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Microbial Diversity and Antimicrobial Resistance Patterns in Diabetic Foot Infections: A Cross-Sectional Study

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ABSTRACT

Purpose: The study was designed to characterize the microbial diversity, antibiotic susceptibility patterns, and MDRO prevalence among patients with diabetic foot infections in western Libya.

Materials and Methods: We conducted a descriptive, observational study involving 104 patients with clinically confirmed diabetic foot infections attending three healthcare facilities in western Libya. Pus swabs were collected aseptically and processed using conventional culture techniques. Bacterial identification employed Gram staining, biochemical tests, and API 20E strips for Gram-negative organisms. Antimicrobial susceptibility testing followed CLSI guidelines using the Kirby-Bauer disk diffusion method. Fungal elements were identified via direct microscopy, culture on Sabouraud dextrose agar, and germ tube testing. Statistical analyses examined associations between clinical variables and infection characteristics.

Results: The cohort predominantly comprised males (68.3%) with a mean age of 56.5 years. Type 2 diabetes was most common (84.6%), with median disease duration of 6–15 years. Bacterial infections predominated (65.4%), frequently presenting as polymicrobial infections (26.9%). *Staphylococcus aureus* was the leading Gram-positive isolate (21.2%), while *Pseudomonas* species and *Enterobacter* species were most prevalent among Gram-negatives (8.7% each). *Candida albicans* was identified in 34.6% of cases. In particular, multidrug resistance was significantly higher in Gram-negative bacteria (90.0%) compared with Gram-positive organisms (25.0%) ($p < 0.001$). Previous amputation, hypertension, and diabetes duration exceeding 15 years emerged as significant risk factors for MDR infections.

Conclusion: This study reveals a complex microbial ecology in Libyan diabetic foot infections, characterized by substantial polymicrobial involvement and alarming rates of antibiotic resistance. The pronounced burden of multidrug-resistant Gram-negative organisms underscores the necessity for culture-guided therapy, robust antimicrobial stewardship, and region-specific treatment protocols. (*Open J Biomed Res 2026;5:78-87*)

Keywords: Diabetic foot infection, microbial diversity, antimicrobial resistance, multidrug resistance, *Staphylococcus aureus*.

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INTRODUCTION

Diabetic foot infections constitute a formidable public health challenge that continues to escalate alongside the global diabetes pandemic. These infections arise from the interplay of multiple pathogenic factors peripheral neuropathy, vascular insufficiency, and immunological dysfunction that create a permissive environment for microbial invasion and impaired wound healing.[1,2] The clinical trajectory of untreated or inadequately managed infections frequently culminates in hospitalization, lower extremity amputation, and premature mortality, with five-year survival rates following major amputation approximating those of several malignancies.[3,4]

The microbiological profile of diabetic foot infections has evolved considerably over recent decades, reflecting changing patterns of antibiotic utilization, healthcare exposure, and patient demographics. While *Staphylococcus aureus* remains a globally predominant pathogen, contemporary studies increasingly report substantial contributions from Gram-negative bacilli, anaerobic organisms, and fungal elements particularly in chronic, previously treated, or severe infections.[5,6] This microbial diversification poses considerable therapeutic challenges, as Gram-negative organisms frequently harbor extensive resistance mechanisms including extended-spectrum β-lactamase (ESBL) production, carbapenem resistance, and multidrug efflux pumps.[7,8]

The emergence and dissemination of multidrug-resistant organisms (MDROs) in diabetic foot infections represents a particularly concerning development. These pathogens are associated with prolonged hospitalization, escalated healthcare costs, treatment failure, and adverse clinical outcomes.[9,10] Risk stratification for MDRO carriage enables clinicians to tailor empiric antibiotic selection appropriately, balancing the need for broad-spectrum coverage against antimicrobial stewardship principles.

Regional variations in microbial epidemiology are well documented, influenced by climate, healthcare infrastructure, antibiotic accessibility, and population characteristics.[11,12] However, comprehensive microbiological surveillance from North Africa, including Libya, remains limited in the international literature. This knowledge gap impedes evidence-based guideline development for local practitioners and hinders comparative analyses of global resistance trends.

