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Biofilm formation and antibiotic resistance of clinical isolates from diabetic foot ulcers

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Abstract. Diabetic foot ulcers are among the most debilitating complications of type 2 diabetes mellitus, often leading to persistent infections and lower limb amputations. Microbial colonisation and biofilm formation contribute significantly to the chronicity and antibiotic resistance observed in these wounds. This study aimed to investigate the spectrum of microorganisms isolated from diabetic foot ulcers, assess their antibiotic susceptibility, and evaluate the biofilm-forming capacity of *Staphylococcus aureus* strains. Microbiological examination of wound discharge was performed for 68 patients with clinically diagnosed diabetic foot syndrome. A total of 78 microbial isolates were identified using morphological and biochemical methods. Most wound infections were monocultures (85%), with mixed infections identified in 10 cases. Antibiotic susceptibility was tested using the Kirby-Bauer disk diffusion method. Biofilm formation in *Staphylococcus aureus* isolates was assessed under static conditions using gentian violet staining and semi-quantitative scoring. Gram-positive bacteria predominated (73%), with *Staphylococcus aureus* and *Staphylococcus haemolyticus* being the most frequently isolated. Among Gram-negative organisms (27%), *Klebsiella* spp. and *Pseudomonas aeruginosa* were common. Antibiotic susceptibility testing revealed moderate methicillin sensitivity in *Staphylococcus aureus* (40%) and *Staphylococcus*

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haemolyticus (44%), while vancomycin and tigecycline showed the highest activity. Macrolides were largely ineffective, and *Corynebacterium* spp. demonstrated extensive resistance. Gram-negative isolates displayed higher resistance overall, with *Klebsiella* spp. resistant to most tested antibacterials. Biofilm formation analysis of 25 *Staphylococcus aureus* isolates revealed biofilm formation in 48%, including weak (58%), moderate (17%), and strong (25%) producers. Routine screening for biofilm-producing pathogens may improve clinical management and outcomes in diabetic foot infections

Keywords: antibiotic susceptibility; chronic wounds; multidrug resistance; *S. aureus*; wound microbiota

INTRODUCTION

Type 2 diabetes mellitus (T2DM) is one of the most widespread endocrine disorders globally, characterised by chronic hyperglycemia resulting from impaired insulin action and relative insulin deficiency. The global prevalence of T2DM continues to rise at an alarming rate, driven largely by aging populations, sedentary lifestyles, and increasing rates of obesity. According to the International Diabetes Federation, cited by A. Kumar *et al.* [1], over 530 million people worldwide are currently (2024) living with diabetes, with T2DM accounting for the vast majority of cases, and this number is projected to exceed 643 million by 2030. By K. Nabrdalik *et al.* [2] this chronic condition poses a growing public health concern, significantly increasing the risk of cardiovascular disease, kidney failure, neuropathy, and other long-term complications. In addition to the medical burden, T2DM represents a substantial economic challenge for healthcare systems globally due to the high cost of ongoing treatment, complication management, and disability-related care.

B. Stancu *et al.* [3] stated that among the many complications associated with diabetes mellitus, diabetic foot ulcers (DFUs) represent one of the most serious and prevalent outcomes, significantly contributing to patient morbidity and healthcare burden. These lesions often result from a complex interplay of factors, including peripheral neuropathy, peripheral arterial disease, and impaired microcirculation, all of which compromise wound healing and tissue integrity. Reduced sensation in the feet leads to unnoticed trauma, while diminished blood supply hinders immune response and tissue regeneration. According to Z. Moore *et al.* [4] and K. Parveen *et al.* [5] if not properly managed, DFUs can progress rapidly to soft tissue and bone infections, gangrene, and ultimately, limb amputation. In severe cases, systemic infection and sepsis may occur, posing a direct threat to the patient's life.

