

PREVALENCE AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF BACTERIAL PATHOGENS ISOLATED FROM CLINICAL SAMPLES

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Abstract

Antimicrobial resistance has become a major public health concern, making the identification of prevalent bacterial pathogens and their antibiotic susceptibility patterns essential for effective treatment. This study was conducted to determine the prevalence and antibiotic susceptibility patterns of bacterial pathogens isolated from clinical samples at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan. Clinical specimens, including urine, blood, wound swabs, sputum, and other relevant samples, were collected from patients during the study period. Samples were processed using standard microbiological techniques for bacterial isolation and identification. The identified bacterial isolates were subjected to antibiotic susceptibility testing using the Kirby–Bauer disc diffusion method against commonly prescribed antibiotics. The study demonstrated the presence of both Gram-positive and Gram-negative bacterial pathogens, with variations in their prevalence among different clinical specimens. The isolated organisms showed variable susceptibility to the tested antibiotics, while resistance was observed against several commonly used antimicrobial agents. Differences in susceptibility patterns were also observed among bacterial species and clinical sample types. The findings highlight the importance of routine microbiological investigation and antibiotic susceptibility testing before antimicrobial therapy. Continuous surveillance of bacterial pathogens and their resistance patterns is essential for guiding appropriate antibiotic selection and supporting effective antimicrobial stewardship.

INTRODUCTION

Bacterial infections remain a major cause of morbidity and mortality worldwide and continue to place a substantial burden on healthcare

systems, particularly in developing countries. Clinical infections can be caused by a wide range of bacterial pathogens, including both Gram-positive and Gram-negative organisms [1, 2]. The

distribution of these pathogens may vary according to the type of clinical specimen, patient population, geographical location, and healthcare setting. Therefore, the identification of bacterial pathogens from clinical samples is essential for accurate diagnosis and appropriate antimicrobial therapy [3, 4]. Antibiotics are among the most important therapeutic agents used for the management of bacterial infections. However, their extensive and inappropriate use has contributed to the rapid emergence and spread of antimicrobial resistance (AMR) [5, 6]. Resistant bacterial infections can result in treatment failure, prolonged hospitalization, increased healthcare costs, and higher risks of complications and mortality. The increasing prevalence of multidrug-resistant bacteria has further complicated the selection of effective empirical antimicrobial therapy, making laboratory-based antibiotic susceptibility testing increasingly important [7, 8]. Clinical specimens such as urine, blood, wound swabs, and sputum provide valuable information about the bacterial pathogens responsible for infections [9, 10]. Microbiological examination followed by bacterial identification and antibiotic susceptibility testing helps clinicians select appropriate antimicrobial treatment and reduces the unnecessary use of ineffective antibiotics. The Kirby-Bauer disc diffusion method is a widely used and practical approach for determining the susceptibility of bacterial isolates to different antimicrobial agents [11, 12]. The prevalence of bacterial pathogens and their antibiotic susceptibility patterns can differ considerably between healthcare facilities and geographical regions. Local surveillance is therefore important for understanding the distribution of bacterial pathogens and identifying emerging resistance patterns [13, 14]. Such information can support evidence-based antibiotic selection, improve patient management, and contribute to antimicrobial stewardship and infection-control strategies. In Pakistan, antimicrobial resistance represents an important and growing healthcare challenge. However, data on the prevalence and susceptibility profiles of bacterial pathogens may vary among different hospitals and regions.

Generating local laboratory data is particularly valuable for healthcare facilities serving populations with different clinical and epidemiological characteristics [15, 16]. Therefore, the present study was undertaken at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan, to determine the prevalence of bacterial pathogens isolated from different clinical samples and to evaluate their antibiotic susceptibility patterns. The findings of this study may provide useful baseline information for clinicians and healthcare professionals regarding local bacterial infections and antimicrobial resistance, while supporting rational antibiotic use and effective antimicrobial stewardship.

