

Bacteriological Profile and Antibiotic Resistance in Diabetic Foot Infections: A 7-Year Retrospective Study

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Abstract

Diabetic foot is a severe complication of diabetes, the management of which depends on the microbiological profile and antibiotic resistance patterns. This study aimed to describe the bacteriological profile and antibiotic susceptibility of the isolated bacteria. A retrospective study conducted from 2019 to 2025 at the Mohamed V Military Training Hospital in Rabat included 100 patients hospitalised for diabetic foot infection. Clinical and bacteriological data, along with antibiograms, were analysed. The study population was predominantly male (80%; M/F sex ratio = 4), with a mean age of 68.2 years. Among the 125 isolates identified, Gram-negative bacilli predominated (50.4%), followed by Gram-positive cocci (46.4%). The main species isolated were *Staphylococcus aureus* (18.4%), *Klebsiella pneumoniae* (13.6%), *Proteus mirabilis* (11.2%), *Enterococcus faecalis* (9.6%) and *Pseudomonas aeruginosa* (8.8%). Among the *Staphylococcus aureus* strains, 17.4% were methicillin-resistant (MRSA). Among Enterobacteriaceae, 16.0% were producers of extended-spectrum beta-lactamases (ESBL), and a single isolate was a carbapenemase producer. Multidrug-resistant strains of *Pseudomonas aeruginosa* were observed in 27.3% of cases. By documenting the local bacterial flora and resistance burden, this study highlights the high prevalence of multidrug-resistant pathogens in diabetic foot infections, demonstrating the essential need to adapt empirical antibiotic regimens to regional epidemiology and systematically guide targeted therapy using antibiogram results.

Keywords: Antibiogram, antibiotic therapy, bacterial resistance, bacteriological profile, diabetic foot, extended-spectrum beta-lactamases, infection, *Staphylococcus aureus*.

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INTRODUCTION

Diabetes represents a major global public health problem. According to the most recent estimates from the World Health Organization, more than 830 million people worldwide are affected by this condition. In 2024, this disease and its complications were responsible for approximately 3.4 million deaths, accounting for nearly 9.3% of overall adult mortality. Furthermore, the prevalence of diabetes among adults is estimated at 11.1%, compared with approximately 7% in 1990, reflecting a sustained and concerning increase over recent decades [World Health Organization, 2024].

In Morocco, in 2024, the prevalence of diabetes among adults aged 20 to 79 years is estimated at 11.9%, corresponding to nearly 2.88 million people, according

to the International Diabetes Federation [International Diabetes Federation, 2024].

Beyond its systemic effects, diabetes gives rise to numerous complications, among which diabetic foot holds a prominent place, representing a frequent cause of morbidity, hospitalisation and amputation. The lifetime risk of developing a diabetic foot infection affects approximately 15% of diabetic patients [Qu *et al.*, 2024].

This infection generally occurs in patients whose condition is compromised by peripheral polyneuropathy and arterial disease, both of which are linked to the duration of diabetes and the effectiveness of glycaemic control [Zanella *et al.*, 2016].

Thus, the management of diabetic foot infections constitutes a major clinical challenge, and

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precise knowledge of the microbiological profile of these infections is essential for implementing a strategic antibiotic therapy in the face of the growing presence of multidrug-resistant strains.

This study aims to investigate the epidemiological and bacteriological profile, as well as the antibiotic resistance patterns, of isolates responsible for diabetic foot infections at the Mohammed V Military Training Hospital in Rabat.

MATERIALS AND METHODS

This was a descriptive retrospective study conducted over seven years (January 2019 - December 2025) among 100 patients hospitalised for diabetic foot at the Mohamed V Military Training Hospital in Rabat.

The study included all adult diabetic patients hospitalised for a diabetic foot infection who underwent a microbiological sample collection. Patients with a history of diabetic foot were also included, in order to account for recurrent cases.

Exclusion criteria comprised patients with foot infections unrelated to diabetes, incomplete medical records, and the absence of a usable microbiological sample.

Bacteriological samples were collected using various techniques: fine-needle aspiration of deep pus, intraoperative bone biopsy, swabbing, or collection of superficial pus.

Samples received at the bacteriology laboratory first underwent macroscopic evaluation.

Direct examination after Gram staining was performed to provide an initial diagnostic orientation.

Superficial samples were inoculated onto Columbia agar enriched with 5% horse blood, Polyvitex chocolate agar, and Mannitol salt agar (Chapman). For possible yeast detection, inoculation onto Sabouraud Chloramphenicol agar was also performed. All media were incubated at 37°C under an aerobic atmosphere enriched with 5% CO₂ for 48 hours. Deep samples were inoculated onto Columbia agar enriched with 5% horse blood and Polyvitex chocolate agar. Additional inoculation was performed onto Schaedler agar and onto blood agar supplemented with colistin and nalidixic acid,

incubated under strictly anaerobic conditions. All cultures were maintained at 37°C for 48 hours.

Brain-heart infusion enrichment broths from deep samples were subcultured onto CNA and Polyvitex chocolate agar plates and then incubated at 37°C in an aerobic atmosphere containing 5% CO₂ to optimise the isolation of low-abundance or slow-growing organisms.

Bacterial identification was performed using conventional culture methods and biochemical tests. Antibiotic susceptibility was assessed by the agar diffusion method, and antibiogram interpretation was carried out in accordance with the CASFM-EUCAST 2024 recommendations.

Clinical and microbiological data were collected from medical records and the laboratory information system.

Data entry and processing were carried out using Microsoft Word and Excel (Microsoft 365, version 2604), while statistical analysis was performed using Jamovi software (version 2.6.44).

RESULTS

We collected data on 100 patients, including 80 men and 20 women, corresponding to a male-to-female sex ratio of 4. The mean age of our patients was 68.2 ± 11.4 years, with a range from 25 to 91 years.

Among the 100 patients included in the study, 75% presented with wet gangrene, while 25% had osteitis. Furthermore, 23% of patients (n=23) had a history of amputation, of whom 74% developed stump superinfection (n=17).

The mean glycated haemoglobin (HbA1c) level was $8.74 \pm 2.19\%$, with values ranging from 5.3% to 16.0%.

The study population mainly consisted of patients with type 2 diabetes (92%, n = 92), with type 1 diabetes accounting for 8% (n = 8) of cases. The main comorbidities were hypertension (38%, n = 38), ischaemic heart disease (14%, n = 14), and end-stage chronic kidney disease, including haemodialysis patients (8%, n = 8). A history of smoking, active or discontinued, was found in 7% of patients (n = 7), ischaemic stroke in 6% (n = 6), valvular heart disease in 3% (n = 3), and atrial fibrillation in 1% (n = 1) (Figure 1).

