Bacterial Profile and Antimicrobial Resistance Patterns in Infected Diabetic Foot Ulcers in Gulf Cooperation Council Countries (2005–2025): A Systematic Review and Meta-Analysis of Observational Studies

Salma M. Alsayed
King Abdulaziz University
Muhammad Yasir
Fakeeh College for Medical Sciences
Aiah M. Khateb
Taibah University
Shahira A. Hassoubah
King Abdulaziz University
Reem M. Farsi
King Abdulaziz University
Ahmed M. Aljabri
King Fahd Armed Forces Hospital
Ahmed A. Afandi
King Fahad Hospital Jeddah
Safaa A. Turkistani
Fakeeh College for Medical Sciences
Mohammed Salleh M. Ardawi
Fakeeh College for Medical Sciences
Esam Ibraheem Azhar
eazhar@kau.edu.sa

King Abdulaziz University

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Abstract

Diabetic foot ulcers (DFUs) are substantially increasing in parallel with the rapidly rising prevalence of diabetes mellitus (DM) worldwide. The regional epidemiological data of infected diabetic foot ulcers and their antimicrobial resistance (AMR) patterns are essential for optimal management of these health challenges. This systematic review and meta-analysis aimed to determine the pooled prevalence of bacterial profiles and antimicrobial resistance patterns of infected DFUs in Gulf Cooperation Council (GCC) countries. A comprehensive search of the literature was conducted on PubMed/MEDLINE, Web of Science, Embase (via Ovid), and Google Scholar databases. Critical appraisal was performed using the Joanna Briggs Institute tool for prevalence studies. A single-arm meta-analysis was conducted using RStudio to estimate the pooled prevalence of bacterial pathogens and their AMR rates using a random-effects model. The I^2 statistic and Cochran's Q test were used to assess the heterogeneity. P-values less than 0.05 were considered statistically significant. Sixteen studies comprising 3260 participants were included; the mean number of bacterial isolates per study was 196.1 ± 265.9. The pooled prevalence of the most common bacterial isolates obtained from DFU were *Staphylococcus aureus* (29%, 95% CI: 20–40%), *Pseudomonas aeruginosa* (16%, 95% CI: 13–20%), and *Escherichia coli* (14%, 95% CI: 10–19%). The highest pooled antibiotic resistance rate was observed for ampicillin (67%), followed by tetracycline (59%), gentamicin (58%), and ciprofloxacin (52%). In contrast, resistance rates were relatively low for carbapenem antibiotics. Our findings provide evidence to help guide appropriate antibiotic selection and infection prevention strategies in the GCC region. Given the high microbial diversity and antimicrobial resistance observed, locally informed stewardship efforts and evidence-based alternative therapeutics may be warranted, particularly in light of the growing global antimicrobial resistance challenge.

1. Introduction

According to the International Diabetes Federation (IDF), the global prevalence of diabetes mellitus (DM) has been rising rapidly, reaching an estimated 589 million individuals (11.1%) in 2024, and is projected to increase further to 852.5 million by 2050, posing a substantial public health and economic burden [1]. Diabetic foot ulcer (DFU) is considered the most serious complication of this disease [2,3]. According to the International Working Group on the Diabetic Foot (IWGDF), up to one in three diabetic patients is expected to develop a DFU during their lifetime [4]. Globally, DFUs are estimated to affect 6.4% of diabetic patients annually and 15–25% in their lifetime [5]. Diabetic foot infections (DFIs) are commonly associated with lower extremity amputations occurring in approximately 17–36% of affected individuals, as well as increased morbidity and mortality [6,7]. In addition to their clinical impact, DFUs also impose a considerable economic burden on healthcare systems. The estimated cost of treating an uncomplicated DFU is approximately $ 16,000, increasing to more than 30,000 for patients requiring major amputation [8]. Outpatient wound care accounts for approximately 51% of total treatment costs, compared with 4% for antibiotics, while surgical interventions account for up to 95% of healthcare expenditures [8,9].

DFU is chronic and polymicrobial; it harbors multiple microorganisms. Understanding the diabetic foot environment and its microbial complexity is critical for developing diagnostic and treatment strategies and improving patient outcomes. Numerous studies conducted in different countries have highlighted different aspects of DFU microbiology, demonstrating considerable variation in microbial composition and antimicrobial susceptibility patterns. A meta-analysis of 40 studies involving 20 countries revealed methicillin-resistant *Staphylococcus aureus* (MRSA) prevalence of 17% in DFU globally, with significant regional variation: 61% in South America, 20% in North America, 19% in Europe, 13% in Africa, and 11% in the remaining regions [10]. Makeri et al. reviewed studies from 13 African countries and identified *S. aureus* as the most prevalent pathogen (19.9%), followed by *Pseudomonas aeruginosa* at 11.8% [11]. Garousi et al. (2023) reported *P. aeruginosa* prevalence rate 18.5%, 16.3%, and 11.1% in Asia, Africa, and Western countries, respectively [12]. In Brazil, Palomo et al. found that Gram-negative bacilli were more prevalent (88%) compared to Gram-positive cocci, which had a prevalence of 68% [13]. Likewise, a study revealed that the distribution of *S. aureus* in Asian countries such as China, India, Saudi Arabia, Kuwait, and Iran varied from 11.4% to 44% [14]. According to the World Health Organization (WHO), Saudi Arabia has the second-highest prevalence of DM in the Middle East and ranks seventh globally, with approximately 7 million people living with diabetes [15,16]. As the prevalence of diabetes increases, the burden of DFUs is expected to increase accordingly. One report estimated that 3.3% of Saudi diabetic patients were diagnosed with DFU [17–19]. In addition, a systematic review by Mairghani et al. examining DFU prevalence and incidence across five Arab countries found that the mean prevalence in Saudi Arabia was 11.85%, with reported rates ranging from 4.7% to 19% [20]. Around 50–60% of these ulcers develop infection; among moderate-to-severe infections, about 20% result in lower extremity amputation [21].

In Saudi Arabia, several studies have shown distinct microbial profiles, with *S. aureus* consistently reported as the most isolated bacteria in DFIs, aligning with previous studies in different geographical regions [22,23]. In addition, *P. aeruginosa* is also commonly isolated, consistent with reports from the Middle East and North Africa [22–24]. For example, a retrospective study conducted in Jeddah identified *S. aureus* as the most common infectious agent in DFUs, followed by *E. coli* and *P. aeruginosa*[25]. These geographical differences in pathogen distribution and antimicrobial susceptibility influence empirical antibiotic selection [26–28]. Therefore, local epidemiological data are essential for developing therapy recommendations, particularly in the context of the global antimicrobial resistance (AMR) crisis, and highlight the need for region-specific research on the microbial composition of DFIs. While antimicrobial management is important, effective DFU care requires a

multidisciplinary approach that includes glycemic control, surgical debridement, vascular assessment, offloading, and, importantly, primary prevention strategies to reduce the occurrence of ulcers altogether. Nonetheless, understanding regional microbial and resistance patterns remains essential for optimizing the antimicrobial component of this broader care pathway

Despite the growing prevalence of DFUs and associated infections in the Arabian Gulf Region, there is a lack of comprehensive studies detailing the bacterial profiles and AMR patterns specific to this region [29]. Most studies are limited in scope or focus on individual countries, and there is no consolidated evidence on the prevalence of specific bacterial pathogens and the emerging trends of AMR in infected DFUs in the Gulf Cooperation Council (GCC) countries. Therefore, we conducted a systematic review and meta-analysis to address this knowledge by providing a comprehensive overview of the bacterial pathogens and resistance patterns prevalent in DFIs across the GCC countries. These findings may support region-specific treatment strategies and guide future research and antimicrobial stewardship efforts.

