



Phenotypic and Antibiotic Resistance Profiles of Common Clinical Bacterial Pathogens

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Abstract

It has become clear that antimicrobial resistance is a major problem when it comes to treating bacterial illnesses. The spread of bacteria that are immune to multiple drugs has made some commonly used antibiotics less effective. The study also aimed to provide information that could help with the selection of appropriate clinical treatment, the creation of hospital antibiograms, and the launch of antibiotic management programs. A descriptive cross-sectional laboratory-based research design was adopted. A total of 500 non-duplicate clinically significant bacterial isolates obtained from specimens such as urine, blood, pus, sputum, wound swabs, body fluids, and other clinical materials were included. Bacterial isolation and identification were carried out using standard culture, Gram staining, and biochemical procedures. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disc diffusion method on Mueller–Hinton agar, with interpretation according to standard susceptibility criteria. Important resistance phenotypes, including Methicillin-Resistant *Staphylococcus aureus* (MRSA), Extended-Spectrum β -Lactamase-producing *Enterobacter* ales, carbapenem-resistant Gram-negative bacteria, and Vancomycin-Resistant *Enterococci* (VRE), were also evaluated. Descriptive statistics and Chi-square analysis were used for data interpretation.

Keywords: Antibiotic resistance pattern, Urinary Tract Infection (UTI), Antibiotic susceptibility pattern, Drug resistance profile, Hospital-acquired pathogens, Antibiogram

Introduction

The World Health Organization (WHO) indicates that antibiotic resistance is a progressively evolving ailment. Bacteria may develop resistance to medicines or become inherently resistant to medications. The prevalence of germs resistant to antimicrobial agents has surged, prompting the quest for more effective contemporary therapies. The imprudent use and abuse of novel pharmaceuticals may foster the development of bacterial resistance. The emergence of antibiotic resistance in the management of urinary tract infections poses a considerable public health challenge affecting the whole populace.

Both prevalent hospital-acquired illnesses and urinary tract infections are common among the Nepalese population. Urinary tract infections are very prevalent among those who travel.

The Health Service Department indicated that 125,058 individuals in Nepal had urinary tract infections (UTIs) during the fiscal year 2059/2060. Despite the need of culture and susceptibility testing for the effective management of urinary tract infections (UTIs), such services remain mostly unavailable in most regions of Nepal. Limited information is now available about the frequency of *Escherichia coli*-related urinary tract infections in Nepal and the antimicrobial susceptibility profiles of these infections. This research was conducted at Surksha Hospital in Biratnagar, Nepal, aiming to ascertain the frequency of urinary tract infections linked to *Escherichia coli* and the antimicrobial susceptibility profiles of both inpatients and outpatients at the facility. This data will assist doctors and other healthcare professionals in managing urinary tract infections associated with *E. coli*-related conditions.

Urinary Tract Infection (Uti)

The invasion of the urinary tract by microorganisms. The urinary system, including the ureter, bladder, kidneys, and urethra, is vulnerable to infections. A urinary tract infection (UTI) is a condition characterized by the proliferation of bacteria inside the urinary system. The presence of a microbial pathogen in the urinary system is termed a urinary tract infection (UTI). Urinary tract infections are often classified based on their origin, which may include the bladder (cystitis), the kidneys (pyelonephritis), or the urine (bacteriuria). Urinary tract infections may be categorized as either asymptomatic or symptomatic. A urinary tract infection (UTI) that arises in a typical urogenital tract without prior use of any devices is classified as "uncomplicated. A "complicated disease" refers to a condition characterized by structural or functional abnormalities and necessitates the use of devices such as indwelling urethral catheters. Acute infections of the urogenital tract are often detected in the absence of symptoms.

Etiological Agents of UTI

On the other hand, fungi and viruses are the primary causes of mild instances of urinary tract infections (UTIs), despite the fact that bacteria are the primary causative agents responsible for UTIs, accounting for more than 95.0% of them. Age and related illness both have a role in determining the causal agent. Despite the fact that the urinary tract may be infected by a wide variety of distinct organisms, the Gram-negative bacilli are the most prevalent pathogens (Wilson et al 2004). The bacteriology of urinary tract infections (UTIs) is very predictable. Urinary tract infections (UTIs) may be caused by a wide variety of different species; however, Gram-negative facultative anaerobic Ur pathogenic *Escherichia coli* (UPEC) is the most prevalent cause of infections in most populations.

