

Isolation, Identification and Antibiotic Susceptibility Profiling of Bacterial Pathogen from Post-Surgical Wounds

Ayub Jadoon¹, Aiman Sultan¹, Muhammad Nazir Uddin², Sidra Saeed³, Iftikhar Alam¹, Keziah Shaheen⁴, Aroosa¹, Waseem Sajjad^{1*}

¹Department of Microbiology, Abbottabad University of Science and Technology, Abbottabad, Khyber Pakhtunkhwa, Pakistan

² Department of Biotechnology, Genetics, Forensic and Microbiology University of Swat, 19130 Pakistan

³ Department of Zoology, Faculty of Life Sciences, University of Okara, Okara, 56130, Pakistan

⁴ Faculty of Pharmacy, Hamdard University, Islamabad Campus

ARTICLE INFO

*Correspondence to

Ayub Jadoon

Department of Microbiology, Abbottabad University of Science and Technology, Abbottabad, Khyber Pakhtunkhwa, Pakistan

Email: waseemsajjad303@gmail.com

Article History

Received: 13-06-2026

Revised: 16-08-2026

Accepted: 22-08-2026

Published: 30-08-2026

How to Cite

Jadoon A, Sultan A, Sajjad W, Alam I, Aroosa. Isolation, Identification and Antibiotic Susceptibility Profiling of Bacterial Pathogens from Post-Surgical Wounds. Pak J Clin Res. 2025;3(8):48-54 doi:10.65761/pjcr.2026.290

DOI: <https://doi.org/10.65761/pjcr.2026.290>

ABSTRACT

Background: Postoperative wound infections are a major cause of morbidity and mortality and may complicate surgical recovery. The emergence of antimicrobial-resistant pathogens further increases the clinical burden. To determine the frequency of bacterial pathogens responsible for postoperative wound infections in surgical wards and assess their antibiotic susceptibility patterns.

Methods: During a six-month study period, 200 wound samples were collected from patients in surgical wards. Samples were cultured for bacterial isolation and identification, followed by biochemical characterization and antibiotic susceptibility testing. Molecular characterization was performed following DNA extraction and PCR amplification using ITS primers, with subsequent sequencing and phylogenetic analysis.

Results: Of the 200 wound samples, 150 (75%) yielded bacterial pathogens, whereas 50 (25%) were bacteriologically sterile. Among the 120 samples obtained from males, 100 (83.3%) were positive, while 50 (62.5%) of 80 samples from females were positive. The predominant isolates were methicillin-resistant *Staphylococcus aureus* (MRSA), *Pseudomonas aeruginosa*, and *Escherichia coli*. All isolates were catalase-positive. *P. aeruginosa* and *E. coli* were coagulase-negative, whereas MRSA was coagulase-positive; *P. aeruginosa* was also oxidase-positive. Antibiotic susceptibility testing demonstrated substantial resistance, particularly to cefepime in *P. aeruginosa*, ceftriaxone in *E. coli*, and clindamycin in MRSA. PCR amplification produced an approximately 800-bp band, while sequencing and phylogenetic analysis showed up to 90% similarity with *P. aeruginosa*, *E. coli*, and *S. aureus*.

Conclusion: Postoperative wounds remain an important reservoir of pathogenic and antimicrobial-resistant bacteria, highlighting the need for appropriate infection-control practices, microbiological surveillance, and targeted antimicrobial therapy.

Keywords: Antibiotic Susceptibility, Bacterial Pathogens, Post-Surgical Wounds

INTRODUCTION

Skin is one of our innate immune systems. Sweat and sebaceous secretions, which offer protection due to their acidic pH (3–5) and chemicals like fatty acids and lysozyme, which have antifungal properties and dissolve bacterial cells, respectively, prevent infections of subcutaneous and systemic tissues. A wound is a break in the skin that exposes subcutaneous tissues after the integrity of the skin is lost.¹ This creates an environment that is warm, moist, and favorable to the colonization and growth of microorganisms. The successful infiltration and growth of one or more organisms anywhere in the body's sterile tissues, often leading to the development of pus, is known as infection of the wound. There are three types of wounds: post-operative, pathological, and accidental.² Infection, regardless of the type of wound, is the result of bacteria adhering to host cells, multiplying, colonizing, and improving their ability to harm host tissues. Wound colonization or infection may result from the pollutants'

particular growth, division, and establishment rather than their persistence. An infection in a wound can result in wound disintegration, wound herniation, and total wound dehiscence in addition to delaying recovery.³