2. Methods

2.1. Protocol and Registration

This systematic review was prospectively registered in the International Prospective Register of Systematic Reviews (PROSPERO; CRD42025118352) and followed the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines, as illustrated in the flow diagram [30] (Fig. 1).

2.2. Search Strategy

We conducted the literature search for this systematic review on February 19, 2025. A systematic search was conducted in PubMed/MEDLINE, Web of Science, Embase (via Ovid), and Google Scholar databases to identify peer-reviewed publications reporting on the microbial profiles of diabetic foot infections in diabetic patients from GCC countries between 2005 and 2025. The search strategy combined MeSH terms and relevant keywords related to diabetic foot ulcers, diabetic foot infections, antibiotic resistance, and microbial patterns, including all applicable subheadings, along with country-specific terms (Supplementary Table S1). Additionally, the reference lists of all included studies were manually screened to identify any additional relevant articles. Original studies conducted in GCC were included.

2.3. Inclusion Criteria

All observational studies conducted in GCC countries that reported on bacterial profile and/or AMR patterns of infected diabetic foot ulcers and were published in English were included.

2.4. Exclusion Criteria

Studies conducted outside GCC countries were excluded. In addition, reviews, commentaries, letters to the editor, encyclopedia, book chapters, and case reports were excluded. To prevent bias towards a specific pathogen study focusing on only one type of bacteria, or those using metagenomic analysis without clear species-level identification, were also excluded.

2.5. Data Extraction and Quality Assessment of Included Studies

Data was extracted using a pre-designed Excel spreadsheet. The data extraction tool included the following variables: authors, year of publication, country, sample size, study design, setting, type of specimen, study period, mean age of participants, sex distribution, HbA1c levels, BMI, types and number of bacterial isolates, and antibiotic resistance patterns. The methodological quality of the included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Analytical Cross-Sectional Studies [31]. Based on methodological quality, all included studies had at least five "YES" answers, indicating that they qualified for inclusion (Table 1). Articles were reviewed through title, abstract, and full-text screening by two independent reviewers, with any disagreements resolved by discussion or consultation with a third reviewer.

Table 1
Quality assessment of included studies using the JBI Appraisal Tools.

Study Number	Authors, Year	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Overall Score
1	Al Benwan et al., 2012 [32]	Y	Y	Y	Y	N	NA	Y	U	5
2	Alhubail, A., et.al; 2020 [33]	Y	Y	Y	Y	U	NA	Y	Y	6
3	Messenger, G., et al., 2018 [34]	Y	Y	Y	Y	U	NA	Y	Y	6
4	Abdulrazak et al., 2005 [35]	Y	Y	Y	Y	U	NA	Y	Y	6
5	Hassan Amir et al., 2020 [36]	Y	Y	Y	Y	U	NA	Y	Y	6
6	Sannathimmappa, M. B., et al., 2021 [37]	Y	Y	Y	Y	U	NA	Y	Y	6
7	Malone, M., et al., 2013 [38]	Y	Y	Y	Y	U	NA	Y	Y	6
8	Johargy, A. K., 2016 [39]	Y	Y	Y	Y	U	NA	Y	Y	6
9	Orfali, R., et al., 2024 [40]	Y	Y	Y	Y	U	NA	Y	Y	6
10	Al-Mijalli, S. H. S., 2021 [41]	Y	Y	Y	Y	U	NA	Y	Y	6
11	Saleem, M., et al., 2025 [24]	Y	Y	Y	Y	U	NA	Y	Y	6
12	Alkhatieb, M., et al., 2022 [42]	Y	Y	Y	Y	U	NA	Y	Y	6
13	Alkhatieb, M. T., et al., 2024 [25]	Y	Y	Y	Y	U	NA	Y	Y	6
14	El-Hazmi M. M., 2015 [43]	Y	Y	Y	Y	U	NA	Y	Y	6
15	Aldawish, M., & Alayed, M., 2018 [44]	Y	Y	Y	Y	U	NA	Y	Y	6
16	Aldhfyan, Y., et al., 2018 [45]	Y	Y	Y	Y	U	NA	Y	Y	6

2.6. Data Analysis

All statistical analyses were performed using RStudio (version 2023.09.1 + 494; Posit Software, PBC). A single-arm meta-analysis was conducted to estimate the pooled prevalence of individual bacterial pathogens isolated from DFU samples. For each bacterium, we calculated prevalence as the proportion of total isolates or patients per study, using the metaprop function from the meta package. A random-effects model (DerSimonian–Laird method) was applied due to anticipated heterogeneity. The same pooling approach was used to estimate resistance rates for specific antibiotics, based on the number of resistant isolates relative to the total number tested in each study. Forest plots were generated to visualize the pooled estimates with corresponding 95% confidence intervals (CIs), and heterogeneity was quantified using the I^2 statistic and p-values derived from Cochran's Q test. Data synthesis and bias assessment tables were prepared using the dplyr and ggplot2 packages. P-values less than 0.05 were considered statistically significant.

3. Results

3.1. Study Characteristics

Systematic searching yielded 437 articles from different databases (PubMed/MEDLINE, Web of Science, Embase (via Ovid), and Google Scholar), of which 173 were removed as duplicates. Of the 264 remaining articles, 231 were excluded during the title and abstract screening. Leaving 33 full-text articles for retrieval. Three articles could not be retrieved, and the remaining 30 were assessed for eligibility. Of these, 14 were excluded for the following reasons: focusing on a single bacterial species (n = 7), not meeting the eligibility criteria (n = 6), or using molecular methods without species-level identification (n = 1). Ultimately, only 16 studies that fulfilled the eligibility criteria were included in this systematic review and meta-analysis (Fig. 1). The distribution of studies across the GCC region was uneven, with Saudi Arabia (n = 10) and Kuwait (n = 4) contributing the majority, while only one study each was identified from Oman and the UAE, and no eligible studies were identified from Qatar or Bahrain (Fig. 2).

In terms of study design, of the 16 included studies, 12 (75%) were retrospective, while the remaining 4 (25%) were prospective. The included studies were conducted in different healthcare settings, including tertiary care hospitals (n = 7, 43.8%), university-affiliated medical centers (n = 5, 31.3%), teaching hospitals (n = 2, 12.5%), and specialized outpatient centers (n = 2, 12.5%) (Table 2). Clinical sites varied across studies, with

data collected from diabetic foot clinics (n = 3, 18.8%), podiatry departments (n = 1, 6.3%), orthopedic departments (n = 1, 6.3%), DM clinics (n = 1, 6.3%), high-risk foot or emergency clinics (n = 2, 12.5%), and hospital laboratory or medical records (n = 6, 37.5%). The clinical setting was not reported in two studies (12.5%) (Table 2). Clinical sample types varied across studies, with the wound swabs and tissue biopsies being the most commonly used specimens (n = 7, 43.8%), followed by unspecified DFU samples (n = 4, 25%), deep tissue or aspirate specimens (n = 1, 6.3%), bone biopsies (n = 1, 6.3%), and combined or mixed sampling techniques including swabs, pus, and necrotic tissue (n = 3, 18.8%) (Table 2).