1. Materials and Methods

A descriptive cross-sectional study was conducted to determine the prevalence and antibiotic susceptibility patterns of bacterial pathogens isolated from clinical samples. The study was carried out at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan. The hospital provides healthcare services to patients from Takht Bhai and surrounding areas and receives patients with a variety of infectious conditions.

1.1 Study Design and Study Area

A descriptive cross-sectional study was conducted to determine the prevalence and antibiotic susceptibility patterns of bacterial pathogens isolated from clinical samples. The study was carried out at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan. The hospital provides healthcare services to patients from Takht Bhai and surrounding areas and receives patients with a variety of infectious conditions.

1.2 Study Population and Study Period

Clinical samples were collected from patients attending different clinical departments of the hospital during the study period from December 2025 to March 2026. Patients of different age groups and both sexes were included according to

the study criteria. Samples were collected from patients suspected of having bacterial infections and for whom microbiological investigation was requested by the attending physician.

1.3 Sample Collection

Different types of clinical specimens, including urine, blood, wound swabs, sputum, and other relevant clinical samples, were collected using standard aseptic procedures. Appropriate sterile and labeled containers or transport systems were used for specimen collection. Each specimen was labeled with the required patient and sample information and transported promptly to the microbiology laboratory for processing. Samples that were improperly collected, inadequately labeled, contaminated, or unsuitable for analysis were excluded from the study.

1.4 Isolation and Identification of Bacterial Pathogens

Clinical specimens were processed using standard microbiological procedures. Depending on the type of specimen, samples were inoculated onto appropriate culture media, including blood agar, MacConkey agar, and other selective or differential media where required. The inoculated culture plates were incubated under appropriate conditions according to the suspected bacterial pathogen and specimen type. Following incubation, bacterial growth was examined for colony morphology, including colony size, shape, color, texture, hemolytic characteristics, and other relevant features. Representative colonies were subjected to Gram staining to differentiate Gram-positive and Gram-negative bacteria. Further identification was performed using conventional biochemical tests appropriate for the suspected bacterial species. The bacterial isolates were identified according to their cultural, microscopic, and biochemical characteristics.

1.5 Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method. Fresh bacterial cultures were used to prepare standardized bacterial suspensions equivalent to

approximately 0.5 McFarland turbidity. The standardized suspension was evenly inoculated onto the surface of Mueller-Hinton agar using a sterile swab. Antibiotic discs representing commonly prescribed antimicrobial agents were placed aseptically on the inoculated agar surface. The plates were incubated under appropriate conditions, and the zones of inhibition around each antibiotic disc were measured in millimeters after incubation. The isolates were categorized as susceptible, intermediate, or resistant according to the interpretive criteria of the applicable Clinical and Laboratory Standards Institute (CLSI) guidelines.

2.7 Quality Control

Quality-control procedures were followed throughout specimen processing, bacterial identification, culture, and antimicrobial susceptibility testing. Culture media were checked for sterility and appropriate performance before use. Standard quality-control bacterial strains, where available, were used to verify the performance of culture media and antibiotic susceptibility testing. Laboratory procedures were performed using standard microbiological practices to minimize contamination and technical errors.

2.8 Data Collection and Statistical Analysis

Relevant information regarding clinical specimens, bacterial isolates, and antibiotic susceptibility results was recorded on standardized data collection forms. Data were entered and analyzed using IBM SPSS Statistics version 24.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics, including frequencies and percentages, were used to summarize the distribution of bacterial isolates and antibiotic susceptibility patterns. The results were presented in tables and figures. Where applicable, the chi-square test was used to determine associations between categorical variables, and a p-value < 0.05 was considered statistically significant.

