DIAGNOSTIC CHARACTERIZATION OF MULTIDRUG-RESISTANT PATHOGENS IN CHRONIC WOUNDS AT MERU TEACHING AND REFERRAL HOSPITAL, KENYA

Rael Gacheri[1], Moses Mahugu Muraya[1], Christopher Mutuku[1], Christine Bii[2]
[1]Department of Biological Sciences, Chuka University, P.O. Box 109-60400,
Chuka, Kenya.
[2]Kenya Medical Research Institute, Box 2632-00202, Nairobi-Kenya.
Corresponding author Email: tabithagacheri@gmail.com, moses.muraya@chuka.ac.ke,
cmutuku@chuka.ac.ke

Abstract

Chronic wound infections remain a significant public health concern, driven by trauma, diabetes, and inadequate hygiene, often with polymicrobial colonization and rising antibiotic resistance. This study at Meru Teaching and Referral Hospital, in Kenya, used a cross-sectional design to analyse 68 wound swabs from 293 patients (8 months) for outlining bacteria in chronic wound infections to identify and understand both known and new pathogens, thereby enhancing diagnosis, treatment, and expanding knowledge of infectious agents, using standard culture and automated identification/AST, with ethics approvals from all relevant ethical committees.The findings revealed that the highest infection rates were among patients aged 21–30 years (22%) and 51–60 years (19.2%). The most frequently isolated organism was *Staphylococcus aureus* (26.6%), followed by *Pseudomonas aeruginosa* (13.2%) and *Escherichia coli* (10.3%). Less common but clinically significant multidrug-resistant (MDR) isolates included *Klebsiella pneumoniae*, *Proteus hauseri*, *Morganella morganii*, *Acinetobacter baumannii*, and *Enterococcus faecalis*. Despite clinical signs of infection, 20.5% of the wound samples had no bacterial growth. This could be as a result of non-infectious causes or fastidious organisms that were not detectable with the media used, though other bacterial or microbial agents that have not been identified may also be at play. This study demonstrates 50% of *Staphylococcus aureus* strains are resistant to beta-lactams and fluoroquinolones, while resistance in Meropenem ranges from 0% to 11%. *E. coli* recorded 78% resistance to ciprofloxacin and 100% resistance to ampicillin/sulbactam and amoxicillin/clavulanate. Despite exhibiting 50–100% resistance, *Klebsiella* sp. and *Pseudomonas* sp. are still mostly sensitive to meropenem, a reserve antibiotic. Meropenem resistance was rare in coagulase-negative staph; however, it ranged from 60% to 100%. Morganella was resistant to ciprofloxacin and trimethoprim/sulfamethoxazole (%?? respectively), whereas Proteus exhibited 40–60% resistance. These findings highlight the complexity and resistance of persistent wound infections, the high prevalence of antibiotic resistance, and the pressing need for advanced diagnostic instruments to guarantee precise pathogen identification. Strengthening diagnostic abilities, endorsing antibiotic stewardship, and implementing regular regional surveillance are essential to combat resistant infections effectively, guide suitable therapy, and improve patient outcomes in resource-limited settings.

Keywords: Bacterial pathogens, Chronic wounds, Multidrug resistance, biofilm formation, VITEK 2 system, Kenya

INTRODUCTION

Chronic wound infections are a major health concern, including diabetic foot ulcers, pressure ulcers, and venous leg ulcers, representing a significant health burden worldwide, mainly due to their propensity for persistent infections and complications (Sen et al., 2020). These wounds are infected by multidrug-resistant pathogens, complicating treatment outcomes and subsequently increasing healthcare costs (World Health Organization [WHO], 2021). Globally, the upsurge of antimicrobial resistance poses a formidable challenge, reducing the efficacy of standard antimicrobial therapies and leading to higher morbidity and mortality rates (Laxminarayan et al., 2020).

Numerous studies conducted in Africa have shown that *Pseudomonas aeruginosa* and *Staphylococcus aureus* are the most common bacteria in chronic wounds, with a worrying increase in multidrug-resistant strains that make therapy more difficult (Adegoke et al., 2020). Inadequate infection control procedures, extensive over-the-counter access to antibiotics, and a lack of antimicrobial stewardship are all major contributors to these resistance trends, which in turn fuel the rise in the incidence of resistant organisms (Aboset et al., 2021).

