HIGH BURDEN AND WARD-SPECIFIC PATTERNS OF MULTIDRUG RESISTANCE IN BACTERIA FROM CHRONIC WOUND INFECTIONS AT MERU TEACHING AND REFERRAL HOSPITAL, KENYA

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Abstract
The emergence of multidrug-resistant (MDR) bacterial pathogens in chronic wounds presents escalating therapeutic challenges, particularly in resource-limited settings such as Kenya, where ward-level resistance surveillance data remain scarce. This study aimed to investigate multiple antibiotic resistance patterns among bacterial isolates from chronic wound infections at Meru Teaching and Referral Hospital. A cross-sectional study analyzed 68 bacterial isolates from chronic wound infections collected between October 2024 to June 2025. A bimodal age distribution (21 - 30 years: 22%; 51 - 60 years: 19.2%) and near-equal gender prevalence (53% male, 47% female) were observed. Identification and antimicrobial susceptibility testing were performed using standard microbiological methods and the VITEK 2 system according to CLSI guidelines. Multiple Antibiotic Resistance (MAR) indices were calculated, with values >0.2 indicating high-risk resistance sources. Findings revealed marked resistance heterogeneity, with MAR indices ranging from 0.00 to 1.00. Klebsiella pneumoniae (MAR = 0.76–1.00) and Acinetobacter baumannii (MAR = 1.00) exhibited the highest resistance levels, predominantly in burn units. *Enterococcus faecalis* (MAR = 0.65) and *Morganella morganii* (MAR = 0.75) were also highly resistant across multiple wards. The burn unit recorded the highest resistance burden, while the wound clinic displayed the widest MAR spectrum (0.0–1.0). These results underscore the urgent need for ward-specific antimicrobial stewardship and infection control interventions, particularly in burn and wound care units, to prevent further resistance escalation.

Keywords: Chronic wound infections; multidrug resistance; pan-drug resistant bacteria; antimicrobial stewardship; hospital-acquired pathogens; ward-level resistance patterns; resistance surveillance; Multiple Antibiotic Resistance (MAR) index

INTRODUCTION
Chronic wound infections represent a significant global health burden, affecting 1–2% of populations in high-income countries, with substantially greater impact in resource-limited settings where surveillance and antimicrobial stewardship remain inadequate (Frykberg and Banks, 2015; Sen et al., 2009). The proliferation of multidrug-resistant (MDR) bacterial pathogens in these infections has transformed chronic wound management from a therapeutic challenge into a critical public health concern. Rising diabetes prevalence, aging populations, and weak infection control systems continue to amplify this burden globally.

Hospital wards function as distinct ecological niches, each characterized by unique antibiotic exposure patterns, patient vulnerability profiles, and infection prevention practices (Dancer, 2014). Burn units and intensive care units have emerged as epicenters for MDR organism selection and transmission, yet institutional surveillance systems often fail to capture ward-specific resistance dynamics. The Multiple Antibiotic Resistance (MAR) index, developed by Krumperman (1983), provides a standardized metric for quantifying resistance burden in bacterial populations. MAR values exceeding 0.2 indicate significant antibiotic selection pressure and high-risk contamination sources, while values approaching 1.0 signal near-complete therapeutic failure.

The MAR index is particularly valuable for detecting differential selection pressures across hospital wards, where variations in antibiotic use and patient exposure shape resistance ecology.

In sub-Saharan Africa, including Kenya, the convergence of weak surveillance infrastructure, resource constraints, and limited antimicrobial stewardship has created conditions conducive to resistance emergence and persistence. Emerging evidence also indicates shifting chronic wound epidemiology, with rising incidence among younger adults due to trauma, diabetes, and occupational exposures (Mahmoudi et al., 2020). Despite extensive global documentation of MDR in chronic wound pathogens, data on ward-level resistance ecology in Kenyan healthcare facilities remain scarce, and the contribution of hospital microenvironments to chronic wound infection dynamics remains unclear. This study aimed to determine the burden and ward-specific distribution of multidrug-resistant bacteria isolated from chronic wound infections at Meru Teaching and Referral Hospital, Kenya, using the MAR index as a metric for resistance intensity.

Materials and Methods

Study Site and Design

This hospital-based cross-sectional study was conducted at Meru Teaching and Referral Hospital (MeTRH), located in Meru County, Kenya (0.05°S, 37.65°E), between October 2025 to June 2025. The facility serves as the primary referral center for a catchment population of approximately 1.46 million people. The study targeted patients with chronic wounds from seven hospital units: the diabetic clinic, burn unit, postnatal ward, medical ward, surgical ward, wound clinic, and outpatient consultation rooms. A cross-sectional design was chosen to capture the current burden and distribution of resistant bacteria across wards at a single time point, allowing for the determination of bacterial prevalence, diversity, and resistance patterns.

Sample Size and Sampling Procedure

The sample size was calculated using Nassiuma (2000) formula, yielding 68 cases from a total population (N) of 293 patients presenting with chronic wounds during the study period. Parameters included a coefficient of variation of 24% (within the recommended 21–30%) and a standard error of 0.025. Stratified random sampling was applied, with sample sizes proportionately allocated based on the number of chronic wound cases recorded per unit: medical ward (6), surgical ward (7), burn unit (2), postnatal ward (9), wound clinic (16), diabetic clinic (7), and outpatient consultation rooms (21), the latter being reflective of patient case load. Within each ward, eligible patients were selected using simple random sampling from daily patient registers. Each stratum was assigned a unique identifier to prevent duplication during analysis.