The present study was designed to characterize the microbial diversity, antibiotic susceptibility patterns, and MDRO prevalence among patients with diabetic foot infections in western Libya. By establishing foundational epidemiological data, we aim to inform clinical practice, support antimicrobial stewardship initiatives, and contribute to the broader understanding of diabetic foot infection microbiology in resource-constrained settings.

MATERIALS AND METHODS

Study Design and Setting

We employed a descriptive, cross-sectional observational design incorporating microbiological and clinical correlation components. The study was conducted across three healthcare facilities in western Libya: Sabratha Teaching Hospital, Alain Center for Diabetes Management, and Royal Clinic in Zawia. These institutions serve diverse urban and semi-urban populations, providing primary through tertiary care for diabetes-related complications. The study protocol received ethical approval from the institutional review boards of participating facilities. Written informed consent was obtained from all

participants. Confidentiality was maintained through anonymized data coding.

Participant Selection

Consecutive patients presenting with clinically infected diabetic foot ulcers between December 2023 and July 2024 were eligible for inclusion. Infection was defined according to Infectious Diseases Society of America (IDSA) criteria, requiring the presence of purulence or at least two signs of inflammation (erythema, warmth, tenderness, pain, or induration).[13] Exclusion criteria comprised antibiotic therapy within the preceding 72 hours, non-diabetic etiology of foot lesions, and refusal to participate. The final analytical sample comprised 104 patients with positive microbial growth from 130 initially enrolled participants.

Data Collection

Trained research personnel conducted structured face-to-face interviews using a standardized questionnaire. Demographic variables included age, sex, residence, education, and occupation. Clinical parameters encompassed diabetes type and duration, glycemic control history, comorbid conditions (hypertension, retinopathy, nephropathy, cardiovascular disease), smoking status, previous foot ulceration or amputation, and current wound management practices. Surgical history and antibiotic exposure within the past three months were documented.

Specimen Collection and Transportation

Pus swabs were obtained aseptically from the deepest accessible portion of each wound following surface debridement with sterile normal saline. Swabs were immediately immersed in Amies transport medium and transferred to the microbiology laboratory within two hours using portable cooler boxes. Temperature maintenance between 2–8°C was verified throughout transportation.

Microbiological Processing

Bacterial isolation and identification:

Specimens were inoculated onto blood agar, MacConkey agar, and mannitol salt agar plates, incubated aerobically at 37°C for 24 hours. Colony morphology, hemolytic patterns, and swarming characteristics were recorded. Gram staining distinguished Gram-positive from Gram-negative organisms. Biochemical identification employed catalase testing, coagulase testing (tube method), oxidase testing, and API 20E strips for Gram-negative bacilli according to manufacturer protocols.[14]

Fungal identification:

Direct microscopic examination of 10% potassium hydroxide preparations assessed yeast cells and pseudohyphae. Sabouraud dextrose agar with chloramphenicol supported primary isolation, with incubation at 37°C for 24–48 hours. The germ tube test (human serum, 37°C, 2–3 hours) presumptively identified *Candida albicans*.[15]

Antimicrobial susceptibility testing:

The Kirby-Bauer disk diffusion method on Mueller-Hinton agar followed CLSI guidelines.[16] Inocula were standardized to 0.5 McFarland turbidity. Tested antibiotics included: ampicillin, amoxicillin-clavulanate, cefuroxime, ceftriaxone, cefotaxime, ceftazidime, cefoperazone, cefoxitin, imipenem, meropenem, amikacin, gentamicin, tobramycin, ciprofloxacin, norfloxacin, erythromycin, clindamycin, azithromycin, doxycycline, tetracycline, vancomycin, linezolid, sulfamethoxazole, and polymyxin. Zone diameters were interpreted using CLSI breakpoints. Methicillin-resistant *Staphylococcus aureus* (MRSA) was defined by cefoxitin resistance or oxacillin MIC ≥4 µg/mL. Multidrug resistance (MDR) was operationalized as acquired non-susceptibility to at least three antimicrobial categories.[17]

Antifungal susceptibility:

Disk diffusion testing assessed susceptibility to amphotericin B, fluconazole, and nystatin.

Statistical Analysis

Data were analyzed using IBM SPSS Statistics version 25. Descriptive statistics summarized demographic and clinical characteristics. Categorical variables were

compared using chi-square or Fisher's exact tests. Continuous variables were analyzed via independent samples t-tests or one-way ANOVA. Pearson correlation examined relationships between diabetes duration and resistance parameters. Binary logistic regression identified independent risk factors for MDR infection, with results expressed as odds ratios (OR) and 95% confidence intervals (CI). Statistical significance was set at $p < 0.05$.