Local information on pathogen prevalence and antibiotic susceptibility profiles is necessary due to the difficulties presented by antimicrobial resistance (AMR). Programs for antibiotic stewardship and empirical therapy depend on such data (O'Neill et al., 2016). Similar trends have been observed in Kenya, where *Staphylococcus aureus*, including methicillin-resistant strains, is commonly isolated from chronic wounds (Omondi et al., 2019). Additionally, studies have revealed polymicrobial nature of chronic wound microbiota, often involving multidrug-resistant bacteria that complicate management (Wambui et al., 2020). However, there is limited localized epidemiological data from regional facilities such as Meru Teaching and Referral Hospital

Despite national concern over MDR, defined as resistance to more than three antibiotic classes in wound infections, no published data currently exist on the prevalence or resistance profiles of chronic wound pathogens at MeTRH, underscoring the importance of conducting dedicated microbiological surveys to inform empirical treatment protocols and curb antimicrobial resistance. Therefore, this study aimed to identify the bacterial pathogens associated with chronic wound infections at MeTRH and assess their antimicrobial resistance profiles to inform local treatment guidelines and antimicrobial stewardship efforts.

MATERIALS AND METHODS

Area of the Study

The study was conducted at the laboratory of Meru Teaching and Referral Hospital (MeTRH), located in Meru County, Kenya (0.05° S, 37.65° E). Meru Teaching and Referral Hospital serves as a major healthcare facility in the region, offering diagnostic and treatment services to a large catchment population. The area’s moderate temperatures, typically ranging from 15°C to 25°C, may influence microbial ecology and resistance dynamics.

Study Design and Population

The study employed a cross-sectional survey design among consenting patients diagnosed with chronic wound infections at MeTRH. Eligibility criteria included all individuals with chronic wound infections who provided informed consent to participate in the study.

Sample Size and Sampling Procedure

Using Wang and Ji's (2020) statistical technique, the entire sample size was calculated with a 95% confidence level, a 5% margin of error, and an estimated prevalence of 85.8% based on previous research at Kenyatta National Hospital. The initial sample size of 187 participants was determined through this calculation. We applied the finite population correction (FPC) because the patients with chronic wounds at Meru Level 5 Hospital comprise the entire population of interest, which is less than 10,000. After adjusting for a population size of 293 chronic wound patients, the corrected sample size was 68 individuals. The total sample size of 68 was proportionally distributed according to the expected number of patients in each stratum to ensure representative sampling across inpatient and outpatient departments. To prevent repeated sampling from the same anatomical site, each wound was assigned a unique identifier and sampled only once. Verification protocols were applied to confirm the distinctness of each sample. The 68 participants were proportionally distributed across inpatient and outpatient departments, with 2 from the burn unit, 21 from outpatient consultation rooms, 6 from the Medical Ward, 7 from the Surgical Ward, 16 from the Wound Clinic, 9 from the Postnatal Ward, and 7 from the Diabetic Clinic, reflecting their particular patient populations within the total of 293 chronic wound infections

Sample Collection, Bacterial Isolation, and Characterisation

Sixty-eight wound swab samples were collected aseptically from patients with chronic wounds, and each was assigned a unique identifier to ensure accurate tracking and prevent duplication. Samples were transported at room temperature to the microbiology department in sterile transport medium within 30 minutes and processed immediately. The culture media included MacConkey, chocolate, blood, and nutrient agar to identify bacteria according to their lactose metabolism, hemolytic characteristics and colony shape. Following culture, bacterial colonies were identified based on morphotypes, Gram staining, and biochemical testing under standard microbiological protocols. Additionally, the VITEK 2 system, an automated identification and testing system, was used to confirm bacterial species and to identify uncommon isolates.

The VITEK 2 system was used for antibiotic susceptibility testing of each bacterial isolate, which entailed preparing standardized bacterial suspensions, inoculating specific AST cards based on Gram stain reaction, and automatically filling the cards with the inoculum. The system evaluated bacterial growth through optical sensors to determine the minimum inhibitory concentration for the antibiotics. Interpretation of the results was as per Clinical and Laboratory Standards Institute (CLSI) breakpoints to categorize strains as susceptible, intermediate, or resistant, providing a comprehensive antibiotic susceptibility profile for each isolate.

Data Analysis

Demographic, bacterial isolate, and antibiotic distribution profiles were coded and entered into IBM SPSS Statistics Version 27 for analysis. Descriptive statistics were used to characterize the study population and determine the prevalence of multidrug-resistant organisms. The heatmap was generated using the hierarchical clustering method with Euclidean distance as the distance metric and complete linkage for agglomeration. Data were pre-processed and visualized in R using the pheatmap and reshape2 packages. The colour gradient reflects the relative abundance of each organism per hospital unit, with darker shades representing higher isolate frequencies.