2. Results and discussions

2.1 Distribution of Clinical Specimens and Culture Results

A total of 300 clinical samples were investigated during the study period from December 2025 to March 2026 at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan. The clinical specimens included urine, blood, wound/pus swabs, sputum, and other relevant clinical samples. Of the 300 samples examined, 184 (61.3%) were culture-positive, whereas 116 (38.7%) showed no bacterial growth. The highest culture positivity was observed in wound/pus swab specimens, with 38 of 55 samples (69.1%) yielding bacterial growth [17]. Urine samples showed the second-highest positivity, with 92 of 140 samples (65.7%), followed by sputum 15/25 (60.0%), other specimens 8/15 (53.3%), and blood samples 31/65 (47.7%). The overall culture positivity of 61.3% indicates a substantial burden of bacterial infection among the patients investigated in this study. The highest positivity was observed in wound/pus specimens (69.1%). This may be related to the direct exposure of wounds to environmental and hospital-associated microorganisms and the favorable conditions for bacterial colonization and infection. The high positivity among urine specimens (65.7%) also indicates that urinary tract infections represented

an important source of bacterial infection in the study population [18]. The predominance of urine and wound/pus samples is comparable with findings reported from other Pakistani clinical settings. A large antibiotic susceptibility surveillance study from Punjab reported that pus and urine were among the major sources of bacterial isolates, while another Pakistani hospital study also identified pus, blood, urine, and sputum as important clinical specimen types. Blood showed the lowest culture positivity among the major specimen categories (47.7%). The relatively lower recovery rate from blood may be associated with several factors, including lower bacterial concentrations in bloodstream infections, previous antibiotic administration before sample collection, intermittent bacteremia, and differences in the underlying clinical conditions of patients [19]. Therefore, negative blood culture results should be interpreted together with the patient's clinical findings. The relatively high proportion of culture-positive samples emphasizes the importance of microbiological investigation in patients with suspected bacterial infections. Identification of the causative organism is particularly important in settings where empirical antibiotic treatment may be affected by increasing antimicrobial resistance.

Table 1. Distribution of clinical specimens and culture results.

Clinical specimen	Total samples	Culture positive n (%)	Culture negative n (%)
Urine	140	92 (65.7)	48 (34.3)
Blood	65	31 (47.7)	34 (52.3)
Wound/pus swab	55	38 (69.1)	17 (30.9)
Sputum	25	15 (60.0)	10 (40.0)
Other specimens	15	8 (53.3)	7 (46.7)
Total	300	184 (61.3)	116 (38.7)

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2.2 Prevalence of Bacterial Pathogens

Among the 184 culture-positive samples, several clinically important bacterial pathogens were isolated. *Escherichia coli* was the most frequently isolated organism, accounting for 65 isolates (35.3%). It was followed by *Staphylococcus aureus* with 38 isolates (20.7%), *Klebsiella pneumoniae* with

25 isolates (13.6%), and *Pseudomonas aeruginosa* with 19 isolates (10.3%). *Proteus* spp. accounted for 14 isolates (7.6%), *Acinetobacter* spp. for 10 isolates (5.4%), while other bacterial species accounted for 13 isolates (7.1%). The results demonstrate that Gram-negative bacteria constituted the major proportion of the bacterial

isolates, with *E. coli* being the predominant pathogen [20]. The predominance of *E. coli* may be explained by its role as an important cause of urinary tract infections and other extraintestinal infections. Its high prevalence in the current study is also consistent with findings from Pakistani clinical laboratories, where *E. coli* is frequently reported among the leading bacterial pathogens. A study conducted in Karachi identified *E. coli* as one of the most common clinical bacterial isolates. The second most prevalent organism was *S. aureus* (20.7%) [21]. The relatively high frequency of this Gram-positive pathogen indicates that Gram-positive bacteria also represent an important component of the bacterial infection burden. *S. aureus* is commonly associated with skin and soft-tissue infections, wound infections, bloodstream infections, and other clinical conditions. Pakistani surveillance studies have also reported substantial proportions of *S. aureus* among clinical bacterial isolates. *K. pneumoniae* was the third most frequent isolate (13.6%). This organism is clinically important because it can cause urinary, respiratory, wound, and bloodstream infections and has considerable potential for acquiring antimicrobial resistance [22]. Previous studies from Khyber Pakhtunkhwa have reported