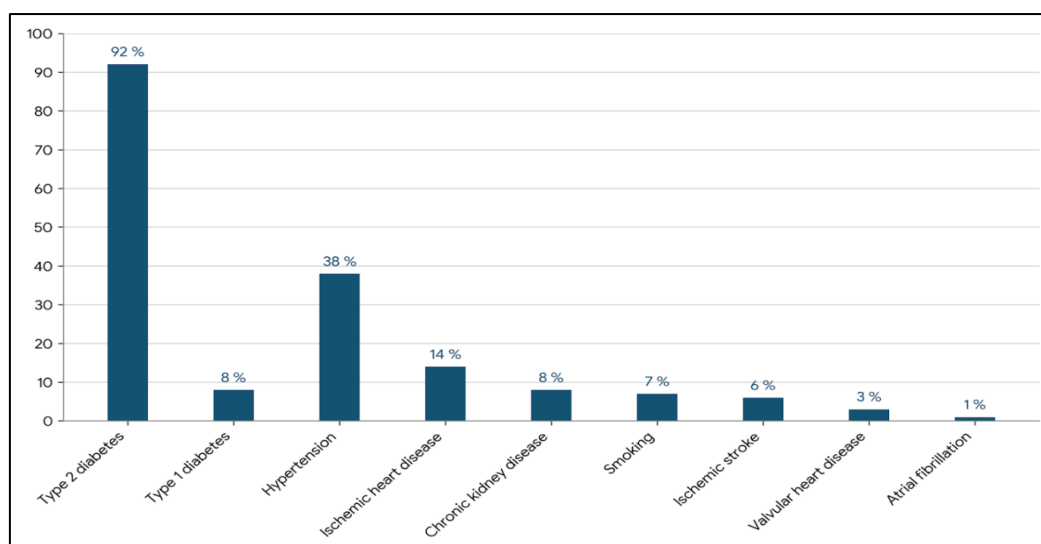


Figure 1: Medical history of patients with diabetic foot infection

56% (n = 56) of patients had a white blood cell count above 12,000 cells/mm³, indicating severe or grade 4 infection [Senneville *et al.*, 2024].

The distribution of samples was dominated by intraoperative deep samples in 94% of cases, followed by superficial samples obtained by swabbing (6%). Among the deep samples, 62% were fine-needle aspirations, 23% were bone biopsies, and 9% were tissue obtained from necrosectomy.

Of the 100 samples analysed, 85% of cultures were positive, while 15% were sterile. Among the 85 positive cultures, 56.5% (n = 48) were monomicrobial and 43.5% (n = 37) were polymicrobial, encompassing bi-, tri-, and quadrimicrobial cultures.

Among the 125 microbiological isolates analysed overall, Gram-negative bacilli were slightly predominant, accounting for 50.4% of isolates (n = 63), followed by Gram-positive cocci, which represented 46.4% (n = 58). The remaining isolates (3.2%, n = 4) comprised strict anaerobic bacteria and yeasts (Figure 2).

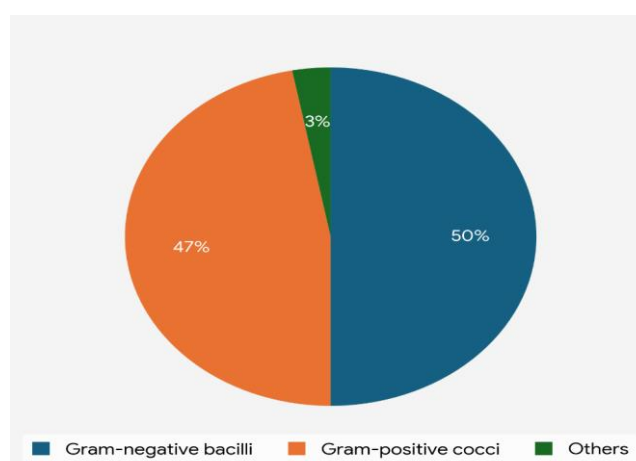


Figure 2: General distribution of isolated bacterial strains

Regarding the distribution of isolates by species, *Staphylococcus aureus* was the most frequently isolated organism (18.4%, n = 23), followed by *Klebsiella pneumoniae* (13.6%, n = 17), *Proteus mirabilis* (11.2%, n = 14), *Enterococcus faecalis* (9.6%, n = 12), *Pseudomonas aeruginosa* (8.8%, n = 11), *Streptococcus agalactiae* (7.2%, n = 9), and alpha-haemolytic streptococci (5.6%, n = 7).

The other bacteria and yeasts were represented at lower rates: *Enterobacter cloacae* and *Morganella morganii* (4.0% each, n = 5), *Escherichia coli* (2.4%, n = 3), followed by *Acinetobacter baumannii*, *Candida spp*, *Citrobacter freundii*, *Proteus vulgaris*, *Providencia rettgeri*, and *Streptococcus constellatus* (1.6% each, n = 2). Strict anaerobic isolates also accounted for 1.6% of cases (n = 2). Other minor organisms were isolated at lower rates (Figure 3).