Table 2
Characteristics of articles included in the meta-analysis to assess bacterial profile and antimicrobial resistance patterns of infected DFU in the GCC region.

Study No.	Authors, Year	Country	Setting	Sample Site / Type†	Study Design	Period
1	Al Benwan et al., 2012 [32]	Kuwait	Teaching hospital	N/M / Deep tissue or aspirate	Retrospective	Jun 2007 – Jul 2008
2	Alhubail et al., 2020 [33]	Kuwait	Specialized center	Podiatry clinic / Swab or biopsy	Retrospective	Jan 2011 – Dec 2017
3	Messenger et al., 2018 [34]	Kuwait	Tertiary outpatient	N/M / DFU	Retrospective	Oct 2014 – Dec 2016
4	Abdulrazak et al., 2005 [35]	Kuwait	Teaching hospital	Diabetic foot clinic / DFU	Prospective	Jun 2002 – Mar 2003
5	Hassan Amir et al., 2020 [36]	UAE	Tertiary care hospital	Orthopedic dept / N/M	Prospective	Mar 2019 – Mar 2020
6	Sannathimmappa et al., 2021 [37]	Oman	Tertiary hospital	Lab records / Base scraping, pus, tissue	Retrospective	Jan 2013 – Dec 2018
7	Malone et al., 2013 [38]	Saudi Arabia	Tertiary hospital	ER or foot clinic / Bone, swabs, tissue	Retrospective	Jan – Dec 2011
8	Johargy, 2016 [39]	Saudi Arabia	N/M	N/M / DFU	Prospective	Jun 2011 – Jun 2012
9	Orfali et al., 2024 [40]	Saudi Arabia	KFMC	DM clinic / Swab	Prospective	Mar 2023 – Sep 2023
10	Al-Mijalli, S. H. S, 2021 [41]	Saudi Arabia	KFMC	N/M / Deep swab	Prospective	N/M
11	Saleem et al., 2025 [24]	Saudi Arabia	Tertiary care center	DFU clinic / Swabs and biopsy	Retrospective	Jan 2021 – Dec 2023
12	Alkhatieb et al., 2022 [42]	Saudi Arabia	Univ. hospital	N/M / Swabs and tissue	Retrospective	Sep – Oct 2021
13	Alkhatieb et al., 2024 [25]	Saudi Arabia	Specialized center	Lab records / Tissue culture	Retrospective	Oct 2021 – Jan 2022
14	El-Hazmi M. M., 2015 [43]	Saudi Arabia	University hospital	Lab records / Swab, tissue, pus	Retrospective	Dec 2009 – Dec 2011
15	Aldawish & Alayed, 2018 [44]	Saudi Arabia	Tertiary hospital	N/M / Tissue culture	Retrospective	Feb 2015 – Oct 2017
16	Aldhfyan et al., 2018 [45]	Saudi Arabia	King Khaled Hospital	Medical records / Tissue	Retrospective	2010–2015

† *Sample types include swab, tissue biopsy, bone specimen, aspirate, and pus. N/M = Not Mention; KFMC = King Fahad Medical City; ER = Emergency Room.*

3.2. Patient Demographics and Clinical Profiles

The included studies comprised 3260 participants, with a mean age of approximately 58 years, with ages ranging from 44 to 76 years. Male predominance was observed in 13 studies (81.3%), with proportions ranging from 60% to 72.4%. Most studies focused on patients with type 2 diabetes mellitus (T2DM) (81.3%), some also included type 1 diabetes mellitus (T1DM) (25%), and commonly reported comorbidities included peripheral neuropathy, hypertension, retinopathy, nephropathy, peripheral arterial disease, and cardiovascular disease. HbA1c was reported in 6 studies (37.5%), with values ranging from 6.95% to 12.7%. The average duration of diabetes was reported in 3 studies (18.8%), ranging from 8.6

to 14.6 years. Body mass index (BMI) was reported in 4 studies (25%), with values ranging from 24.9 to 33.2. BMI was not reported in the remaining 12 studies (75%).

3.3. Microbiological Profiles

The total number of isolates was reported in 7 studies (43.8%), with a mean of 196.1 ± 265.9 isolates per study and a range of 12 to 777. Polymicrobial infections were observed in all included studies. The most commonly reported pathogens were *S. aureus* (n = 14, 87.5%), *P. aeruginosa* (n = 12, 75.0%), *E. coli* (n = 11, 68.8%), and *Klebsiella pneumoniae* (n = 10, 62.5%), while *Proteus* spp. were reported in 9 studies (56.2%). *Streptococcus* spp., *Enterococcus* spp., *Acinetobacter* spp., and *Candida* spp. were also reported. Multidrug-resistant (MDR) bacteria were noted in 6 studies (37.5%), while Methicillin-resistant *S. aureus* (MRSA) was identified in 7 studies (43.8%). Biofilm formation was reported in four studies (25.0%) (Table 3; Supplementary Table S2).

Table 3
Summary of patient characteristics and microbiological findings in included studies in the meta-analysis

Study No.	Authors, Year	Population (T2DM/T1DM)	Sample Size	Mean Age (Year)	HbA1c (%)	BMI	No. of Isolates	Common Pathogens †	Resistance Summary
1	Al Benwan et al., 2012 [32]	432/8	440	56.7	NM	NM	777	*S. aureus* (18.5%), *P. aeruginosa* (17.4%)	VAN effective; MRSA 41.6%
2	Alhubail et al., 2020 [33]	DM	513	62 ± 11	8.6 ± 1.9	NM	NM	*S. aureus* (19.9%), *P. aeruginosa* (12.8%)	Low VAN resistance; high AMP/ERY resistance
3	Messenger et al., 2018 [34]	95%/NM	150	62.6 ± 9.5	8.8 ± 2.02	33.2 ± 6.7	NM	Gram-neg (16%), MRSA (3%)	NM
4	Abdulrazak et al., 2005 [35]	DM	86	61 ± 1.7	NM	NM	140	*S. aureus* (38.4%), *P. aeruginosa* (17.5%)	VAN effective; AMP, CIP resistant
5	Hassan Amir et al., 2020 [36]	92.4%/7.6%	370	53.8 ± 10	7.3 ± 3.3	NM	NM	MRSA (20.3%), *P. aeruginosa* (20.3%)	100% susceptibility to VAN, LZD
6	Sannathimmappa et al., 2021 [37]	DM	74	65 ± 11	NM	NM	233	Polymicrobial (56%), *S. aureus* (19%)	Doxy & CARB effective
7	Malone et al., 2013 [38]	98%/1.5%	66	62.9 ± 11.3	9.9 ± 2.0	NM	93	*S. aureus* (36%), *E. coli* (21%)	NM
8	Johargy, 2016 [39]	DM	138	NM	NM	NM	55	*S. aureus, E. coli, P. aeruginosa*	VAN & AMK effective
9	Orfali et al., 2024 [40]	72.8%/27.1%	70	54	12.7 ± 3.4	NM	63	*S. marcescens* (20.6%), *E. coli* (9.5%)	MDR prevalent
10	Al-Mijalli, 2021 [41]	T2DM %NM	44	59.4 ± 7.6	NM	29.7 ± 7.7	12	*S. aureus* (65.9%), *S. agalactiae*	High VAN, CIP resistance
11	Saleem et al., 2025 [24]	T1DM/T2DM	200	63.5 ± 10.5	8.6 ± 1.5	24.9 ± 5.7	NM	*S. aureus* (33%), *P. aeruginosa* (20%)	MDR, KPC/NDM genes prevalent
12	Alkhatieb et al., 2022 [42]	71.5%/19.6%	260	63.04 ± 13	6.95¬±5.88	26.88¬±7.4	NM	*E. coli* (16.9%), *S. aureus* (10.8%)	MDR & ESBL prevalent
13	Alkhatieb et al., 2024 [25]	96.90%	96	63.03 ± 10.88	NM	NM	NM	*S. aureus* (27.7%), *P. aeruginosa* (15.4%)	30% no growth; 58.2% MDR
14	El-Hazmi M. M., 2015 [43]	DM	268	59.6	NM	NM	308	*S. aureus* (21.4%), *P. aeruginosa* (13.3%)	High MDR prevalence, ESBL (19.4%)
15	Aldawish & Alayed, 2018 [44]	DM	126	NM	NM	NM	NM	*S. aureus* (37.3%), *P. aeruginosa*	ERY, GEN resistance