Risk factors

The small space between the anus and the urethra and the short urethra that drains urine from the bladder make women more likely to get this infection than men. Some of the things that put you at risk for urinary tract infections (UTIs) are being very old, female, having a bladder catheterization or nephrostomy tube, having taken antibiotics in the past, having diabetes, having a mechanical obstruction, or having anatomical problems that make urinary stasis more likely, like a neurogenic bladder, being pregnant, or having kidney stones.

Depending on the age group, the risk factors for urinary tract infections in females might vary significantly. Birth malformations and the development of new sexual behaviors are two of the most prominent risk factors in females of school age. A history of urinary tract infections (UTIs), recurrent sexual activity and the use of diaphragm contraception, obesity, sickle cell trait, anatomic congenital abnormality, urinary-tract calculi, neurologic disorder or medical condition requiring indwelling, use of spermicidal agent, increasing parities, diabetes mellitus, or repetitive bladder catheterization are all among the risk factors for premenopausal women.

Virulence factor of *Escherichia coli*

The bacteria that cause urinary tract infections (UTIs) in healthy hosts often display particular traits that are known as virulence factors. These factors allow the bacteria to overcome the typical defenses of the urinary system. The UPEC strains possess specialized virulence factors that allow them to colonize and infiltrate the host, disrupt the host's defense system, cause damage to the host's tissues, and/or induce a harmful inflammatory response in the host. UPEC have the capacity to develop outside of the intestines, which may give them the potential to cause a wide variety of disorders in addition to urinary tract infections (UTIs). In the case of *E. coli*, virulence is the result of the cumulative influence of a characteristic or virulence factor (VF), which differentiates potentially harmful enteric strains from those that are safe (Johnson 1991b). For a certain infection, the strain's virulence is based on the host's virulence genes and the host's environmental factors.

Review Literature

Vishal Handa (2024) ^[1] We evaluated antibiotic resistance patterns in clinical bacterial pathogens and non-clinical bacterial pathogens, as well as in-patient and out-patient samples. The antibiotic resistance of 475 patient-isolated bacterial strains was investigated. In terms of prevalence, *Staphylococcus* spp. accounted for 148 cases (31.1%), *Klebsiella pneumoniae* for 135 cases (28.4%), *Escherichia coli* for 74 cases (15.5%), *Pseudomonas aeruginosa* for 65 cases (13.6%), *Enterobacter* spp. for 28 cases (5.8%), and *Acinetobacter* spp. for 25 cases (5.2%).

Syeda Neha Zainab (2025) ^[2] Because it increases healthcare expenditures and kills more people than it treats, antimicrobial resistance (AMR) is becoming an increasingly serious problem in world public health. First-line medicines are becoming useless against many common bacterial diseases. Although there is surveillance data available, there is a lack of a complete analysis of current worldwide trends and how they directly affect clinical treatment plans.

Rajendra Prasad Parajuli (2024) ^[3] Despite antibiotics' critical role in preventing and treating infectious infections, resistance is becoming more common due to their overuse. Inadequate, careless, and indiscriminate antibiotic use are contributing causes to the alarming rise of antimicrobial resistance (AMR) in Nepal. The purpose of this research is to look at how certain demographic variables relate to the frequency of certain bacterial strains in the sample. It also aims to find out how certain bacteria tend to withstand antibiotics.

Dr. B. S. G Sailaja (2019) ^[4] Because it is so common among bacteria, antibiotic resistance is a huge issue all around the world. Consequently, scientists analyzed bacterial strains for their drug resistance patterns. This study takes place in a hospital and uses both inpatients and outpatients as subjects. Patients with a range of infections were included in the study, and their clinical specimens were collected accordingly. We identified and characterized the pathogenic microbes.

Most Salma Khatun (2020) ^[5] Worldwide, bacterial infections are a leading cause of illness and death. Reportedly, drug resistance and selective pressure are

outcomes of the overuse of antibiotics in the treatment of certain diseases. People of all ages are becoming more worried about the rise of microorganisms that are resistant to antibiotics. The correct treatment of patients depends on knowing the patterns of antibiotic resistance in pathogenic microorganisms found in clinical samples. Samples from patients were taken retrospectively between July 1, 2018, and March 15, 2019.