RESULTS

Demographic and Clinical Characteristics

The study population exhibited substantial male predominance (68.3% vs. 31.7% female), with mean ages of 56.9 ± 13.7 and 56.1 ± 17.5 years respectively ($p = 0.812$). Age distribution peaked in the 55–69 year bracket (39.4%), followed by 40–54 years (30.8%). Geographic distribution revealed highest case concentration in Sabratha (25.0%), Surman (18.3%), and Zawia (14.4%).

Type 2 diabetes constituted 84.6% of cases, with 60.5% of participants reporting 6–15 years disease duration. Hypertension was the most prevalent comorbidity (31.7%), followed by isolated retinopathy (8.7%) and hypertensive chronic kidney disease (8.7%). Among male participants, 19.2% were current smokers and 16.3% former smokers. Surgical interventions were common: debridement (43.2%), amputation (39.4%), and incision with drainage (17.3%). Normal saline dressings predominated (69.2%), with silver colloid-hyaluronic acid used in 26.9% (Fig. 1).

Microbial Diversity and Infection Types

Bacterial monomicrobial infections were most frequent (65.4%), followed by mixed bacterial-fungal infections (26.9%) and isolated fungal infections (7.7%). Among bacterial isolates, Gram-positive organisms marginally predominated (45.1%) over Gram-negative organisms (40.0%), with polymicrobial bacterial infections in 6.7%.

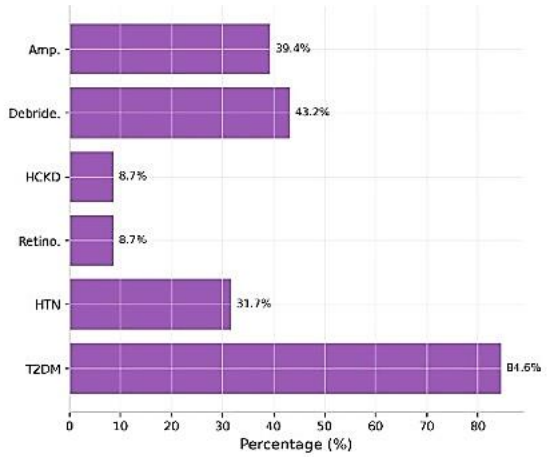


Fig. 1: Key Clinical Features.

Staphylococcus aureus was the single most common isolate (21.2%), with *Streptococcus* species (10.6%) and coagulase-negative staphylococci (6.7%) contributing substantially to Gram-positive diversity. Among Gram-negatives, *Pseudomonas aeruginosa* and *Enterobacter cloacae* were equally prevalent (8.7% each), followed by *Escherichia coli* (6.7%), *Klebsiella pneumoniae* (5.8%), and *Acinetobacter baumannii* (2.9%). *Candida* species predominantly *C. albicans* were identified in 34.6% of all cases when including mixed infections (Fig. 2).

Age stratification revealed significant variation in infection patterns ($F = 3.125$, $p = 0.048$). Mixed infections were more prevalent among older patients (mean age 63.4 years) compared with bacterial (58.7 years) or fungal (57.0 years) infections alone. No significant associations emerged between infection type and gender ($p = 0.780$), diabetes type ($p = 0.902$), or diabetes duration ($p = 0.950$).

Antimicrobial Susceptibility Profiles

Staphylococcus aureus demonstrated excellent susceptibility to linezolid (100%) and retained moderate sensitivity to cefoxitin (68.3%) and vancomycin (63.6%). However, considerable resistance was observed for erythromycin (45.5%), ciprofloxacin (40.9%),

and clindamycin (31.8%). MRSA prevalence reached 31.8% among *S. aureus* isolates.

Gram-negative organisms exhibited more concerning resistance patterns. *Pseudomonas* species showed high resistance to cefuroxime (66.7%) and amoxicillin-clavulanate (77.8%), while retaining better susceptibility to imipenem (77.8%) and gentamicin (66.7%). *Enterobacteriaceae* collectively demonstrated extensive β-lactam resistance, with preserved carbapenem activity.