Operationally, chronic wounds were defined as wounds failing to show signs of healing after 4–6 weeks of standard treatment. Eligible participants were patients aged ≥18 years, with wounds persisting ≥4 weeks, who provided written informed consent, and had not received antibiotic therapy within the preceding 48 hours. Exclusion criteria included known immunocompromising conditions, ongoing antibiotic treatment beyond 48 hours, acute wounds of <4 weeks duration, and inability to provide informed consent.

Specimen Collection and Processing

Wound specimens were collected using rigorous aseptic techniques following standardized protocols (Murray et al., 2021). The wound surface was initially cleansed of debris and superficial contaminants using sterile saline irrigation. One swab per patient was collected from the deepest viable tissue or regions demonstrating active infection signs after debridement to minimize surface contamination. Culture media utilized included MacConkey agar for gram-negative bacterial isolation, Chocolate agar for fastidious organism cultivation, Blood agar for hemolytic pattern differentiation, and Nutrient agar for general bacterial isolation. Specimens were incubated at 37°C for 18–24 hours under appropriate atmospheric conditions.

Standard ATCC control strains (Escherichia *coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, and *Pseudomonas aeruginosa* ATCC 27853) were used for quality assurance of culture and susceptibility testing.

Bacterial colonies underwent systematic characterization based on macroscopic morphology, followed by standard identification procedures including Gram staining and comprehensive biochemical testing panels. The VITEK 2 automated identification system provided definitive bacterial species identification and antimicrobial susceptibility testing, particularly for uncommon or difficult-to-identify isolates. This standardized platform ensures reliable identification through validated biochemical and enzymatic test batteries.

Antimicrobial susceptibility testing was performed against a panel of antibiotics including β-lactams (ampicillin, amoxicillin-clavulanate), cephalosporins (ceftriaxone, cefotaxime, ceftazidime), carbapenems (imipenem, meropenem), aminoglycosides (gentamicin, amikacin), fluoroquinolones (ciprofloxacin, levofloxacin), glycopeptides (vancomycin), and others as appropriate for each bacterial species. Antimicrobial susceptibility was interpreted according to Clinical and Laboratory Standards Institute (CLSI) 2023 guidelines.

Multiple Antibiotic Resistance Index Calculation

Resistance profiles were quantified using the Multiple Antibiotic Resistance (MAR) index (Krumperman, 1983):

Isolate-level MAR was obtained as,

$$MAR = \frac{a}{b}$$

where a = number of antibiotics to which the isolate is resistant, and b = total number of antibiotics tested against the isolate.

Ward-level MAR was obtained as,

$$MAR = \frac{a}{b\ x\ c}$$

where a = total number of resistant responses among all isolates within a ward, b = total number of antibiotics tested, and c = number of isolates from the specific ward.

A MAR index >0.2 was interpreted as indicative of high-risk environments with intensive antibiotic use and high selective pressure.

Data Analysis

Data were cleaned and validated to ensure consistency prior to analysis using SPSS version 27 (IBM Corporation, Armonk, NY, USA). Descriptive statistics, including frequencies, percentages, means, and standard deviations, were used to summarize patient demographics, antibiotic resistance patterns, and Multiple Antibiotic Resistance (MAR) indices. Prevalence estimates were reported with 95% confidence intervals where appropriate. Inferential statistical tests, including the Chi-square test for categorical variables and the Kruskal-Wallis test for non-parametric comparisons of MAR indices across wards were employed to identify significant differences in resistance patterns. Statistical significance was set at $p < 0.05$.

Ethical Considerations

All study procedures adhered strictly to Good Clinical Practice guidelines and universal precautions for infectious specimen handling. Ethical approval was obtained from Chuka University Ethics Committee, the National Commission for Science, Technology and Innovation (NACOSTI; Approval No. NACOSTI/P/24/39429), and the Meru County Health Research Committee. Written informed consent was obtained from all participants by trained research assistants following a comprehensive explanation of study objectives, procedures, potential risks, and benefits in either English or Kiswahili, depending on participant preference. Participant confidentiality was maintained throughout the study, and all data were anonymized using unique identifiers

Results and Discussion

Demographic Characteristics

Among 68 participants, age distribution demonstrated bimodal peaks at 21-30 years (22%, n=15) and 51-60 years (19.2%, n=13), with intermediate prevalence in 31-40 (16.2%, n=11) and 41-50 years (14.7%, n=10), and declining prevalence thereafter (Fig. 1). This pattern contradicts conventional chronic wound epidemiology, which predominantly affects elderly populations, suggesting multifactorial contributions including early-onset diabetes, urbanization-related trauma, occupational hazards, and healthcare access barriers characteristic of sub-Saharan African contexts.