† *% as reported in article; N/M = Not Mentioned; DM =* Diabetes Mellitus; T2DM = Type 2 Diabetes Mellitus; T1DM = Type 1 Diabetes Mellitus; *MDR = Multidrug-Resistant; ESBL = Extended-Spectrum Beta-Lactamase producing; MRSA = Methicillin-Resistant Staphylococcus aureus; ERY = Erythromycin; GEN = Gentamicin; VAN = Vancomycin; CIP = Ciprofloxacin; AMK = Amikacin; Doxy = Doxycycline; CARB = Carbapenem; LZD = Linezolid; AMP = Ampicillin; KPC/NDM = Carbapenemase genes (Klebsiella pneumoniae carbapenemase / New Delhi metallo-beta-lactamase)*

Study No.	Authors, Year	Population (T2DM/T1DM)	Sample Size	Mean Age (Year)	HbA1c (%)	BMI	No. of Isolates	Common Pathogens †	Resistance Summary
16	Aldhfyan et al., 2018 [45]	DM	81	NM	NM	NM	NM	*S. aureus* (30%), *E. coli* (22%)	Aerobe-anaerobe mixed

† *% as reported in article; N/M = Not Mentioned; DM =* Diabetes Mellitus; T2DM = Type 2 Diabetes Mellitus; T1DM = Type 1 Diabetes Mellitus; *MDR = Multidrug-Resistant; ESBL = Extended-Spectrum Beta-Lactamase producing; MRSA = Methicillin-Resistant Staphylococcus aureus; ERY = Erythromycin; GEN = Gentamicin; VAN = Vancomycin; CIP = Ciprofloxacin; AMK = Amikacin; Doxy = Doxycycline; CARB = Carbapenem; LZD = Linezolid; AMP = Ampicillin; KPC/NDM = Carbapenemase genes (Klebsiella pneumoniae carbapenemase / New Delhi metallo-beta-lactamase)*

3.4. Antimicrobial Resistance Patterns

The pooled prevalence of antimicrobial resistance among DFU isolates varied across antibiotics (Fig. 2). Ampicillin showed the highest resistance at 67% (95% CI: 55–80), followed by tetracycline (59%, 95% CI: 47–71), gentamicin (58%, 95% CI: 40–75), and ciprofloxacin (52%, 95% CI: 25–79). In contrast, the lowest resistance rates were observed for vancomycin (0%, 95% CI: 0–3), linezolid (2%, 95% CI: 0–6), and piperacillin–tazobactam (9%, 95% CI: 4–16). Resistance to imipenem and meropenem remained low at 13% (95% CI: 7–22) and 12% (95% CI: 6–24), respectively.

3.5. Data Synthesis and Prevalence Estimates

A single-arm meta-analysis of seven studies including 1,116 isolates estimated the pooled prevalence of *S. aureus* in infected DFUs at 29% (95% CI: 20%–40%) using a random-effects model. Substantial heterogeneity was observed ($I^2 = 89.6\%$, $\tau^2 = 0.3467$, $p < 0.0001$) (Fig. 4-A). Similarly, a meta-analysis of six studies including 1,056 isolates estimated the pooled prevalence of *E. coli* at 14% (95% CI: 10%–19%), with moderate heterogeneity ($I^2 = 70.2\%$, $\tau^2 = 0.1318$, $p = 0.0050$) (Fig. 4-B). For *P. aeruginosa*, six studies including 1,142 isolates yielded a pooled prevalence of 16% (95% CI: 13%–20%). Moderate heterogeneity was observed ($I^2 = 53.9\%$, $\tau^2 = 0.0621$, $p = 0.0430$) (Fig. 4-C).

Heterogeneity was moderate ($I^2 = 53.9\%$, $\tau^2 = 0.0621$, $p = 0.0430$), reflecting variability attributable to study-level factors. Less frequently isolated pathogens included *K. pneumoniae* (12%), *Proteus mirabilis* (11%), *Enterococcus* spp. (9%), *Acinetobacter baumannii* (8%), *Streptococcus agalactiae* (7%), and *Candida* spp. (5%) (Fig. 5; Supplementary Figure S1).

3.6. Quality Assessment of Included Studies

The methodological quality of the 16 included studies was assessed using the Joanna Briggs Institute's (JBI) Critical Appraisal Tool for Analytical Cross-Sectional Studies. Overall, most included studies (n = 15) scored 6 out of 8, while one study scored 5 out of 8. All included studies were considered to have acceptable methodological quality to be included in the meta-analysis (Table 1).

4. Discussion

DFIs are among the most serious, disabling, and costly complications of DM, contributing to substantially reduced patients' quality of life, prolonged hospitalization, and lower extremity amputations [2,3]. This systematic review and meta-analysis represent, to our knowledge, the first comprehensive regional synthesis of bacterial profile and AMR patterns associated with DFIs in the Arabian Gulf. Sixteen studies involving 3260 participants were included. Our findings revealed that DFIs in the GCC are predominantly polymicrobial, with a broad spectrum of bacterial pathogens. *S. aureus* was the most frequently isolated pathogen, reported in 87.5% of the included studies. This finding is consistent with previous global meta-analyses, which have also identified *S. aureus* as the predominant pathogen in DFIs, with a pooled prevalence estimate of approximately 18.0% [46]. Moreover, several studies reported an increased abundance of *S. aureus* in chronic wounds with age, which can form biofilms and hinder the healing process [46,47]. In the present study, the mean age of participants was 58 years, consistent with previous studies. Aging is associated with a decline in both innate and adaptive immune responses, reducing the ability to fight and eliminate bacterial infections effectively. Furthermore, the aged frequently have diminished perfusion, compromised skin integrity, and comorbidities including diabetes and vascular disease. These factors combine to create an ideal environment for colonization by *S. aureus* and other opportunistic pathogens. Together, these factors may contribute to the persistence of *S. aureus* and chronic wound infections in the aged population [48–50]. The second most dominant pathogens were Gram-negative bacteria, including *P. aeruginosa* (75.0%), *E. coli* (68.8%), and *K. pneumoniae* (62.5%), which is consistent with previously reported studies [51–53]. The diversity in bacterial profiles across the studies may be attributed to several factors, such as patient comorbidities, clinical ulcer characteristics, sampling strategies, antibiotics previously administered, and the use of different diagnostic techniques [53–55]. These findings show a large variation in bacterial profiles of DFUs in the Gulf region, supporting the necessity for region-specific surveillance to guide antibiotic treatment protocols and limit the emergence of resistance.