RESULTS AND DISCUSSION

Demographic Characteristics

Demographic data of the population was obtained in terms of age, gender, and strata, in order to help in understanding patterns of chronic wounds, identifying risk factors, and developing targeted interventions.

Distribution of Study Participants by Age

The findings of this study indicate that chronic wound infections affect a wide age range, with the highest prevalence observed among individuals aged 21–30 years (22%) and 51–60 years (19.2%), as illustrated in Figure 1 below.

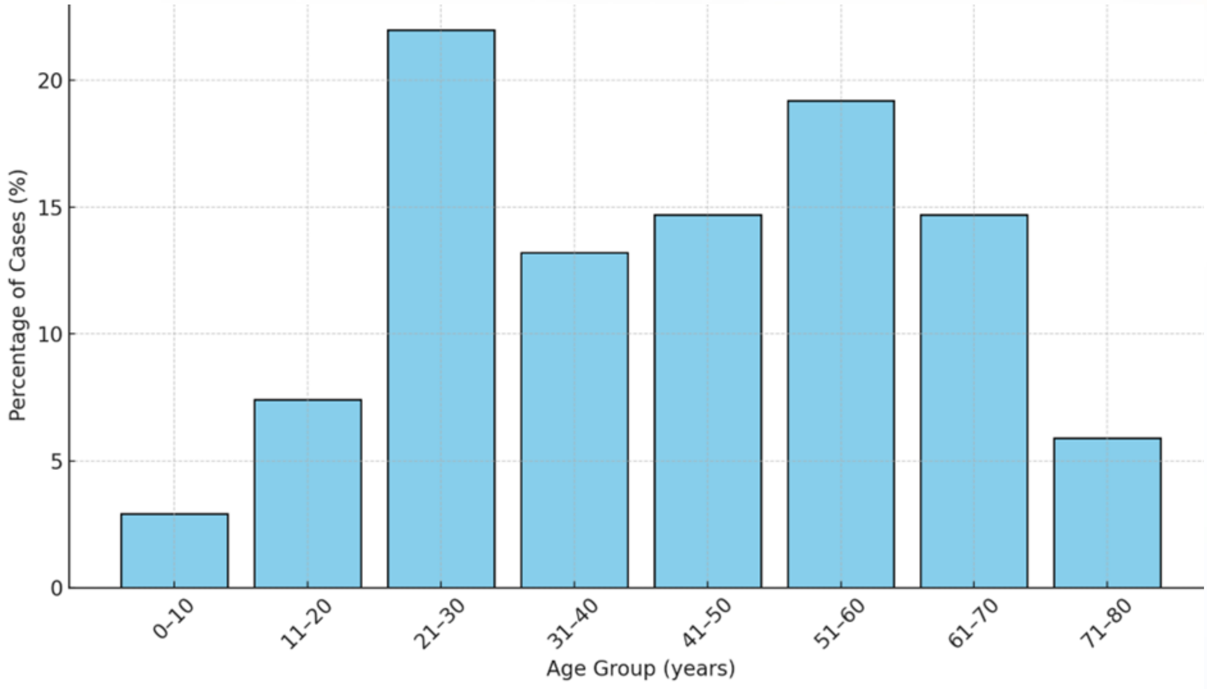

Figure 1: Age distribution of patients with chronic wound infections

Interestingly, a considerable proportion of the cases occurred in younger persons, particularly those in their 20s and 30s.These findings challenge the conventional perception that chronic wounds primarily affect the elderly. Studies by Mahmoudi et al. (2020) and Song et al. (2021) similarly reported increased susceptibility among younger populations, attributing this trend to factors such as traumatic injuries, diabetes-related complications, and poor wound care practices. In contrast, older individuals, especially those over 60, remain at elevated risk due to comorbidities, impaired immune function, and delayed wound healing.

The proportion of cases in the oldest age group (71–80 years) was relatively low, accounting for only 5.9% of the total. This contradicts the findings by Frykberg and Banks (2015), which reported that chronic wounds mainly affect older adults, especially those over 60 years of age. The lower percentage seen in this age group may be due to regional differences, the small sample size, or possibly better wound care practices and preventive health behaviours among the elderly in the study setting.

In contrast, Mahmoudi et al. (2020) reported a growing incidence of chronic wounds among younger individuals, particularly in low and middle-income countries where trauma, infections, and diabetes-related complications are increasingly common. Conversely, Lee et al. (2019) found that in high-income countries, chronic wounds are more prevalent among older adults, reflecting differences in healthcare infrastructure, disease burden, and population demographics. These contrasting findings underscore the broader age distribution of chronic wound infections than previously recognized, emphasizing the need for early detection and intervention in younger age groups. While older adults remain a high-risk population, the significant prevalence among young and middle-aged individuals highlights the importance of developing prevention and management strategies that address all age groups.