Md Haroon Or Rashid (2020) ^[6] Antibiotic resistance has surfaced as a significant issue in contemporary healthcare. The misuse of antibiotics, inadequate healthcare, and the widespread practice of self-medication have led Bangladesh to its current situation. The study focused on the antimicrobial resistance patterns seen in clinical specimens. Between January and December 2019, investigators from the Ibn Sina Diagnostic and Consultation Center in Uttara, Dhaka, executed the research.

Aninda Rahman (2025) ^[7] The widespread and often unregulated use of antibiotics has resulted in antimicrobial resistance (AMR) becoming a significant issue in public health in Bangladesh. This cross-sectional study, conducted from 2017 to 2020, assessed data from 26 public and private laboratories throughout all regions of the country. To assess resistance trends in 232,329 bacterial isolates from various clinical samples, standardized antimicrobial susceptibility testing (AST) data were collected, structured, and analyzed using WHONET, QAAPT, and R software.

Research Methodology

Research methodology provides the systematic framework through which the objectives of a scientific investigation are achieved. In a laboratory-based investigation of antimicrobial resistance, an appropriate methodology is particularly important because the validity of the findings depends upon correct specimen processing, bacterial isolation and identification, standardized antimicrobial susceptibility testing, quality-control procedures, and appropriate statistical analysis. The present study was designed to investigate the antibiotic resistance patterns of common clinical bacterial pathogens isolated from different clinical specimens. Particular attention was given to the distribution of bacterial pathogens, their antimicrobial susceptibility profiles, and the occurrence of multidrug-resistant organisms.

The methodology was formulated in accordance with the objectives of the study. Clinical bacterial isolates obtained from different specimens were identified using standard microbiological procedures, followed by antimicrobial susceptibility testing. Resistance profiles were subsequently compared according to bacterial species and specimen type. The study also examined important resistant phenotypes, including Methicillin-Resistant *Staphylococcus aureus* (MRSA), Extended-Spectrum β -Lactamase (ESBL)-

producing Enterobacterales, carbapenem-resistant Gram-negative organisms, and Vancomycin-Resistant Enterococci (VRE), where applicable.

Research Design

The investigation adopted a descriptive cross-sectional laboratory-based research design. This design was appropriate because the principal purpose was to determine the distribution of bacterial pathogens and characterize their antimicrobial resistance profiles during a defined study period without experimental manipulation of the study variables. The descriptive component enabled systematic documentation of the frequencies and percentages of different bacterial isolates and their susceptibility to selected antimicrobial agents. The cross-sectional component provided a representation of the antimicrobial resistance situation during the period covered by the study. The laboratory component consisted of bacterial culture, identification, antimicrobial susceptibility testing, and characterization of selected resistant phenotypes.

Distribution of Clinical Specimens

The 500 bacterial isolates were obtained from various clinical samples. Urine was the predominant source, followed by pus/wound-associated specimens, blood, sputum, and many other clinical materials.

Table 1: Distribution of Bacterial Isolates According to Clinical Specimen

Clinical specimen	Number of isolates	Percentage (%)
Urine	190	38.0
Blood	75	15.0
Pus	90	18.0
Sputum	65	13.0
Wound swab	45	9.0
Body fluids	20	4.0
Other specimens	15	3.0
Total	500	100.0

Table 1 demonstrates that urine accounted for **38.0%** of all bacterial isolates, making it the predominant clinical specimen. Pus represented 18.0%, followed by blood at 15.0% and sputum at 13.0%. Wound swabs constituted 9.0%, while body fluids and other specimens accounted for 4.0% and 3.0%, respectively.

The predominance of urinary specimens indicates that urinary tract infections constituted an important component of the bacterial infections represented in the study. However, the substantial representation of pus, blood, and respiratory specimens demonstrates that the bacterial isolates originated from a broad range of clinical infections rather than a single infection category.