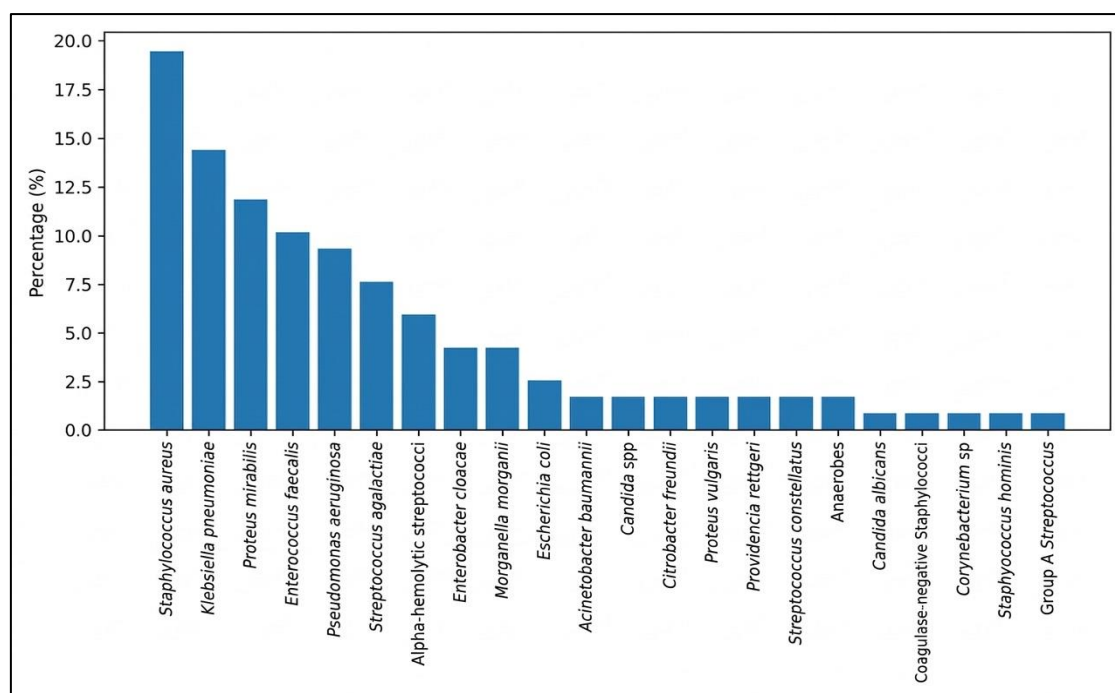


Figure 3: Overall distribution of isolated organisms

1-Resistance profile of Gram-negative bacteria

1-1 Resistance profile of Enterobacteriaceae

✓ Overall profile of Enterobacteriaceae

Enterobacteriaceae accounted for 40% of bacterial isolates (n = 50). Among these, an ESBL phenotype was identified in 16.0% of isolates (n = 8), while a single isolate (2.0%) produced a carbapenemase.

Enterobacteriaceae isolates showed high resistance to amoxicillin-clavulanic acid (59.1%) as well as to fluoroquinolones (34.1%). Lower resistance rates were observed for third-generation cephalosporins (15.9%), while resistance remained minimal for imipenem (4.5%) and amikacin (2.3%) (Figure 4).

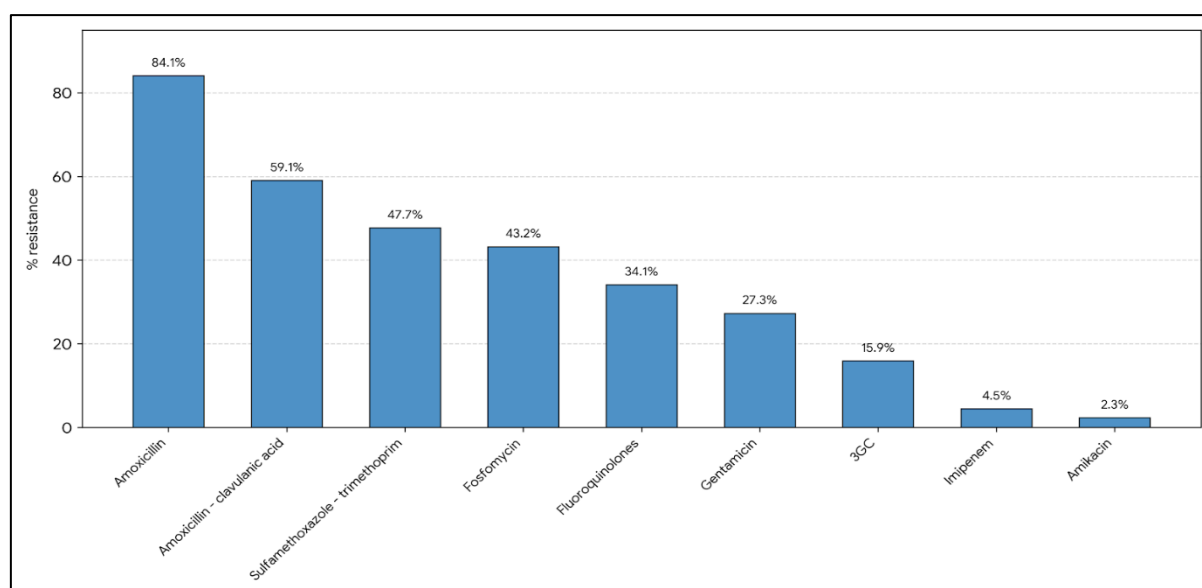


Figure 4: Antibiotic resistance rates of Enterobacteriaceae isolates

✓ Resistance profile by species

➤ *Klebsiella pneumoniae*

The susceptibility study showed a resistance rate to AMC of 70.6% (n=12), to third-generation cephalosporins (cefotaxime) of 35.3% (n=6), to gentamicin of 41.2% (n=7), to imipenem of 5.9% (n=1),

to fluoroquinolones of 58.8% (n=10), and to SXT of 64.7% (n=11). The ESBL phenotype accounted for 35.3% of isolates (n=6), among which one case of carbapenemase co-production was identified (5.9%, n=1) (Figure 5).

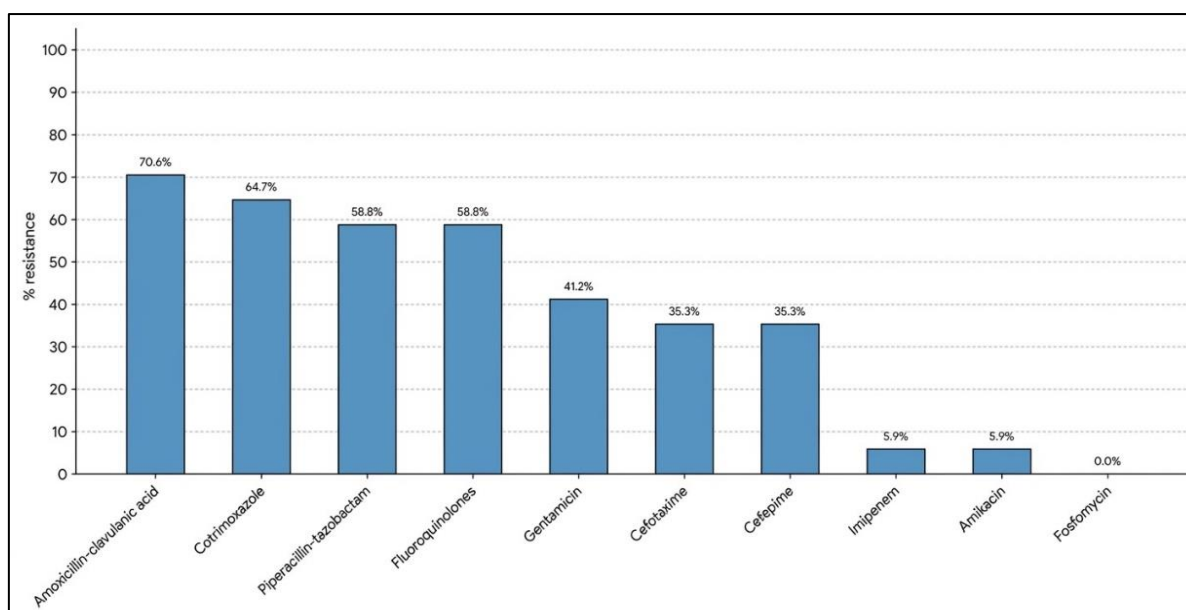


Figure 5: Resistance rate of isolated *Klebsiella pneumoniae* strains

➤ ***Proteus mirabilis***

The susceptibility study showed a resistance rate to amoxicillin of 50.0% (n=7), to AMC of 14.3%