In this study, we found that the heterogeneity was substantially higher for *S. aureus* (I^2 = 89.6%) compared to *E. coli* (I^2 = 70.2%), and *P. aeruginosa* (I^2 = 53.9%) (Fig. 4). These findings reflect differences in the methodological approaches used across included studies, ranging from conventional culture-based techniques to more advanced automated and molecular diagnostic methods. In addition, differences in clinical sampling, healthcare settings, and geographical location may have further affected the bacterial detection rates. In addition, variability in the timing of specimen collection and prior antibiotic exposure may have further contributed to the inconsistent prevalence of *S. aureus*, given its well-established role as both a colonizing and pathogenic organism in DFUs. Together, these methodological and clinical differences may explain the variability in pathogen prevalence observed across the included studies. Moreover, the reported BMI values across studies ranged from approximately 24.9 to 33.2, with most patients being overweight or obese. HbA1c, a marker of long-term glycemic control, ranged from 6.95% to 12.7%, indicating poor to moderate glycemic control in most cases. Higher BMI is also associated with poorer glycemic control, particularly in patients with T2DM [56–58]. Consequently, these factors, along with advancing age, increase the risk of wound infection and impair wound healing and increase susceptibility to bacterial DFU colonization [56–58]. This may explain the observed increased abundance and diversity of pathogens such as *S. aureus* and *P. aeruginosa* in these patients.

Importantly, we observed higher resistance rates to several commonly used antibiotics, particularly ampicillin, tetracycline, gentamicin, and ciprofloxacin (67%, 59%, 58%, and 52%, respectively). In contrast, resistance remained low for imipenem, meropenem, piperacillin–tazobactam, linezolid, and vancomycin (13%, 12%, 9%, 2%, and 0%), consistent with previous studies [52,53,59]. However, the growing global prevalence of AMR threatens the long-term effectiveness of these agents, particularly with prolonged or repeated use often required in DFU management [53]. This underscores the importance of continued national surveillance and judicious antibiotic use guided by Antimicrobial Susceptibility Testing (AST) to preserve the effectiveness of these agents, particularly in the era of rising AMR. For example, Saudi Arabia introduced a prescription-only antibiotic dispensing policy in 2018, which was associated with a measurable initial decline in antimicrobial sales [60]. Unfortunately, subsequent data suggest that this reduction was not sustained over time [60,61]. As this meta-analysis included studies spanning the period from 2005 to 2025, the reported AMR patterns may reflect the cumulative impact of antimicrobial prescribing practices both before and after these regulatory shifts. This example emphasizes the broader need for standardized and sustained implementation of antimicrobial regulations throughout GCC countries. Coordinated, regionally standardized treatment guidelines may further support the translation of these findings into routine clinical practice.

Recently, Multidrug-Resistant Organisms (MDROs) have become an increasing concern, particularly in chronic and recurring DFUs with previous antibiotic exposure. These resistant bacteria, including MRSA and carbapenem-resistant Gram-negative bacteria (CR-GNB), are increasingly reported in DFUs and are associated with more challenging clinical management and poorer outcomes [52,62]. The present meta-analysis sought to estimate the prevalence of MDR bacterial infections within the region. MDROs were reported in six of the 16 included studies (37.5%), while MRSA was identified in seven studies (43.8%). However, the limited number of eligible studies and inconsistent reporting of AMR data prevented pooled prevalence estimates for specific MDR phenotypes. These findings indicate that MDR bacterial pathogens are present across the GCC, while also highlighting the need for more standardized surveillance and reporting to better define their regional burden. Biofilm formation also contributes to AMR in DFIs by protecting bacteria from host defenses and antibiotics, and by facilitating resistance gene transfer between species [47]. In this study, biofilm was reported in only 4 of 16 studies (25.0%), highlighting the need for its routine assessment alongside susceptibility testing.

Despite the substantial and rising burden of DM across the GCC countries, among the highest globally [1], the regional evidence base on DFI microbiology and AMR remains limited, with only 16 eligible studies identified over 20 years (2005–2025) across the six GCC countries (Fig. 1). Additionally, research output remained low and uneven over time, with only 5 of 16 studies published between 2005 and 2016 compared with 11 between 2018 and 2025, suggesting a modest, gradual increase in regional research activity. The relatively limited volume of regional evidence highlights the urgent need for greater investment in microbiology research infrastructure.

Several limitations should be acknowledged. The majority of the included studies were retrospective, which may influence the reliability, accuracy, and completeness of reported data. Another limitation is the geographical imbalance in the regional evidence base, with Saudi Arabia contributing most of the included studies, while Bahrain and Qatar had no qualifying studies (Fig. 2). Many studies also lacked essential details needed to understand DFI dynamics, such as ulcer chronicity, clinical grading, biofilm formation, and prior antibiotic exposure. Furthermore, the distinction between bacterial colonization and true clinical infection could not be consistently verified across the included studies, as most studies did not uniformly apply standardized clinical infection criteria (e.g., IWGDF/IDSA). Furthermore, anaerobic bacteria and fungi were rarely documented, resulting in significant gaps in characterizing the DFUs across the GCC region. There was significant heterogeneity among included studies due to differences in study design, patient characteristics, sampling methods, and antibiotic use. This heterogeneity was compounded by inconsistencies in reporting: pooled prevalence estimates were calculated using patient counts when studies reported patient-level data, or isolate counts when only microbiological isolate data were available. The use of diverse denominators among included studies may have influenced the observed between-study variability, which should be considered when interpreting the pooled prevalence estimates. The restriction to English-language publications may have resulted in language bias by excluding eligible studies published in other languages. Furthermore, publication bias cannot be ignored, given the increased likelihood of publication for studies showing higher pathogen prevalence

or more dramatic AMR patterns. Beyond these methodological considerations, it is also critical to understand the larger picture of bacterium-host interactions. DFU outcomes are also influenced by ulcer characteristics (depth and severity), host immune responses, and host–microbiome interactions. An imbalance in protective skin microbiota, along with the expansion of opportunistic species, may shift colonization towards infection. To better understand how diabetes load and complications, particularly poor blood perfusion, comorbidities, and regional climates, affect bacteria-host dynamics in DFUs, future studies integrating metagenomics and host-immune profiling may provide a more comprehensive understanding of DFI pathogenesis in the GCC.

Collectively, these limitations underscore the need for large, comprehensive, multi-country research to track resistance trends and provide more up-to-date data to inform future policy decisions related to public health and infection control. With ongoing progress in the healthcare sectors in the GCC, national and regional data-sharing platforms are important for continuous monitoring of DFU cases, real-time laboratory surveillance, identification of causative agents, and determination of their AMR profile. Our findings are complementary to worldwide efforts to control both DM and AMR, and they may help shape clinical management strategies, guide infection control policies, and support calls to increase investment in improving DFU care across the Arabian Gulf region through enhanced education and awareness for both diabetic patients and healthcare providers.