Gram-positive cocci (GPC) such as Enterococci, *Staphylococcus epidermidis*, *S. aureus*, and *Streptococcus pyogenes*, as well as gram-negative bacilli (GNB) like *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Escherichia coli*, and *Proteus*, make up the bulk of organisms found in wounds. Higher wound classes (dirty-infected wounds) and higher bacterial loads increase the likelihood of a wound infection. Microbes are humans' invisible enemies, causing havoc on both the human body and other living things.⁴ The leading cause of morbidity and mortality is still bacterial infections. Human skin, the nasopharynx, the gastrointestinal tract, and other parts of the body are home to a variety of bacterial species, but because of the body's first line of defense, they are less likely to cause illness.⁵ Human skin and soft



tissue infections (SSTIs) are caused by microbial pathogens during or following trauma, burns, abrasions, minor cuts, lacerations, crush injuries, gunshot injuries, and surgical procedures. Pus, a white or yellow fluid containing dead leukocytes, cellular debris, and devitalized tissue, is produced when the first line of defense is compromised due to bacterial contamination.⁶

An environment that is favorable to the colonization and growth of microorganisms is created when skin integrity is lost for a number of reasons. Wound infection occurs when pathogens from the cutaneous surface, surroundings, or the patient's own flora are drawn to the wound by humidity, heat, and nourishment. These pathogens develop and release different virulence factors. The body's defense system draws immune cells to the site of infection to combat infections.⁷ One of the most worrisome problems in terms of mortality and financial burden is antimicrobial resistance (AMR). Antimicrobial agents, often known as pharmaceuticals, are compounds that can either eradicate bacteria or prevent them from growing. Until the culture report is produced, you can treat the patient empirically by knowing which bacteria are susceptible to certain antibiotics. Unintentional and improper use of antibiotics causes the development of drug-resistant bacteria, which can result in a protracted hospital stay, a large financial loss, and major health issues.⁷

A patient may transmit drug-resistant bacteria to other patients, family members, or even medical staff during an extended hospital stay. As bacteria evolve and patterns of antibiotic use or misuse shift over time, so does the sensitivity of these organisms to antibiotics in a particular environment. The emergence of pathogenic microorganisms resistant to antibiotics is considered a serious threat to public health worldwide. The issue has also been made worse by patient self-medication, doctors prescribing needless antibiotics without properly assessing the bacteria's susceptibility, and the quick and unchecked use of antimicrobials in farming and agriculture. Long-term, careless antibiotic use results in significant genetic alterations in bacteria, which lowers the efficacy of numerous antibiotics and promotes the emergence of AMR. Because of the concerning increase in infections brought on by the introduction of antibiotic-resistant bacteria, managing wound infections has become a major concern.⁸

METHODOLOGY

A hospital-based descriptive microbiological study was conducted at Ayub Teaching Hospital, Abbottabad, Pakistan, from November 2025 to April 2026. The study investigated bacterial pathogens recovered from postoperative wound infections and characterized the isolates according to their phenotypic characteristics, antimicrobial susceptibility profiles, and molecular identification. A total of 200 adult patients admitted to the surgical wards who developed postoperative wound infection within 30 days of surgery were included. Patients aged ≥ 18 years with clinical evidence of surgical-site infection, particularly the presence of purulent discharge from the surgical wound, were considered eligible. Patients with wound infections unrelated to surgical procedures, those who had received antibiotics within 72 hours before specimen collection, and patients without demonstrable bacterial or fungal infection were excluded.

Data were collected using a structured questionnaire adapted from relevant literature and contextualized to the local clinical setting. Information regarding sociodemographic characteristics, clinical history, surgical procedures, hospitalization, and potential risk factors was recorded. Relevant clinical information was additionally obtained from patient medical records. The principal variables and their measurement domains are presented in Table 1.

Table 1. Study variables and data-collection domains

Domain	Variable	Measurement/response
Sociodemographic	Participant ID	Unique identification number
Sociodemographic	Age	Years
Sociodemographic	Sex	Male/Female
Clinical	Type of surgery	Recorded surgical procedure
Clinical	Duration of hospital stay	Days
Clinical	Surgical-site infection	Yes/No
Clinical	Antibiotic use before hospitalization	Yes/No
Risk factors	Personal hygiene	Good/Average/Poor
Risk factors	Contact with infected individuals	Yes/No

Before specimen collection, the surgical wound was cleansed with sterile normal saline to remove superficial contaminants, exudate, and devitalized material. Pus or purulent wound exudate was then collected aseptically using sterile cotton swabs. Specimens were processed promptly and inoculated onto blood agar, MacConkey agar, and chocolate agar, followed by incubation at 37°C for 24–48 hours. Bacterial isolates were initially characterized according to colony morphology and Gram-staining characteristics and were subsequently identified using appropriate biochemical reactions.