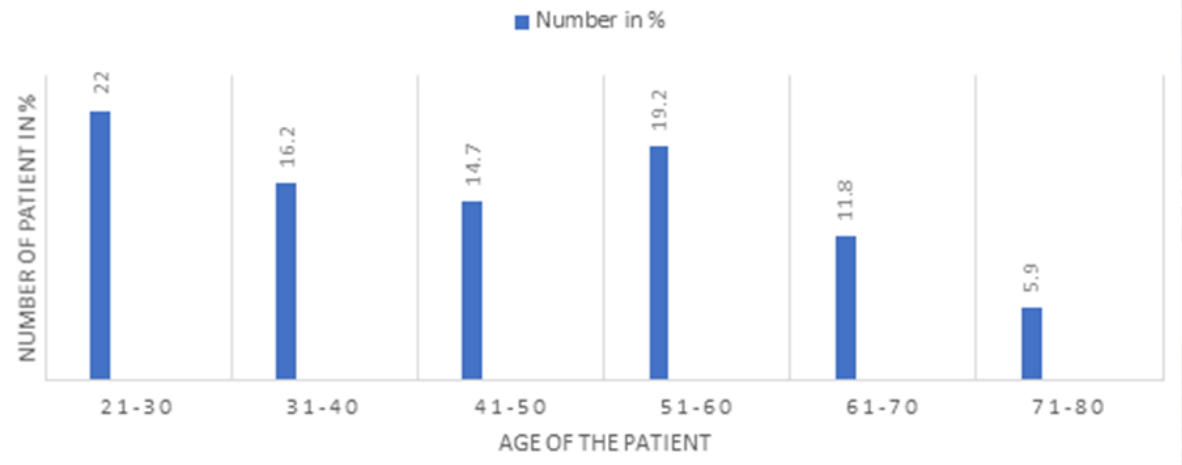

Figure 1: Age distribution of study participants

Distribution of chronic wounds by gender

Gender distribution was balanced (53% male, 47% female), with younger males and older females showing slight predominance (Fig. 2). Age-stratified patterns likely reflect differential exposure risks, trauma and occupational hazards in younger males, and comorbidities with increased longevity in older females, rather than inherent gender susceptibility. These findings align with Patel et al. (2020), who reported comparable gender susceptibility with increased female prevalence in older cohorts due to vascular disease and hormonal changes, and Kumar et al. (2022), who noted higher prevalence in younger males associated with trauma. Collectively, chronic wound distribution appears largely gender-neutral, with variations attributable to behavioral, biological, and socioeconomic determinants.

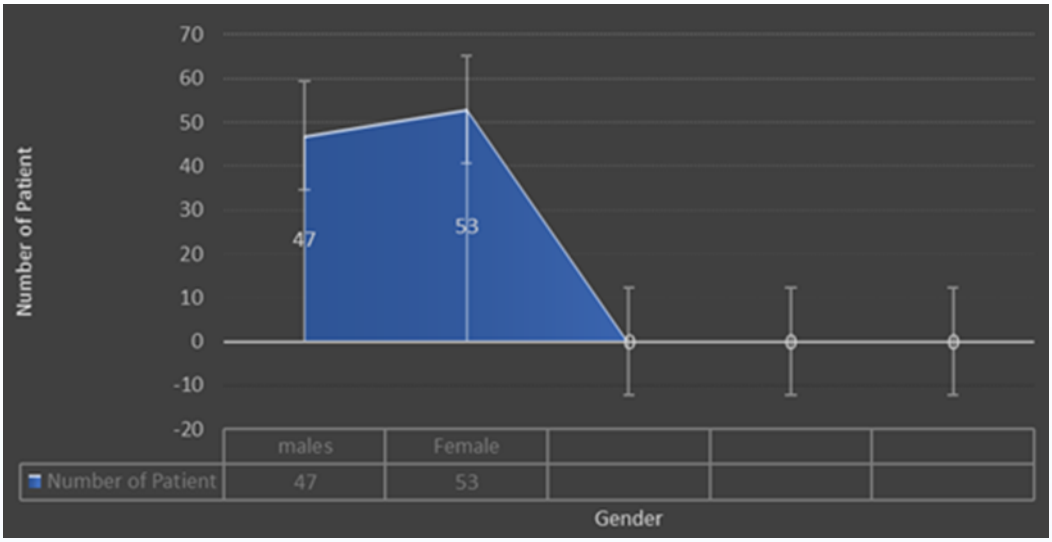

Figure 2: Distribution of chronic wounds by gender

Multiple Antibiotic Resistance Profiles and Emerging Pan-Resistant Threats

Marked variation was observed in Multiple Antibiotic Resistance (MAR) indices, ranging from complete susceptibility (0.00) to total pan-resistance (1.00) to total susceptibility (0.00). The most alarming findings were *Acinetobacter baumannii* (1.00) and *Klebsiella pneumoniae* (MAR 1.00), both exhibiting pan-drug resistance and representing critical therapeutic crises. Similarly, *Morganella morganii* (0.75), Staphylococcus aureus (0.736), and Enterococcus faecalis (0.65) demonstrated moderate-to-high resistance, underscoring their potential to complicate treatment.

Escherichia coli displayed the widest variability (MAR: 0.00-0.66), reflecting the coexistence of community-acquired susceptible strains alongside highly hospital-adapted resistant variants. Notably, *Pseudomonas aeruginosa* exhibited only moderate resistance (MAR 0.22 - 0.37), a finding that was unexpectedly lower than anticipated for this intrinsically resistant pathogen.

Overall, the coexistence of pan-resistant, multidrug-resistant, and susceptible strains across both Gram-positive and Gram-negative bacteria emphasizes the urgent need for enhanced infection control measures, antimicrobial stewardship programs, and context-specific treatment strategies. Comparisons with global data confirm these patterns. Brazilian surveillance reported carbapenem-resistant Enterobacteriaceae (19.3%) and *Acinetobacter baumannii* (9.6%) as priority pathogens, consistent with the present findings of pan-resistant *K. pneumoniae* and *A. baumannii* (Lobo et al., 2025). However, the variability observed in *E. coli* (MAR 0.00 - 0.66) contrasts with Bangladesh (96% with MAR >0.3) and Nigeria (MAR 1.00) (Okwu et al., 2019; Rahman et al., 2021). The moderate resistance in *P. aeruginosa* (MAR 0.22 - 0.37) closely mirrors Jamaican data (mean MAR 0.34) (Phillips et al., 2016).

Collectively, these findings highlight a dual challenge: while some organisms retain susceptibility, others have already reached pan-resistance, narrowing treatment options to last-resort drugs. This spectrum of resistance reflects not only bacterial adaptability but also the regional heterogeneity of antimicrobial pressure.