Comparative analysis confirmed significantly higher resistance rates among Gram-negative bacteria to vancomycin (90% vs. 20%, $p < 0.001$) and linezolid (90% vs. 0%, $p < 0.001$), while Gram-positive organisms showed elevated ciprofloxacin resistance (50% vs. 30%, $p = 0.032$).

Candida isolates exhibited favorable antifungal susceptibility: amphotericin B (87%), fluconazole (79%), with modest nystatin resistance (23.3%) (Fig. 3).

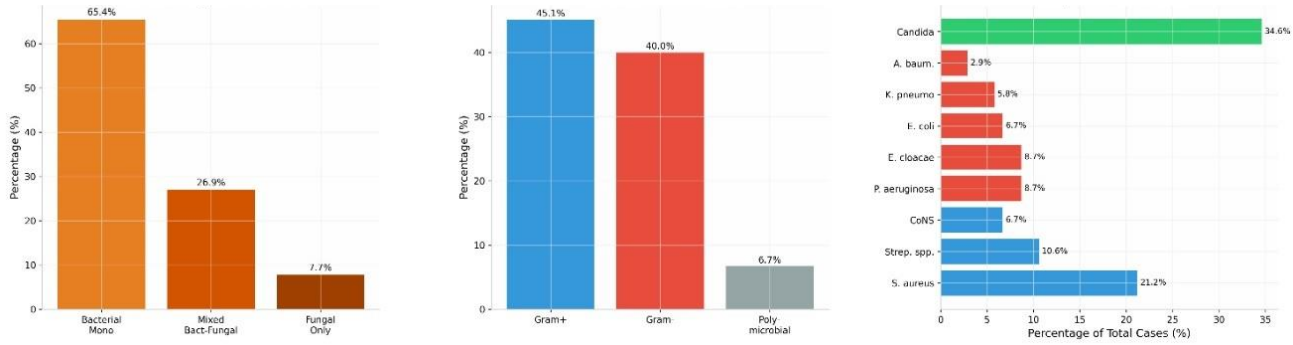
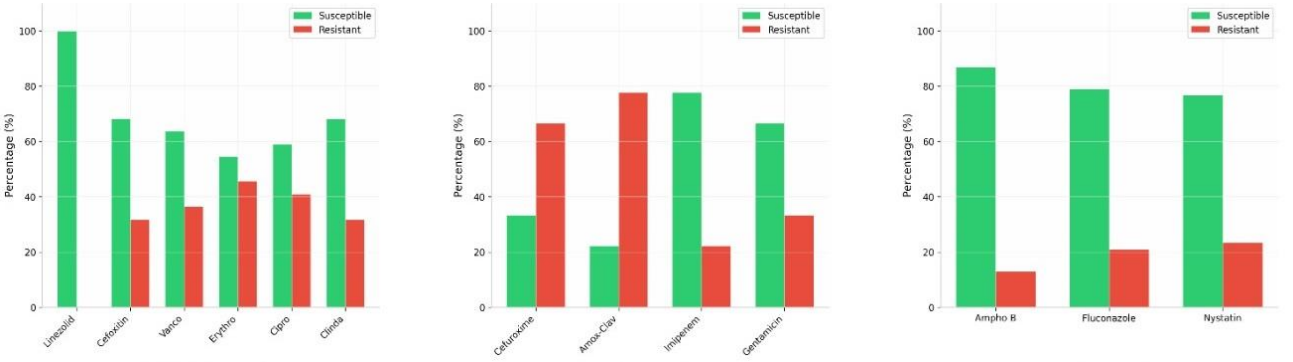


Fig. 2: Microbial diversity and infection types.



A-S. *aureus* susceptibility (n=22) B- *Pseudomonas* susceptibility (n=9) B- *Candida* susceptibility (n=36)

Fig. 3: Antimicrobial susceptibility profiles

Multidrug Resistance Patterns

MDR was dramatically more prevalent among Gram-negative bacteria (90.0%) than Gram-positive organisms (25.0%) ($Z = 19.76$, $p < 0.001$). Within Gram-negatives, *Proteus* species and *Acinetobacter* species demonstrated near-universal MDR (99.0% each), followed by *Citrobacter* (98.4%), *Pseudomonas* (88.9%), *Klebsiella* (83.3%), and *E. coli* (71.4%).

