

MICROBIOLOGICAL PROFILE AND ITS ANTIBIOTIC SUSCEPTIBILITY IN DIABETIC FOOT ULCERS

Usman Iqbal^{1*}, Muhammad Imran Anwar², Hafiz M Naeem³, Fariha Ali⁴, Haseeb Ghaffar⁵

^{1,5} MBBS, FCPS-II, Postgraduate Resident (PGR) at Department of General Surgery and Surgical Oncology Unit-I Shaikh Zayed Hospital, Lahore

² MBBS, FCPS, Professor & HOD of Department of General Surgery and Surgical Oncology Unit-I Shaikh Zayed Hospital, Lahore

³ MBBS, FCPS, Consultant General Surgery and Surgical Oncology Unit-I Shaikh Zayed Hospital, Lahore

⁴ MBBS Student Islam Teaching Hospital Sialkot

Correspondence to Usman Iqbal, Email: osmaniqbal293742@gmail.com

Received: 17 May, 2026; Revised: 22 May 2026; Accepted: 12 June, 2026; Published: 22 June 2026

ABSTRACT

Background: Diabetic foot ulcers are a major complication of diabetes mellitus and are associated with increased morbidity, prolonged hospital stay, and risk of lower limb amputation. Identification of bacterial pathogens and their antibiotic susceptibility patterns is essential for effective treatment and prevention of antimicrobial resistance.

Objectives: To isolate and identify the bacterial pathogens associated with diabetic foot ulcers and to assess their antibiotic susceptibility patterns.

Study Design & Setting: This descriptive cross-sectional study was conducted in the General Surgery and Surgical Oncology Unit of Sheikh Zayed Hospital, Lahore from 16 November 2025 to 16 May 2026.

Methodology: A total of 95 patients aged 18 years or older with diabetic foot ulcers and purulent discharge were included through non-probability consecutive sampling. Pus samples or wound scrapings were collected for Gram staining and culture on chocolate agar and CLED agar. Bacterial isolates were identified through biochemical tests, and antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method according to CLSI guidelines. Data were analyzed using SPSS version 20.0.

Results: The mean age of patients was 56.8 ± 11.4 years, and 61 (64.2%) patients were male. Monomicrobial infections were identified in 63 (66.3%) patients, while gram-negative organisms accounted for 57 (60.0%) isolates. *Staphylococcus aureus* was the most common isolate followed by *Pseudomonas aeruginosa* and *Escherichia coli*. Vancomycin and Linezolid showed the highest sensitivity among gram-positive organisms, whereas Meropenem and Piperacillin-Tazobactam were most effective against gram-negative organisms. Significant associations were observed between polymicrobial infections with older age and poor glycemic control.

Conclusion: Gram-negative bacteria were predominant in diabetic foot ulcers, with significant antimicrobial resistance against commonly used antibiotics. Early culture-guided therapy and strict glycemic control may help improve treatment outcomes and reduce complications.

Keywords: Antibiotic susceptibility, Diabetes mellitus, Diabetic foot ulcer, Gram-negative bacteria, Gram-positive bacteria, Microbiological profile

How to cite this article: Iqbal U, Anwar MI, Naeem HM, Ali F, Ghaffar H. Microbiological profile and its antibiotic susceptibility in diabetic foot ulcers. *Int J Drug Deliv Technol.* 2026;16(69s):879-884 DOI: 10.25258/ijddt.16.69s.90

Source of support: Nil.

Conflict of interest: None

INTRODUCTION

Diabetic foot ulcers are among the most common causes of hospital admission related to diabetes mellitus and its complications.¹ Approximately 20–25% of diabetic patients are hospitalized due to foot-related problems.² Diabetic foot infections may range from simple superficial infections such as folliculitis to severe soft tissue and bone infections including cellulitis, abscess formation, necrotizing fasciitis, tendinitis, osteomyelitis, and septic shock.³ Patients with diabetes have nearly a 25% lifetime risk of developing foot ulcers and a significantly increased risk of lower limb amputation compared to non-diabetic

individuals.⁴ The major pathophysiological mechanisms responsible for diabetic foot infections include peripheral neuropathy, peripheral vascular disease, and impaired immune response.⁵