(n=2), to third-generation cephalosporins (cefotaxime) of 0.0% (n=0), to imipenem of 7.1% (n=1), and to fluoroquinolones of 14.3% (n=2) (Figure 6).

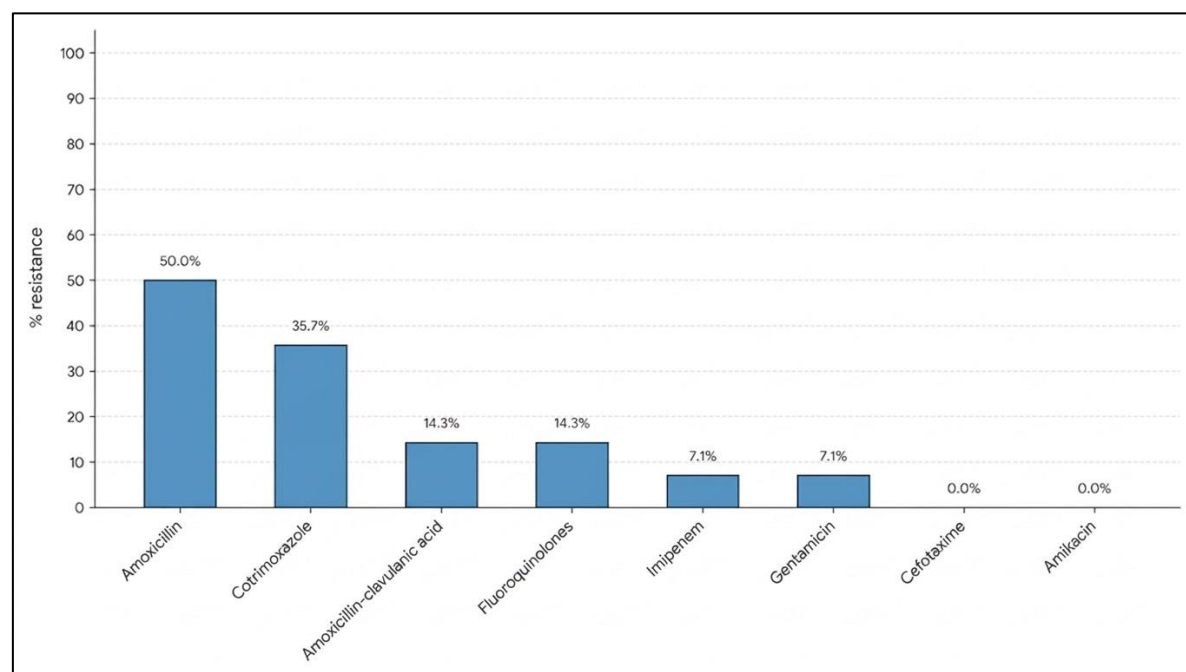


Figure 6: Resistance rate of isolated *Proteus mirabilis* strains

➤ ***Enterobacter cloacae***

Susceptibility testing showed a resistance rate to third-generation cephalosporins (cefotaxime) of 20.0% (n=1), to cefepime of 20.0% (n=1), to gentamicin of 20.0% (n=1), to imipenem of 0.0% (n=0), to fluoroquinolones (ciprofloxacin) of 20.0% (n=1), and to SXT of 40.0% (n=2). A single isolate (20.0%, n = 1)

showed a multidrug-resistant profile including cefotaxime and cefepime. The use of a supplementary agar containing cloxacillin allowed the masking effect of chromosomal cephalosporinase AmpC to be lifted and confirmed the presence of a co-existing ESBL (Figure 7).

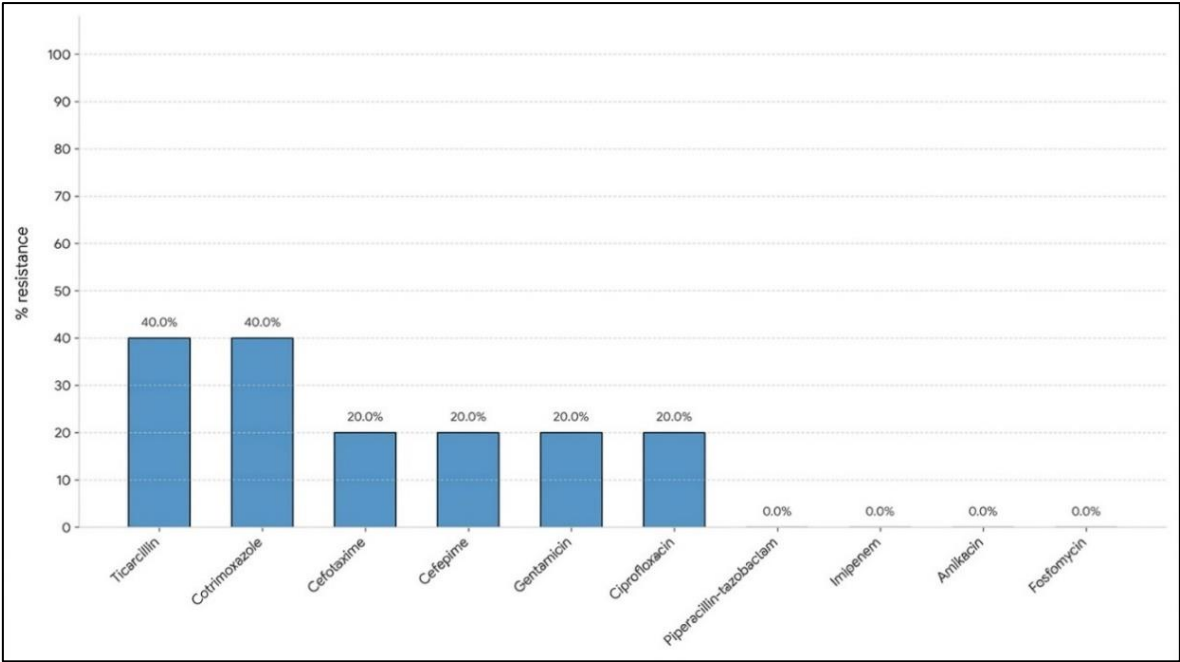


Figure 7: Resistance rate of isolated *Enterobacter cloacae* strains

➤ *Morganella morganii*

Susceptibility testing showed a resistance rate to third-generation cephalosporins (cefotaxime) of 0.0% (n=0), to cefepime of 20.0% (n=1), to gentamicin of

20.0% (n=1), to imipenem of 0.0% (n=0), to fluoroquinolones (ciprofloxacin) of 40.0% (n=2), and to SXT of 20.0% (n=1). No ESBL phenotype was identified (Figure 8).