Phenotypic and biochemical characterization was performed using standard microbiological procedures. Gram staining was conducted using crystal violet, Lugol's iodine, acetone decolorization, and safranin counterstaining, followed by microscopic examination under oil immersion at 100× magnification.⁹ Catalase activity was determined by observing oxygen-bubble formation following exposure of bacterial colonies to hydrogen peroxide.¹⁰ Coagulase testing was performed to identify coagulase-producing staphylococci based on clot or agglutination formation.¹¹ Oxidase testing was used to detect cytochrome c oxidase activity through the development of a characteristic blue-purple reaction.¹²

For molecular characterization, genomic DNA was extracted from pure overnight bacterial cultures using a boiling-based extraction procedure. DNA concentration and purity were assessed using a NanoDrop spectrophotometer, and extracted DNA was stored at -20°C until further analysis.¹³ DNA integrity was evaluated by electrophoresis on a 1% agarose gel prepared in Tris-borate-EDTA buffer, followed by visualization under ultraviolet illumination.¹⁴ Molecular identification was performed by amplification of the bacterial 16S rRNA gene using universal primers. The amplified products were confirmed by agarose gel electrophoresis, purified, and submitted for Sanger sequencing.^{13,14} The reported PCR thermal profile consisted of an initial denaturation at 94°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 52.7°C for 35 seconds, and extension at 72°C for 2 minutes, with a final extension at 72°C for 5 minutes.

Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk-diffusion method on Mueller-Hinton agar.^{15,16} A bacterial suspension equivalent to a 0.5 McFarland turbidity

standard was prepared and uniformly inoculated onto the agar surface. The antimicrobial agents tested included penicillin, amikacin, cefoxitin, piperacillin-tazobactam, erythromycin, ceftriaxone, clindamycin, ceftazidime, vancomycin, cefepime, linezolid, imipenem, tetracycline, meropenem, and ciprofloxacin. Following incubation at 37°C for 16–18 hours, inhibition zones were measured in millimeters and isolates were categorized according to the applicable antimicrobial susceptibility criteria.^{15, 16}

For sequence analysis, chromatograms were examined and edited using Chromas and BioEdit. Homologous nucleotide sequences were identified using the NCBI BLASTn database. Multiple sequence alignment was performed using CLUSTAL Omega, while phylogenetic relationships among the identified bacterial isolates and reference sequences were inferred using MEGA X with the Fast Minimum Evolution method.¹³

Statistical analysis was performed using IBM SPSS Statistics version 20. Categorical variables were summarized using frequencies and percentages, whereas continuous variables were presented as means and standard deviations. Descriptive analyses were used to characterize the study population, determine the distribution of bacterial isolates, and summarize antimicrobial susceptibility patterns.

RESULTS

A questionnaire was used to gather information from 200 patients at Ayub Teaching Hospital in Abbottabad between 2025 and 2026. Participants in the study must be at least 18 years old. 150 out of 200 patients had post-surgical wounds, according to the questionnaire results.

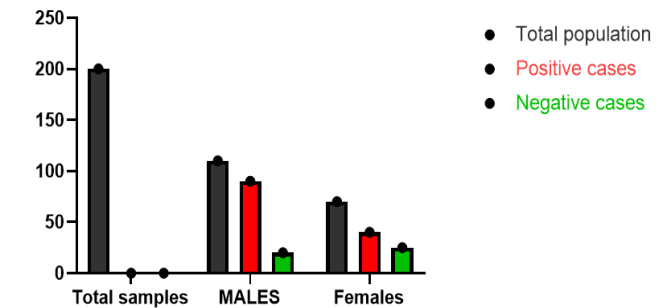
Table 1: Positive and Negative samples distribution

Total samples	200
Positive samples	150
Negative samples	50

Gender wise distribution

The current study investigated samples from 120 males and 80 females. Out of 80 samples, 50 (or 25%) were positive from females, while 100 (or 50%) of the 120 samples from males showed the illness.

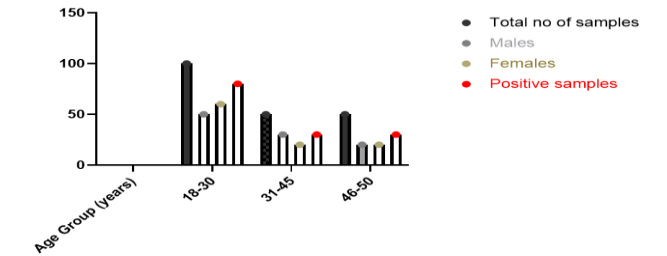
Figure 1: Gender wise distribution post-surgical wounds



Age wise distribution in the study sample set

The participants were divided into four age-based groups for this investigation. These groups ranging from 18-30, 31-45, 46-50.

Figure 2: Age wise distribution of patients in the study sample set



Identification of bacterial isolates

Fifty of the 200 samples were negative, and 150 were positive. Fifty Gram negative isolates and one hundred Gram positive isolates were found from positive samples. The bacteria that were isolated included *Pseudomonas aureginosa*, *E. coli*, and Methicillin-resistant *Staphylococcus aureus*.