Microvascular disease reduces the delivery of neutrophils and other phagocytic cells to the infected tissue, thereby impairing bacterial clearance and wound healing. Diabetic foot infections may be monomicrobial or polymicrobial in nature. Commonly isolated organisms include *Staphylococcus aureus*, methicillin-resistant *Staphylococcus aureus* (MRSA), *Escherichia coli*, *Proteus* species, *Pseudomonas* species, and *Enterococcus* species.⁶ The prevalence of multidrug-resistant organisms in

*Author for Correspondence: osmaniqbal293742@gmail.com

diabetic foot infections has increased considerably over recent years, posing a major therapeutic challenge.⁷

A study conducted in China in 2021 on 102 patients reported that 54.9% of isolates were gram-negative bacteria, whereas 43.1% were gram-positive bacteria. Similar findings have been reported in studies from India and other Asian countries, while gram-positive organisms were found to be predominant in several Western studies. Antibiotic susceptibility testing in that study demonstrated varying resistance patterns among *Staphylococcus*, *Enterococcus*, *Acinetobacter*, and *Pseudomonas* species against commonly used antimicrobial agents.⁷

Approximately 50–60% of patients with diabetic foot ulcers develop superimposed infections, which significantly worsen clinical outcomes and increase the risk of hospitalization and amputation.⁸ Early administration of empirical antibiotics targeting locally prevalent organisms, followed by culture-sensitive antibiotic therapy, has been shown to improve treatment outcomes. Conversely, irrational and unnecessary use of broad-spectrum antibiotics contributes to antimicrobial resistance, which has become a major global public health concern.⁹

Therefore, identification of the microbiological profile and antibiotic susceptibility patterns of organisms isolated from diabetic foot ulcers is essential for developing local antibiotic guidelines and improving patient management. This study aims to identify the common bacterial pathogens associated with diabetic foot ulcers and evaluate their antibiotic susceptibility patterns in the local population. The objectives of the study were to isolate and identify the bacterial pathogens associated with diabetic foot ulcers and to assess the antibiotic susceptibility patterns of these pathogens.

METHODS

This descriptive cross-sectional study was conducted in the General Surgery and Surgical Oncology Unit of Sheikh Zayed Hospital Lahore from 16 November 2025 to 16 May 2026. The sample size of 95 patients was calculated using the WHO sample size calculator by taking the population proportion of gram-positive bacteria as 43%, confidence level of 95%, and precision of 10%. Non-probability consecutive sampling technique was used. Patients aged 18 years or older with diabetic foot ulcers of any grade and having pus or purulent discharge requiring culture and sensitivity testing were included in the study.¹⁰ Patients who had taken antibiotics for more than 24 hours during the previous 72 hours, had incomplete clinical data, or refused participation were excluded.

The study was conducted after approval from the institutional ethical review board, and informed consent was obtained from all participants. Diabetic patients presenting with foot ulcers in the outpatient, emergency, and inpatient departments were assessed for eligibility through history and clinical examination. Pus samples or wound scrapings were collected and sent for culture and sensitivity testing. Samples were screened by Gram staining and cultured on chocolate agar and CLED agar. Organisms were identified through biochemical tests

including TSI, citrate, SIM, catalase, DNase, oxidase, and bile esculin tests. Antibiotic susceptibility testing was performed by the Kirby–Bauer disc diffusion method according to CLSI guidelines using the 0.5 McFarland standard. Results were reported as susceptible, intermediate, or resistant. Data regarding age, gender, type of bacterial isolate, and antibiotic susceptibility patterns were recorded on a predesigned proforma while maintaining confidentiality.