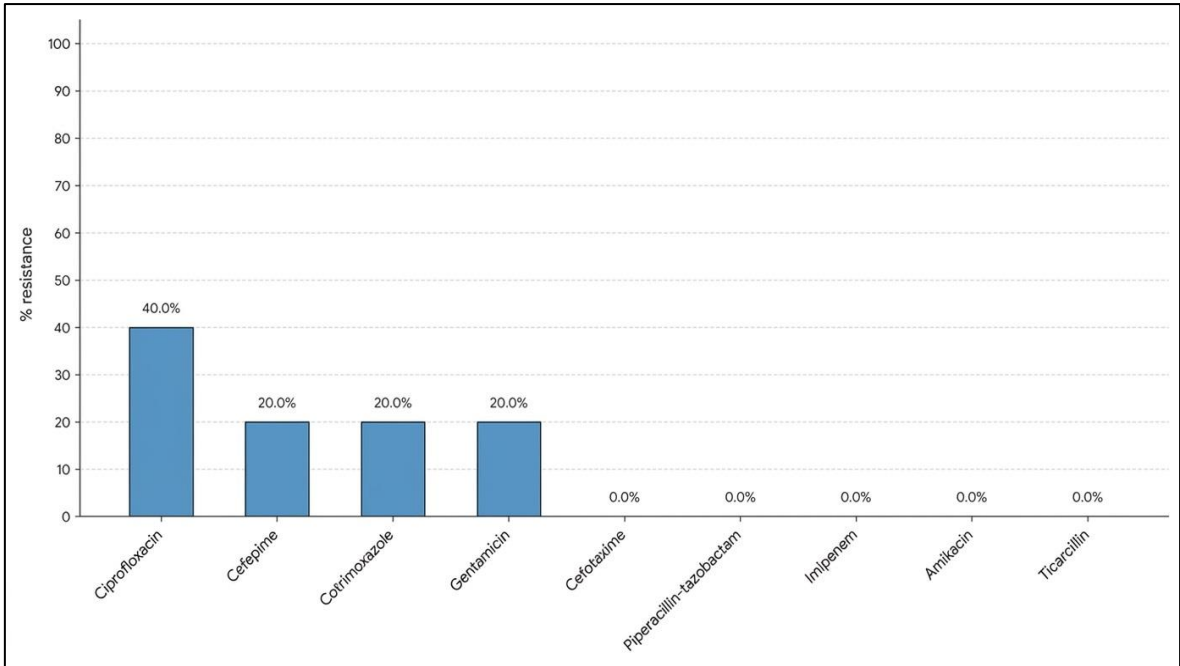


Figure 8: Resistance rate of isolated *Morganella morganii* strains

➤ *Escherichia coli*

Susceptibility testing showed a resistance rate to AMC of 66.7% (n=2), to third-generation cephalosporins (cefotaxime) of 0.0% (n=0), to

gentamicin of 66.7% (n=2), to imipenem of 0.0% (n=0), to fluoroquinolones (ciprofloxacin) of 0.0% (n=0), and to SXT of 66.7% (n=2). No ESBL phenotype was identified (Figure 9).

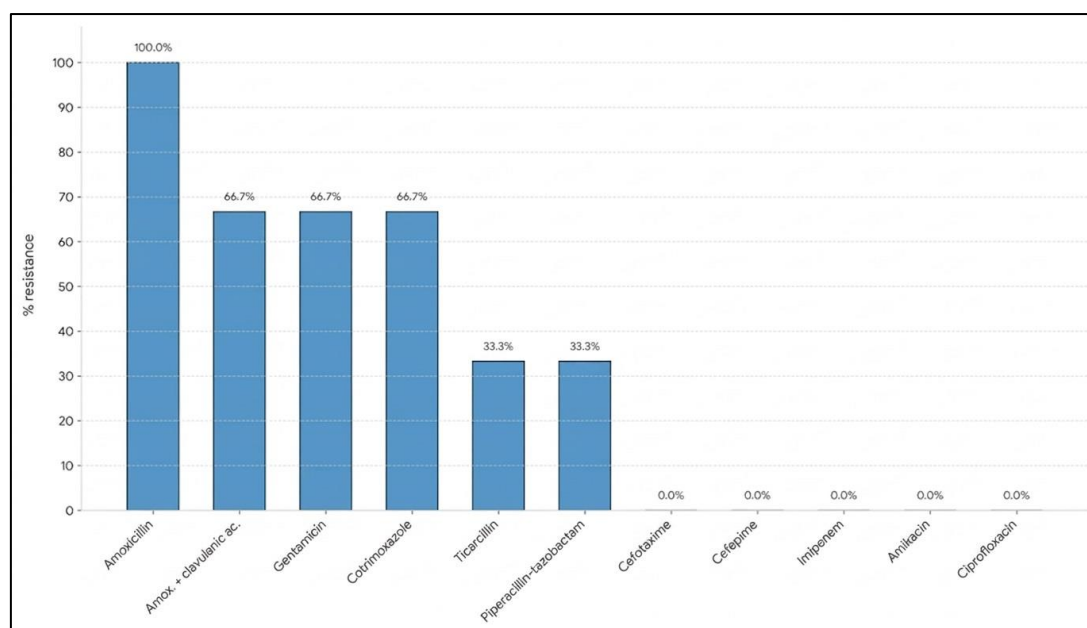


Figure 9: Resistance rates of isolated *Escherichia coli* strains

1-2 Resistance profile of non-fermenting Gram-negative bacteria

➤ *Pseudomonas aeruginosa*

Pseudomonas aeruginosa isolates showed a resistance rate of 45.5% to ceftazidime (n = 5) and 36.4% to carbapenems (n = 4). Fluoroquinolones showed

resistance rates of 63.6% for levofloxacin and 54.5% for ciprofloxacin. Multidrug-resistant strains were identified in 27.3% of cases (n = 3), and one isolate produced a metallo-beta-lactamase (9.1%, n = 1). Colistin remained active against all strains (Figure 10).