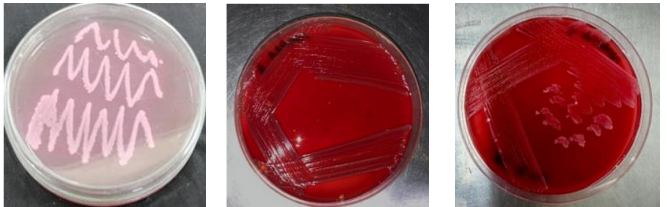
Table 2: Distribution of the causative organisms among positive patients at ATH

Organisms	Total isolated organism
Methicillin resistant <i>Staphylococcus aureus</i>	55
<i>E. coli</i>	70
<i>Pseudomonas aureginosa</i>	25
Total positive samples	150

Morphological characterization

The morphology of the bacterial isolates was then described using several media, including MacConkey medium, blood agar, and chocolate agar. *E. Coli* produces pink colonies on MacConkey agar, *Pseudomonas aureginosa* develops grayish colonies on blood agar, while MRSA forms creamy white colonies on blood agar.

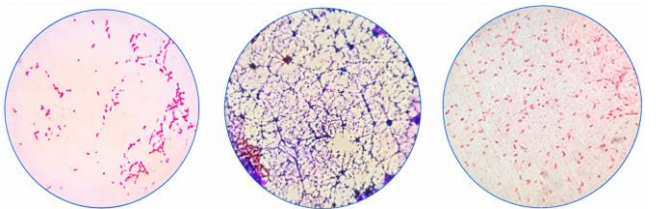
Figure 3: Bacterial growth on media



Gram staining

Following the utilization of the Gram-staining technique, microscopic analysis revealed that *Pseudomonas aureginosa* and MRSA strains were gram-negative rod-shaped bacteria, while *E. Coli* strains were gram-positive cocci grouped in clusters resembling grapes.

Figure 4: Microscopy of bacterial isolates

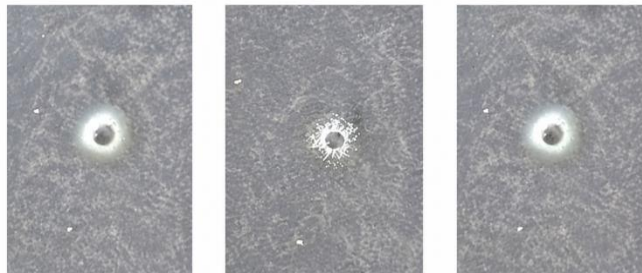


Biochemical characterization of bacterial isolate

Catalase test

After being treated with a few drops of 3% H₂O₂, the isolated bacteria produced gas bubbles on a glass slide, signifying a positive catalase test. More bacterial isolates tested positive for catalase. When a drop of hydrogen peroxide was introduced to its isolates, oxygen bubbles were created. Every strain of bacteria tested positive for catalase.

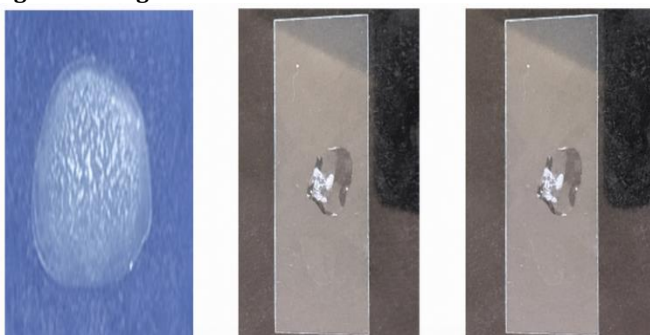
Figure 5: Catalase test results for all bacterial isolates



Coagulase test

A positive test result is indicated by the adherence of bacterial cells following the addition of plasma. If there is no agglutination, the test is negative. *Pseudomonas aureginosa* and *E. coli* strains tested negative for coagulase, however MRSA strain tested positive.

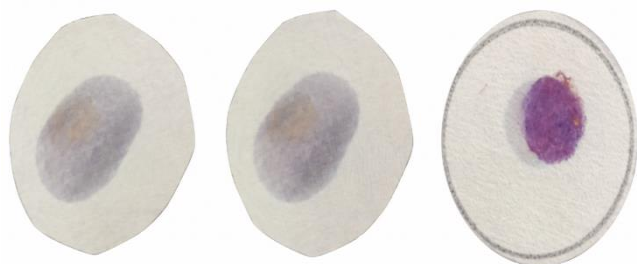
Figure 6: Coagulase test results for all bacterial isolates



Oxidase test

The oxidase test was used to determine the organism's capacity to produce cytochrome c oxidase. In order to determine whether the purple color formed in 30 to 60 seconds, the bacterium tested positive. The oxidase test was performed on each isolated bacterium. *Pseudomonas aureginosa* tested positive for oxidase, although MRSA and *E. coli* strains tested negative.