Ward-Specific Resistance Analysis

Multiple Antibiotic Resistance Index of Bacterial Isolates from the Medical Ward

Multiple Antibiotic Resistance (MAR) indices of isolates from the medical ward ranged from 0.00 to 0.33 (median: 0.22) (Figure 3). The threshold MAR index of 0.2, commonly used to indicate high-risk contamination sources, was exceeded by several isolates, reflecting concerning antibiotic selection pressure within this ward environment.

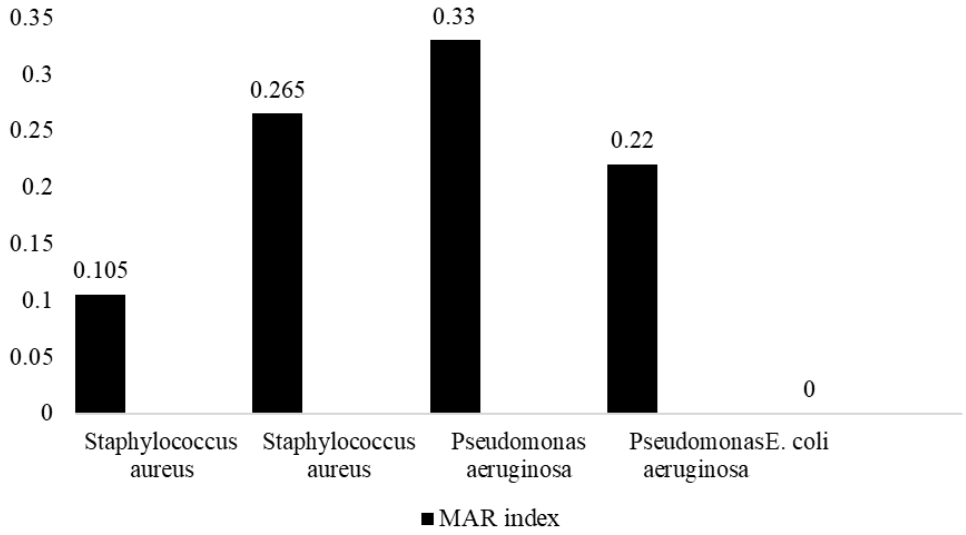

Figure 3: Multiple Antibiotic Resistance Indices of Bacterial Isolates Obtained from Patient Medical Ward

Staphylococcus aureus exhibited heterogeneity (MAR 0.105 - 0.265), consistent with the coexistence of methicillin-susceptible (MSSA) and methicillin-resistant (MRSA) strains. The higher MAR values of MRSA align with global surveillance data, where co-resistance mechanisms frequently elevate resistance levels (Oliveira et al., 2018). This mixed pattern highlights the persistence of both phenotypes in hospital settings and the associated risk of transmission.

Pseudomonas aeruginosa isolates consistently exceeded the high-risk threshold (MAR 0.22 - 0.33), underscoring the pathogen's intrinsic and adaptive resistance mechanisms, including efflux pumps, β-lactamase production, and biofilm formation (Pang et al., 2019). Its uniformly elevated MAR values reinforce its status as a major healthcare-associated pathogen.

In contrast, *Escherichia coli* isolates displayed complete susceptibility (MAR 0.00), suggesting the presence of wild-type strains or community-acquired variants with minimal exposure to broad-spectrum antibiotics. This contrasts sharply with the global rise of extended-spectrum β-lactamase (ESBL)-producing *E. coli* (Pitout & Laupland, 2008), indicating that these isolates may originate from environments with relatively low antimicrobial selective pressure.

Taken together, these findings reveal distinct species-specific resistance patterns within the medical ward. *Staphylococcus aureus* demonstrated intermediate heterogeneity, reflecting the co-circulation of both susceptible and resistant strains. In contrast, *Pseudomonas aeruginosa* exhibited consistently high-level resistance, consistent with its well-documented ability to adapt through diverse resistance mechanisms. Meanwhile, *Escherichia coli* remained fully susceptible, a finding that suggests differences in ecological niches or acquisition pathways compared with the other pathogens. This variation highlights the critical need for ward-focused surveillance and species-specific antimicrobial stewardship, as resistance dynamics appear to be shaped not only by local antibiotic practices but also by intrinsic pathogen biology.

Multiple antibiotic resistance index of bacterial isolates from the surgical ward

The five isolates illustrated in Figure 4 ranged from 0.00 to 0.37 (median: 0.25). Coagulase-negative staphylococci recorded the highest resistance (MAR: 0.37), considering their role as resistance gene reservoirs. *Staphylococcus aureus* demonstrated typical hospital-associated resistance (MAR: 0.105-0.25), while *Pseudomonas aeruginosa* showed moderate resistance (MAR: 0.33). *Escherichia coli* again demonstrated complete susceptibility.