Diabetic foot ulcers are particularly susceptible to microbial colonisation due to compromised tissue integrity, impaired immune responses, and poor vascularisation. According to I. Volch *et al.* [6], chronic diabetic foot ulcers are often colonised by a wide range of microorganisms, including both Gram-positive and Gram-negative bacteria. Among them, *Staphylococcus aureus* and *Klebsiella* spp. were found to predominate, but other frequently isolated pathogens included *Staphylococcus haemolyticus*, *Pseudomonas aeruginosa*, *Corynebacterium* spp., *Escherichia coli*, and *Proteus* spp., as well as opportunistic fungi such as *Candida* spp. Similarly, A.C. Afonso *et al.* [7] documented a polymicrobial nature of diabetic foot infections, noting that the pathogens involved may range from aerobic to anaerobic species and include both Gram-positive and Gram-negative bacteria. Reported biofilm-producing organisms included members of the *Enterobacteriaceae* family (*E. coli, Klebsiella pneumoniae, Klebsiella oxytoca, Proteus mirabilis, Proteus vulgaris, Morganella morganii, Citrobacter* spp., and *Vibrio* spp.), as well as *P. aeruginosa, Acinetobacter baumannii*, and other *Acinetobacter* spp. Among Gram-positive isolates, *S. aureus* (including MRSA), coagulase-negative *Staphylococcus* spp., *Streptococcus* spp., *Enterococcus faecalis*, and *Corynebacterium* spp. were highlighted. In a separate study, Y.V. Ivanova *et al.* [8] also reported a wide microbial spectrum in chronic diabetic foot ulcers, with frequent recovery of *S. aureus, A. baumannii, E. coli, K. pneumoniae,* and *Candida albicans*. Importantly, the authors emphasised that these clinical isolates exhibited markedly higher adhesive properties than reference strains. Once colonised, bacteria in diabetic foot ulcers may adopt survival strategies that include the development of antibiotic resistance. As highlighted by M. Piksa *et al.* [9], this complication is of particular concern because the diabetic foot provides a favorable environment for chronic infection, sometimes extending to the bone, and is frequently associated with pathogens resistant to conventional therapy. Another important mechanism described by T. Naaz *et al.* [10] is the ability to form biofilms, which are complex, structured communities of microorganisms surrounded by a self-produced extracellular matrix, composed of polysaccharides, DNA, and proteins. As stated by N.Y. Kravets *et al.* [11], within these biofilms, bacteria are protected from various environmental stresses, including host immune defenses and antimicrobial agents, making them significantly more difficult to eradicate than planktonic cells.

The biofilm mode of growth has been strongly associated with chronic, recurrent infections and increased antibiotic resistance, particularly in individuals with diabetes, whose compromised healing capacity further exacerbates the risk. According to C. Pouget *et al.* [12], biofilm-associated infections often do not respond to conventional antibiotic therapy, leading to prolonged treatment courses and frequent recurrence. Consequently, identifying and characterising biofilm-producing clinical isolates from diabetic foot ulcers is crucial for guiding more effective treatment strategies. Despite its clinical relevance, biofilm formation is not routinely assessed in microbiological diagnostics, potentially contributing to persistent infections in patients who repeatedly fail to respond to antibiotic therapy alone. The purpose of this study was to assess the antibiotic resistance and biofilm-forming ability of pathogens isolated from diabetic foot ulcers.

MATERIALS AND METHODS

This study builds upon authors' previous research on the microbiota of diabetic foot ulcers and its patterns of antibiotic resistance [6]. It included 68 patients diagnosed with type 2 diabetes mellitus and diabetic foot syndrome, who were treated at the Municipal Non-Profit Enterprise "Ternopil City Emergency Hospital" in 2024-2025. The inclusion criteria were: patients of both sexes, age over 18 years, verified diagnosis of type 2 diabetes mellitus, presence of diabetic foot syndrome. The exclusion criteria were: presence of chronic diseases in the acute phase or in the phase of decompensation, current treatment with glucocorticosteroids, pregnancy, mental disorders, confirmed or suspected cancer. All included patients were diagnosed with complicated diabetic foot syndrome, characterised by purulent-necrotic lesions and ulcers, and were indicated for surgical intervention. As part of the preoperative assessment, microbiological testing of wound discharge was performed.