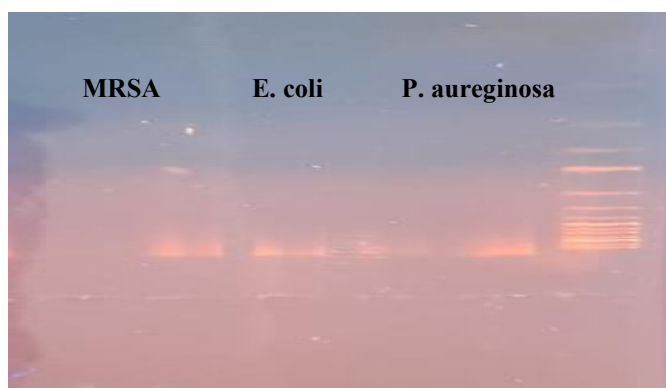
Figure 7: Oxidase test results for all bacterial isolates



DNA extraction

Bacterial strains DNA was isolated using the kit extraction method. After DNA isolation, a gel electrophoresis technique was used to examine the DNA on a 1% agarose gel. The presence of DNA was shown by clear bands. The outcome indicates that the band size of is approximately 800 bp.

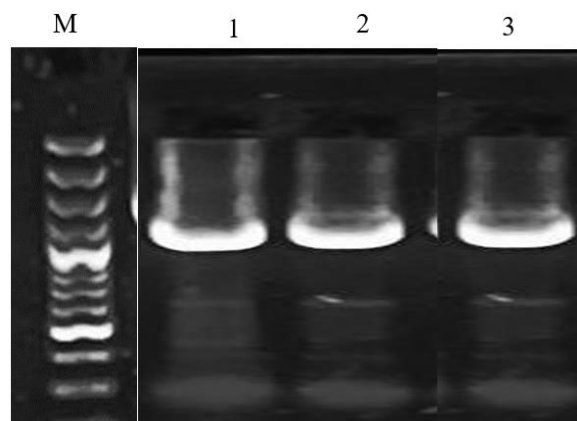
Figure 8: Genomic DNA extraction of Bacterial strains showing clear DNA bands on agarose gel electrophoresis.



PCR

PCR was carried out to molecularly confirm the pathogen using specific primers. The conserved region of MRSA, *E. coli* and *P. aureginosa* was amplified by PCR. The PCR product of about 800 bp bands were obtained using a DNA ladder of 1000 bp (Figure 7).

Figure 9: 16s RNA amplification results for all bacterial isolates



Phylogenetic Analysis

Each bacterial isolate's ITS sequences were blasted using NCBI Nucleotide Blast, and the phylogenetic tree was constructed as earlier described. Bacterial strain found during the investigation was shown to belong to the corresponding *E. coli*, *P. aureginosa* and MRSA by the phylogram topology.

PQ423 731.1	Escherichia coli	1480	550	750	100	768	00	878/927	95%
OQ168 635.1	Pseudomonas aeruginosa	1657	447	567	100	567	00	888/927	95%
OQ626 075.1	MRSA	1345	237	657	100	789	00	894/927	95%

Figure 10: The phylogenetic tree of all bacterial isolates and other relative species based on a neighbor joining method analysis of ITS sequences.