Diabetic foot ulcer was defined according to the International Working Group on the Diabetic Foot (IWGDF) criteria. Patients fulfilling any two of the following were considered to have diabetic foot ulcers: erythema >0.5 cm around the ulcer, white blood cell count >12,000/mm³ or <4,000/mm³, absence of vibration sensation with a 128 Hz tuning fork on both sides of the hallux, or absence of pressure sensation with a 10 g monofilament at two or more plantar sites. Isolation and identification of bacterial pathogens were performed using pus samples or wound scrapings, which were Gram stained and cultured on chocolate agar and CLED agar. Growth of at least one colony was considered positive. Organisms were identified by biochemical tests including TSI, citrate, SIM, catalase, DNase, oxidase, and bile esculin tests. Antibiotic susceptibility testing was performed by the Kirby–Bauer disc diffusion method according to CLSI guidelines using a 0.5 McFarland standard. Antibiotics showing a zone of inhibition >4 mm were considered susceptible.

Data were analyzed using SPSS version 20.0. Numerical variables such as age were presented as mean $\pm$ standard deviation, while median and interquartile range were used for non-normally distributed data after assessment by the Shapiro–Wilk test. Categorical variables including gender, type of bacterial pathogen, and antibiotic susceptibility patterns were presented as frequencies and percentages. Stratification was performed for age, gender, and glycemic control, and the chi-square test was applied. A p-value ≤ 0.05 was considered statistically significant.

RESULTS

The mean age of the patients was 56.8 ± 11.4 years, while the mean HbA1c level was $8.9 \pm 1.7\%$. Most of the patients were older than 50 years, accounting for 61 (64.2%) cases, whereas 34 (35.8%) patients belonged to the 18–50 years age group. Male patients were predominant with 61 (64.2%) cases, while females comprised 34 (35.8%) of the study population, as given in Table 1.

Table 1: Demographic and Clinical Characteristics of Patients with Diabetic Foot Ulcers (n=95)

Variable	Mean $\pm$ SD / n (%)
Age (years)	56.8 $\pm$ 11.4
18–50 years	34 (35.8)

>50 years	61 (64.2)
HbA1c (%)	8.9 ± 1.7
Male	61 (64.2)
Female	34 (35.8)

Monomicrobial infections were observed in 63 (66.3%) patients, whereas polymicrobial infections were present in 32 (33.7%) patients. Gram-negative bacterial isolates were more common and accounted for 57 (60.0%) isolates, while gram-positive organisms were identified in 38 (40.0%) cases, as given in figure 1.

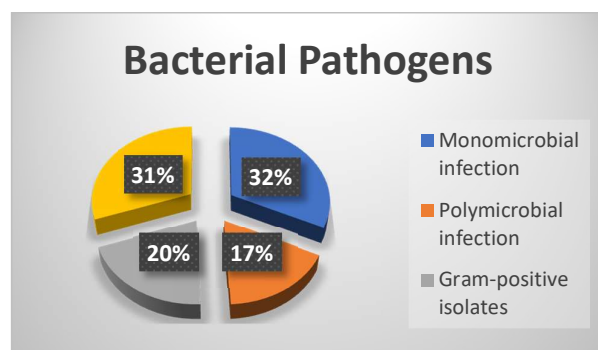


Figure 1: Distribution of Bacterial Pathogens Isolated from Diabetic Foot Ulcers (n=95)

Among the isolated organisms, *Staphylococcus aureus* was the most frequently isolated pathogen found in 24 (25.3%) patients, followed by *Pseudomonas aeruginosa* in 19 (20.0%) and *Escherichia coli* in 17 (17.9%) patients. MRSA was identified in 11 (11.6%) cases, while *Proteus* species, *Klebsiella pneumoniae*, and *Enterococcus* species were isolated in 10 (10.5%), 8 (8.4%), and 6 (6.3%) patients respectively, as given in figure 2.