Sterile cotton swabs were used to collect samples from the wound discharge under aseptic conditions. The collected material was inoculated onto selective culture media and incubated at 37°C for 24-48 hours. Pure microbial cultures were identified based on their morphological characteristics and a series of biochemical tests. Gram-negative rods were identified using the following assays: fermentation in Kligler Iron Agar, Simmons' citrate agar (Farmaktiv, LLC, Kyiv, Ukraine), indole production, catalase activity, and motility testing. Gram-positive cocci were identified by evaluating catalase, lecithinase, and coagulase activity (Biolik Pharma LLC, Kharkiv, Ukraine). In addition, blood agar (Farmaktiv, LLC, Kyiv, Ukraine) was used to assess hemolytic activity. The antibiotic susceptibility of the isolated microbial strains was assessed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, following standard protocols. The tested antibiotics included ciprofloxacin, ceftazidime, chloramphenicol, amikacin, azithromycin, ceftriaxone, doxycycline, erythromycin, methicillin, tigecycline, vancomycin, and ertapenem. Zone diameters were measured after incubation and interpreted according to CLSI [13].

The ability of the isolated strains to form biofilms was studied under static conditions by growing the cultures on sterile glass coverslips. After incubation, the coverslips were stained with gentian violet and examined under a light microscope (TM MICROmed, Poltava, Ukraine), which was equipped with a Swift 5.0 Megapixel Digital Camera (Swiftmicroscopes, China). Biofilm formation was semi-quantitatively evaluated using a 0-3 point scale based on the density and morphology of adherent cells [14, 15]. *S. aureus* was selected as a representative Gram-positive pathogen for biofilm assessment due to its high prevalence and well-established role in diabetic foot infections. The collected data were organised and tabulated using Microsoft Excel (Microsoft Corporation, Redmond, WA, USA). Descriptive statistics were applied, and the results were presented as percentages and proportions.

This study was conducted in accordance with the principles outlined in the UNESCO Universal Declaration on Bioethics and Human Rights [16] and the Declaration of Helsinki "Ethical principles of medical research involving human subjects" [17]. The research was approved by the Ethics Committee of Ternopil National Medical University (Protocol No. 81, April 3, 2025), and all participants provided written informed consent prior to participation. This study focused on biofilm formation in *S. aureus* isolates only, despite the presence of other clinically relevant species such as *S. haemolyticus* and *P. aeruginosa*. The selection was based on the high prevalence and clinical importance of *S. aureus* in diabetic foot infections. Additionally, microbial identification was qualitative in nature, and therefore the presence of a microorganism does not necessarily imply a causative role in infection.

RESULTS AND DISCUSSION

Microbiological testing was performed for all 68 patients enrolled in the study, resulting in a total of 78 microbial isolates. The majority of patients (n = 58) had monoculture infections, while mixed infections involving two distinct pathogens were identified in 10 cases. Gram-positive bacteria predominated, accounting for 57 isolates (73.08%), while 21 isolates (26.92%) were Gram-negative. *Staphylococcus* spp. were the most prevalent Gram-positive organisms, with *S. aureus* and *S. haemolyticus* being the most commonly isolated species. Among the Gram-negative bacteria, *Klebsiella* spp. were the most frequently detected. The complete distribution of isolated pathogens is presented in Table 1.