significant recovery of *K. pneumoniae* from urine, pus, blood, and other clinical specimens, together with considerable resistance to commonly used antibiotics. The prevalence of *P. aeruginosa* (10.3%) is also clinically relevant because this organism is an important opportunistic pathogen and is frequently associated with hospital-acquired infections. Its ability to develop resistance through multiple mechanisms makes antimicrobial susceptibility testing particularly important [23]. The isolation of *Proteus* spp. and *Acinetobacter* spp. further demonstrates the diversity of bacterial pathogens present in the study population. *Acinetobacter* spp. are particularly concerning in healthcare settings because multidrug-resistant strains can persist in hospital environments and may cause difficult-to-treat infections. Overall, Figure 1 demonstrates that the bacterial population was dominated by a relatively small number of clinically important organisms, particularly *E. coli*, *S. aureus*, *K. pneumoniae*, and *P. aeruginosa*. This pattern supports the need for routine bacterial identification and local surveillance because the distribution of pathogens can vary according to geographic location, patient population, specimen type, and healthcare setting.

Table 2. Prevalence of bacterial pathogens isolated from clinical samples.

Bacterial pathogen	Number of isolates	Prevalence (%)
<i>Escherichia coli</i>	65	35.3
<i>Staphylococcus aureus</i>	38	20.7
<i>Klebsiella pneumoniae</i>	25	13.6
<i>Pseudomonas aeruginosa</i>	19	10.3
<i>Proteus</i> spp.	14	7.6
<i>Acinetobacter</i> spp.	10	5.4
Other bacteria	13	7.1
Total	184	100

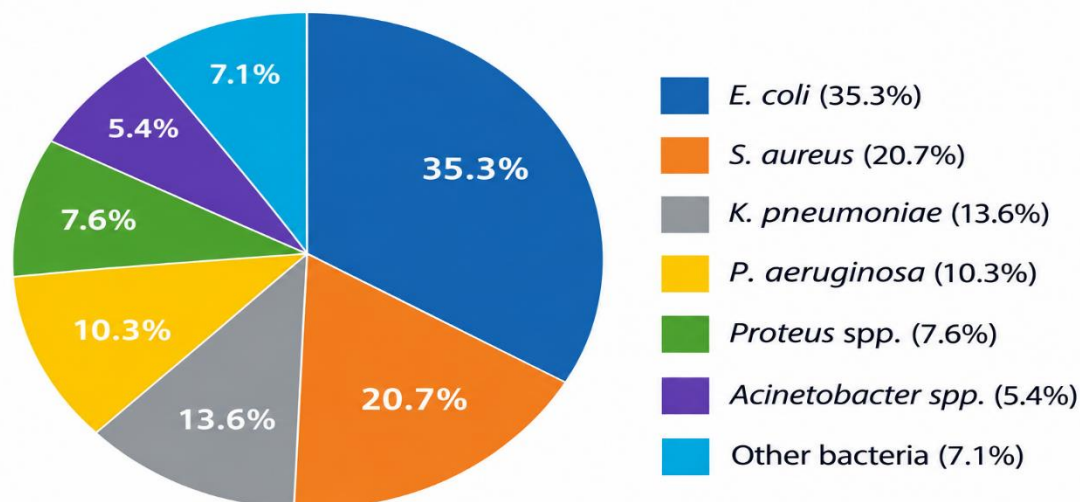


Figure 1. Prevalence and distribution of bacterial pathogens isolated from clinical samples collected at THQ Hospital Takht Bhai during the study period. *E. coli* was the most frequently isolated pathogen, followed by *S. aureus* and *K. pneumoniae*.