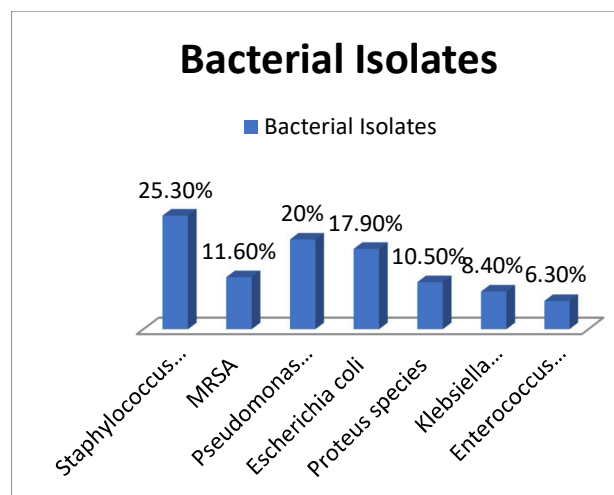


Figure 2: Frequency of Specific Bacterial Isolates in Diabetic Foot Ulcers (n=95)

Among gram-positive organisms, the highest sensitivity was observed against Vancomycin in 35 (92.1%) isolates, followed by Linezolid in 33 (86.8%) isolates. Resistance was highest against Amoxicillin-Clavulanate in 22 (57.9%) isolates and Ciprofloxacin in 20 (52.6%) isolates, as given in Table 2.

Table 2: Antibiotic Susceptibility Pattern of Gram-Positive Organisms (n=38)

Antibiotic	Sensitive n (%)	Resistant n (%)
Vancomycin	35 (92.1)	3 (7.9)
Linezolid	33 (86.8)	5 (13.2)
Clindamycin	24 (63.2)	14 (36.8)
Ciprofloxacin	18 (47.4)	20 (52.6)
Amoxicillin-Clavulanate	16 (42.1)	22 (57.9)

Among gram-negative organisms, Meropenem showed the highest sensitivity in 49 (86.0%) isolates, followed by Piperacillin-Tazobactam in 44 (77.2%) and Amikacin in 41 (71.9%) isolates. The highest resistance was observed against Ciprofloxacin in 36 (63.2%) isolates, followed by Ceftriaxone in 34 (59.6%) isolates, as given in Table 3.

Table 3: Antibiotic Susceptibility Pattern of Gram-Negative Organisms (n=57)

Antibiotic	Sensitive n (%)	Resistant n (%)
Meropenem	49 (86.0)	8 (14.0)
Piperacillin-Tazobactam	44 (77.2)	13 (22.8)
Amikacin	41 (71.9)	16 (28.1)
Ceftriaxone	23 (40.4)	34 (59.6)
Ciprofloxacin	21 (36.8)	36 (63.2)

Stratification analysis showed a statistically significant association between age group and type of infection ($p=0.048$), with polymicrobial infections being more frequent in patients older than 50 years. Glycemic control also demonstrated a significant association with type of infection ($p=0.032$), as patients with HbA1c >8% had a higher proportion of polymicrobial infections. However, no significant association was observed between gender and type of infection ($p=0.421$), as given in Table 4.

Table 4: Stratification of Type of Infection According to Age, Gender, and Glycemic Control (HbA1c) (n=95)

Variable	Type	Monomicro n (%)	Polymicro n (%)	p- value
Age Group	18–50 years (n=34)	26 (76.5)	8 (23.5)	0.048
	>50 years (n=61)	37 (60.7)	24 (39.3)	
Gender	Male (n=61)	39 (63.9)	22 (36.1)	0.421
	Female (n=34)	24 (70.6)	10 (29.4)	
Glycemic Control (HbA1c)	≤8% (n=36)	28 (77.8)	8 (22.2)	0.032
	>8% (n=59)	35 (59.3)	24 (40.7)	

DISCUSSION

T Diabetic foot ulcers are among the most serious complications of diabetes mellitus and are a major cause of morbidity, hospitalization, and lower limb amputations worldwide. Impaired immunity, peripheral neuropathy, and vascular insufficiency predispose diabetic patients to severe foot infections.¹¹ These infections are commonly caused by both gram-positive and gram-negative organisms, with increasing emergence of multidrug-resistant bacteria. Early identification of causative pathogens and their antibiotic susceptibility patterns is essential for appropriate management and prevention of complications.¹² Empirical antibiotic therapy without culture guidance may contribute to antimicrobial resistance and poor clinical outcomes. Therefore, understanding the local microbiological profile and resistance patterns in diabetic foot ulcers is important for developing effective treatment strategies and antibiotic policies.