Table 1. Distribution and frequency of pathogens isolated from diabetic foot ulcers

Pathogen	Number of isolates	Frequency of isolation, %
Staphylococcus aureus	25	36.76
Staphylococcus haemolyticus	25	36.76
Klebsiella spp.	9	13.24
Corynebacterium spp.	7	11.76
Pseudomonas aeruginosa	8	10.29
Escherichia coli	4	5.88

Source: compiled by the authors

This distribution of pathogens reflects the well-recognised predominance of Gram-positive cocci, particularly *Staphylococcus* spp., in diabetic foot infections, while the presence of Gram-negative organisms such as *Klebsiella* spp. highlights the role of encapsulated bacteria that complicate host immune clearance and contribute to the chronicity of these wounds. Antibiotic susceptibility testing revealed distinct resistance patterns among Gram-positive and Gram-negative pathogens isolated from diabetic foot ulcers (Table 2). Among the Gram-positive isolates, *S. aureus* and *S. haemolyticus* demonstrated moderate sensitivity to methicillin (40% and 44%, respectively), with tigecycline and vancomycin showing the highest activity. In contrast, macrolides such as erythromycin and azithromycin exhibited poor efficacy, with only 36% of strains being sensitive. *Corynebacterium* spp. exhibited resistance to the majority of tested antibiotics, showing full susceptibility only to tigecycline and amikacin. This finding of extensive resistance in *Corynebacterium* spp. is noteworthy, as this organism is often underestimated in clinical practice yet may contribute substantially to treatment failures in chronic wounds.

Table 2. Antibiotic sensitivity of pathogens isolated from diabetic foot ulcers

Antibiotic	*S. aureus* (n = 25)	*S. haemolyticus* (n = 25)	*Klebsiella* spp. (n = 9)	*Corynebacterium* spp. (n = 7)	*P. aeruginosa* (n = 8)	*E. coli* (n = 4)
Methicillin	10 (40.0%)	11 (44.0%)	R	R	R	R
Tigecycline	25 (100%)	22 (88.0%)	4 (44.4%)	7 (100%)	R	4 (100%)
Vancomycin	22 (88.0%)	24 (96.0%)	1 (11.1%)	3 (42.9%)	8 (100%)	R
Ciprofloxacin	14 (56.0%)	14 (56.0%)	R	R	8 (100%)	4 (100%)
Ceftazidime	13 (52.0%)	12 (48.0%)	R	R	R	2 (50.0%)
Levomycetin	17 (68.0%)	20 (80.0%)	R	5 (71.4%)	R	4 (100%)
Amikacin	21 (84.0%)	19 (76.0%)	4 (44.4%)	7 (100%)	7 (87.5%)	3 (75.0%)
Azithromycin	9 (36.0%)	9 (36.0%)	R	R	R	4 (100%)
Ceftriaxone	17 (68.0%)	14 (56.0%)	R	R	R	R
Erythromycin	9 (36.0%)	9 (36.0%)	R	R	R	R

Note: R – all tested isolates were resistant (0% sensitivity)
Source: compiled by the authors

Gram-negative isolates showed a higher degree of resistance overall. *Klebsiella* spp. were resistant to most antibiotics tested, including methicillin, ciprofloxacin, and ceftriaxone. *P. aeruginosa* was fully sensitive to ciprofloxacin and vancomycin but resistant to several other antibiotics, including tigecycline and ceftazidime. *E. coli* strains demonstrated good susceptibility to multiple agents such as ciprofloxacin, levomycetin, azithromycin, and tigecycline, but were completely resistant to vancomycin and ceftriaxone. Out of the 25 *S. aureus* isolates obtained from patients with diabetic foot ulcers, 12 (48%) demonstrated the ability to form biofilms under static conditions. Among these biofilm-producing strains, 7 (58.3%) exhibited weak biofilm formation (1 point), 2 strains (16.7%) showed moderate formation (2 points), and 3 strains (25.0%) demonstrated strong biofilm-forming ability (3 points), as shown in the sectoral distribution (Fig. 1).