Distribution of pathogens by Gender

The results obtained on pathogen distribution by gender indicate a fairly balanced representation, with males accounting for 53% and females 47% of the cases, and a slight predominance of females observed in the older age groups.

The obtained data on gender distribution points to a fairly balanced representation, with a small bias in favor of women in older age groups. According to recent studies by Patel et al. (2020), unique risk factors like vascular disease and hormonal impacts frequently influence gender differences in chronic wound prevalence. Some studies suggest that women may be more affected in particular situations, particularly post-menopause. However, wounds associated with behavioral factors, including trauma or occupational hazards, are more common in male patients (Kumar et al., 2022). These results demonstrate that chronic wounds have a substantial influence on both sexes, with differences depending on biological and socioeconomic circumstances.

Studies have highlighted gender-specific risk factors influencing the prevalence of chronic wounds. Patel et al. (2020), reported that vascular conditions and hormonal changes, particularly those occurring post-menopause, may increase susceptibility among women in certain contexts. In contrast, Kumar et al. (2022) found that wounds linked to behavioural and environmental factors, such as trauma and occupational hazards, are more commonly observed in male patients. These findings suggest that chronic wounds significantly affect both sexes, with variations influenced by a combination of biological, behavioural, and socioeconomic factors.

Pathogenic Bacteria Isolated from Chronic Wound Infections

As indicated in table 1 below, the most prevalent isolates were *Staphylococcus aureus,*18 isolates (26.6%), *Pseudomonas aeruginosa*, 9 (13.2%), *Escherichia coli,* 7 (10.3%), *Corynebacterium striatum*, 5 (7.3%) and coagulase -negative Stapylococci (CoNS), 5 (7.3%). Among the less prevalent isolates included *Proteus hauseri,* 4 (5.8%), *Klebsiella pneumoniae 2* (2.9%), *Morganella morganii* 2 (2.9%), *Acinetobacter baumannii,* 1 (1.5%) and *Enterococcus faecalis* 1(1.5%). Notably, no growth was observed in 14 (20.5%) of the 68 samples.

Table 1: Pathogenic bacteria isolated from chronic wound infections

Isolated bacterial pathogen	Number isolated	Percentage (%)
Staphylococcus aureus	18	26.6
Pseudomonas aeruginosa	9	13.2
E. coli	7	10.3
Corynebacterium striatum	5	7.3
Coagulase-negative staphylococci (CoNS)	5	7.3
Proteus hauseri	4	5,8
Klebsiella pneumoniae	2	2,9
Morganella morganii	2	1.5
Acinetobacter baumannii	1	1.5
Enterococcus faecalis	1	1.5
Samples with no growth obtained	14	20.5
Total	68	100

The findings on microbial prevalence confirm *Staphylococcus aureus* as the most frequently isolated pathogen in chronic wound infections, accounting for 26.6% of all isolates. Its high prevalence underscores its critical role in biofilm formation, tissue invasion, and persistence within the wound environment (Thangamani et al., 2020; Zhang et al., 2023). The detection of *Staphylococcus aureus,* including strains resistant to methicillin (MRSA), raises significant concerns regarding antimicrobial resistance. Strains resistant to methicillin's ability to form biofilms further complicates treatment, as biofilm-associated infections are notoriously resistant to antibiotics and contribute to delayed wound healing (Fusi et al., 2021; Wright & Schaefer, 2023)

Cluster Heatmap Analysis of Pathogen Distribution across Hospital Units

The cluster heatmap illustrates the distribution of bacterial pathogens across various hospital strata (Figure 2). *Staphylococcus aureus* and *Pseudomonas aeruginosa* are widely represented, with the highest concentrations observed in samples from the Wound Clinic and Outpatient Consultation Rooms. This suggests a consistent presence of these pathogens in community-acquired and outpatient-associated infections. The clustering of multiple pathogens, such as *Escherichia coli, Corynebacterium striatum, Proteus spp*., and coagulase-negative staphylococci, within this setting further supports the polymicrobial nature of chronic wounds. The relatively low pathogen diversity in the Burn Unit and Diabetic Clinic could reflect specific patient profiles or limited sampling. These findings support previous studies emphasizing the importance of clinical context in interpreting microbial load and underline the value of stratified surveillance in infection control and antimicrobial stewardship.

