) and Enterococci spp. 19(9.8%). Gram negative organisms show highest resistance to cefixime, ceftriaxone, cefuroxime, azithromycin, amox iclav and ciprofloxacin and highest sensitivity to Colistin, nitrofurantoin and imipenem. Gram positive bacteria were highly resistant against cefixime, Cotrimoxazole, ceftriaxone, cefuroxime, azithromycin, amoxiclav and ciprofloxacin. Conclusion: This stu dy indicates that gram -negative bacteria, particularly E. coli are the commonest isolated organism, and all isolates show resistance to commonly used antimicrobial agents. Urinary tract infections as well as the significant growth and spread of resistant b acterial pathogens in children should be monitored regularly .

Keywords: Paediatric Age Group, Urinary Tract Infection, Uropathogens, Antimicrobial Resistance .

Article at a glance:
Study Purpose : To contribute to existing knowledge or propose new ideas.
Key findings: Among gram-negative bacteria, predominant gram-positive bacteria were isolated in children Escherichia Coli 113 (57.9%).
Newer findings: In this study, Gram negative bacteria showed higher resistance to commonly used antibiotics from previous study.
Abbreviations: UTI: Urinary Tract Infection .

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Original Research Article

Current Microbial Isolates from Wound Swab and Their Susceptibility Pattern in Rajshahi Medical College Hospital

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Abstract: ***Background*** : Wound infection is one of the major health issues that are caused and aggravated by harmful microorganisms where empiric treatment is routine. Objective: To find out current microbial isolates from wound swab and their susceptibility pattern in Rajshahi Medical Colleg e Hospital. Materials and Method: A total of 409 wound swab and pus samples were collected during the period from July 2024 to December 2024 at Rajshahi Medical College Hospital, Rajshahi, Bangladesh. Swabs from the wound were inoculated on appropriate med ia and cultured and the isolates were identified by standard procedures as needed. Antimicrobial susceptibility testing was performed by disk diffusion method according to 'The Clinical and Laboratory Standard Institute' guidelines. Results: In this study 266 bacterial isolates were recovered from 409 samples showing an isolation rate of 65%. The predominant bacteria isolated from infected wounds were Staphylococcus aureus 96 (36%) followed by Pseudomonas aeruginosa 64(24%), Escherichia coli 58 (22%), Klebs iella 28 (11%), CoNS 11(4%) and Proteus 9 (3%). Staphylococcus aureus was sensitive to Vancomycin (100%), Doxycycline (99.5%), Linezolid (97.1%). Among the Gram -negative Pseudomonas aeruginosa was predominant and showed sensitivity to imipenem (100%), pipe racillin and tazobactam (79.6%), amikacin (70.39 %) and E coli showed sensitivity to imipenem (94.52%), levofloxacin (93.58%) Amikacin (88.1%). Conclusion: Staphylococcus aureus was the most frequently isolated pathogen from wound swab and the antibiotic s ensitivity pattern of various isolates help to assist the clinician in appropriate selection of empirical antibiotics against wound infection .

Keywords: Wound Swab, Microbial Isolates, Antimicrobial Sensitivity Pattern .

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Prevalence and epidemiologic features of nontuberculous mycobacteria causing persistent surgical site infections in Bangladesh
Article: *https://pmc.ncbi.nlm.nih.gov/articles/PMC12391278/pdf/main.pdf*

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Prevalence and epidemiologic features of nontuberculous mycobacteria causing persistent surgical site infections in Bangladesh

Mosammat Rezaun Nahar [1], Syeda Anjuman Nasreen [1], Shyamal Kumar Paul [2], Mohammed Abedul Hoque [3], Meiji Soe Aung [4], Nazia Haque [1], Tasmia Hossain [1], Sheikh Anika Tasnim [1], Sultana Jahan Tuly [1], Nashid Sultana Ishi [1], Iffat Ara Ifa [5], Abdullah Al Mamun [1], Parvez Arafa [1], Nobumichi Kobayashi [4,*]

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M. abscessus
hsp65
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ABSTRACT

Objectives: Nontuberculous mycobacteria (NTM) are an increasing cause of extrapulmonary infections affecting skin and soft tissue. This study aimed to determine the involvement of NTM in persistent surgical site infections (SSIs) in Bangladesh.

Methods: Specimens of SSIs (wound swab, pus, sinus discharge) were collected from patients who attended a tertiary care hospital during a 6-month period in 2024. NTM were detected by phenotypic methods (microscopic examination, culture, biochemical tests), immunochromatography, and polymerase chain reaction. Species of NTM were identified by sequence analysis of hps65 gene. Antimicrobial susceptibility was determined by broth microdilution test.

Results: Among a total of 155 samples collected, NTM were detected in 12 samples (7.7%), which were identified to be Mycobacterium abscessus (n = 5), Mycobacterium fortuitum (n = 4), Mycobacterium intracellulare, Mycobacterium engbaekii and Mycobacterium kubicae (one specimen each). NTM were detected in patients aged 0-50 years who were showing variable durations of non-healing wound (3 to >14 weeks), more commonly after surgery of laparoscopic cholecystectomy and laparotomy. Resistance to amikacin, ciprofloxacin, and clarithromycin was noted for M. abscessusand M. fortuitum.

Conclusions: NTM represented by M. abscessusand M. fortuitum were revealed to be a significant cause of persistent SSIs of various patient groups in Bangladesh, associated with specific types of surgery.