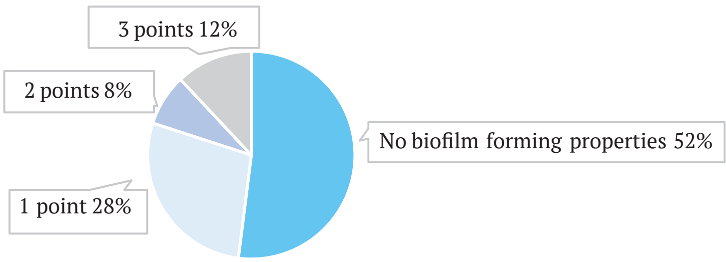

Figure 1. Distribution of biofilm-forming ability among *S. aureus* isolates from diabetic foot ulcers
Source: compiled by the authors

Although less than half of the *S. aureus* isolates demonstrated biofilm-forming ability and their overall resistance profile was moderate, the presence of strong biofilm producers within this group highlights that even a relatively small subset of strains may disproportionately drive persistence and treatment failure in diabetic foot ulcers. Representative microscopic images of each biofilm formation category are presented in Figure 2.

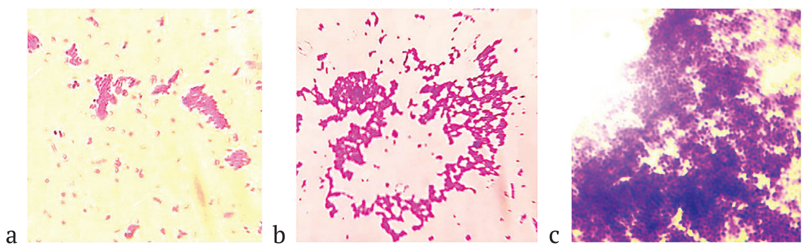

Figure 2. Biofilm formation in *Staphylococcus aureus* isolated from diabetic foot ulcer discharge in patients with type 2 diabetes mellitus. Gentian violet, ×1000
Note: a – weak biofilm formation (1 point); b – moderate biofilm formation (2 points); c – strong biofilm formation (3 points)
Source: compiled by the authors

The findings of this study demonstrated that diabetic foot ulcers harbor a diverse microbial community composed of both Gram-positive and Gram-negative organisms, with notable differences in antimicrobial susceptibility profiles. The high prevalence of multidrug resistance together with the biofilm-forming ability observed in nearly half of the *S. aureus* isolates, underscores the clinical challenges associated with effective treatment and wound healing. Other studies have shown that diabetic foot ulcers are colonised by a wide range of Gram-positive and Gram-negative microorganisms. For example, A. Banu *et al.* [18] reported that *S. aureus* was the predominant microorganism, followed by *P. aeruginosa*, among 100 samples collected from diabetic foot ulcer contents. These findings are consistent with the current study. The same authors also noted that biofilm formation occurred predominantly in *S. aureus* isolates (20%). In contrast, F. Du *et al.* [19] reported a higher prevalence of Gram-negative bacteria (52.4%) compared to Gram-positive bacteria (43.4%). In their study, the most frequently isolated pathogens included *S. aureus* (17.7%), *E. coli* (10.9%), *P. aeruginosa* (10.5%), *Klebsiella pneumoniae* (6.2%), *Staphylococcus epidermidis* (5.3%), *Enterococcus faecalis* (4.9%), and fungi (3.7%).

Corynebacterium spp. are generally regarded as skin commensals; however, under certain conditions, they may act as opportunistic pathogens and contribute to chronic wound colonisation. In this study, *Corynebacterium* spp. were identified in 7 cases, though the qualitative nature of the analysis does not allow for differentiation between colonisation and infection. Notably, these isolates exhibited resistance to 6 out of 10 tested antibiotics. In investigation of the diabetic foot ulcer microbiome, L. Soldevila-Boixader *et al.* [20] reported a higher abundance of *Corynebacterium* spp. in non-infected DFUs, suggesting a possible commensal or modulatory role. Their findings also indicated that *Corynebacterium* may influence the growth dynamics of *S. aureus*. In the present study, *P. aeruginosa* was isolated in 10.29% of cases. According to M. Garousi *et al.* [21], *P. aeruginosa* is one of the most common causes of diabetic foot infections globally. In their study, 16.6% of diabetic foot wound infections were attributed to *P. aeruginosa*. The clinical relevance of *P. aeruginosa* lies in its intrinsic resistance to many commonly used antibiotics, its ability to thrive in moist wound environments, and its capacity to form biofilms, which complicates eradication. Infections caused by *P. aeruginosa* are often associated with delayed wound healing, prolonged hospital stays, and increased risk of amputation [22].