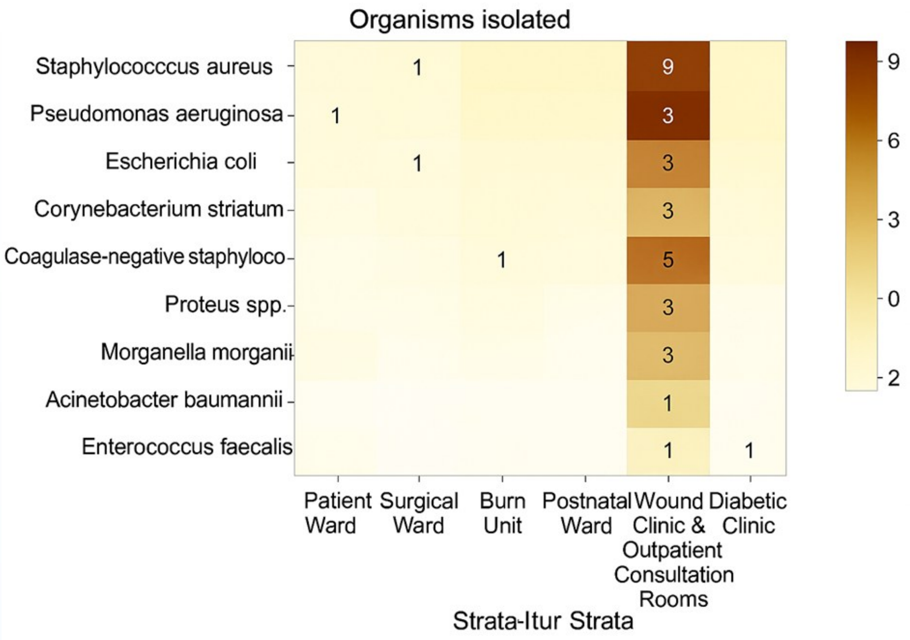

Figure 2: Cluster heatmap of pathogen distribution across hospital units

Pseudomonas aeruginosa was identified as the second most prevalent pathogen, accounting for 13.2% of isolates. This finding is consistent with recent studies that report its frequent occurrence in chronic ulcers, particularly among patients with diabetic foot infections and burn wounds (Malik et al., 2021; Friedlander et al., 2023). As a gram-negative bacterium, *P. aeruginosa* is well recognized for its ability to form biofilms, secrete potent virulence factors, and exhibit resistance to multiple classes of antibiotics, factors that collectively contribute to persistent infections and delayed wound healing (Friedlander et al., 2023). The detection of *Escherichia coli* in 10.3% of samples further underscores the role of Enterobacteriaceae in chronic wounds colonization. Often associated with faecal contamination or translocation from adjacent tissues, *E. coli* presents additional challenges in infection management due to its potential for antimicrobial resistance and its role in promoting polymicrobial synergy within the wound environment (Li et al., 2022).

Other notable isolates included *Corynebacterium striatum* and coagulase-negative staphylococci (CoNS), each comprising 7.3% of the total isolates. Although historically regarded as skin commensals, both organisms are increasingly recognized as opportunistic pathogens, particularly in immunocompromised individuals and patients with chronic infections (Liu et al., 2022; Johnson et al., 2023). Their capacity to form biofilms and persist in compromised tissue environments makes them clinically relevant contributors to delayed healing and recurrent infection. These findings highlight the importance of accurately distinguishing true pathogens from contaminants, especially in chronic wound cases where viable tissue samples may be limited and microbial colonization is complex.

The identification of less common bacteria such as *Proteus hauseri* (5.8%), *Klebsiella pneumoniae* (2.9%), *Morganella morganii* (1.5%), *Acinetobacter baumannii* (1.5%), and *Enterococcus faecalis* (1.5%) highlights the polymicrobial character of chronic wounds. These pathogens are frequently linked to multidrug resistance and biofilm development, which makes treatment more challenging (Kumar et al., 2022; Smith et al., 2022). Their identification underscores the importance of thorough microbiological assessment to map the complete bacterial profile in chronic wounds.

In this study, approximately 20.5% of chronic wound samples showed no bacterial growth despite clinical signs of infection. Although limitations in sample collection techniques could partly account for these findings, other underlying factors are likely involved. These may include the presence of fastidious or anaerobic organisms or viable cultural organisms not supported by conventional culture methods, prior antibiotic use, or the involvement of non-bacterial pathogens such as fungi.

This observation reflects the complex and multifactorial nature of chronic wound pathology and underscores the need for advanced diagnostic approaches, including molecular methods, to detect non-culturable or low-abundance pathogens.