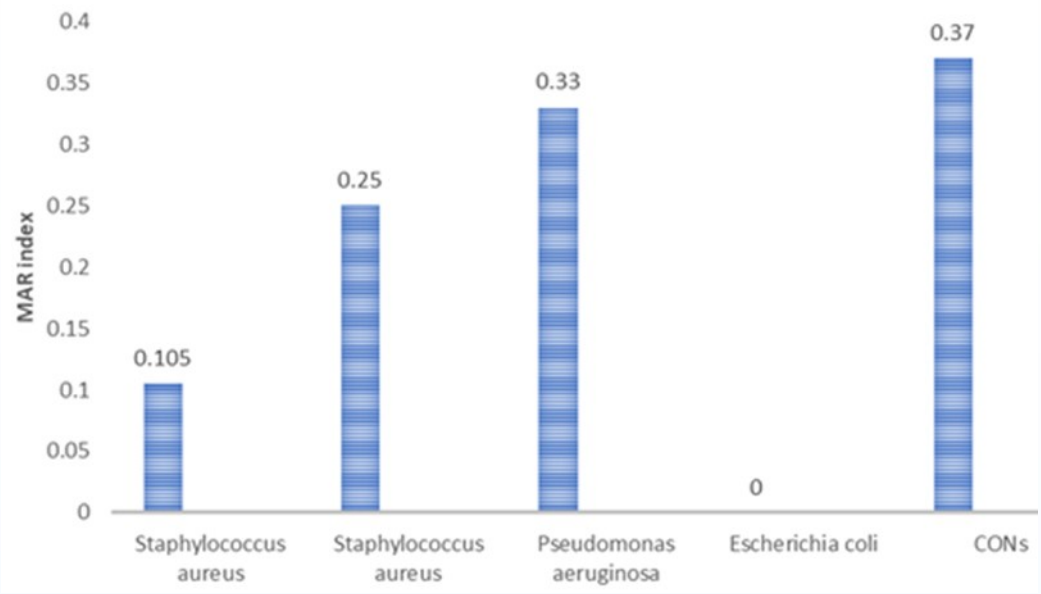

Figure 4: Multiple antibiotic resistance indices of bacterial isolates from the surgical ward

Different bacterial species exhibit different patterns of antibiotic resistance, as indicated by the MAR indices (0.00-0.33, median: 0.22). This study environment exhibits moderate antibiotic selective pressure, as indicated by the median value, which is close to the critical 0.2 threshold specified by Krumperman (1983).

The co-circulation of methicillin-susceptible and methicillin-resistant strains common in healthcare settings was reflected in the heterogeneous resistance (MAR: 0.105-0.265) of *Staphylococcus aureus* (Tong et al., 2015). Through efflux pumps and enzymatic processes, *Pseudomonas aeruginosa* continuously surpassed resistance thresholds (MAR: 0.22-0.33), demonstrating its inherent multidrug resistance capabilities (Moradali et al., 2017). In contrast to global trends of isolates that produce extended spectrum beta-lactamases (ESBL), *Escherichia coli* showed perfect susceptibility (MAR: 0.00), indicating wild-type strains with little exposure to antibiotics (Allocati et al., 2013).

These results indicate species-specific resistance dynamics within the surgical ward: CoNS emerged as the most resistant, *S. aureus* exhibited intermediate variability, *P. aeruginosa* maintained consistently high resistance, and *E. coli* remained fully susceptible. This contrast underscores the complex ecological interactions shaping resistance in surgical wards and highlights the need for species-tailored antimicrobial stewardship strategies to mitigate the spread of resistance genes while preserving treatment efficacy.

Multiple antibiotic resistance index of bacterial isolates from the burn unit

The two *Klebsiella pneumoniae* isolates illustrated in Figure 5 exhibit critically high resistance (MAR: 0.76 and 1.00). The pan-resistant isolate (MAR: 1.00) represents a therapeutic emergency with no viable treatment options among tested antimicrobials. Due to the strong antimicrobial selection pressure found in burn care settings, this unit showed the highest resistance burden in the study.

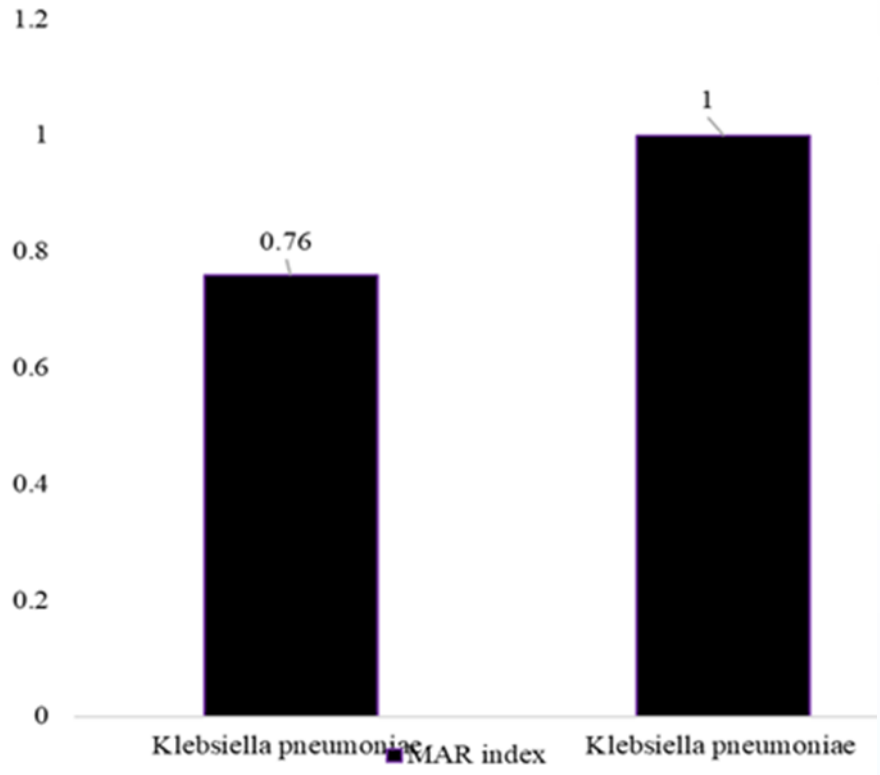

Figure 5: Multiple Antibiotic Resistance Indices of Bacterial Isolates from the Burn Unit

With *Klebsiella pneumoniae* isolates showing extremely high resistance levels (MAR: 0.76 and 1.00), the burn unit showed the most severe antimicrobial resistance burden. The acquisition of several resistance mechanisms, such as carbapenemases, extended-spectrum β-lactamases, and colistin resistance genes frequently found in healthcare-associated *Klebsiella pneumoniae,* makes the pan-resistant isolate (MAR: 1.00) a therapeutic emergency (Navon-Venezia et al., 2017). According to worldwide surveillance data, *Klebsiella pneumoniae* is a critical priority pathogen for the containment of antibiotic resistance, which is consistent with our observation (Tacconelli et al., 2018).