The current study revealed diverse antibiotic resistance profiles among pathogens isolated from diabetic foot ulcers, with Gram-negative isolates generally exhibiting a higher degree of resistance. *S. aureus* and *S. haemolyticus* showed moderate sensitivity to methicillin, while *Corynebacterium* spp. were resistant to most antibiotics, remaining fully susceptible only to tigecycline and amikacin. Among Gram-negative isolates, *Klebsiella* spp. displayed the highest level of resistance, whereas *P. aeruginosa* retained sensitivity to ciprofloxacin and vancomycin. *E. coli* showed favorable susceptibility to multiple agents but demonstrated complete resistance to vancomycin and ceftriaxone. These findings are consistent with those reported in studies and meta-analyses, which have confirmed a high global prevalence of multidrug-resistant (MDR) pathogens in diabetic foot ulcers [23, 24]. According to S. Yang *et al.* [25], the most prevalent MDR Gram-positive bacterium was *S. aureus*, with a reported rate of 12.13%, while *E. coli* (6.93%) and *P. aeruginosa* (6.01%) were the leading MDR Gram-negative pathogens.

In addition to the widespread emergence of multidrug resistance, another major factor contributing to the persistence and poor healing of diabetic foot ulcers is the ability of certain pathogens to form biofilms. In the present study, 48% of *S. aureus* isolates demonstrated biofilm-forming ability, with varying degrees of biofilm density. This proportion is lower than what has been reported in other studies. For instance, H. Mamdoh *et al.* [26] found that all isolated *Staphylococcus* spp. from diabetic foot ulcers were capable of forming biofilms, albeit with differing intensities. Their dataset included *S. aureus* alongside *S. haemolyticus*, *S. epidermidis*, and other coagulase-negative staphylococci. While some studies have reported a high prevalence of biofilm formation among *S. aureus* isolates from diabetic foot ulcers, others have shown much lower rates in different clinical contexts. For example, a study on *S. aureus* strains isolated from the oropharynx of children with chronic tonsillitis found that only 28.6% demonstrated biofilm-forming ability [11].

The findings of this study highlighted the complex microbial ecology of diabetic foot ulcers, where both Gram-positive and Gram-negative organisms contribute to chronicity through antibiotic resistance and biofilm formation. The detection of multidrug-resistant strains such as *Klebsiella* spp., *P. aeruginosa*, and methicillin-sensitive but biofilm-producing *S. aureus* highlights the challenge of antimicrobial resistance and microbial persistence in wound environments. The identification of *Corynebacterium* spp. further illustrates the potential role of less frequently reported organisms in shaping wound microbiota and influencing pathogenic dynamics. This reinforced the need for integrated diagnostic and therapeutic approaches that address not only antimicrobial susceptibility but also microbial interactions and biofilm-related resilience in diabetic foot ulcers.