In the present study, the mean age of patients was 56.8 ± 11.4 years, and most patients were older than 50 years (64.2%), with a male predominance of 64.2%. Monomicrobial infections were more common than polymicrobial infections (66.3% vs. 33.7%). Gram-negative organisms accounted for 60.0% of isolates, whereas gram-positive organisms comprised 40.0%. *Staphylococcus aureus* was the most frequently isolated

pathogen (25.3%), followed by *Pseudomonas aeruginosa* (20.0%) and *Escherichia coli* (17.9%). Among gram-positive organisms, vancomycin showed the highest sensitivity (92.1%), while meropenem demonstrated maximum sensitivity (86.0%) against gram-negative bacteria. Significant associations were observed between polymicrobial infections with older age ($p=0.048$) and poor glycemic control ($p=0.032$). Shanmugam et al. (2013) reported predominance of gram-negative organisms, where 72 out of 92 isolates were gram-negative and only 20 were gram-positive. *Pseudomonas aeruginosa* was the leading isolate (27%), followed by *Klebsiella* species (22%), *E. coli* (19%), and *Staphylococcus aureus* (17%). Our study also demonstrated predominance of gram-negative bacteria (60.0%) with *Pseudomonas aeruginosa* accounting for 20.0% and *E. coli* for 17.9%, although *Staphylococcus aureus* was the most frequent isolate in our population.¹⁴

Jan et al. (2015) from Peshawar observed gram-negative pathogens in more than 60% of diabetic foot infections and reported poor outcomes in advanced disease. These findings closely resemble our results, where gram-negative isolates constituted 60.0% of total pathogens.²³ Miyan et al. (2017) reported that gram-negative organisms accounted for 76.27% of isolates, while polymicrobial infections were observed in 56.87% of patients. *Staphylococcus aureus* was the leading gram-positive isolate, whereas *E. coli* was the commonest gram-negative organism. MRSA was identified in 26.76% of *S. aureus* isolates. Although our study also identified gram-negative predominance and *Staphylococcus aureus* as the leading pathogen, the proportion of polymicrobial infections in our study was comparatively lower (33.7%). Similarly, MRSA was isolated in 11.6% of cases in our study.¹⁹

Amjad et al. (2017) also demonstrated that gram-negative bacteria were more common than gram-positive organisms and observed significant resistance against commonly prescribed antibiotics. Similar resistance trends were observed in our study, where resistance against ciprofloxacin and amoxicillin-clavulanate was high among gram-positive isolates, while ceftriaxone and ciprofloxacin showed poor sensitivity against gram-negative organisms.²¹ Kaimkhani et al. (2018) from Karachi reported predominance of gram-negative organisms, particularly *Pseudomonas aeruginosa* and *E. coli*, along with high resistance against cephalosporins and quinolones. These findings strongly correlate with our study, where ciprofloxacin resistance among gram-negative organisms was 63.2% and ceftriaxone resistance was 59.6%.²²

Ullah et al. (2020) from Peshawar reported predominance of gram-negative aerobes and identified *E. coli* as the commonest pathogen. MRSA was present in 76.6% of *Staphylococcus aureus* isolates, and multidrug-resistant *Pseudomonas* strains were frequently observed. In comparison, our study identified lower MRSA frequency (11.6%), although resistance among gram-negative isolates remained considerably high.¹⁸ Macdonald et al. (2021), in a meta-analysis, concluded that gram-negative organisms

predominated in Asian countries, whereas gram-positive bacteria were more frequent in Western populations. The most common pathogens included *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli*. The microbiological profile observed in our study closely aligns with these findings, supporting the regional predominance of gram-negative pathogens.⁷