Due to extended antibiotic courses, immunocompromised patients, and numerous invasive procedures, the high antimicrobial selective pressure found in burn care settings accelerates the evolution of resistance (Keen et al., 2010). In order to acquire resistance genes and facilitate horizontal transmission between bacterial populations, burn patients usually need prolonged hospitalization with numerous antimicrobial treatments.

The resistance profile of the burn unit exhibits maximum resistance levels that surpass common infection patterns linked to healthcare, which is a stark contrast to other clinical settings. While the second isolate (MAR: 0.76) shows widespread drug resistance that is getting close to pan-resistance, the existence of a fully pan-resistant *Klebsiella pneumoniae* isolate reflects the peak of antimicrobial resistance development. This dual presence highlights the urgent need for improved infection prevention and antimicrobial stewardship treatments by indicating that resistance development is still occurring within the department.

Multiple antibiotic resistance index of bacterial isolates from the postnatal ward

The MAR indices of four isolates ranged from 0.22 to 0.37. Because of the sensitive maternal and neonatal populations, they serve, the resistance burden of three isolates surpassing the 0.2 threshold is alarming. *Pseudomonas aeruginosa* (MAR: 0.22-0.37) and coagulase-negative staphylococci (MAR: 0.22) require special attention in this high-risk setting. The findings are illustrated in Figure 6

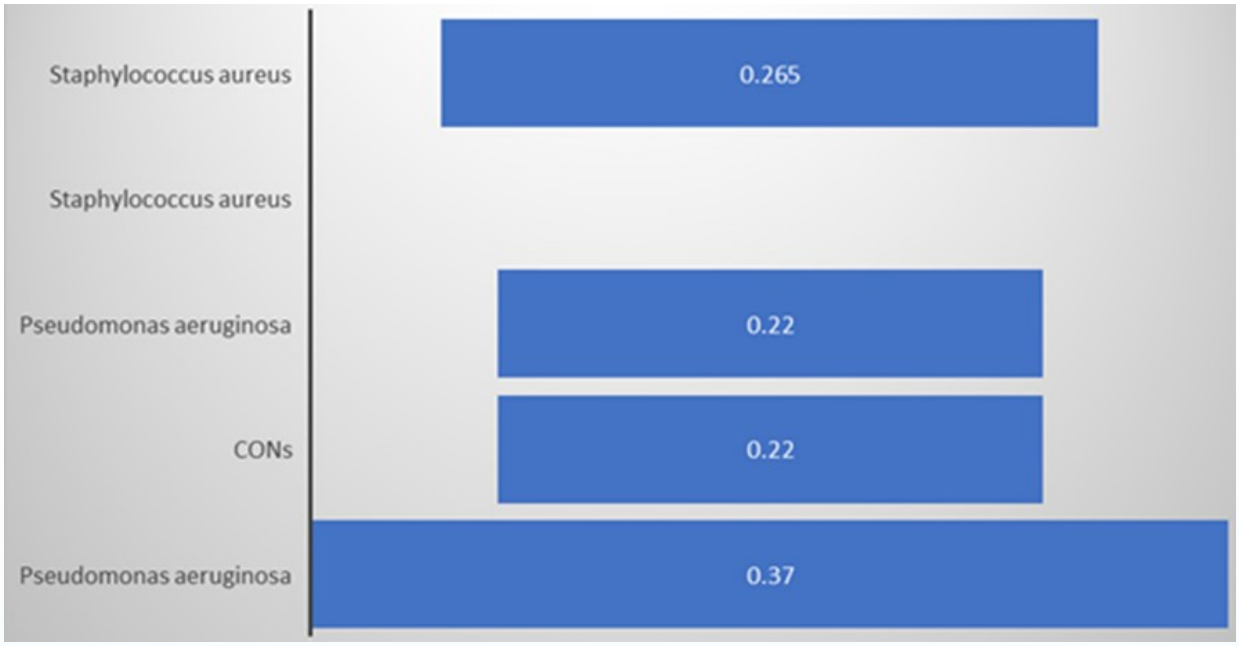

Figure 6: Multiple antibiotic resistance indices of bacterial isolates from the postnatal ward

With MAR indices ranging from 0.22 to 0.37 and three-quarters of isolates surpassing Krumperman's (1983) critical threshold of 0.2, the maternity ward showed alarming levels of resistance. Given that antimicrobial-resistant infections can cause serious consequences like sepsis, meningitis, and elevated mortality rates in the vulnerable maternal and newborn populations they serve, this discovery is especially concerning (Cantey & Baird, 2017).

In line with its inherent resistance mechanisms and capacity to quickly pick up new resistance determinants in hospital settings, isolates of *Pseudomonas aeruginosa* displayed varied resistance (MAR: 0.22-0.37) (Moradali et al., 2017). Because resistant *Pseudomonas aeruginosa* is linked to ventilator-associated pneumonia in neonatal intensive care units and newborn sepsis, its presence in maternity settings is especially worrying.

Given that they are the primary cause of late-onset sepsis in preterm newborns and frequently show methicillin resistance, coagulase-negative staphylococci (MAR: 0.22) pose a growing risk to neonatal treatment (Dong & Speer, 2015).