CONCLUSIONS

This study provided important microbiological insights into the management of diabetic foot ulcers, highlighting both the diversity of isolated pathogens and their complex antimicrobial resistance profiles. The predominance of Gram-positive bacteria (73%), particularly *S. aureus* and *S. haemolyticus*, along with notable Gram-negative isolates such as *Klebsiella* spp. and *P. aeruginosa*, reflects the polymicrobial nature of diabetic foot infections. Antibiotic susceptibility testing confirmed widespread resistance, especially among Gram-negative bacteria, which frequently exhibited multidrug resistance patterns. Importantly, *Corynebacterium* spp., often considered mere commensals, also demonstrated significant resistance, suggesting their potential underrecognised role in chronic infections. The assessment of biofilm formation in *S. aureus* added an important detail, showing that nearly half of the isolates (48%) were capable of forming biofilms of varying intensity. This finding emphasised the role of biofilms in persistent infections and reduced antibiotic efficacy, and supported the consideration of biofilm assessment as part of advanced diagnostic protocols. Taken together, these results stressed the urgent need for integrated diagnostic strategies that combine pathogen identification, susceptibility testing, and biofilm evaluation. Such approaches can inform more targeted therapies, reduce treatment failures, and ultimately improve patient outcomes. In addition to conventional antibiotic-based regimens, future research should also explore the role of adjuvant therapies aimed at reducing microbial load and enhancing wound healing. Among these, ozonated water and oils have shown promising antimicrobial and antibiofilm activity in other clinical contexts, and their potential integration with standard care may represent a valuable complementary approach. Investigating such strategies, alongside novel antibiofilm agents, could expand the therapeutic arsenal available for managing chronic and resistant diabetic foot infections.

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Біоплівкоутворення та антибіотикорезистентність клінічних ізолятів з виразок діабетичної стопи

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Анотація. Виразки діабетичної стопи є одними з найбільш виснажливих ускладнень цукрового діабету 2 типу, які часто призводять до стійких інфекцій та ампутації нижніх кінцівок. Мікробна колонізація та утворення біоплівок значно сприяють хронічності перебігу та резистентності до антибіотиків, що спостерігаються у цих ранах. Мета цього дослідження полягала у вивченні спектру мікроорганізмів, виділених з діабетичних виразок стопи, оцінці їх чутливості до антибіотиків та оцінці здатності штамів *Staphylococcus aureus* до утворення біоплівок. Мікробіологічне дослідження виділень з ран було проведено у 68 пацієнтів з клінічно діагностованим діабетичним синдромом стопи. За допомогою морфологічних та біохімічних методів було ідентифіковано 78 мікробних ізолятів. Більшість ранових інфекцій були представлені монокультурами (85 %), а у в 10 випадках було виявлене полімікробне інфікування. Чутливість до антибіотиків було перевірено за допомогою методу дифузії дисків Кірбі-Бауера. Утворення біоплівки в ізолятах *Staphylococcus aureus* було оцінено в статичних умовах за допомогою фарбування генціан-фіолетовим. Переважали грампозитивні бактерії (73 %), серед яких найчастіше виділяли *Staphylococcus aureus* та *Staphylococcus haemolyticus*. Серед грамнегативних організмів (27 %) поширеними були *Klebsiella* spp. та *Pseudomonas aeruginosa*. Оцінка чутливості до антибіотиків виявила помірну чутливість до метициліну у *Staphylococcus aureus* (40 %) та *Staphylococcus haemolyticus* (44 %), тоді як ванкоміцин та тигециклін показали найвищу активність. Макроліди були значною мірою неефективними, а *Corynebacterium* spp. продемонстрували значну резистентність. Грамнегативні ізоляти загалом продемонстрували вищу резистентність, при цьому *Klebsiella* spp. були стійкими до більшості протестованих антибактеріальних препаратів. Аналіз біоплівкоутворення 25 ізолятів *Staphylococcus aureus* виявив утворення біоплівки у 48 %, включаючи слабких (58 %), помірних (17 %) та сильних (25 %) продуцентів. Регулярний скринінг на наявність збудників, що утворюють біоплівки, може покращити клінічне лікування та наслідки у випадках інфекцій діабетичної стопи

Ключові слова: чутливість до антибіотиків; хронічні рани; множинна стійкість до антибіотиків; *S. aureus*; ранова мікробіота