5. Conclusion

DFUs represent a significant global public health concern, especially in light of the continuing rise in DM prevalence. This is the first systematic review and meta-analysis to determine the prevalence of bacterial profiles and AMR patterns of infected DFUs across the GCC over the past two decades. *S. aureus, E. coli*, and *P. aeruginosa* were the most common bacteria isolated in DFUs in the region, with high resistance to commonly used antibiotics. Our findings can help guide appropriate antibiotic selections and highlight the urgent need for region-specific, effective policies to strengthen infection control and prevent the spread of antibiotic-resistant bacteria. Evidence-based alternative treatment options for DFUs are needed to address these serious and costly complications, particularly amid the rising burden of DM.

Abbreviations

AMR: Antimicrobial Resistance

AST: Antimicrobial Susceptibility Testing

BMI: Body mass index

CR-GNB: carbapenem-resistant Gram-negative bacteria

DFIs: Diabetic Foot Infections

DFUs: Diabetic Foot Ulcers

DM: Diabetes mellitus

GCC: Gulf Cooperation Council

IDF: International Diabetes Federation

IWGDF: International Working Group on the Diabetic Foot

JBI: Joanna Briggs Institute

MDROs: Multidrug-Resistant Organisms

MRSA: Methicillin-resistant *Staphylococcus aureus*

T1DM: Type 1 diabetes mellitus

T2DM: Type 2 diabetes mellitus

UAE: United Arab Emirates

WHO: World Health Organization

Declarations

Ethical approval

Not applicable because the study is a systematic review

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Author Contribution

S.M.A. conceived and designed the study, performed the investigation, curated and analyzed the data, wrote the original draft of the manuscript, reviewed and edited the manuscript, and supervised the study. M.Y. contributed to the study conceptualization and methodology, participated in the investigation, supervised the study, validated the results, and reviewed and edited the manuscript. A.M.K. contributed to the methodology, investigation, data curation, supervision, validation, and manuscript review and editing. S.A.H. and R.M.F. contributed to supervision and validation. A.M.A. reviewed and edited the manuscript. S.A.T. contributed to the investigation, validation, and manuscript review and editing. A.A.A. and M.S.M.A. contributed to the investigation, data curation, and manuscript review and editing. E.I.A. conceived the study, contributed to the methodology, investigation, data curation, validation, and supervision, and reviewed and edited the manuscript. All authors reviewed and approved the final manuscript and agree to be accountable for all aspects of the work.

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Data Availability

The datasets generated and analyzed in this study are available in the Supplemental Dataset

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Figures

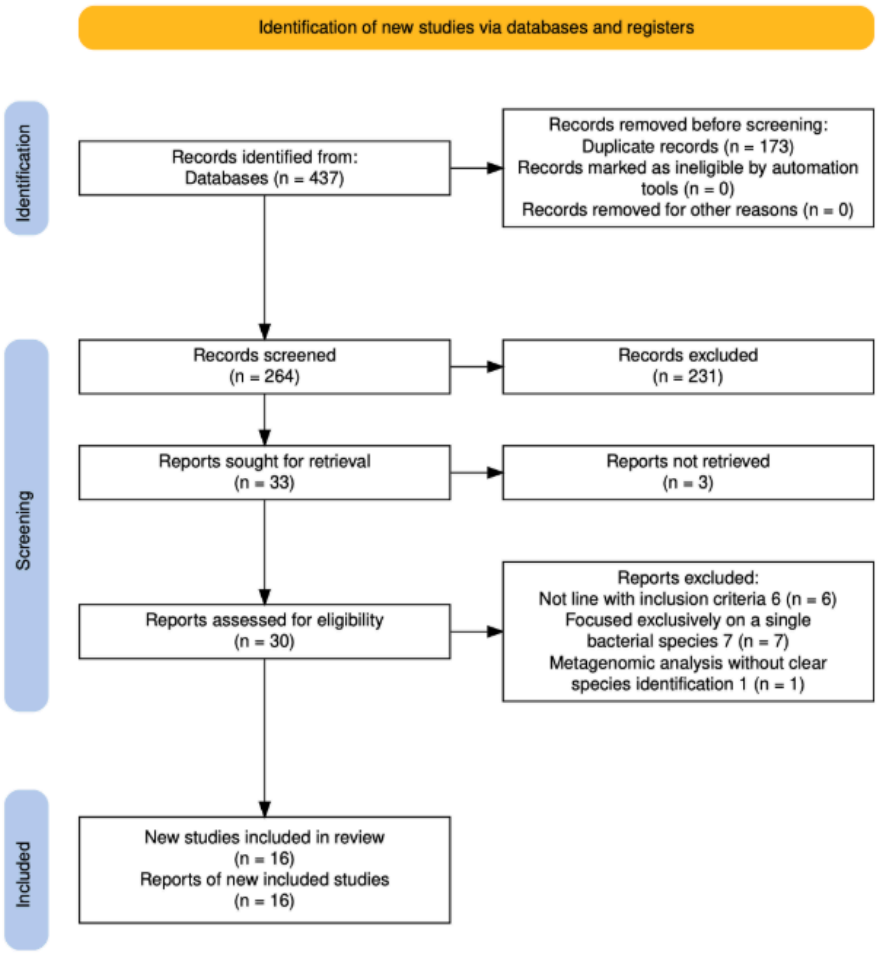

Figure 1

PRISMA flowchart illustrating the study selection process. A total of 437 records were identified through database searching. After duplicate removal and title/abstract screening, 30 full-text articles were assessed for eligibility. Fourteen full-text articles were excluded for the following reasons: failure to meet the inclusion criteria (n = 6), reporting only a single bacterial species (n = 7), and metagenomic analysis without culture-based bacterial species identification (n = 1). Sixteen studies met the eligibility criteria and were included in the systematic review and meta-analysis. The diagram was created using the PRISMA Flow Diagram tool available at PRISMA Flow Diagram - ESTECH. (https://estech.shinyapps.io/prisma_flowdiagram/)