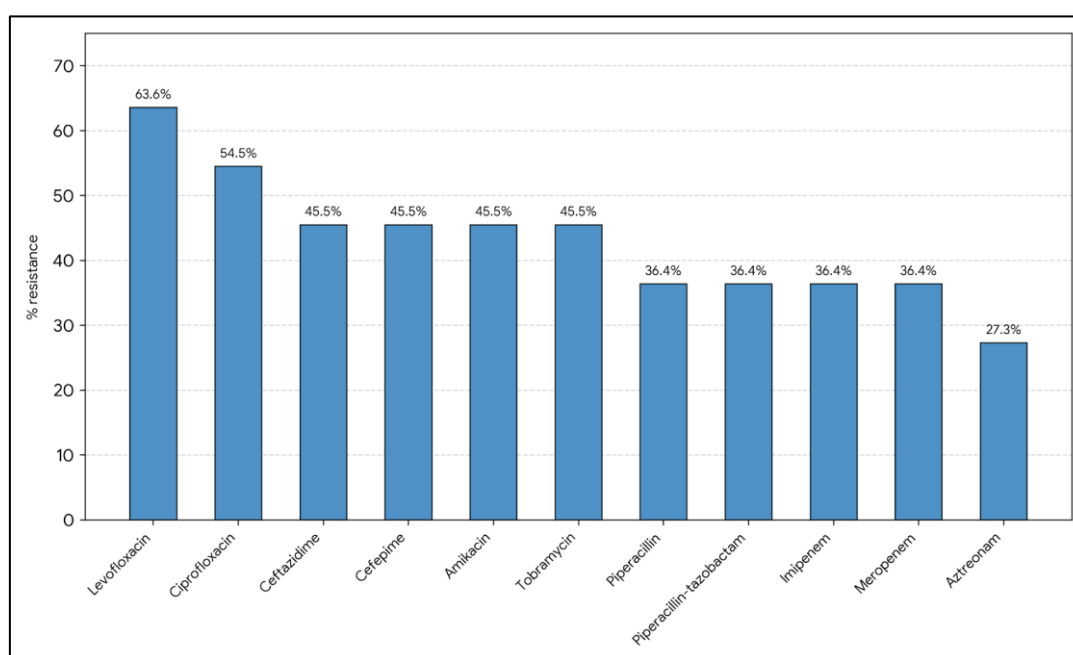


Figure 10: Resistance rates of isolated *Pseudomonas aeruginosa* strains

➤ *Acinetobacter baumannii*

Acinetobacter baumannii isolates showed 100% resistance to most of the molecules tested (beta-lactams, aminoglycosides, fluoroquinolones), while all strains were found to be susceptible to colistin following determination of the minimum inhibitory concentration.

2- Resistance profile of gram-positive cocci

➤ *Staphylococcus aureus*

17.4% of isolates were methicillin-resistant (n=4), while 17.4% of strains (n=4) showed resistance to clindamycin (Figure 11).

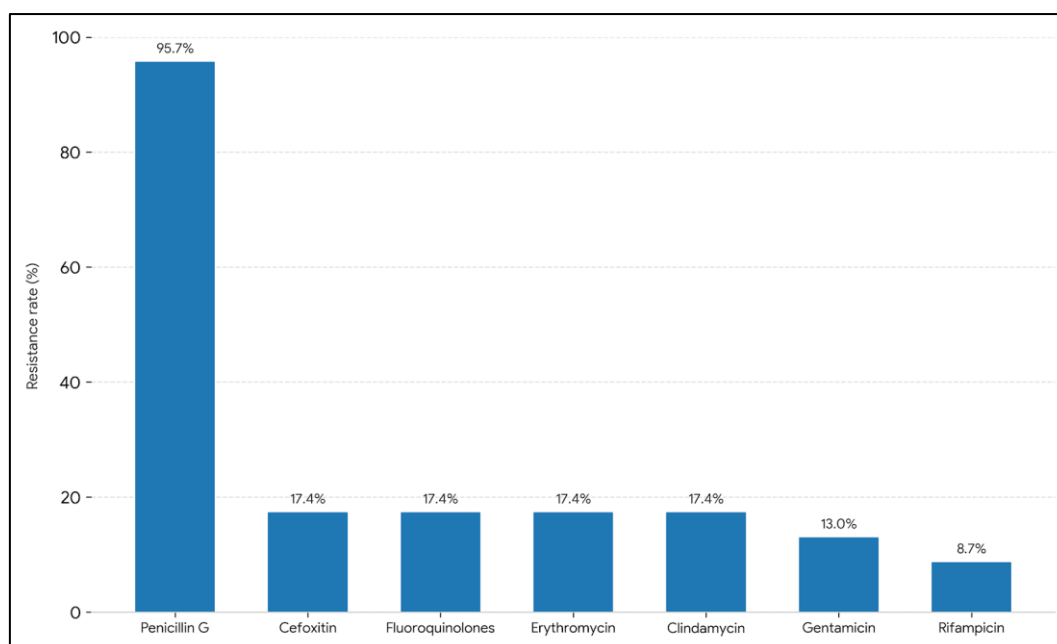


Figure 11: Resistance rates of isolated *Staphylococcus aureus* strains

➤ ***Enterococcus faecalis***

No high-level resistance to aminoglycosides, glycopeptides, or linezolid was observed.

➤ ***Streptococcus agalactiae***

No resistance to penicillin G, ampicillin, glycopeptides, or linezolid was observed.

➤ **α -hemolytic streptococci**

Resistance to penicillin G and ampicillin was observed in 14.3% of isolates (n=1). No resistance to glycopeptides or linezolid was observed.

DISCUSSION

A diabetic foot infection is defined as any skin, soft tissue, or bone infection affecting the tissues below the ankle in diabetic patients [Senneville *et al.*, 2024].

They affect nearly 10 to 15% of people with diabetes and represent the main cause of non-traumatic lower-limb amputations [Ghotaslou *et al.*, 2018].

Infection is most often a secondary phenomenon occurring in a compromised host weakened by peripheral artery disease and peripheral polyneuropathy, both closely linked to the duration of diabetes and the quality of glycemic control [Macdonald *et al.*, 2021].