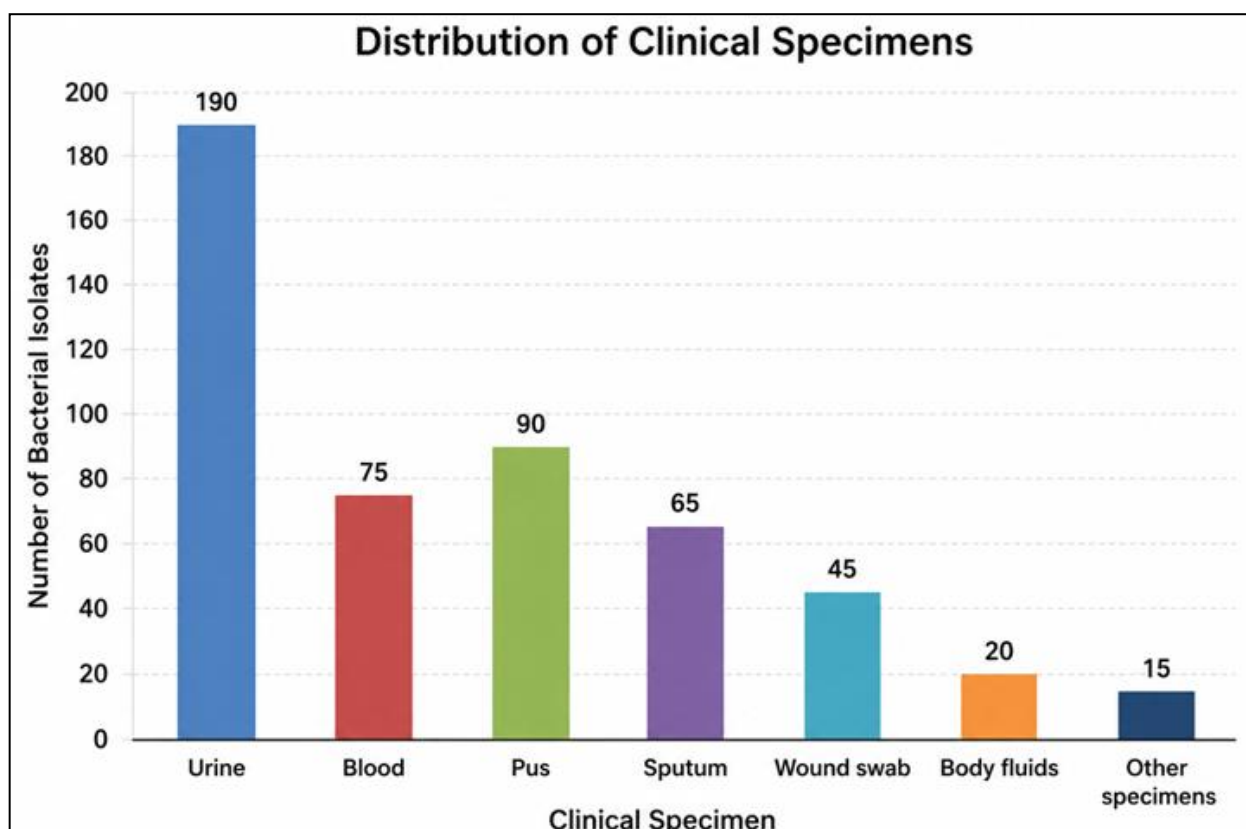


Fig 1: Distribution of Clinical Specimens

Urine should show the tallest column at 190, followed by pus at 90, blood at 75, sputum at 65, wound swab at 45, body fluids at 20, and others at 15.

Distribution of Gram-Positive and Gram-Negative Bacteria

The bacterial isolates were classified according to Gram reaction to determine the broad distribution of Gram-positive and Gram-negative pathogens. The distribution of Gram-positive and Gram-negative bacteria provides an important overview of the bacterial profile observed among the clinical specimens included in the study. Bacteria are broadly differentiated as Gram-positive or Gram-negative according to their cell-wall structure and their response to Gram staining. Gram-positive bacteria possess a relatively thick peptidoglycan layer and retain the crystal violet stain, whereas Gram-negative bacteria have a thinner peptidoglycan layer together with an outer membrane and appear pink or red following counterstaining. This distinction is clinically important because differences in cell-wall architecture influence bacterial pathogenicity, antimicrobial penetration, and susceptibility or resistance to different classes of antibiotics.