Multiple antibiotic resistance index of bacterial isolates from the wound clinic and consultation rooms

As shown in Figure 7, bacterial isolates from the wound clinic and general outpatient consultation rooms exhibited the widest resistance spectrum, with MAR indices ranging from 0.0 to 1.0. This setting, characterized by diverse patient demographics and treatment histories, revealed striking heterogeneity: fully susceptible isolates (MAR 0.0) coexisted alongside pan-resistant strains (MAR 1.0). The most critical findings included pan-resistant *Acinetobacter baumannii* (MAR 1.00), extensively resistant *Morganella morganii* (MAR 0.75), and highly resistant *Enterococcus faecalis* (MAR 0.65). The coexistence of fully susceptible strains with pan-resistant isolates indicates heterogeneous selective pressures.

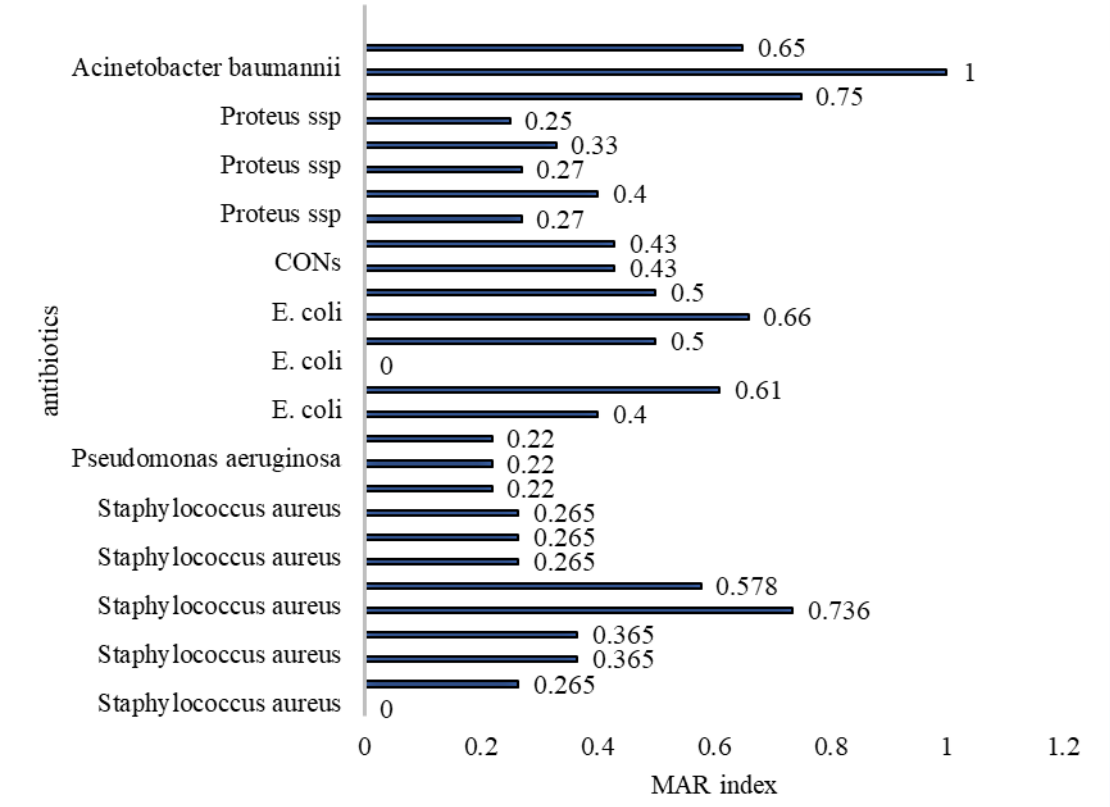

Figure 7: Multiple antibiotic resistance indices of bacterial isolates from the wound clinic and general outpatient consultation rooms

The outpatient setting displayed the widest resistance spectrum, with MAR indices ranging from 0.0 to 1.0, reflecting the diverse patient populations and varied antibiotic exposure histories in this environment. The most critical findings included pan-resistant *Acinetobacter baumannii* (MAR 1.00), extensively resistant *Morganella morganii* (MAR 0.75), and highly resistant *Enterococcus faecalis* (MAR 0.65). These results underscore the clinical threat posed by priority pathogens such as *A. baumannii*, well known for carbapenemase production and efflux-mediated resistance (Doi et al., 2015). Likewise, the detection of highly resistant *M. morganii* mirrors global concerns over carbapenem-resistant Enterobacteriaceae (Pitout et al., 2015), while resistant *E. faecalis* highlights the persistence of vancomycin resistance mechanisms in hospital environments (Arias & Murray, 2012).

The coexistence of fully susceptible strains (MAR 0.0) with pan-resistant isolates (MAR 1.0) in the same outpatient unit points to heterogeneous selective pressures shaped by treatment regimens, patient histories, and infection control practices. This broad spectrum of resistance illustrates the complex antimicrobial ecology of healthcare facilities and underscores the urgency of implementing tailored stewardship interventions to contain resistant strains while preserving antibiotic effectiveness.

Multiple antibiotic resistance index of bacterial isolates from the diabetic clinic

As shown in Figure 8, the four isolates showed modest to moderate resistance (MAR: 0.157-0.25). *Pseudomonas aeruginosa* isolates demonstrated identical resistance profiles (MAR: 0.22), suggesting stable resistance phenotypes. This environment showed the most controlled resistance patterns, potentially reflecting specialized care protocols and targeted antimicrobial use.