Most patients develop a superficial ulceration or wound, which can progress to an abscess, cellulitis, fasciitis, osteomyelitis, and/or joint involvement, with or without systemic infection [World Health Organization, 2024].

In our study, males accounted for the majority of patients (80%), with a mean age of 68.2 years. These findings align with the study by Djibril *et al* conducted in Togo, which also reported a male predominance and a mean age between 60 and 65 years among patients with diabetic foot [Djibril *et al.*, 2018]. Similarly, Stańkowska *et al* and Chai *et al* observed an advanced mean age and a male predominance in their European and Asian series [Stańkowska *et al.*, 2022] [Chai *et al.*, 2021].

An American retrospective study involving over one million cases of diabetic foot infections reported a median age of 67 years and a marked male predominance [Duhon *et al.*, 2016].

Advanced age and male sex are major risk factors for diabetic foot complications due to the accumulation of comorbidities, neuropathies, and peripheral artery disease, altered immunity, as well as differences in healthcare-seeking behaviors and exposures among men [Petrone *et al.*, 2021] [Hu *et al.*, 2024].

The mean HbA1c in our study was 8.74%, with a wide range reaching up to 16%, indicating pronounced glycemic dysregulation in many patients. This is consistent with literature data showing that poor glycemic control promotes the onset and worsening of diabetic foot infections by impairing the immune response and delaying wound healing [Lane *et al.*, 2020].

In our study, 56% of patients had a white blood cell count greater than 12,000 cells/mm³, reflecting a notable systemic inflammatory response. Indeed, according to the International Working Group on the Diabetic Foot (IWGDF) classification, a foot infection in

a diabetic patient is considered Grade 4 (severe) when accompanied by at least two systemic signs (SIRS criteria), including a white blood cell count $> 12,000/\text{mm}^3$ or $< 4,000/\text{mm}^3$ [Senneville *et al.*, 2024].

Table 1 presents the classification of diabetic foot infections according to the Infectious Diseases Society of America (IDSA) and the (IWGDF) [Lipsky *et al.*, 2012].

Table 1: Classification of diabetic foot infections according to the IDSA and IWGDF

Clinical Manifestation of Infection	PEDIS Grade	IDSA Infection Severity
No symptoms or signs of infection	1	Uninfected
Infection present, as defined by the presence of at least 2 of the following items: Local swelling or induration Erythema Local tenderness or pain Local warmth Purulent discharge (thick, opaque to white or sanguineous secretion)		
Local infection involving only the skin and the subcutaneous tissue (without involvement of deeper tissues and without systemic signs as described below). If erythema, must be >0.5 cm to ≤ 2 cm around the ulcer. Exclude other causes of an inflammatory response of the skin (eg, trauma, gout, acute Charcot neuro-osteoarthropathy, fracture, thrombosis, venous stasis).	2	Mild
Local infection (as described above) with erythema > 2 cm, or involving structures deeper than skin and subcutaneous tissues (eg, abscess, osteomyelitis, septic arthritis, fasciitis), and No systemic inflammatory response signs (as described below)	3	Moderate
Local infection (as described above) with the signs of SIRS, as manifested by ≥ 2 of the following: Temperature $>38^\circ\text{C}$ or $<36^\circ\text{C}$ Heart rate >90 beats/min Respiratory rate >20 breaths/min or $\text{PaCO}_2 <32$ mm Hg White blood cell count $>12,000$ or $<4,000$ cells/ μL or $\geq 10\%$ immature (band) forms	4	Severe ^a

C-reactive protein serves as a useful marker for monitoring response to anti-infective therapy. However, it can sometimes be an unreliable parameter, remaining normal even in the presence of severe infections [Zemmouri *et al.*, 2015].

In our study, *Staphylococcus aureus* was the most frequently isolated organism (18.4%), consistent with literature data. Indeed, the meta-analysis by Macdonald *et al.*, which included 112 studies, 16,159 patients, and 22,198 microbial isolates, reports that *Staphylococcus aureus* is the most commonly identified pathogen in diabetic foot infections, with an estimated weighted prevalence between 21 and 23%. It also highlights a significant proportion of methicillin-resistant strains (18%), emphasizing substantial heterogeneity across studies [Macdonald *et al.*, 2021].

17.4% of the identified *Staphylococcus aureus* strains in our study were methicillin-resistant (MRSA). This distribution aligns with literature data, which reports a variable MRSA prevalence typically ranging between 10 and 30%, depending on prior antibiotic exposure, geographical context, and the level of clinical management [Tentolouris *et al.*, 1999] [Zambelli *et al.*, 2025].

The presence of MRSA, although a minority, carries major clinical significance due to its association with more severe infections, prolonged hospital stays, and reduced empirical treatment options [Tentolouris *et al.*, 1999].

In our study, Gram-negative bacilli represented a significant proportion of the isolated bacteria, dominated by Enterobacteriaceae, which accounted for 40% of all isolates. Among these, *Klebsiella pneumoniae* (13.6%), *Proteus mirabilis* (11.2%), *Enterobacter cloacae* (4.0%), and *Escherichia coli* (2.4%) were the most frequently identified species. This predominance of Enterobacteriaceae correlates closely with literature data identifying them as the main Gram-negative bacilli involved in diabetic foot infections, particularly in chronic or severe forms [Garousi *et al.*, 2023] [Macdonald *et al.*, 2021] [Zambelli *et al.*, 2025]. However, their frequency in our series appears higher than that reported in the Moroccan study by Belefquih *et al.* conducted at the Mohammed V Military Hospital in Rabat, where Enterobacteriaceae accounted for 31.8% of bacterial isolates [Belefquih *et al.*, 2016].

In our study, 16% of the Enterobacteriaceae were ESBL producers, mainly *Klebsiella pneumoniae*, while a single isolate produced a carbapenemase. This frequency is close to that reported in a Moroccan study

performed at the Mohammed V Military Hospital in Rabat, where 14.1% of Enterobacteriaceae isolated from diabetic foot infections were ESBL producers, whereas carbapenemase-producing strains represented 3.8% of isolates [Belefquih *et al.*, 2016]. Internationally, a study conducted among patients with diabetic foot infections reported a higher frequency of ESBL-producing bacteria (25% of isolates), with *Klebsiella pneumoniae* also featured among the primary species involved [Leibovitch *et al.*, 2021].