These findings suggest that non-infectious etiologies may account for up to 20.5% of chronic wounds in which no pathogens are detected by culture depended technique. Immune-mediated conditions such as vasculitis and pyoderma gangrenosum often mimic infectious wounds clinically but typically yield negative microbiological results, highlighting the importance of considering autoimmune and inflammatory disorders in differential diagnosis (Vanderplas et al., 2021; Host et al., 2022). Additionally, factors unrelated to infection, such as ischemia and tissue hypoxia, are well-documented contributors to wound chronicity. Impaired perfusion hinders tissue repair and regeneration, underscoring the need for early vascular assessment and appropriate management in patients with non-healing wounds (Sen et al., 2019; Morales & Khan, 2021).

Neuropathic diseases, especially in diabetic patients, and mechanical causes, such as pressure ulcers, are also important. In these cases, tissue damage is caused by prolonged mechanical stress or sensory loss rather than microbial invasion (Harding et al., 2020; Patel & Garcia, 2023). Furthermore, systemic health problems such as comorbid disorders and malnutrition delay healing processes, highlighting the necessity of holistic care approaches that go beyond antimicrobial intervention (Smith & Lee, 2023; Zhang et al., 2024). These findings highlight the importance of considering non-infectious pathophysiological mechanisms in the assessment and management of chronic wounds, and they underscore the need for more individualized, multidisciplinary, and effective treatment approaches.

The bacterial profile observed in this study reflects the typical microbial landscape of chronic wound infections while underscoring the persistent challenge posed by resistant, biofilm-forming pathogens. Consistent with recent findings, these results highlight the critical need for early and accurate identification of causative organisms, along with antimicrobial susceptibility testing, to guide effective treatment strategies and curb the progression of antimicrobial resistance (Fusi et al., 2021; Friedlander et al., 2023). To further improve outcomes in chronic wound management, future studies should prioritize the integration of molecular diagnostics tools and the development of novel anti-biofilm therapies.

Moreover, the findings of this study (Table 2; Fig. 3) reveal distinct clustering patterns among microbial isolates, suggesting significant variation in the composition of wound microbiota. These clusters, characterized by the dominance of specific bacterial species, underscore the complexity of chronic wound microbiomes and their influence on healing trajectories. Understanding these microbial patterns is essential for developing targeted, individualized treatment approaches that address both the microbial and host-related factors affecting wound resolution.

Table 2. Distribution of pathogens by hospital units

Stratum	Sample size	Organisms isolated	Number Isolated
Patient Medical Ward	6	*Staphylococcus aureus*	2
		Pseudomonas aeruginosa	2
		E coli-	1
		Samples with no growth obtained	3
Surgical Ward	7	*Staphylococcus aureus*	2
		Pseudomonas aeruginosa	1
		E. coli	1
		Coagulase-negative *staphylococci* (CoNS)	1
		Samples with no growth obtained	3
Burn Unit:	2	*Klebsiella Pneumoniae*	2
Postnatal Ward	9	*Staphylococcus aureus*	2
		Pseudomonas aeruginosa	1
		Coagulase-negative *staphylococci* (CoNS)	1
		Enterococcus faecalis	1
		Samples with no growth obtained	2

Wound Clinic and Outpatient Consultation Rooms	37	*Staphylococcus aureus*	9
		Pseudomonas aeruginosa	3
		E. coli	5
		Corynebacterium striatum	5
		Coagulase-negative *staphylococci* (CoNS)	3
		Proteus ssp	5
		Morganella morganii	1
		Acinetobacter baumannii	1
		Enterococcus faecalis	1
		Samples with no growth obtained	4
Diabetic Clinic	7	*Staphylococcus aureus*	2
		Pseudomonas aeruginosa	2
		Samples with no growth obtained	2