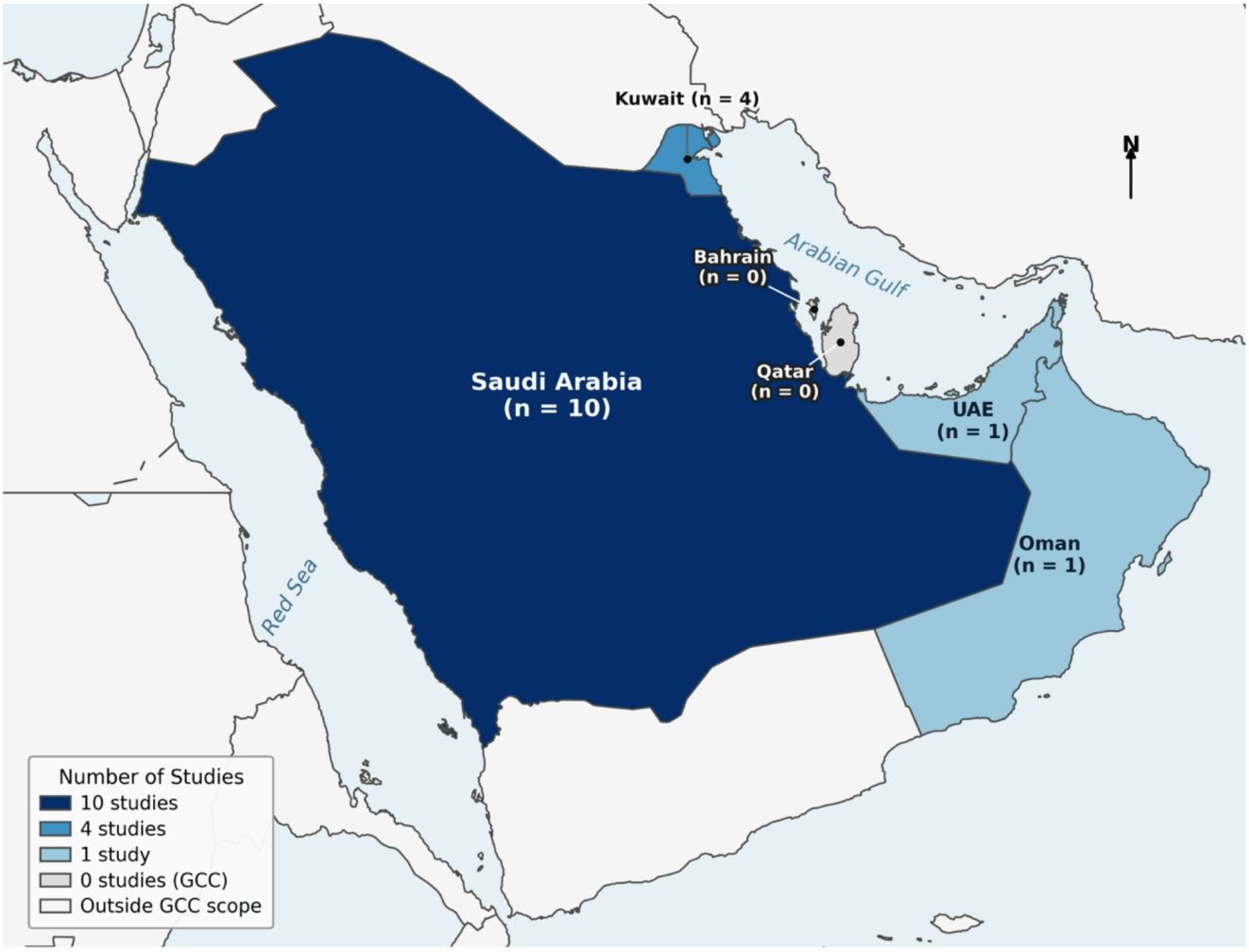

Figure 2

Geographic distribution of the 16 included studies across the Gulf Cooperation Council (GCC) countries. Color intensity corresponds to the number of included studies per country; countries highlighted in grey had no eligible studies identified.

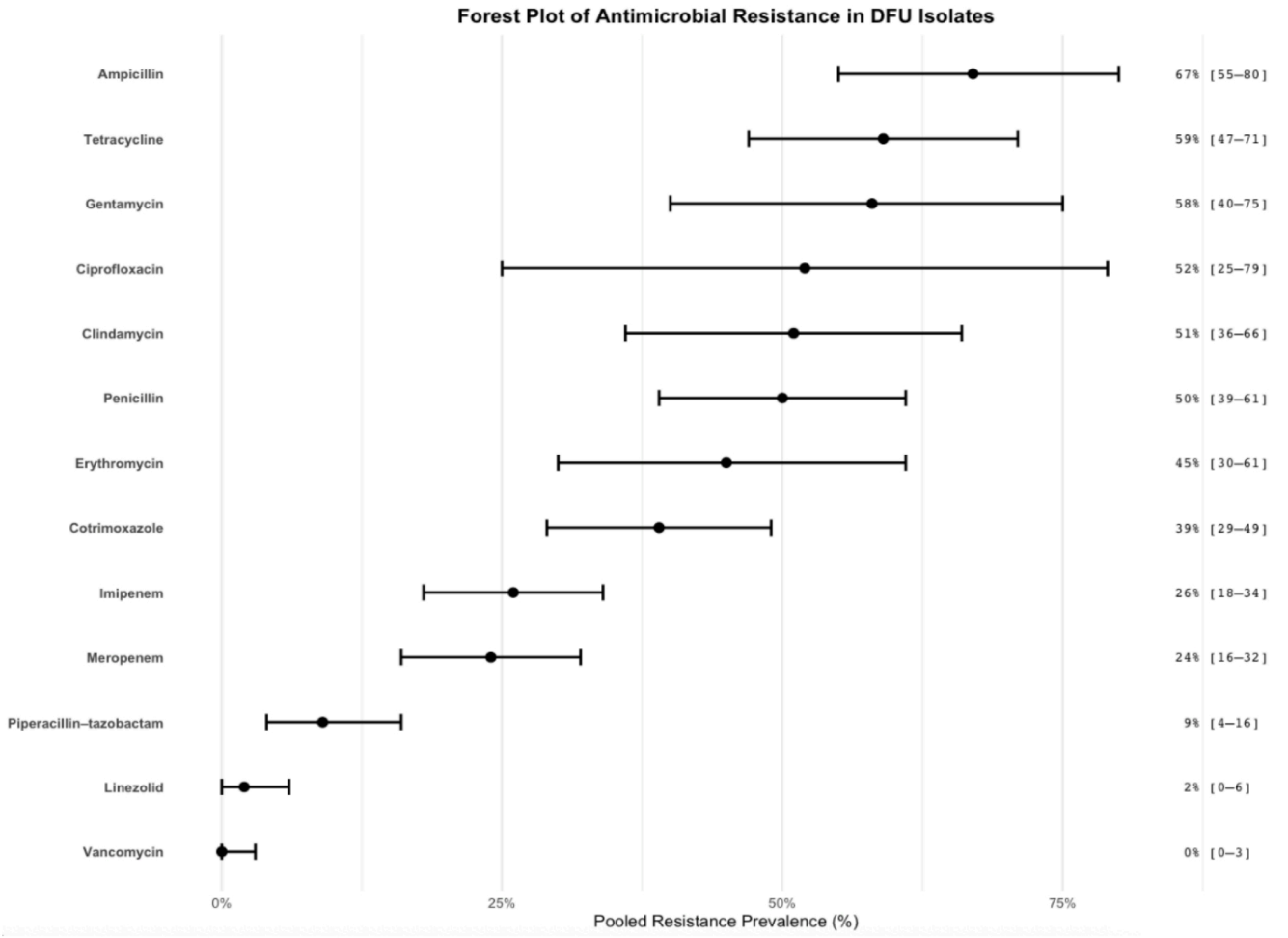

Figure 3

Forest plot of pooled prevalence estimates of antimicrobial resistance among diabetic foot ulcer (DFU) isolates in the GCC region. Points represent pooled prevalence estimates; horizontal lines represent the 95% confidence intervals. Antibiotics are ordered from highest (Ampicillin, 67%) to lowest (Vancomycin, 0%) resistance.