Regarding the susceptibility profile, carbapenems remained the most active antibiotics against the Enterobacteriaceae isolated in our study, whereas higher resistance rates were observed for amoxicillin-clavulanic acid, co-trimoxazole, and fluoroquinolones. These results align with those reported in Morocco by Belefquih *et al* who found high resistance to amoxicillin-clavulanic acid (60.4%) and ciprofloxacin (26.2%) among Enterobacteriaceae isolated from diabetic foot infections, while resistance to ertapenem remained low (5.0%), demonstrating the preserved efficacy of carbapenems [Belefquih *et al.*, 2016]. Internationally, Citron *et al* showed that carbapenems, particularly imipenem and ertapenem, were among the most active antibiotics in vitro against Enterobacteriaceae isolated from moderate to severe diabetic foot infections [Citron *et al.*, 2007].

The resistance profiles of *Proteus mirabilis* were generally consistent with literature data, characterized by good susceptibility to third-generation cephalosporins and carbapenems. The observed resistance mainly involved co-trimoxazole, whereas resistance to fluoroquinolones remained limited in our series, although higher rates have been reported in other studies [Ben Azaiez *et al.*, 2020] [Joseph *et al.*, 2025] [Wang *et al.*, 2014].

The differences observed between species are also explained by their intrinsic characteristics. Thus, the constant resistance of *Enterobacter cloacae*, *Morganella morganii*, and *Citrobacter freundii* to aminopenicillins with or without a β -lactamase inhibitor is consistent with the natural expression of a chromosomal AmpC-type cephalosporinase and does not necessarily reflect the acquisition of a new resistance mechanism. Conversely, the identification of an ESBL-producing *Enterobacter cloacae* strain illustrates the potential accumulation of resistance mechanisms in these species, further complicating their therapeutic management.

In our study, *Pseudomonas aeruginosa* accounted for 8.8% of isolates, a frequency identical to that reported by Belefquih *et al* in Morocco (8.8%) and close to the 10% found by Pellizzer *et al.* In contrast, studies conducted in India report higher frequencies, reflecting geographical variations in the bacterial ecology of diabetic foot infections. Furthermore, this

species is more frequently isolated in chronic infections due to its ability to form biofilms and persist in long-standing wounds [Belefquih *et al.*, 2016]. Regarding resistance, our results highlight a concerning profile, characterized by a significant decrease in susceptibility to ceftazidime, carbapenems, and fluoroquinolones, as well as the presence of 27.3% multidrug-resistant strains and one metallo- β -lactamase-producing isolate. These observations are consistent with the meta-analysis by Garousi *et al* which describes *Pseudomonas aeruginosa* as one of the main multidrug-resistant pathogens in diabetic foot infections, with increasing resistance to antipseudomonal β -lactams, carbapenems, and fluoroquinolones [Garousi *et al.*, 2023].

Streptococcus agalactiae was isolated in 7.2% of cases and demonstrated complete susceptibility to beta-lactams, glycopeptides, and linezolid.

Several international studies indicate that group B streptococci responsible for diabetic foot infections generally remain susceptible to reference antibiotics, particularly beta-lactams, although variations may exist depending on geographical regions and local antibiotic pressure [Raabe & Shane, 2019].

Alpha-hemolytic streptococci accounted for 5.6% of isolates in our series. Their susceptibility profile was overall favorable, albeit with a 14.3% resistance rate to beta-lactams; a phenomenon previously described in chronic diabetic foot infections [Zemmouri *et al.*, 2015].

Bacteria less frequently isolated in our series, though each accounting for less than 2% of cases, displayed concerning resistance profiles. *Acinetobacter baumannii* (1.6%) exhibited complete resistance to carbapenems, confirming the high resistance potential of this species and the limitation of conventional therapeutic options [Zemmouri *et al.*, 2015].

The management of diabetic foot infections relies on a multidisciplinary approach. According to recent guidelines from the IWGDF and the IDSA, superficial infections limited to the skin can be treated orally, primarily targeting *Staphylococcus aureus* and streptococci, with options such as amoxicillin-clavulanic acid, cephalexin, or clindamycin for 1 to 2 weeks [Senneville *et al.*, 2024]. For moderate to severe infections, which are often polymicrobial, it is recommended to initiate broad-spectrum intravenous antibiotic therapy covering both Gram-positive and Gram-negative bacteria as well as anaerobes. For example, piperacillin-tazobactam or ampicillin-sulbactam and then adjust the treatment based on cultures and clinical course [Senneville *et al.*, 2024].

In cases of osteomyelitis, the duration of treatment is extended to at least 4–6 weeks and is generally accompanied by surgical debridement

[Senneville *et al.*, 2024]. The French SPILF guidelines emphasize the importance of collecting deep specimen cultures after debridement and re-evaluating patients after 48 to 72 hours, while accounting for contributing factors such as hyperglycemia, neuropathy, and ischemia [Bonnet *et al.*, 2024]. Thus, optimal management combines appropriate empirical antibiotic therapy, regular clinical follow-up, and proper local wound care [Bonnet *et al.*, 2024].

Hygiene plays a fundamental role in preventing diabetic foot infections in both outpatient and inpatient settings. The diabetic foot represents a particularly high-risk condition due to neuropathy, vascular disorders, and the chronicity of lesions, which foster bacterial colonization and subsequent progression toward infection. In the outpatient setting, prevention relies primarily on patient education and daily foot hygiene. The IWGDF guidelines emphasize regular foot washing with careful drying, particularly in the interdigital spaces, daily inspection for early-stage lesions, wearing appropriate footwear, and avoiding skin trauma. Early management of minor lesions helps limit progression to infected ulcerations, making patient education an essential pillar of prevention [International Working Group on the Diabetic Foot, 2023].

In the hospital setting, patients with a diabetic foot are at increased risk of nosocomial infections, particularly those caused by Gram-negative bacilli such as *Pseudomonas aeruginosa* or multidrug-resistant Enterobacteriaceae. Prevention relies on the strict implementation of hospital hygiene measures, including hand hygiene via alcohol-based hand rubs, standard and contact precautions in cases of multidrug-resistant bacteria, rigorous asepsis during wound care, and the disinfection and sterilization of equipment. Limiting cross-transmission constitutes a major objective, particularly in high-density care units where antibiotic selection pressure is significant [World Health Organization, 2009].

CONCLUSION

This study highlights the substantial clinical burden and complex microbiological profile of diabetic foot infections in our patient population. Our key findings reveal a high prevalence of multidrug-resistant organisms, particularly ESBL producing Enterobacteriaceae and MRSA, which directly complicate empirical therapeutic selection.

In our view, effective management requires updating local empirical treatment guidelines based on continuous regional resistance monitoring, implementing strict antimicrobial stewardship, and maintaining strong multidisciplinary coordination to optimize clinical outcomes and limit further resistance.

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