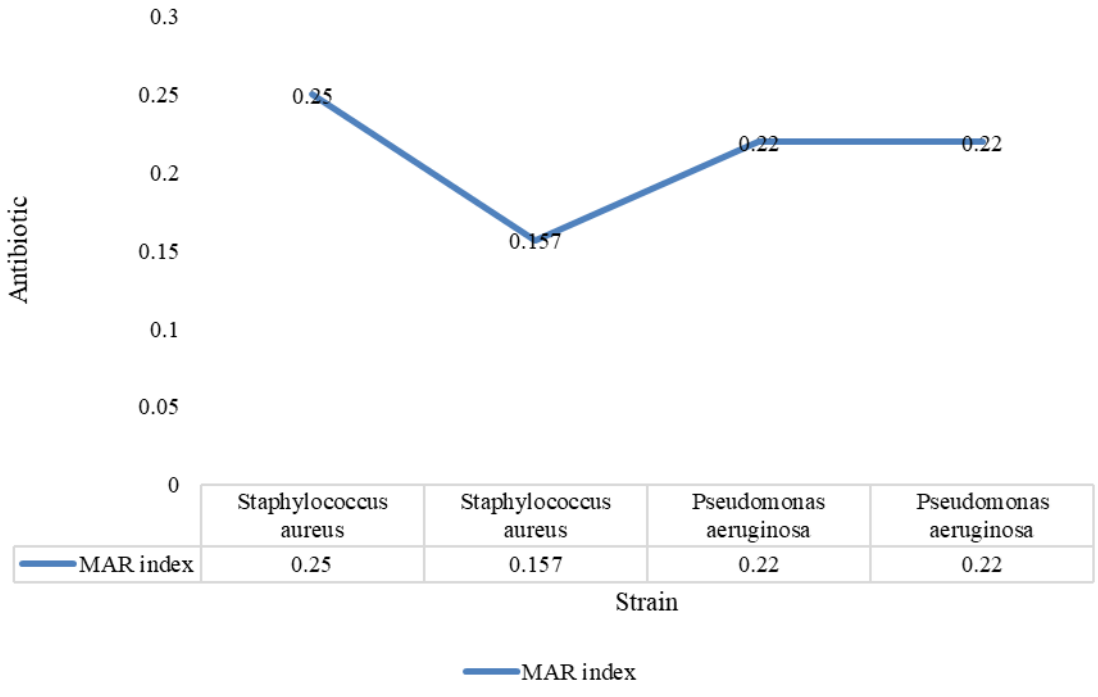

Figure 8: Multiple antibiotic resistance index of bacterial isolates from the diabetic clinic

With MAR indices ranging from 0.157 to 0.25, the four isolates showed modest to moderate resistance to all tested antibiotics. This suggests that the isolates were exposed to antimicrobial pressure rather than widespread pan-resistance. *Pseudomonas aeruginosa* isolates, on the other hand, showed identical resistance profiles (MAR = 0.22), suggesting durable resistance phenotypes that may be the result of uniform antimicrobial management in the environment or a shared clonal lineage. According to targeted antibiotic use and specific care standards, the environment seemed to enforce the most controlled resistance patterns overall. All of these results suggest that *Pseudomonas aeruginosa* has a moderate resistance burden with consistent, repeatable patterns. The *Pseudomonas aeruginosa* group has a single MAR value of 0.22, indicating homogeneous resistance features, while the four isolates have a range of 0.157–0.25, indicating some heterogeneity. Stewardship-driven limits are highlighted by the environment-controlled resistance patterns, which match the reported MAR values and the consistent *Pseudomonas aeruginosa* profile; the range of the four isolates indicates more varied exposures or processes. The persistent resistance observed in *Pseudomonas aeruginosa* implies routine infection-control practices and potential species-tailored stewardship, but the four isolates may require more thorough surveillance to identify any changes in resistance.

Conclusion

This study demonstrates pronounced ward-specific and intra-ward variability in antibiotic resistance among chronic wound pathogens at Meru Teaching and Referral Hospital. Resistance patterns differed not only between wards but also within the same bacterial species and clinical units, reflecting diverse micro-evolutionary processes, patient-specific antibiotic exposure, and strain-level mechanisms of resistance acquisition. The burn unit highlighted the most extreme case, where *Klebsiella pneumoniae* isolates exhibited MAR indices ranging from extensively drug-resistant to pan-resistant phenotypes, underscoring the individualized pathways of resistance development.

These findings reveal that resistance control cannot rely solely on ward-level surveillance but must account for intra-ward heterogeneity. The coexistence of susceptible and highly resistant isolates within shared clinical environments signals the need for targeted antimicrobial stewardship and age-inclusive prevention strategies. The presence of pan-resistant organisms across multiple wards represents an urgent public health emergency requiring immediate, coordinated interventions at both the hospital and broader population levels.

Recommendations

Effective management of antibiotic resistance in chronic wound pathogens requires isolate-specific approaches. Rapid point-of-care resistance testing should be integrated into clinical practice to address intra-ward variability, while pan-resistant management algorithms must be developed for high-risk units. Comprehensive pathogen-specific monitoring systems and selective reporting strategies will help capture ward-level trends, and strain-aware antibiotic cycling protocols should be tailored to individual patient histories.

Enhanced surveillance and data systems are equally critical. This includes integrating decision-support tools with patient antimicrobial exposure records, improving detection of resistant clones, and maintaining standardized resistance databases supported by strain typing. Targeted isolation measures guided by resistance profiles and robust contact investigations should be adopted, while dual-level reporting systems and quality-controlled testing panels will strengthen reliability. Multicenter collaborations are needed to share data, standardize protocols, and compare the efficacy of ward-based versus tailored stewardship strategies.

Finally, molecular epidemiology using whole-genome sequencing should be expanded to track transmission pathways. Longitudinal studies incorporating patient-risk stratification and MAR index tracking will provide valuable insights for stewardship planning.

Integrating antimicrobial stewardship with infection control, prioritizing precision antimicrobial therapy, and developing transmission dynamics models will be essential to guide interventions and safeguard the long-term effectiveness of antibiotics.

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