2.2 Antibiotic Susceptibility Pattern of Major Bacterial Isolates

Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method. The major bacterial isolates demonstrated variable susceptibility to the tested antibiotics. Overall, the highest susceptibility among the Gram-negative organisms was observed against selected aminoglycosides and meropenem, whereas comparatively lower susceptibility was observed against ciprofloxacin and third-generation cephalosporins. *S. aureus* demonstrated high susceptibility to linezolid and vancomycin [24]. The susceptibility profile of *E. coli* showed considerable variation among the tested antibiotics. The highest susceptibility was observed for meropenem (82%), followed by amikacin (78%) and piperacillin-tazobactam (69%). In contrast, susceptibility to ceftriaxone (34%), cefotaxime (36%), and ciprofloxacin (41%) was substantially lower. This pattern indicates that resistance to commonly prescribed cephalosporins

and fluoroquinolones may be an important therapeutic concern. The observed lower susceptibility of *E. coli* to ceftriaxone and cefotaxime is consistent with previous reports from Pakistan. Long-term surveillance of *E. coli* in Lahore documented high resistance to several beta-lactam antibiotics and cephalosporins, whereas carbapenems retained considerably greater activity. Similarly, a Pakistani antimicrobial stewardship study reported low susceptibility of *E. coli* to several commonly prescribed cephalosporins and co-amoxiclav. *K. pneumoniae* demonstrated a comparable resistance pattern. Susceptibility was relatively high to meropenem (78%), amikacin (72%), and piperacillin-tazobactam (64%), while susceptibility to ceftriaxone (30%), cefotaxime (32%), and ciprofloxacin (38%) was low [25]. The reduced susceptibility to cephalosporins is particularly important because *K. pneumoniae* is a well-recognized producer of extended-spectrum beta-lactamases and other resistance mechanisms. A

study conducted in Khyber Pakhtunkhwa reported substantial resistance among clinical *K. pneumoniae* isolates, including resistance to cefotaxime and other commonly used antimicrobial agents. Another Pakistani study also reported high resistance of *K. pneumoniae* to ampicillin, ceftriaxone, gentamicin, and ciprofloxacin, demonstrating that resistance to multiple antibiotic classes is widespread in this organism. For *P. aeruginosa*, susceptibility was highest to meropenem (74%), amikacin (68%), and piperacillin-tazobactam (63%). However, susceptibility to ceftriaxone (35%), cefotaxime (38%), and ciprofloxacin (45%) was considerably lower. The variable susceptibility pattern observed for *P. aeruginosa* emphasizes the importance of performing susceptibility testing before selecting definitive antimicrobial therapy [26]. The susceptibility profile of *S. aureus* was comparatively

favorable. The highest susceptibility was observed against linezolid (95%) and vancomycin (94%). Susceptibility to amikacin (76%) and gentamicin (68%) was also relatively high, whereas lower susceptibility was observed against cefotaxime (49%), ceftriaxone (51%), and ciprofloxacin (55%). Previous Pakistani surveillance has similarly reported high activity of linezolid and other selected agents against *S. aureus*. In a Lahore study, *S. aureus* demonstrated high susceptibility to linezolid, chloramphenicol, rifampicin, and minocycline. The overall susceptibility pattern indicates that commonly used antibiotics such as fluoroquinolones and cephalosporins may have reduced effectiveness against several Gram-negative pathogens. Therefore, empirical antibiotic therapy should be guided by local susceptibility patterns whenever possible.

Table 3. Antibiotic susceptibility pattern of major bacterial isolates.