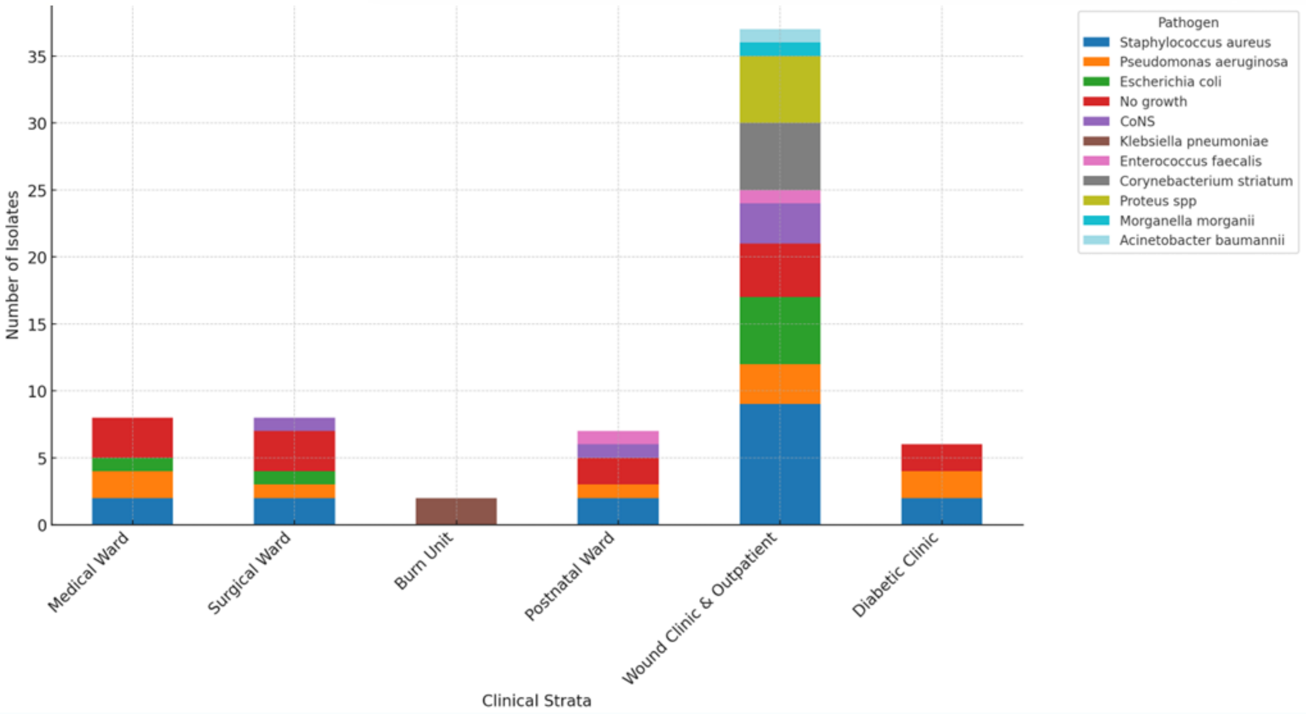

Figure 3: Distribution of pathogen by hospital units

The observed clustering patterns in this study align with previous research demonstrating that the microbial composition of chronic wounds plays a critical role in determining wound chronicity and treatment response (Malhotra et al., 2020). The predominance of *Staphylococcus aureus* and *Pseudomonas aeruginosa* in persistent, non-healing wounds mirrors findings by James et al. (2019), who identified specific bacterial biofilms strongly associated with delayed healing. The clustering identified in this study reflects similar microbial associations, supporting the hypothesis that particular bacterial consortia, especially those involving biofilm-forming and multidrug-resistant species, are linked to poorer clinical outcomes and may require tailored therapeutic strategies.

This study reveals relatively consistent clustering patterns over time, suggesting that specific bacterial profiles may persist and exert a continuous influence on wound healing trajectories. This finding contrasts with earlier work by Øien et al. (2018), who reported that chronic wound microbiota is highly individualized and subject to considerable temporal variability. Such discrepancies may stem from differences in analytical methodologies, wound types, or sampling protocols. Nevertheless, the stable clustering observed in the present study supports the approach advocated by Wolcott et al. (2016), who emphasized individualized treatment strategies tailored to the dominant microbial communities. These results reinforce the potential of targeted antimicrobial interventions aimed at specific bacterial consortia to enhance treatment outcomes. However, given the inherent complexity of microbial diversity and biofilm dynamics in chronic wounds, caution is warranted, and further longitudinal studies are essential to validate these findings and inform precision-based therapeutic approaches.

Susceptibility Profile of the Integrated Isolated Pathogens

According to the susceptibility profile for this study, 50% of *Staphylococcus aureus* strains are resistant to beta-lactams and fluoroquinolones; other antibiotics show better activity although only 11% are resistant to meropenem. *E. coli* has 78% resistance to ciprofloxacin and 100% resistance to ampicillin/clavulanate and amoxicillin/clavulanate largely associated with chromosomally encoded AmpC beta-lactamases. In addition to having limited resistance (0–11%) to meropenem, *Klebsiella pneumoniae* exhibits 50–100% resistance to other drugs. While *Pseudomonas aeruginosa* exhibits 0% resistance to meropenem, it exhibits 50–100% resistance to the majority of tested antibiotics. Despite having no resistance to meropenem, coagulase-negative staphylococci exhibit 60–100% resistance to a number of medications. *Morganella morganii* exhibits 100% resistance to ciprofloxacin and trimethoprim/sulfamethoxazole, but *Proteus* species have only 40% to 60% resistance to some antibiotics.