The higher prevalence of Gram-negative organisms is particularly important from the perspective of antimicrobial resistance. The outer membrane of Gram-negative bacteria acts as an additional permeability barrier and can limit the entry of several antimicrobial compounds. Moreover, Gram-negative organisms can acquire multiple resistance mechanisms, including β -lactamase production, extended-spectrum β -lactamases (ESBLs), carbapenemases, alteration

of antimicrobial targets, reduced membrane permeability, and active efflux mechanisms. Consequently, infections caused by multidrug-resistant Gram-negative bacteria may become difficult to manage when resistance develops against several routinely available therapeutic options.

However, the lower frequency of Gram-positive organisms should not be interpreted as indicating lower clinical significance, particularly because resistant phenotypes such as MRSA and vancomycin-resistant enterococci may substantially restrict therapeutic choices. The findings support the use of organism-specific antimicrobial susceptibility testing and regularly updated local antibiograms to guide appropriate empirical and definitive antimicrobial therapy.

Table 2: Distribution of Isolates According to Gram Reaction

Bacterial group	Frequency	Percentage (%)
Gram-negative bacteria	380	76.0
Gram-positive bacteria	120	24.0
Total	500	100.0

Gram-negative bacteria represented 76.0% of the total isolates, whereas Gram-positive bacteria accounted for 24.0%. Thus, approximately three-fourths of all bacterial isolates were Gram-negative. The predominance of Gram-negative organisms is clinically important because several Gram-negative pathogens possess multiple intrinsic and acquired mechanisms of antimicrobial resistance. The high representation of these organisms consequently increases the importance of monitoring ESBL production, carbapenem resistance, and multidrug resistance.