Taki et al. (2022) reported that 63.8% of isolates were gram-negative bacteria, with *Pseudomonas aeruginosa* and *E. coli* as the predominant pathogens. They further observed excellent sensitivity of gram-negative organisms to meropenem and amikacin, whereas vancomycin and linezolid were highly effective against gram-positive organisms. Our findings are in close agreement, as meropenem (86.0%) and amikacin (71.9%) showed high sensitivity among gram-negative organisms, while vancomycin (92.1%) and linezolid (86.8%) were highly sensitive against gram-positive isolates.¹³ Ahmad et al. (2022) observed predominance of gram-negative organisms and reported that polymicrobial infections were more frequent among patients with poor glycemic control and advanced age.¹⁶ Similar findings were observed in our study, where statistically significant associations existed between polymicrobial infections with age greater than 50 years ($p=0.048$) and HbA1c $>8\%$ ($p=0.032$). Naem et al. (2023), in a study conducted at Mayo Hospital Lahore, reported predominance of polymicrobial growth and identified *Staphylococcus aureus* as the most abundant isolate. They also highlighted increasing antimicrobial resistance among commonly isolated pathogens. Although our study demonstrated monomicrobial predominance, *Staphylococcus aureus* remained the leading pathogen, and substantial antimicrobial resistance was similarly observed.²⁰

Qasim et al. (2024) reported *Pseudomonas aeruginosa* in 46.6% of diabetic foot ulcer samples and found high resistance against amoxicillin-clavulanic acid, whereas cefoperazone-sulbactam and gentamicin showed good sensitivity. Our findings partially correspond with this study, as *Pseudomonas aeruginosa* was isolated in 20.0% of cases and gram-negative organisms demonstrated marked resistance to commonly used antibiotics.¹⁵ Das et al. (2025) documented a very high prevalence of MRSA, with approximately 92% of *Staphylococcus aureus* isolates being methicillin resistant, indicating rapidly increasing antimicrobial resistance in diabetic foot infections. Although MRSA frequency in our study was lower (11.6%), the emergence of resistant gram-positive organisms remains a significant clinical concern.¹⁷

STUDY LIMITATIONS

This study was conducted at a single tertiary care center with a relatively small sample size, which may limit the generalizability of the findings. Anaerobic bacterial and fungal cultures were not performed, therefore some pathogens may have been missed. Prior undocumented antibiotic use by patients could have affected culture and sensitivity results. In addition, long-term clinical outcomes and treatment response were not evaluated in this study.

CONCLUSION

Gram-negative organisms were more frequently isolated than gram-positive bacteria in diabetic foot ulcers, with monomicrobial infections being predominant. Meropenem and Vancomycin showed the highest sensitivity against gram-negative and gram-positive organisms respectively. Poor glycemic control and older age were significantly associated with polymicrobial infections

REFERENCE

1. Diabetology Bekele F, Chelkeba L, Fekadu G, Bekele K. Risk factors and outcomes of diabetic foot ulcer among diabetes mellitus patients admitted to Nekemte referral hospital, western Ethiopia: Prospective observational study. *Ann Med Surg.* 2020;51:17-23.
2. Jouhar L, Jaafar RF, Nasreddine R, Itani O, Haddad F, Rizk N, et al. Microbiological profile and antimicrobial resistance among diabetic foot infections in Lebanon. *Int Wound J.* 2020;17(5):1764-73.
3. Pitocco D, Spanu T, Di Leo M, Vitiello R, Rizzi A, Tartaglione L, et al. Diabetic foot infections: a comprehensive overview. *Eur Rev Med Pharmacol Sci.* 2019;23.
4. Hurlow JJ, Humphreys GJ, Bowling FL, McBain AJ. Diabetic foot infection: A critical complication. *Int Wound J.* 2018;15(5):814-21.
5. Edmonds M, Manu C, Vas P. The current burden of diabetic foot disease. *J Clin Orthop Trauma.* 2021;17:88-93.
6. Chang M, Nguyen TT. Strategy for treatment of infected diabetic foot ulcers. *Acc Chem Res.* 2021;54(5):1080-93.
7. Macdonald KE, Boeckh S, Stacey HJ, Jones JD. The microbiology of diabetic foot infections: a meta-analysis. *BMC Infect Dis.* 2021;21(1):1-10.
8. Ghotaslou R, Memar MY, Alizadeh N. Classification, microbiology and treatment of diabetic foot infections. *J Wound Care.* 2018;27(7):434-41.
9. Zubair M. Prevalence and interrelationships of foot ulcer, risk-factors and antibiotic resistance in foot ulcers in diabetic populations: A systematic review and meta-analysis. *World J Diabetes.* 2020;11(3):78.
10. Monteiro-Soares M, Russell D, Boyko EJ, Jeffcoate W, Mills JL, Morbach S, et al. Guidelines on the classification of diabetic foot ulcers (IWGDF 2019). *Diabetes Metab Res Rev.* 2020;36:e3273
11. Rathnayake A, Saboo A, Malabu UH, Falhammar H. Lower extremity amputations and long-term outcomes in diabetic foot ulcers: A systematic review. *World journal of diabetes.* 2020 Sep 15;11(9):391.
12. Morris S, Cerceo E. Trends, epidemiology, and