Antibiotic	<i>E. coli</i> S (%)	<i>S. aureus</i> S (%)	<i>K. pneumoniae</i> S (%)	<i>P. aeruginosa</i> S (%)
Amikacin	78	76	72	68
Gentamicin	62	68	58	61
Ciprofloxacin	41	55	38	45
Cefotaxime	36	49	32	38
Ceftriaxone	34	51	30	35
Amoxicillin-clavulanate	43	57	39	—
Piperacillin-tazobactam	69	—	64	63
Meropenem	82	—	78	74
Linezolid	—	95	—	—
Vancomycin	—	94	—	—

Overall Susceptibility, Intermediate Response and Resistance

To provide an overall comparison of antimicrobial response, the major bacterial isolates were categorized into susceptible, intermediate, and resistant groups. The resulting distribution is presented in Figure 2. Figure 2 demonstrates that antimicrobial resistance was substantial among the major bacterial pathogens. *K. pneumoniae* showed the highest overall resistant proportion (46%),

followed by *E. coli* (41%) and *P. aeruginosa* (37%). *S. aureus* showed a comparatively lower resistant proportion (31%) and the highest susceptible proportion (55%). The high resistance observed in *K. pneumoniae* is of particular clinical concern [27]. This organism has a strong ability to acquire resistance determinants and can become resistant to multiple antibiotic classes. Studies from Pakistan have reported high rates of multidrug resistance among clinical *K. pneumoniae* isolates. In

a study from Khyber Pakhtunkhwa, substantial resistance was observed against several commonly used antibiotics, with multidrug-resistant isolates representing an important proportion of the bacterial population. The resistant proportion observed for *E. coli* is also consistent with the broader antimicrobial resistance problem reported in Pakistan. Previous long-term surveillance studies have demonstrated very high resistance of *E. coli* to several commonly used beta-lactam antibiotics and cephalosporins. The resistance observed in *P. aeruginosa* is similarly important because this organism possesses several intrinsic and acquired resistance mechanisms [28]. Pakistani surveillance studies have reported substantial resistance among *P. aeruginosa*,

although the exact pattern varies between hospitals and geographical regions. Although *S. aureus* showed a lower overall resistant proportion than the Gram-negative organisms, the presence of 31% resistance remains clinically significant. Continuous monitoring is necessary because resistance among *S. aureus* can change over time and may vary considerably between hospitals. It should be noted that the values presented in Figure 2 represent an overall summary of susceptibility categories and should not be interpreted as the susceptibility to a single antibiotic. Table 3 provides the antibiotic-specific susceptibility percentages, whereas Figure 2 summarizes the broader susceptibility/resistance pattern.