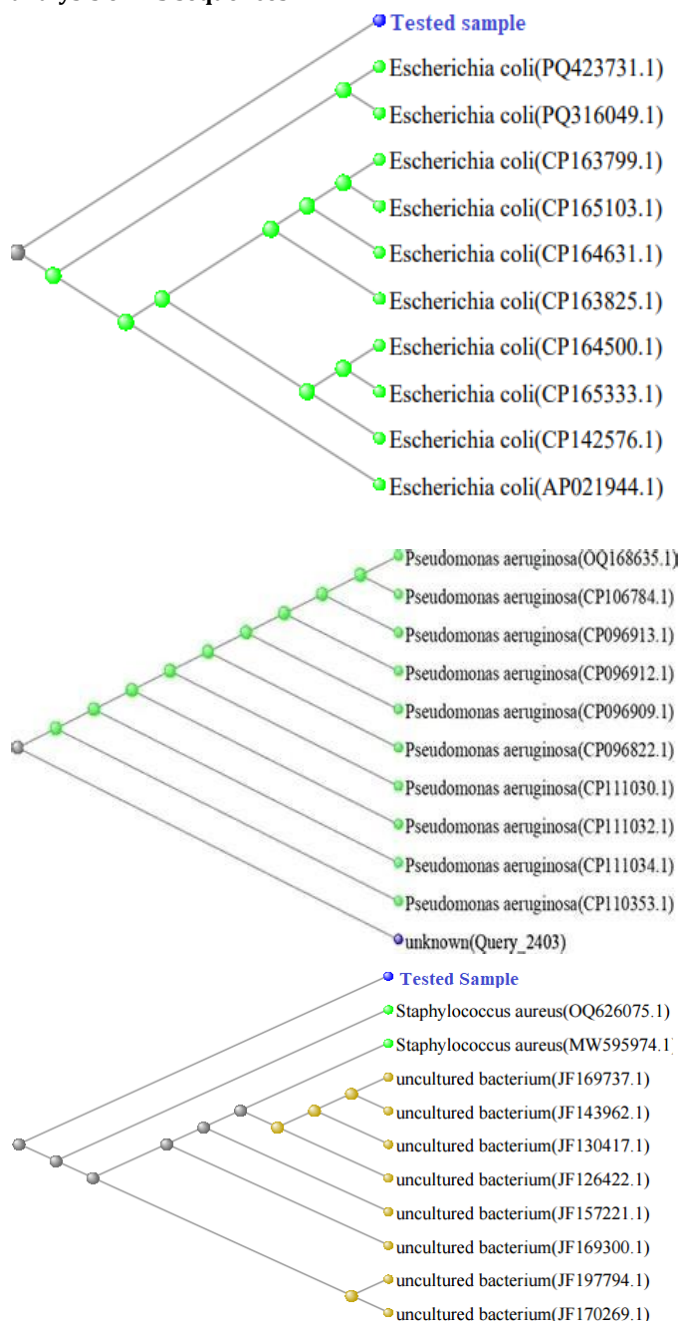


Figure 11: Antibiotic susceptibility testing on Mueller-Hinton agar utilizing the disc diffusion technique. The isolate's susceptibility and resistance to particular antibiotics are indicated by the zones of inhibition surrounding antibiotic discs

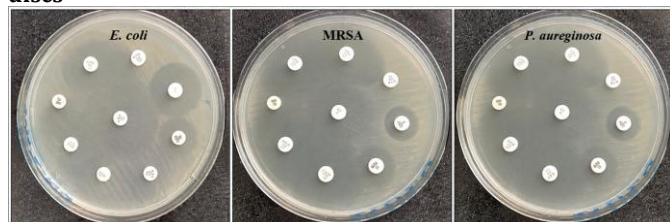


Table 3: Resistant and susceptible Pattern of MRSA

Antibiotic	Sensitivity (%)	Resistance (%)
Penicillin (10U)	7%	93%
Cefoxitin (30µg)	8%	94%
Erythromycin (15µg)	12%	88%
Clindamycin (2µg)	3%	97%
Vancomycin (30µg)	9%	91%
Linezolid (30µg)	15%	85%
Tetracycline (30µg)	12%	88%

Table 1: Resistant and susceptible Pattern of E. coli

Antibiotic	Sensitivity (%)	Resistance (%)
Amikacin (30µg)	8	93
Piperacillin-tazobactam (100/10µg)	7	94
Ceftriaxone (30µg)	0	100
Ceftazidime (30µg)	2	98
Cefepime (30µg)	1	99
Imipenem (10µg)	7	93
Meropenem (10µg)	8	94
Ciprofloxacin (5µg)	7	93

Table 5: Resistant and susceptible Pattern of Pseudomonas aeruginosa

Antibiotic	Sensitivity (%)	Resistance (%)
Amikacin (30µg)	10%	90%
Piperacillin-tazobactam (100/10µg)	20%	80%
Ceftriaxone (30µg)	7%	93%
Ceftazidime (30µg)	8%	94%
Cefepime (30µg)	3%	97%
Imipenem (10µg)	7%	93%
Meropenem (10µg)	8%	94%
Ciprofloxacin (5µg)	12%	88%

DISCUSSION

Postoperative wound infection is an important complication of surgical procedures and may involve the superficial or deep incisional tissues or extend to an organ or body space.⁷ Such infections can delay wound healing, prolong hospitalization, increase healthcare costs, and complicate antimicrobial management, particularly when the causative organisms exhibit antimicrobial resistance. The emergence of multidrug-resistant (MDR) bacterial pathogens has consequently become an important concern in the management of surgical-site infections.¹⁸

The present study focused on the isolation, identification, and antimicrobial susceptibility profiling of bacterial pathogens recovered from post-surgical wounds at Ayub Teaching Hospital, Abbottabad. Pus, purulent exudates, and other wound specimens were collected and transported promptly to the microbiology laboratory for processing. Bacterial isolation was performed using MacConkey agar, blood agar, and chocolate agar. *Pseudomonas aeruginosa* produced grayish colonies on blood

agar, MRSA produced creamy-white colonies on blood agar, whereas *Escherichia coli* produced pink colonies on MacConkey agar. Similar culture-based approaches for recovering bacterial pathogens from postoperative wounds have been reported previously.^{2,5} Gram staining was subsequently performed for preliminary differentiation of bacterial isolates according to their Gram reaction and morphology. Gram-negative organisms are frequently reported among pathogens responsible for postoperative wound infections, although Gram-positive organisms, particularly *Staphylococcus aureus*, also represent important causative agents.^{1,6}