- management of multi-drug resistant gram-negative bacterial infections in the hospitalized setting. *Antibiotics*. 2020 Apr 20;9(4):196.
13. Taki E, Abou Chakra CN, Rekhtman D, et al. Microbial profile and antibiotic susceptibility pattern in diabetic foot ulcer infections. *J Clin Med*. 2022;11(8):2156. doi:10.3390/jcm11082156.
 14. Shanmugam P, Jeya M, Linda SS. The bacteriology of diabetic foot ulcers, with a special reference to multidrug resistant strains. *J Clin Diagn Res*. 2013;7(3):441-5. doi:10.7860/JCDR/2013/5091.2794.
 15. Qasim M, Ahmad N, Rasheed M, et al. Frequency and antimicrobial susceptibility pattern of *Pseudomonas aeruginosa* isolated from diabetic foot ulcers. *J Health Rehabil Res*. 2024;4(2):112-8.
 16. Ahmad S, Khan I, Ali S, et al. Antimicrobial susceptibility patterns in infected diabetic foot ulcers and associated risk factors. *Cureus*. 2022;14(10):e30211. doi:10.7759/cureus.30211.
 17. Das L, Sharma P, Gupta R, et al. Prevalence of methicillin-resistant *Staphylococcus aureus* in diabetic foot infections and associated antimicrobial resistance patterns. *Sci Rep*. 2025;15:42418. doi:10.1038/s41598-026-42418-x.
 18. Ullah I, Ali SS, Ahmed I, Khan MN, Rehman MU, Malik SA. Bacteriological profile and antibiotic susceptibility patterns in diabetic foot infections, at Lady Reading Hospital, Peshawar. *J Ayub Med Coll Abbottabad*. 2020;32(3):383-9.
 19. Miyan Z, Fawwad A, Sabir R, Basit A. Microbiological pattern of diabetic foot infections at a tertiary care center in a developing country. *J Pak Med Assoc*. 2017;67(5):665-9.
 20. Naeem H, Siddiqui MA, Ali MM, Randhawa FA, Nazir S, Farooqui F. Microbial profile and antimicrobial resistance among the diabetic foot ulcers at a tertiary care hospital in Lahore, Pakistan. *BioSci Res*. 2023;20(1):145-52.
 21. Amjad SS, Zafar J, Shams N. Bacteriology of diabetic foot in tertiary care hospital; frequency, antibiotic susceptibility and risk factors. *J Ayub Med Coll Abbottabad*. 2017;29(2):234-40.
 22. Kaimkhani GM, Siddiqui AA, Rasheed N, Rajput MI, Kumar J, Khan MH, et al. Pattern of infecting microorganisms and their susceptibility to antimicrobial drugs in patients with diabetic foot infections in a tertiary care hospital in Karachi, Pakistan. *Cureus*. 2018;10(6):e2872.
 23. Jan Y, Khan SA, Khan M, Gul T, Ahmad I. Presentation, microbiological profile and outcome of diabetic foot ulcers in a tertiary care hospital. *Khyber J Med Sci*. 2015;8(1):25-30.