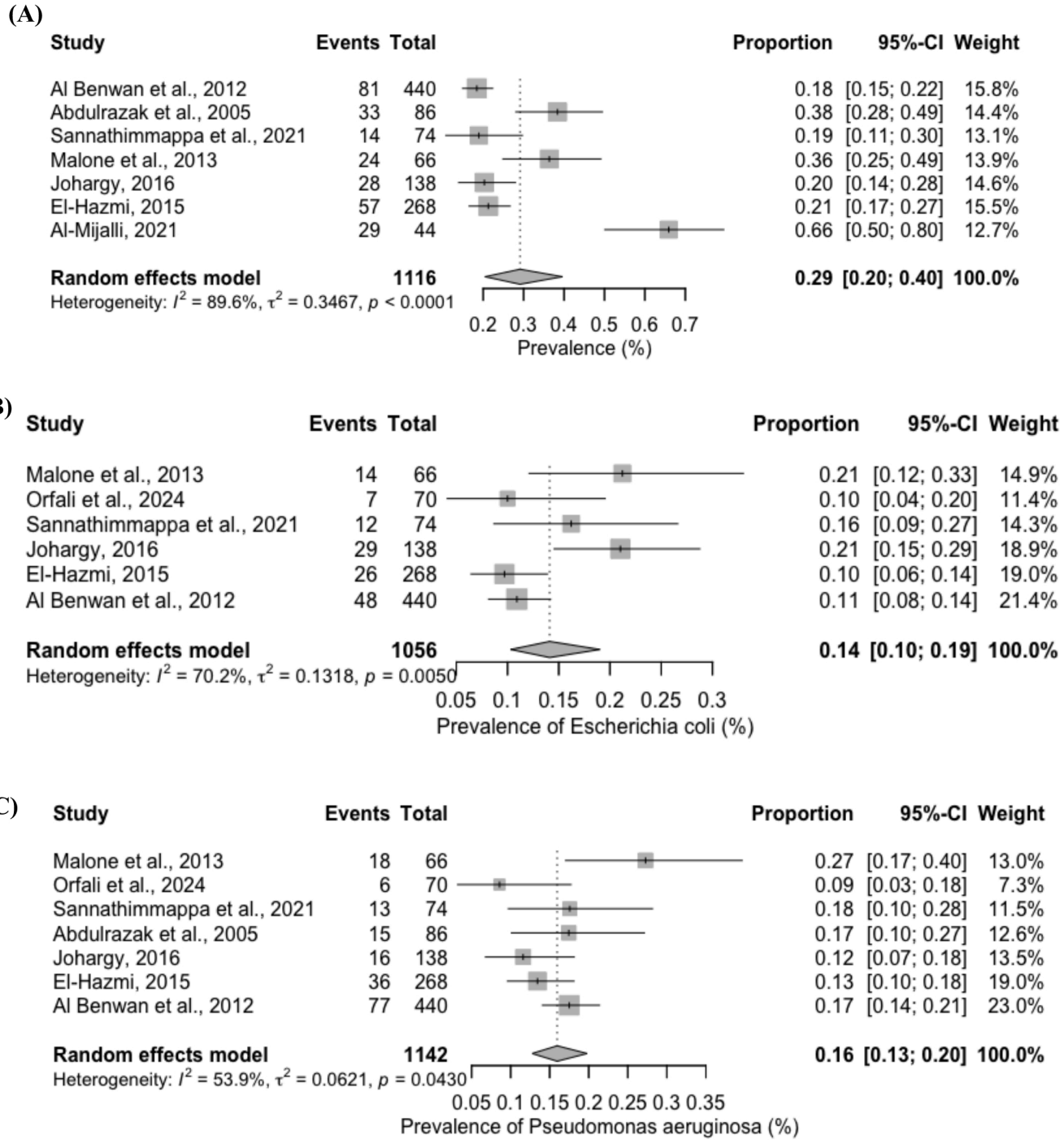

Figure 4

Forest plots of pooled prevalence estimate for the three most isolated bacterial pathogens from DFUs across GCC countries, derived from random-effects meta-analysis with 95% confidence intervals. (A) *S aureus* (14 studies; pooled prevalence 29%, 95% CI: 20–40%; I² = 89.6%). **(B)** *E. coli* (6 studies; pooled prevalence 14%, 95% CI: 10–19%; I² = 70.2%). **(C)** *P. aeruginosa* (6 studies; pooled prevalence 16%, 95% CI: 13–20%; I² = 53.9%).

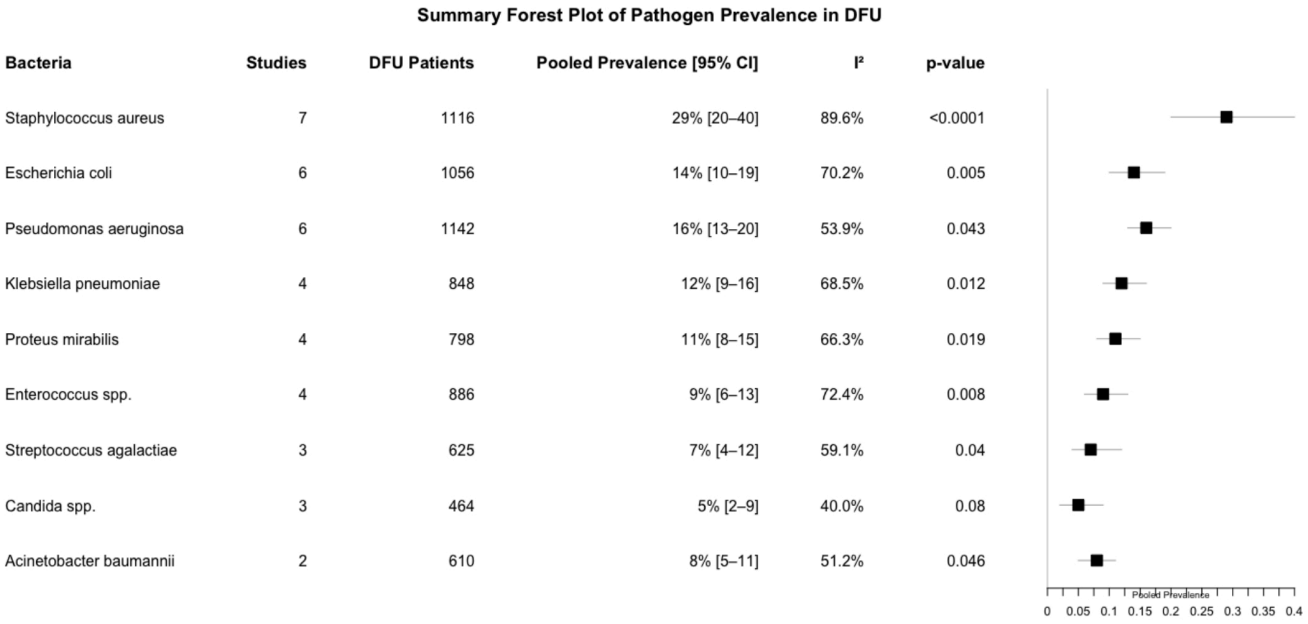

Figure 5

Summary forest plot of the pooled prevalence estimates of the most common bacterial pathogens isolated from DFUs in the GCC region led by *S. aureus* (29%), *P. aeruginosa* (16%), and *E. coli* (14%). Squares represent pooled prevalence; horizontal lines represent 95% confidence intervals.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementaryDFUinGCC.docx