Biochemical characterization further supported the identification of the bacterial isolates. All three principal isolates examined in the present study were catalase-positive. The MRSA isolate was coagulase-positive, whereas *E. coli* and *P. aeruginosa* were coagulase-negative. MRSA and *E. coli* were oxidase-negative, while *P. aeruginosa* demonstrated a positive oxidase reaction. These findings are consistent with the established biochemical characteristics used for differentiating staphylococci, enteric Gram-negative bacilli, and *Pseudomonas* species.^{8,10,11} The observed coagulase positivity of the MRSA isolate and oxidase positivity of *P. aeruginosa* further supported their phenotypic identification.¹¹

Molecular characterization was subsequently performed to strengthen bacterial identification. DNA was extracted from the bacterial isolates, and electrophoretic analysis demonstrated an approximately 800-bp amplified product. The isolates were identified using 16S rRNA gene sequence analysis, an established molecular approach for bacterial identification and phylogenetic characterization.^{12,13} The phylogenetic analysis supported identification of the isolates as *Staphylococcus aureus* (MRSA), *E. coli*, and *P. aeruginosa*. BLASTn analysis further demonstrated sequence similarity between the study isolates and reference sequences corresponding to these bacterial taxa. The application of 16S rRNA sequencing for bacterial identification and comparative sequence analysis has been described in previous investigations.^{12,14}

Antimicrobial susceptibility testing revealed variable susceptibility patterns among the bacterial isolates. In the present study, comparatively greater susceptibility was observed to erythromycin, linezolid, tetracycline, amikacin, and meropenem. In contrast, the most prominent resistance patterns were observed in *P. aeruginosa* against cefepime, *E. coli* against ceftriaxone, and MRSA against clindamycin. Previous investigations have also demonstrated considerable variation in antimicrobial susceptibility among bacterial pathogens recovered from postoperative wounds.¹⁶ The reported resistance patterns emphasize the importance of microbiological culture and antimicrobial susceptibility testing in guiding appropriate treatment.

The presence of antimicrobial-resistant organisms in postoperative wounds is clinically important because inappropriate antimicrobial exposure can favor the selection and persistence of resistant bacterial populations.^{4,18} Differences in resistance patterns between studies may reflect variations in patient populations, bacterial distribution, antimicrobial prescribing practices, local antimicrobial consumption, and infection-prevention measures. Studies from Pakistan and other settings have reported substantial antimicrobial resistance among bacterial isolates recovered from surgical wounds.^{6,17} Such findings highlight the need for continuous local antimicrobial-resistance surveillance and periodic assessment of susceptibility patterns.

The findings of the present study have important implications for postoperative infection management. The recovery of clinically important organisms, including MRSA, *E. coli*, and *P. aeruginosa*,

together with their variable antimicrobial susceptibility profiles, indicates that empirical antimicrobial therapy should be selected cautiously and modified according to culture and susceptibility results whenever possible. Appropriate infection-prevention and control practices, rational antibiotic prescribing, microbiological surveillance, and antimicrobial stewardship are therefore essential components of strategies aimed at reducing postoperative wound infections and limiting the further emergence of antimicrobial resistance.^{1,18}

CONCLUSION

MRSA, *P. aeruginosa* and *E. coli* was the most common pathogen in this investigation, Multidrug resistant isolates are increasingly common in wound infections caused by resistance bacteria. To prevent resistance, hospital antibiotic treatment and disinfection procedures should be strictly followed and routinely reviewed. For post-operative wound infection prevention and management in rural settings, improved preoperative optimization of comorbidities, high-quality healthcare, and thorough surveillance are required. Therefore, it is crucial to periodically monitor infections and antibiotic susceptibility in order to stop the spread of multidrug resistant bacteria.

Ethical Approval

The study was conducted in accordance with the Declaration of Helsinki and was approved by the relevant Institutional Review Board/Ethics Committee of Abbottabad University of Science and Technology (AUST), Abbottabad, Khyber Pakhtunkhwa, Pakistan.

Data Availability

The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Author Contributions

Conceptualization: Ayub Jadoon, Aiman Sultan
Methodology: Ayub Jadoon, Aiman Sultan, Waseem Sajjad
Data Collection: Aiman Sultan, Waseem Sajjad, Aroosa
Formal Analysis: Ayub Jadoon, Waseem Sajjad, Iftikhar Alam
Writing – Original Draft: Muhammad Danyal, Samina Habib
Writing – Review & Editing: Ayub Jadoon, Aiman Sultan, Waseem Sajjad, Iftikhar Alam, Aroosa
All authors take responsibility for all aspects of the research, ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Informed Consent

Written informed consent was obtained from all participants before enrollment in the study.

Funding

This research received no external funding.

Conflict of Interest

The authors declare that they have no competing interests.

Acknowledgments

The authors sincerely acknowledge the cooperation and support of the healthcare professionals and administrative staff of the participating tertiary care hospitals for their assistance during data collection and completion of this study.