Logistic regression identified powerful independent risk factors for MDR infection: previous amputation (OR 67.67, 95% CI 19.22–238.27), hypertension (OR 61.00, 95%

CI 15.62–238.20), and diabetes duration exceeding 15 years (OR 36.11, 95% CI 11.02–118.29) (all p < 0.001) (Fig. 4).

A striking positive correlation emerged between diabetes duration and aggregate antibiotic resistance rates (r = 0.983, p < 0.001), suggesting cumulative exposure effects or progressive immunological deterioration.

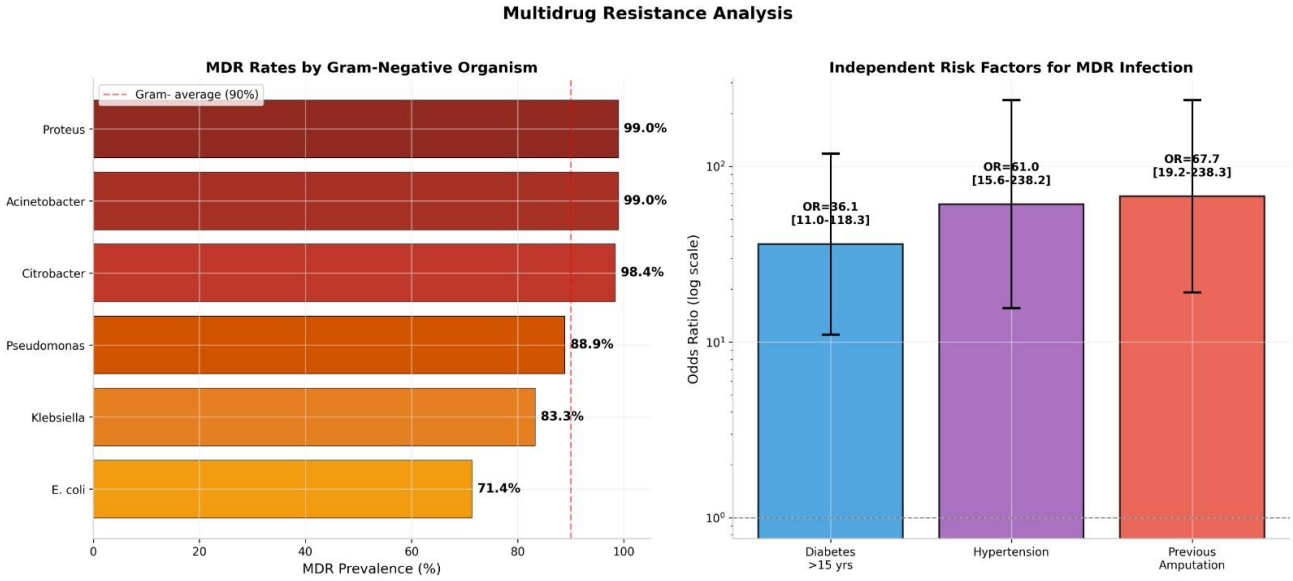


Fig. 4: Multidrug resistance analysis.

DISCUSSION

This comprehensive investigation of diabetic foot infections in western Libya reveals a microbial landscape characterized by substantial diversity, frequent polymicrobial involvement, and alarming resistance to commonly employed antibiotics. Our findings align with global reports emphasizing the complexity of diabetic foot microbiology while highlighting region-specific patterns that demand tailored therapeutic approaches.

The pronounced male predominance observed in our cohort (68.3%) mirrors international epidemiological patterns.[18,19] This disparity likely reflects multifactorial influences including occupational hazards, footwear practices, delayed healthcare-seeking behavior, and potentially biological factors such as more severe peripheral neuropathy in male patients.[20,21] The concentration of cases in middle-to-late adulthood (70.2% aged ≥40 years) underscores the time-dependent nature of diabetic microvascular complications and the cumulative burden of glycemic exposure.[22]

Our microbiological findings both confirm established patterns and reveal notable variations. *Staphylococcus aureus* predominance aligns with meta-analytic evidence identifying this organism as the most frequent global isolate from diabetic foot infections.[5,23] The substantial MRSA prevalence (31.8%) exceeds estimates from some European and North American settings but approximates reports from India, sub-Saharan Africa, and prior Libyan studies.[24,25] This finding carries critical therapeutic implications, necessitating MRSA-active empiric coverage for moderate-to-severe infections in our setting.