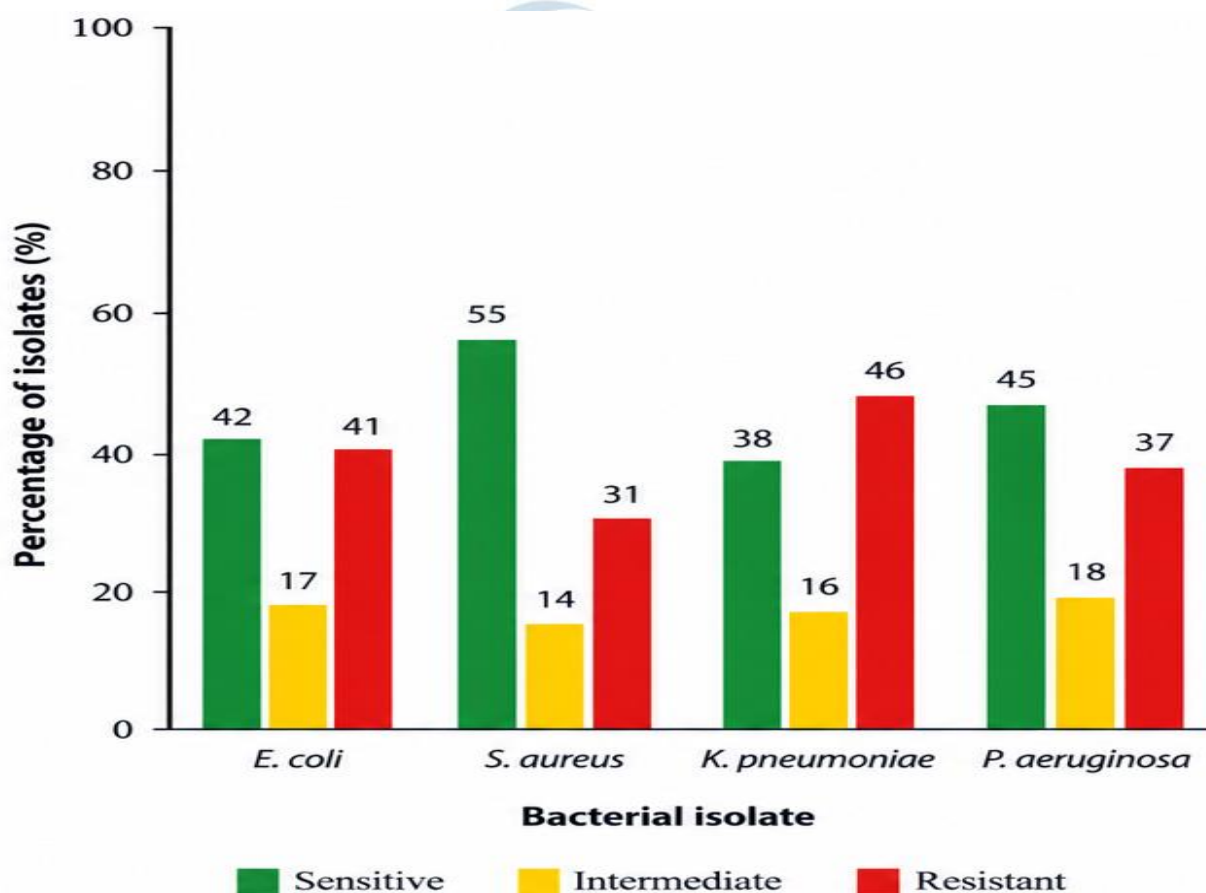


Figure 2. Overall antibiotic susceptibility profile of the major bacterial pathogens isolated from clinical samples, showing the percentages of susceptible, intermediate, and resistant isolates.

Table 4. Overall antibiotic susceptibility, intermediate response, and resistance patterns of major bacterial pathogens isolated from clinical samples.

Bacterial pathogen	Susceptible (%)	Intermediate (%)	Resistant (%)
<i>E. coli</i>	42	17	41
<i>S. aureus</i>	55	14	31
<i>K. pneumoniae</i>	38	16	46
<i>P. aeruginosa</i>	45	18	37

2.3 Comparison of Major Resistance Findings with Previous Pakistani Studies

The antimicrobial susceptibility pattern observed in this study generally follows the broader resistance trends reported from Pakistan. Previous surveillance has demonstrated high resistance among Gram-negative organisms to commonly used beta-lactams, cephalosporins, and fluoroquinolones. For example, a large surveillance study from Punjab reported considerable multidrug resistance among *E. coli*, *K. pneumoniae*, *P. aeruginosa*, and *S. aureus*. The study also identified substantial activity of selected agents such as amikacin, carbapenems, linezolid, and other reserve antibiotics, depending on the bacterial species. The present findings also show relatively better activity of meropenem and amikacin against the major Gram-negative organisms [28]. However, the use of these antibiotics should be carefully controlled because increasing exposure to broad-spectrum and reserve antibiotics can contribute to the development and selection of resistant organisms. The lower susceptibility to ciprofloxacin and third-generation cephalosporins observed in the present dataset is also consistent with resistance trends reported in several Pakistani hospitals. Differences between the present findings and individual published studies may occur because antimicrobial susceptibility patterns are influenced by geographical location, hospital type, patient characteristics, specimen distribution, antibiotic prescribing practices, infection-control measures, and previous antibiotic exposure.