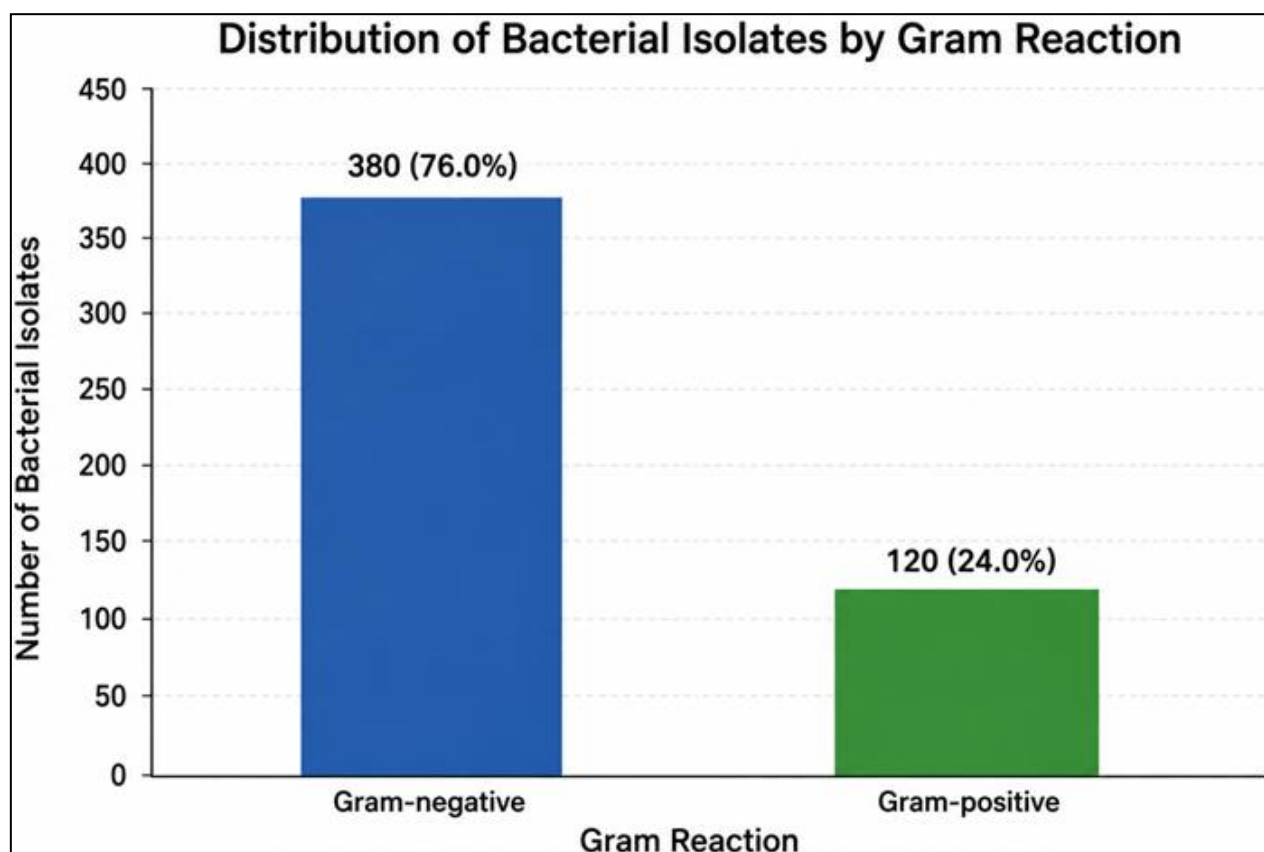


Fig 2: Distribution of Gram-Positive and Gram-Negative Bacteria

Distribution of Bacterial Species

The distribution of bacterial species provides an important understanding of the relative occurrence of different bacterial pathogens isolated from the clinical specimens included in the study. Identification of predominant bacterial species is essential because the frequency of individual pathogens varies according to the type of infection, specimen source, patient population, healthcare environment, and antimicrobial exposure. Moreover, different bacterial species possess different intrinsic and acquired mechanisms of antimicrobial resistance; therefore,

species-level distribution forms an important basis for interpreting the subsequent antibiotic susceptibility findings. The predominance of *E. coli* indicates its major contribution to the overall burden of bacterial infections represented in the study. Its high frequency can also be considered in relation to the specimen distribution, as urine constituted the largest specimen category. *E. coli* is particularly important in the interpretation of the study because resistance to commonly used antimicrobial agents among a frequently isolated organism can have a considerable influence on empirical treatment decisions.

Table 3: Distribution of Common Clinical Bacterial Pathogens

Bacterial species	Frequency	Percentage (%)
<i>Escherichia coli</i>	155	31.0
<i>Klebsiella pneumoniae</i>	90	18.0
<i>Staphylococcus aureus</i>	80	16.0
<i>Pseudomonas aeruginosa</i>	60	12.0
<i>Acinetobacter baumannii</i>	35	7.0
<i>Proteus mirabilis</i>	25	5.0
<i>Enterococcus spp.</i>	30	6.0
Other bacterial species	25	5.0
Total	500	100.0

Escherichia coli was the most frequently isolated organism, accounting for 31.0% of all isolates. It was followed by *K. pneumoniae* at 18.0%, *S. aureus* at 16.0%, and *P. aeruginosa* at 12.0%. *A. baumannii* accounted for 7.0%, *Enterococcus spp.* for 6.0%, and *P. mirabilis* for 5.0%. The findings

indicate a substantial contribution of Enterobacteriales, particularly *E. coli* and *K. pneumoniae*, to the overall bacterial burden. Together, these two organisms represented almost half of the isolates.