Table 2. Integrated bacteria susceptibility profile of pathogenic bacteria

Antibiotic	*Staphylococcus aureus*	*E. coli*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	Con (Coagulase-negative staph)	*Proteus* spp.	*Morganella morganii*
Ampicillin	0%	33%	0%	0%	0%	40%	0%
Amoxicillin/Clav	50%	100%	50%	100%	100%	60%	0%
Amp/Sulbactam	50%	100%	50%	100%	100%	60%	0%
Piperacillin/ Tazobactam	50%	89%	50%	100%	50%	60%	0%
Cefazolin	0%	67%	0%	100%	0%	0%	0%
Cefuroxime	0%	67%	50%	100%	100%	60%	0%
Cefoxitin	0%	67%	50%	60%	50%	60%	0%
Ceftazidime	50%	78%	50%	50%	50%	50%	0%
Ceftriaxone	50%	67%	50%	50%	50%	50%	0%
Cefepime	50%	67%	50%	50%	50%	50%	0%
Aztreonam	50%	67%	50%	50%	50%	50%	0%
Meropenem	11%	89%	0%	0%	0%	0%	0%
Amikacin	0%	100%	0%	0%	0%	0%	0%
Gentamicin	0%	100%	0%	0%	0%	0%	0%
Ciprofloxacin	22%	78%	50%	50%	50%	50%	100%
Trimethoprim/ Sulfamethoxazole	0%	33%	50%	60%	50%	60%	100%
Tetracycline	0%	100%	50%	50%	50%	50%	0%

In line with recent research, the data indicate that *E. coli* is highly susceptible to aminoglycosides, fluoroquinolones, and beta-lactam/beta-lactamase inhibitors (Bonomo et al., 2017). On the other hand, *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* show notable resistance, particularly to aminoglycosides and carbapenems, which reflects current worries about strains of the bacteria that are resistant to many drugs (Sader et al., 2020; Nordmann et al., 2019). As MRSA rates rise, *Staphylococcus aureus* and coagulase-negative staphylococci exhibit decreased susceptibility, particularly to beta-lactams (Chambers & DeLeo, 2018).

Targeted antimicrobial methods are necessary since, on the whole, Gram-negative bacteria are still more vulnerable than Gram -positive ones, which are becoming more resistant (WHO, 2021).

Conclusion

This study provides new insights into the epidemiology and microbiology of chronic wound infections at Meru Teaching and Referral Hospital. Contrary to the traditional view that chronic wounds predominantly affect the elderly, a substantial number of cases were observed among young and middle-aged adults, emphasizing the need for age-inclusive prevention strategies. While gender distribution was relatively balanced, observed differences in risk factors highlight the importance of tailored interventions. Microbiological analysis confirmed the polymicrobial nature of chronic wounds, with *Staphylococcus aureus*, *Pseudomonas aeruginosa,* and *Escherichia coli* as the most common pathogens. The presence of multidrug-resistant organisms, including *Acinetobacter baumannii* and *Klebsiella pneumoniae*, underscores the importance of robust diagnostic tools and antimicrobial susceptibility testing. These findings support the integration of advanced diagnostic platforms such as the VITEK 2 system to enhance targeted therapy. Although limited by a small sample size and single-centre design, this study contributes critical data for guiding empirical treatment and highlights the need for antimicrobial stewardship in resource-limited settings.

Recommendations

To improve outcomes for patients with chronic wound infections, this study recommends several key strategies. First, the integration of molecular diagnostic tools in clinical settings should be prioritized to enable rapid and accurate identification of pathogens, including non-culturable or polymicrobial organisms. This would enhance early detection and guide appropriate therapy. Second, research into anti-biofilm therapies and the development of novel antimicrobial agents is crucial to address the persistence of multidrug-resistant organisms identified in this study. Third, public health education should target younger and middle-aged individuals, emphasizing wound care, diabetes management, and prevention of trauma-related injuries. Finally, capacity building is essential in resource-limited settings. This includes training healthcare professionals in infection control and diagnostics and equipping facilities with tools like the VITEK 2 system. Routine microbial surveillance and AMR reporting should be integrated into hospital policy to guide empirical treatment protocols.

Ethical Approval

All procedures performed in this study adhered to established ethical standards and followed good clinical practice guidelines. Standard operating procedures and universal precautions for handling potentially infectious biological samples were strictly observed. Ethical clearance for the study was granted by the Chuka University Ethics Committee. A research permit was obtained from the National Commission for Science, Technology and Innovation (NACOSTI), Licence No. NACOSTI/P/24/39429 and formal authorization to conduct the study and utilize hospital facilities was obtained from the Meru County Health Research

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