2.4 Clinical Significance and Antimicrobial Stewardship

The findings of the present study have important implications for clinical practice at THQ Hospital Takht Bhai. The presence of substantial resistance

among common bacterial pathogens indicates that empirical antibiotic treatment should be selected carefully and, whenever possible, modified according to culture and susceptibility results. The high frequency of *E. coli*, *S. aureus*, *K. pneumoniae*, and *P. aeruginosa* demonstrates the need for continued local microbiological surveillance. A hospital-specific antibiogram can provide clinicians with information regarding the most appropriate empirical antimicrobial options while reducing unnecessary exposure to ineffective antibiotics [29]. The relatively high susceptibility observed for meropenem and amikacin should not be interpreted as justification for their routine empirical use. These agents should be preserved for appropriate clinical indications and used according to microbiological evidence whenever possible. Similarly, linezolid and vancomycin should be used judiciously because they are important agents for the management of serious Gram-positive infections. Antimicrobial stewardship programs should emphasize appropriate antibiotic selection, correct dosing, appropriate duration of therapy, de-escalation following culture results, and avoidance of unnecessary antimicrobial exposure. Regular surveillance of resistance patterns can help identify emerging resistance and guide hospital antibiotic policies.

2.5 Statistical Analysis

Descriptive statistical analysis showed that 184 (61.3%) of the 300 clinical samples were culture-positive, whereas 116 (38.7%) showed no bacterial growth. The distribution of culture-positive samples varied among specimen types, with the highest positivity observed in wound/pus swabs (69.1%), followed by urine samples (65.7%), sputum (60.0%), other specimens (53.3%), and blood samples (47.7%). A chi-square test was

performed to determine whether culture positivity was significantly associated with the type of clinical specimen. The analysis yielded a χ^2 value of 8.05 with 4 degrees of freedom and a p-value of 0.090. Since the p-value was greater than 0.05, the association between specimen type and culture positivity was not statistically significant. Although the differences were not statistically significant, the higher culture positivity observed in wound/pus and urine specimens may reflect the greater bacterial burden commonly associated with localized wound infections and urinary tract infections [30]. In contrast, the relatively lower positivity in blood samples may be related to factors such as low bacterial load, intermittent bacteremia, prior antibiotic exposure, or limitations in blood culture recovery. These findings indicate that specimen type may influence the observed recovery of bacterial pathogens, although the present dataset did not demonstrate a statistically significant association. Overall, the statistical findings support the descriptive results of the study and emphasize the importance of interpreting bacterial prevalence and antibiotic susceptibility patterns within the clinical and specimen-specific context. Continued surveillance using larger datasets may provide greater statistical power to identify significant differences in pathogen distribution and antimicrobial resistance patterns.

Conclusion

This study demonstrated a substantial burden of bacterial infections and variable antibiotic susceptibility patterns among clinical isolates collected at THQ Hospital Takht Bhai, District Mardan, Khyber Pakhtunkhwa, Pakistan. Among the 300 clinical samples analyzed, 184 (61.3%) yielded bacterial growth, with *Escherichia coli* being the most frequently isolated pathogen, followed by *Staphylococcus aureus* and *Klebsiella pneumoniae*. The bacterial isolates exhibited considerable variation in their susceptibility to commonly used antibiotics, with relatively higher susceptibility observed toward selected aminoglycosides and carbapenems, whereas reduced susceptibility was observed against several cephalosporins and

fluoroquinolones. The observed resistance patterns highlight the growing challenge of antimicrobial resistance in the hospital setting. These findings emphasize the importance of routine culture and antibiotic susceptibility testing before initiating or modifying antimicrobial therapy. Regular hospital-based surveillance, development of local antibiograms, appropriate infection-control practices, and implementation of antimicrobial stewardship programs are recommended to reduce inappropriate antibiotic use and limit the emergence and spread of resistant bacterial pathogens. Continued monitoring of resistance trends at THQ Hospital Takht Bhai will be important for guiding evidence-based antibiotic selection and improving patient outcomes.

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