Photo Gallery

Consultative Meeting

Consultative meeting on dissemination of the evaluation report

Consultative meeting of Finalization of the updated Antibiogram Preparation and Microbiology Laboratory Data Analysis Training Manual

Inception Programs

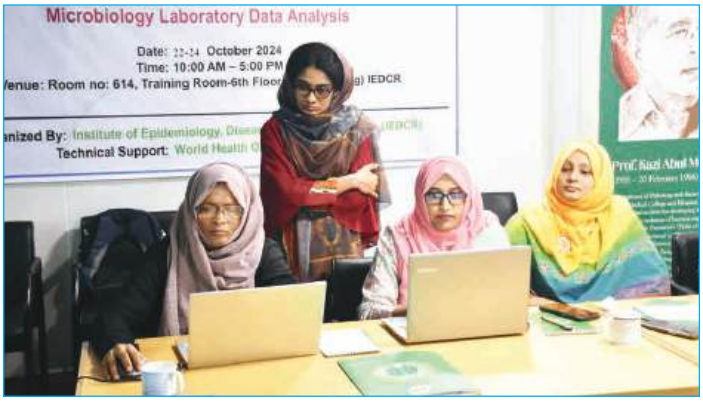
Faridpur Medical College Hospital

Jahurul Islam Medical College Hospital

Trainings

Hands-on-training of the AMR Surveillance site Microbiologists and Medical Technologists on Updated Laboratory SOP

Training of the Microbiologist on Antibiogram Preparation & Microbiology Laboratory Data Analysis



Training on Preparation of PT Panel and conduction of NEQA

Hands on Training Biosafety & Biosecurity

Hands on Training on Whole Genome Sequencing

Monitoring Visit

Chattogram Medical College Hospital

Rohingya Camp

Cox Bazar Field Lab

Sylhet MAG Osmani Medical College Hospital

Rajshahi Medical College

Workshop on Clinical Engagement and Antimicrobial Stewardship

Sylhet MAG Osmani Medical College and Hospital

Chittagong Medical College and Hospital

Sectoral Working Group (Human Health)

Consultative Meeting of Sectoral Working Group (Human Health) of Antimicrobial Resistance Surveillance

Others

Exploring Challenges and Enablers for Effective One Health Policy and Integrated Surveillance of Antibiotic Resistance in Bangladesh (PASS AMR)

Focus Group Discussion (FGD) on Integrated AMR/AMU/AMC Data Analysis in One Health Approach among DGDA, DLS and IEDCR

Healthcare Associated Infections (HAI) Surveillance

Consultative meeting

Consultative Meeting for Development of Healthcare Associated Infections (HAI) Surveillance Protocol

Consultative Meeting for Finalization of Healthcare Associated Infections (HAI) Surveillance Protocol

Exploratory site visit for Healthcare associated Infections (HAIs) Surveillance - Khulna Medical College & Hospital

Orientation Meeting on Healthcare associated Infections (HAIs) Surveillance- Khulna Medical College & Hospital

Training

Training of Intern Doctors on Antimicrobial Resistance and Healthcare- Associated Infections (HAIs)

Khulna Medical College Hospital

Rajshahi Medical College Hospital

Training: Training of the Surveillance Physicians, Nurses and Project Facilitators of the Surveillance Sites on Healthcare Associated Infections (HAIs) in Bangladesh

Monitoring Visit

Khulna Medical College & Hospital

Dissemination Program

Rajshahi Medical College Hospital

Khulna Medical College Hospital

World AMR Awareness Week-2024

Dissemination Program

Institute of Epidemiology, Disease Control & Research (IEDCR)

Dissemination On AMR Surveillance Findings in Rohingya population

Dhaka Medical College & Hospital

Uttara Adhunik Medical College Hospital

Chittagong Medical College Hospital

Cox's Bazar Medical College

Khulna Medical College Hospital

Mymensingh Medical College Hospital

Rajshahi Medical College Hospital

Rangpur Medical College Hospital

Sher-E-Bangla Medical College & Hospital

Sylhet MAG Osmani Medical College and Hospital

Leaflet distribution

Chittagong Medical College and Hospital

Cox's Bazar Medical College and Sadar Hospital

Rangpur Medical College and Hospital


Uttara Adhunik Medical College and Hospital

Mymensingh Medical College and Hospital


Bangladesh Institute of Tropical and Infectious Disease


Rally

Institute of Epidemiology Disease Control and Research

Chittagong Medical College and Hospital

Rangpur Medical College and Hospital

Rajshahi Medical College and Hospital

Sher-E-Bangla Medical College and Hospital

Bangladesh Institute of Tropical and Infectious Disease

Dhaka Medical College and Hospital

Sylhet MAG Osmani Medical College and Hospital

Hospital Wall Graffiti

Institute of Epidemiology Disease Control And Research

Khulna Medical College and Hospital

Bangladesh Institute of Tropical and Infectious Disease

Awareness Program for Students

Institute of Epidemiology Disease Control And Research

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Program for Students on
Antimicrobial Resistance
Auditorium, IEDCR (New building, 1st Floor)
29 November 2024
Sverige
Awareness Program for Students on
Antimicrobial Resistance

Bangladesh Medical College

US Bangla Medical College




Faridpur Medical College





BSMMC

Note:

অ্যান্টিমাইক্রোবিয়াল অকার্যকারিতা: এখনই পদক্ষেপ নিন
বর্তমান সুরক্ষিত রাখুন, ভবিষ্যৎ নিরাপদ করুন।

Act Now: Protect Our Present, Secure Our Future.

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