The significant representation of Gram-negative organisms (40% of bacterial isolates), particularly *Pseudomonas* and *Enterobacter* species, diverges somewhat from classic descriptions emphasizing Gram-positive

predominance. This pattern likely reflects the chronicity of infections in our cohort, previous antibiotic exposure selecting for resistant flora, and possibly climatic factors favoring environmental Gram-negative colonization.[26,27] The comparable prevalence of *Pseudomonas* and *Enterobacter* to *S. aureus* challenges simplistic empiric regimens and supports culture-guided therapy whenever feasible.

Perhaps most striking is our documentation of extensive fungal involvement, with *Candida* species identified in over one-third of cases. While often dismissed as commensal colonization, accumulating evidence supports the pathogenic potential of *Candida* in chronic, antibiotic-exposed wounds, particularly through biofilm formation and synergistic interactions with bacterial pathogens.[28,29] Our high detection rate may reflect the warm, humid climate, prolonged antibiotic histories, and enhanced diagnostic attention in our protocol.

The resistance patterns we document are deeply concerning. The near-universal MDR among Gram-negative organisms (90%) vastly exceeds global pooled estimates of approximately 50%.[9,30] Even allowing for potential selection bias toward more complex cases in our referral population, this finding signals a critical local resistance crisis. The exceptional MDR rates in *Acinetobacter* (99%) and *Proteus* (99%) approach pan-resistance, severely constraining therapeutic options and likely contributing to the high amputation rates we observed.

Our identification of robust risk factors for MDR infection previous amputation, hypertension, and extended diabetes duration provides clinically actionable intelligence. These markers enable risk stratification at presentation, informing decisions regarding empiric antibiotic breadth, need for hospitalization, and urgency of surgical consultation. The particularly strong association with previous amputation (OR >67) likely reflects recurrent infection cycles, repeated antibiotic exposure, and healthcare-associated colonization with resistant organisms. [31,32]

The remarkable correlation between diabetes duration and resistance severity (r = 0.983) suggests that long-standing diabetes represents not merely a risk factor for infection, but for *resistant* infection. This probably operates through multiple mechanisms: cumulative immunological dysfunction, progressive vascular compromise limiting antibiotic tissue penetration, extended exposure to healthcare environments, and repeated antibiotic courses for prior infections.[33,34]

Several limitations warrant acknowledgment. Our cross-sectional design precludes causal inference and outcome tracking. The moderate sample size, while adequate for primary analyses, may limit precision for subgroup comparisons. Anaerobic culture was not systematically performed, potentially underestimating polymicrobial complexity. We did not employ molecular diagnostic techniques, possibly missing fastidious or slow-growing organisms. Finally, our single-region focus may limit generalizability to other Libyan settings or North African countries.

Clinical implications of our findings are substantial. Empiric antibiotic selection for moderate-to-severe diabetic foot infections in western Libya should anticipate MRSA among Gram-positives and extensive β-lactam resistance (including ESBL and carbapenem resistance) among Gram-negatives. Initial regimens might reasonably combine agents with reliable MRSA coverage (vancomycin, linezolid, or daptomycin) with antipseudomonal β-lactam/β-lactamase inhibitor combinations or carbapenems, reserving broader combinations for high-risk patients identified by our predictive factors. The substantial fungal involvement suggests considering antifungal therapy, particularly for chronic, non-responsive wounds with extensive antibiotic exposure.

Antimicrobial stewardship imperatives are equally clear. The resistance crisis we document demands urgent implementation of prescription auditing, formulary restriction, infection control reinforcement, and prescriber education. Without such interventions, the therapeutic armamentarium for these common, devastating infections will continue to erode.

CONCLUSION

This study establishes foundational microbiological and resistance surveillance data for diabetic foot infections in western Libya. We demonstrate a complex, frequently polymicrobial infectious ecology with exceptional rates of multidrug resistance, particularly among Gram-negative organisms. The identification of robust clinical predictors for MDR infection supports risk-stratified empiric therapy, while our findings overall emphasize the critical importance of culture-guided management, antimicrobial stewardship, and preventive strategies to address this growing public health challenge.

Conflicts of Interest

The authors declare no conflicts of interest.

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