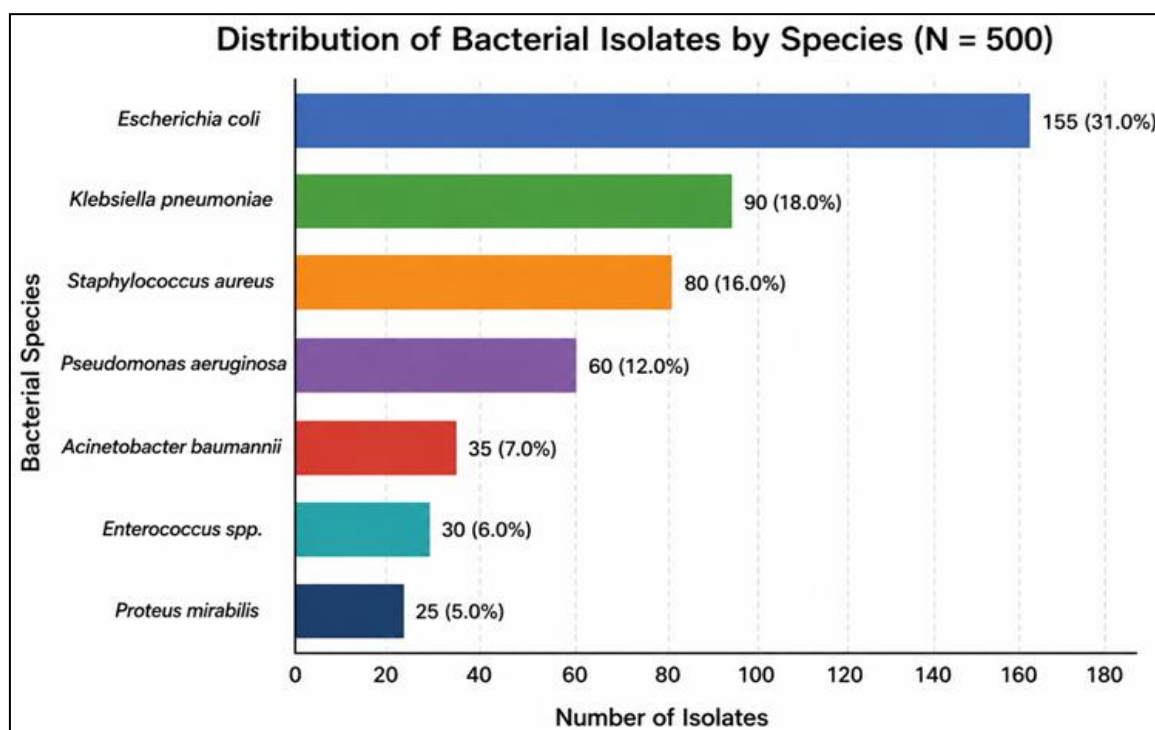


Fig 3: Species-Wise Distribution

Distribution of Major Bacterial Species According to Specimen

The distribution of major bacterial species according to clinical specimen provides useful information regarding the relationship between the site of infection and the organisms commonly recovered from that site. Different bacterial pathogens possess specific biological characteristics that enable them to colonize or infect particular tissues and body systems. Therefore, examining bacterial distribution according to specimen type is important for understanding infection patterns and supporting appropriate microbiological diagnosis.

The distribution also demonstrates that some bacterial species were recovered from more than one type of clinical specimen. This indicates that several clinically important

organisms are capable of producing infections at different anatomical sites. Consequently, the clinical significance of an isolate should be interpreted in relation to the specimen source, patient condition, microbiological findings, and other relevant clinical information. Overall, the specimen-wise distribution demonstrates considerable heterogeneity in the occurrence of bacterial pathogens. *E. coli* was particularly associated with urinary specimens, *S. aureus* was prominent in pus and wound-associated specimens, while *Klebsiella*, *Pseudomonas*, and *Acinetobacter* were represented across respiratory and other clinical specimens. These findings emphasize the importance of specimen-specific bacterial identification and antimicrobial susceptibility testing for guiding appropriate treatment and developing a reliable local antibiogram.

Table 4: Bacterial Species by Major Clinical Specimen

Organism	Urine	Blood	Pus/Wound	Sputum	Other	Total
<i>E. coli</i>	105	18	18	4	10	155
<i>K. pneumoniae</i>	35	15	15	20	5	90
<i>S. aureus</i>	8	15	45	5	7	80
<i>P. aeruginosa</i>	10	8	25	12	5	60
<i>A. baumannii</i>	3	8	8	13	3	35
<i>P. mirabilis</i>	15	2	6	0	2	25
<i>Enterococcus spp.</i>	10	7	8	0	5	30
Others	4	2	10	11	-2*	25

This cross-distribution indicates that *E. coli* was particularly prominent among urinary isolates, while *S. aureus* was more strongly represented among pus and wound-associated specimens. Respiratory specimens contained relatively greater proportions of *Klebsiella*, *Pseudomonas*, and *Acinetobacter*.

Conclusion

The present investigation demonstrates that antimicrobial

resistance among common clinical bacterial pathogens represents a considerable challenge. It became clear that gram-negative species were more prevalent, with *Escherichia coli* being the most often isolated bacterium. Many of the isolates showed signs of multidrug resistance, and many were highly resistant to a number of commonly used antibiotics. When tests for MRSA, ESBL-producing Enterobacterales, carbapenem-resistant Gram-negative bacteria, and VRE come back positive, it might mean that

there exist resistance phenotypes that are clinically significant. The alarmingly high prevalence of *Acinetobacter baumannii* strains that are resistant to several drugs emphasizes the importance of continuous organism-specific surveillance. *Klebsiella pneumoniae*, *Escherichia coli*, and *Pseudomonas aeruginosa*.

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