Declaration of AI-Assisted Language Editing

Grammarly AI used for language and sentence correction.

REFERENCES

1. Akinkunmi EO, Adesunkanmi AR, Lamikanra A. Pattern of pathogens from surgical wound infections in a Nigerian

- hospital and their antimicrobial susceptibility profiles. *Afr Health Sci.* 2014;14(4):802-9. doi:10.4314/ahs.v14i4.5.
2. Alshara JM. Isolation and identification of bacterial wound infection isolates and their antibiotic susceptibility pattern. *Al-Kufa Univ J Biol.* 2018;10(2):9-19. doi:10.36320/ajb/v10.i2.8126.
3. Amjad D, Rehman A, Malik R, Amjad L, Ullah A, Dalail M, et al. Prevalence and antibiotic susceptibility of MDR bacteria isolated from post-surgical wounds. *Indus J Biosci Res.* 2026;4(2):186-91. doi:10.70749/ijbr.v4i2.2947.
4. Atiang PM. Surgical wound sepsis and respective resistance profiles of the bacterial isolates among post operative patients at Case Hospital [undergraduate dissertation]. 2026.
5. Brown DF, Edwards DI, Hawkey PM, Morrison D, Ridgway GL, Towner KJ, et al. Guidelines for the laboratory diagnosis and susceptibility testing of methicillin-resistant *Staphylococcus aureus* (MRSA). *J Antimicrob Chemother.* 2005;56(6):1000-18. doi:10.1093/jac/dki372.
6. Ennab R, Al-Momani W, Al-Titi R, Elayan A. Antibiotic profile of pathogenic bacteria isolated from postsurgical site infections in public hospitals in Northern Jordan. *Infect Drug Resist.* 2022;15:359-66. doi:10.2147/IDR.S350406.
7. Feier CVI, Teodor A, Muntean C, Faităr OC, Cilibiu CI, Jianu N, et al. Surgical site infections and antimicrobial resistance: six years of data from a Western Romanian hospital. *Medicina (Kaunas).* 2026;62(1):108. doi:10.3390/medicina62010108.
8. Gajic I, Kabic J, Kekic D, Jovicevic M, Milenkovic M, Mitic Culafic D, et al. Antimicrobial susceptibility testing: a comprehensive review of currently used methods. *Antibiotics (Basel).* 2022;11(4):427. doi:10.3390/antibiotics11040427.
9. Gangania PS, Singh VA, Ghimire SS. Bacterial isolation and their antibiotic susceptibility pattern from post-operative wound infected patients. *Indian J Microbiol Res.* 2015;2(4):231. doi:10.5958/2394-5478.2015.00020.5.
10. Hoorzook KB, Barnard TG. Comparison of DNA extraction methods for the direct quantification of bacteria from water using quantitative real-time PCR. *Water.* 2022;14(22):3736. doi:10.3390/w14223736.
11. Hubab M, Ullah O, Hayat A, Rehman MU, Sultana N. Antibiotic susceptibility profile of bacterial isolates from post-surgical wounds of patients in tertiary care hospitals of Peshawar, Pakistan. *J Pak Med Assoc.* 2018;68(10):1517-21.
12. Hudzicki J. Kirby-Bauer disk diffusion susceptibility test protocol. Washington (DC): American Society for Microbiology; 2009. p.1-23.
13. Izadiyan M, Taghavi SM. Isolation and characterization of the citrus canker pathogen *Xanthomonas citri* subsp. *citri* pathotype A, occurring in imported tangerine (*Citrus reticulata* Blanco) fruits. *J Plant Pathol.* 2020;102:671-9. doi:10.1007/s42161-020-00568-5.
14. Kaabi HKJA, Al-Yassari AKS. 16S rRNA sequencing as tool for identification of *Salmonella* spp isolated from human diarrhea cases. *J Phys Conf Ser.* 2019;1294:062041. doi:10.1088/1742-6596/1294/6/062041.
15. Mengesha RE, Kasa BG-S, Saravanan M, Berhe DF, Wasihun AG. Aerobic bacteria in post surgical wound infections and pattern of their antimicrobial susceptibility in Ayder Teaching and Referral Hospital, Mekelle, Ethiopia. *BMC Res Notes.* 2014;7:575. doi:10.1186/1756-0500-7-575.
16. Paray AA, Singh M, Mir MA, Kaur A. Gram staining: a brief review. *Int J Res Rev.* 2023;10(9):336-41. doi:10.52403/ijrr.20230934.
17. Pateriya A, Agrawal M, Sharma R. Microbiological profile in post surgical wound infections and pattern of antimicrobial susceptibility at a tertiary care teaching hospital. *Int J Pharm Clin Res.* 2024;16(3):701-7.
18. Reiner K. Catalase test protocol. Washington (DC): American Society for Microbiology; 2010. p.1-6.